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Graphical Analysis of Multi-Environment Trials for Barley Yield Using AMMI and GGE-Biplot Under Rain-Fed Conditions

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Abstract

The AMMI and SREG GGE are among the models that effectively capture the additive and multiplicative components of genotype × environment interaction (GEI) and provide meaningful interpretation of multi-environment trials' data set in the breeding programs. The objective of this study was to assess the effect of GEI on grain yield of barely advanced lines and exploit the positive GEI effect using AMMI and SREG GGE biplot analysis. Therefore, 18 lines were evaluated at four research stations (Gorgan, Mogan, Lorestan and Gachsaran) of Dryland Agricultural Research Institute (DARI), located in the semi-warm regions in Iran, in 2004, 2005 and 2006 cropping seasons under rain-fed conditions. Analysis of variance showed that grain yield variation due to environments, genotypes and GEI were highly significant ($p<0.01$), which accounted for 70.4%, 6.8% and 22.8% of treatment combination sum of squares, respectively. To determine the effects of GEI on yields, the data were subjected to AMMI and GGE biplot analysis. The first four AMMI model terms were highly significant ($p<0.01$) and of which the first two terms explained 48% of the GEI. There were two mega-environments according to the SREG GGE model. The best genotype in one location was not always the best in other test locations. According to AMMI1 biplot, the ideal-genotype biplot and by visualizing the mean yield and stability of the genotypes, lines G2 and G11 were better than all other lines across environments. G11 was the ideal genotype to plant in Gachsaran and Lorestan and G2 was the best for Gorgon and Mogan.

Keywords: AMMI, GE interaction, GGE biplot, Stability

Introduction

Multi-environment yield trials (MEYTs) are essential because of the presence of genotype × environment (GE) interactions. The GE interaction that results from the differential responses of genotypes across a range of environments reduces the correlation between phenotypic and genotypic values and complicates the selection of the best genotypes (Ebdon and Gauch 2002). Plant breeding programs should take GE interaction into consideration as well as the estimate of its magnitude, relative to the magnitude of genotype and environment effects, which affects grain yield. Furthermore, the identification of genotypes that yield best across a number of environments would be useful to breeders and producers. Therefore, experimental research needs to be carried out over multiple environments in order to identify and analyze the major factors that are responsible for genotype adaptation (De Lacy *et al.* 1996). For the accurate analysis of MEYTs, the additive main effects and multiplicative interaction (AMMI) model is a valuable tool due to the accuracy that it provides in GE interaction studies (Gauch 2006; Li *et al.* 2006). AMMI analysis combines the additive parameters of traditional ANOVA with multiplicative parameters of PCA (principal component analysis). It is very useful in visualizing multi-environment data and gaining accuracy (Gauch 2006). Another method that has gained importance in investigating the role of genotype, environment and GE interaction effects in MEYTs is the genotype main effects plus genotype × environment interaction (GGE) biplot. Using a site regression model (SREG), Yan (2001) combined G and GE and provided to the agricultural research community an excellent scientific method of visual analysis, called ‘GGE biplot analysis’ and developed a sophisticated Windows-based software called ‘GGEbiplot’ to summarize the G and GE and to address the issue of cultivar recommendation in multi-environment trials. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation as well as sources of variation in GE interaction (Yan *et al.* 2000, 2001). The GGE biplot emphasizes two concepts. First, although the measured yield is the combined effect of G, E and GE interaction, only G and GE interaction are relevant to, and must be considered simultaneously in genotype evaluation, hence the term GGE. Second, the biplot technique is employed to approximate and display the GGE of a MEYT, hence the term GGE biplot. This GGE-biplot is constructed by the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data to singular value decomposition. It clearly shows which genotype won in which environments, and thus facilitates mega-environments (MEs) identification (Yan *et al.* 2000). The AMMI and GGE biplot models are defined as powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programs (Yan *et al.* 2000; Ebdon and Gauch 2002; Samonte *et al.* 2005). The AMMI and GGE biplot have frequently been used for explaining GE interaction and to identify high yielding and adapted cultivars. Also the effectiveness of this methods in analyzing MEYTs data have been well documented (Yan *et al.* 2000, 2001; Kaya *et al.* 2002; Yan and Kang 2002; Morris *et al.* 2004; Yan and Tinker 2005; Samonte *et al.* 2005; Kang *et al.* 2006; Dehghani *et al.* 2006; Gauch 2006; Fan *et al.* 2007; Setimela *et al.* 2007; Mohammadi *et al.* 2007; Yan *et al.* 2007; Sabaghnia *et al.* 2008).

Accordingly, the aim of this study was (i) to apply AMMI and GGE biplot models to evaluate the significance and magnitude of GE interaction effect on grain yield of 18 advanced lines of barely tested across 12 rain-fed environments and (ii) to identify the best performing lines for selection environments by using and comparing the AMMI and GGE biplot methods.

Material and Methods

This study was carried out to determine the yield performances of 18 advanced lines of barely across four rain-fed locations undertaken in Mogan, Gachsaran, Gorgan and Lorestan during the 2004, 2005 and 2006 cropping seasons under non-irrigated conditions. These multi-environment yield trials were conducted in four research stations of Dryland Agricultural Research Institute (DARI), located in the semi-warm regions of Iran. These sites widely differ in terms of geographic position, altitude and rainfall (Table 1). The code of 18 lines and their pedigrees are given in Table 2. The experimental layout was a randomized complete block design with four replications at each site and year. Sowing was done in 1.05 m × 7.03 m plots, consisting of 6 rows with 17.5 cm distance between the rows. The central four rows were harvested for grain yield measurement in order to exclude border effects. Following harvest, grain yield was determined for each line in each test environment, and mean yield averages were computed in accordance with the experimental design. Combinations of three years and four locations were treated as 12 environments. The SAS software was used to partition yield variation into E, G and GE interaction. The grain yield data were subjected to AMMI and GGE biplot analyses. The GGEbiplot software (Yan 2001) was used to generate graphs showing (i) “which-won-where” pattern, (ii) ranking of cultivars on the basis of yield and stability, (iii) ranking of environments on the basis of discriminating ability and representativeness, (iv) environment vectors, and (v) comparing relative genotype performance in different locations (Yan and Kang 2003).

Table 1. Site description and rainfall data of experimental sites in Iran where the experiments were conducted

Station	Longitude (E)	Latitude (N)	Altitude (m)	Rainfall (mm)		
				2004	2005	2006
Gachsaran	50.5	30.17	710	515.2	560.7	511.2
Gorgan	37.16	55.12	45	539.4	377.9	441.7
Lorastan	48.28	33.39	1125	477.1	438.3	554.1
Mogan	47.88	39.39	100	254.2	182.8	143.7

Table 2. Code and pedigree of 18 barely advanced lines used in the study

Code	Pedigree
G1	Alger/Ceres//Sls/3/ER/Apm/4/Wi2197/Mazurkal ICB92-0944-OAP-OAP(10-B-Moghan-2003)
G2	Moroco9-75/Wi2291/Wi2269(13-B-Moghan-2003)
G3	Rhn-03//Lignee 527/As45 CB93-0815-OAP-5AP-OAP-OAP(2-B-Moghan-2003)
G4	Wi2291/TipperICB93-1156-OAP-22AP-OAP-OAP(6-B-Moghan-2003)
G5	Hyb 85-6//As46/Aths×2 ICB91-0736-OAP-OAP-OAP(12-B-Moghan-2003)
G6	Arizona5968/Aths//Avt/Attiki(16-B-Moghan-2003)
G7	BKF/Maguelone1604/3/Apro//SV(14-B-Moghan-2003)
G8	Alanda/5/Aths/4/Pro/Toli//Cer×2/Toli/3/5106/6/Avt/. -8G -3 G(7-B-Gachsaran-2003)
G9	Bda/Cr. 115/Pro/Bc/3/Api/Cm67/4/ Giza121/... -9G -2 G(9-B-Gachsaran-2003)
G10	Emir/Nacta//As907/3/Avt_(9-9)ACSAD-1290-6AP-OTR-OAP-6AP-OAP-OAP(11-BNYT-Gachsaran-2003)
G11	Lth/3/Nopal//Prol/11012-2/4/Kabaa-03ICB94-0498-OAP-3AP-OAP-OAP(8-BNYT-Gachsaran-2003)
G12	Himalaya-12/Plaisant ICBH95-0630-OAP-OAP-16AP(6-BNYT-Gachsaran-2003)
G13	MoB1337/Wi2291//Bonita//Weeah/3/AtahualpaICB98-0563(5-BNYT-Gachsaran-2003)
G14	Weeah11/wi2291/Bgs/3/ER/Apm//Ac253 ICB94-0707-OAP-OAP(7-B-Gonbad-2003)
G15	26216/4/Arar/3/Mari/Aths×2//M-ATT-73-337-1ICB94-0517-37AP-OAP(11-B-Gonbad-2003)
G16	MK1272//Manker/Arig8/3/AlandaICB93-0448-OAP-6AP-OAP(12-Bgonbad-2003)
G17	LB
G18	IZEH

Results and Discussion

Analysis of variance

The analysis of variance and AMMI for grain yield of 18 advanced lines of barely tested across 12 environments is presented in Table 3. The ANOVA for grain yield showed that mean squares of environments, genotypes and genotype × environment interaction (GEI) were highly significant ($p<0.01$) which accounted for 70.4%, 6.8% and 22.8% of model sum of squares (SS), respectively (Table 3). This case, along with a highly significant GEI, indicated the need for the stability analysis. The genotype and the environment means for each location and each genotype are given in Table 4. The environment was the main cause of variations in grain yield, explaining 70.4% of the model (G + E+ GEI) SS (Table 3). A large yield variation explained by environments indicated that the environments were diverse, because large differences among environmental means caused most of the variation in grain yield. The environment yield means (averaged across genotypes) varied from 3412 kgha^{-1} at Gorgan in 2005 (Gor5) to 4866 kgha^{-1} at Gachsaran in 2005 (Gac5) (Table 4). Only the small portion, 6.8% of the total SS, was attributed to genotypic effects. The yields of the lines (averaged across environments) varied from 3290 kgha^{-1} for G6 to 4256 kgha^{-1} for G1 (Table 4). GEI significantly explained 22.8% of model variation in grain yield. The magnitude of the GEI sum of squares was about 3.5 times larger than that for genotypes. It is very common for MEYTs data to embody a mixture of crossover and non-crossover types of GEI. Gauch and Zobel (1997) reported that E accounts for about 80% of the total variation, while G and GE each account for about 10% in normal MEYTs. More pronounced influence of environment on the grain yield compared to the genotype or the GEI effects has been documented in many crops (Akcura *et al.* 2005). Similar results were found in our study since the E effect was about 2.5 times higher than G + GE effects. On the other hand, the differential rankings of genotypes observed across test environments revealed a plausible existence of crossover GEI.

Analysis of genotype by environment interaction is vital for breeders in order to design the dissemination strategies for new varieties. It is important to identify cultivars with specific and general adaptation. Precise recommendation of lines for general and specific adaptation requires clear understanding of the real pattern of genotype by environment interaction. Thus, GE sum of squares was partitioned into “noise” and “real structure” following the procedure by Gauch and Zobel (1997). This computation ignores irrelevant environmental effects and much interaction noise while focusing mainly on the relevant genotype and real interaction effects (Campbell and Jones 2005). The AMMI analysis partitioned the SS of GEI into four significant interaction principal components axes (IPCA) (Table 3). The first principal axis (AMMI1) captured 28% of the SS GEI, the second 20%, the third 17% and the fourth 11%. Accordingly, the GEI contained 71357.7 (pooled error mean square) × 187 (degree of freedom for GEI) = 13343889.9 noise SS (32.6%) and 40862400 - 13343889.9 = 27518510.1 pattern SS (67.3%). This contribution of pattern SS (67.3%) was larger than that retained by the first two multiplicative terms that together accounted for 48% of the GEI sum of squares. Moreover, the first two terms had SS greater than that of genotypes and were highly significant ($p<0.01$). This suggested that the AMMI model with the first and second multiplicative terms was adequate for cross-validation of the yield variation explained by GEI in the present data set since it excludes most of its actual noise. Admassu *et al.* (2008) proposed that two interactions PCA for AMMI model was sufficient for the predictive model. Other interaction PCA captured mostly non-predictive random variation (noise) and did not fit to predict validation observations. Therefore, the approximation of factual interaction pattern of the 18 barely advanced lines with 12 environments was best cross-validated with the first two multiplicative terms of genotypes and environments that easily was visualized with the aid of a biplot.

Table 3. AMMI analysis of variance and partitioning of the sum of squares (SS) for grain yield (kgha^{-1}) of 18 barely advanced lines evaluated across 12 environments

Source of variation	df	SS	MS	Explained % of model & GEI SS[a]
Model	215	179474000	834762.8	
Genotypes (G)	17	12241600	720094**	6.8
Environments (E)	11	126370000	11488181**	70.4
GEI	187	40862400	218515**	22.8
AMMI1	27	11303800	418659**	28
AMMI2	25	8098030	323921**	20
AMMI3	23	7064300	307143**	17
AMMI4	21	4559200	217105**	11
GE Residual	91	9837030	108099.2^{ns}	24
Pooled error	612	43670913.2	71357.7	

a: % of model sum of squares for genotypes, environments and GEI; % (underlined numbers) of GEI sum of squares for IPCAs.
**: Significant at the 0.01 probability level; ns: non-significant; df: degree of freedom; SS: sum of squares; MS: mean squares.

Table 4. Mean grain yield (kgha^{-1}) of 18 barely advanced lines across 12 environments (combination of four locations and three years) in Iran

Environment Genotype	Gor4	Mog4	Lor4	Gac4	Gor5	Mog5	Lor5	Gac5	Gor6	Mog6	Lor6	Gac6	Mean
G1	4102	3790	4962	4104	4094	5421	4135	5775	3602	1417	4881	4791	4256
G2	4000	4557	4490	4367	3817	5366	4027	5639	3196	2247	3465	3993	4097
G3	3577	4018	3969	4055	3700	4370	4298	4490	3090	2276	3235	5263	3862
G4	3315	4678	4692	3394	3412	4683	4460	4561	2490	1485	4152	4471	3816
G5	3517	4712	4938	3935	3363	4999	4362	5035	3229	1514	3608	4467	3973
G6	3221	3933	4390	2809	2802	3621	3540	3951	2860	1455	3394	3498	3290
G7	2444	4349	3967	4130	3367	4820	4102	5280	2762	3072	3960	3698	3912
G8	3188	3581	3831	3796	3141	4074	3862	3834	3817	1753	3633	4370	3573
G9	3390	5550	4858	4228	3367	4975	4681	4292	4165	2061	3185	3108	3988
G10	3225	3866	3171	4502	2790	3813	4267	5065	2890	2504	2646	4029	3564
G11	4223	4206	4529	3984	3722	4819	4279	4693	4085	2158	4712	4057	4122
G12	3302	3848	4942	4282	2965	4735	4102	5278	3617	2063	4629	4288	4004
G13	3644	3760	4150	3529	3502	4490	3996	5222	4135	1804	3660	4622	3876
G14	3640	3948	4877	4509	3449	5300	4238	5138	3983	1591	3929	5868	4206
G15	3669	3950	5271	3620	3541	4567	3960	5639	3619	1290	3823	4117	3922
G16	4160	4420	4031	4041	3637	4702	3944	4908	3367	1522	2394	4680	3817
G17	3806	4646	3379	3091	3381	5519	4298	4190	3773	1216	2406	3602	3610
G18	3600	4544	4075	4351	3359	5004	4415	4607	3248	1773	3800	4550	3944
mean	3612	4242	4362	3930	3412	4738	4165	4866	3440	1845	3640	4304	3880

Underlined values are the maximum yield at each test environment.
Environment is designated as locations first letters (Gorgan, Mogan, Lorestan and Gachsaran) followed by 4, 5 or 6 (i.e. 2004, 2005 and 2006) to indicate year.

AMMI biplot analysis

To visualize the lines' performance in relation to stability, main effects (mean performance) was plotted against IPCA1 (Figure 1). Displacement along the vertical axis indicated interaction differences between lines and between environments, and displacement along the horizontal axis indicated difference in line and environment main effects. This biplot (Figure 1) based on AMMI1 model explained treatments SS, with 6.82% due to Genotype SS, 70.41% due to Environment SS, and 6.3% due to PC1 SS. Thus, it is very informative since it explains 83.5 % of the treatment SS. The lines with PC1 scores close to zero expressed general adaptation whereas the larger scores depicted more specific adaptation to environments with PC1 scores of the same sign (Ebdon and Gauch 2002). Therefore, a line such as G9 with larger PC1 score was better adapted to Mogan in 2004 with larger PC1 score with the same sign (Figure 1). In contrast, line G1, was adapted to Lorestan in 2004 and Gachsaran in 2006 with larger negative PC1 scores. The relative magnitude and direction of lines along the abscissa and ordinate axis in biplot is important to understand the response pattern of genotypes across environments. The best genotype should combine high yield and stable performance across range of production environments. Therefore, the four high yielding (averaged over environments) lines G1, G14, G11 and G2 (with 4256, 4206, 4122 and 4097 kgh^{-1}, respectively) can best judged based on their stability. G2 and G11 that combined low absolute PC1 score and high yield would be best overall winners with relatively less variable yield across environments. Gorgan had relatively smaller variation in the interaction (PC1 score) from year to year while year differences were very high for Lorestan, Mogan and Gachsaran. This underlines the importance of evaluating multi-location yield trials over different seasons. Also, Figure 1 indicated that the relative ranking of genotypes were stable at Gorgan than other locations.

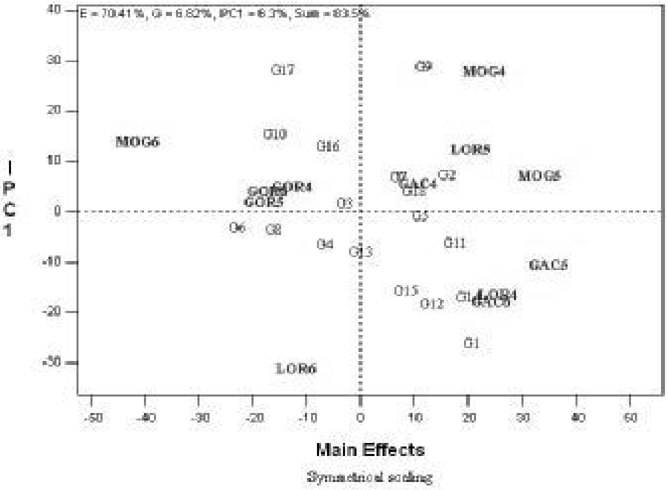

Figure 1. AMMI1 biplot for IPCA1 vs main effect, to show genotype performance in relation to stability of 18 barely advanced lines evaluated across 12 environments

Winning genotype and mega-environment

The Figure 2 polygon is a summary of the GEI pattern of the 18 barely lines with 12 environments. According to this analysis, ideal cultivars are those that should have large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability). Also, ideal test environments should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments) (Yan *et al.* 2000). This polygon is formed by connecting the lines that are further away from the biplot origin in a way that all other lines are contained in the polygon. With the present data set, the lines G1, G2, G9, G17, G10, G6 and G8 expressed a highly interactive behavior. The genotypes at vertex are the winners in the sites included in that sector. Six rays in Figure 2 divided the biplot into six sectors and the environments fall into two of them. Three (or four) environments, Mogan2004, Mogan2005 (probably also Mogan2006) and Lorestan 2005, fell into the first sector and the vertex line for this sector was G9. Therefore, Mogan in all years clustered in one sector indicating repeatable performance of the lines observed in this location and it could be considered as separate mega-environment for barely variety evaluation and recommendation. The rest of environments (Gorgan in three years, Gachsaran in three years and Lorestan on two years) fell into the second sector. The vertex line for this sector was the G1. The length of an environmental vector is an estimation of discriminating power of the environment (Yan *et al.* 2007). Test environments with longer vectors (Lor6 in Figure 2) are more discriminating of the genotypes. A test environment close to the biplot origin (Mog6 and Lor5 in Figure 2) means that it exhibited low interaction and relative performance of all genotypes is similar. Therefore, Mog6 and Lor5 provided little or no information about the genotype differences. On the hand, the nearly additive behavior of Mogan in 2006 indicated that genotypic yield in that environment was highly correlated with the overall genotypic means across environments. Gorgan was relatively closer to biplot origin in all years and hence less interactive location and could be a suitable location for the selection of genotypes with average adaptation.

Visualizing the mean yield and stability of the genotypes

The mean yield and stability of genotypes are evaluated by defining an average tester coordinate (ATC) method (Yan 2001). In this method, the average environment is indicated by a circle and shows the positive end of the ATC *x* axis (Figure 3). A line known as the average environment axis and serves as the abscissa of the AEC is then drawn to pass through this average environment and the biplot origin. The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa (Figure 3). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is indicated by double arrows, and either direction away from the biplot origin indicates greater GEI effect and lower

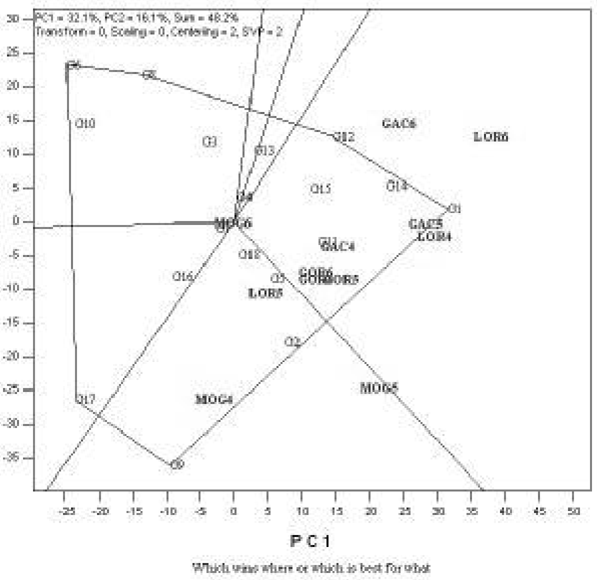

Figure 2. Polygon views of the GGE biplot based on symmetrical scaling for which won where pattern for genotypes and environments.

stability. The AEC ordinate separates genotypes with below-average means from those with above-average means. Furthermore, the average yield of genotypes is approximated by the projections of their markers to the AEC abscissa. For this study, lines with above-average means (i.e. G1, G14, G2, G11, G5, G15, G12, G9 and G18) were selected, whereas the rest (i.e. G4, G7, G13, G16, G3, G17, G8 and G10) were discarded. On the other hand, a longer projection to the AEC ordinate, regardless of the direction, represents a greater GEI of a genotype, which means it is more variable and less stable across environments or vice versa. For instance, lines G5, G18, G11 and G2 were more stable as well as high yielding. Conversely, G9, G1, G12, G14 and G15 were more variable, but high yielding. The requirement for the use of SREG based GGE biplots in the identification of superior genotypes is to facilitate the identification of such genotypes (Crossa *et al.* 2002).

Ideal genotype and ideal environment

An ideal genotype is defined as one that is the highest yielding across test environments and is absolutely stable in performance (Yan and Kang 2003). Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation. 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. When an "ideal" cultivar view was drawn (Figure 4), the lines G2, G11 and G1 were the closest to the ideal cultivar (center circle) and may be regarded as desirable genotypes, followed by G14, G5 and G15 as a group. Ranking of other genotypes as ideal was G18 >

G12 > G7 > G4 > G13 > G16 > G9 > G3 > G17> G8 > G10 > G6. On the other hand, the lower yielding genotypes i.e. G7, G4, G13, G16, G9, G3, G17, G8, G10 and G6, 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 using the ideal genotype procedure of the GGEbiplot are similar to those found in other crop stability studies such as rice (Samonte *et al.* 2005), wheat (Kaya *et al.* 2006), barley (Dehghani *et al.* 2006) and maize (Fan *et al.* 2007).

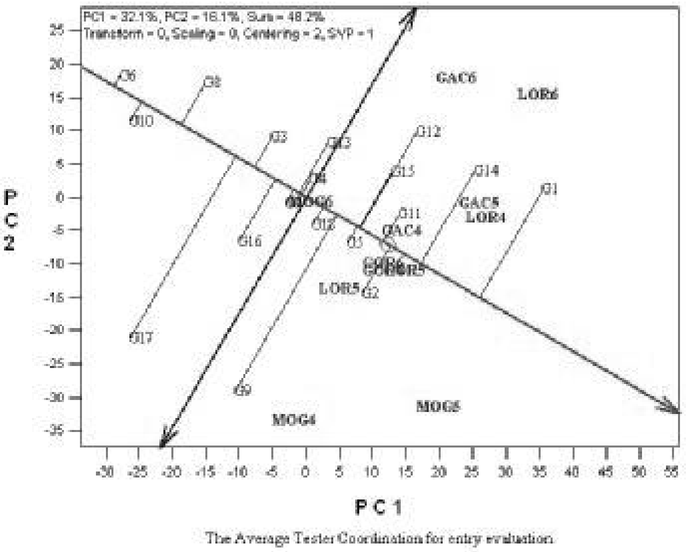

Figure 3. GGE biplot obtained from sites regression (SREG) analysis showing mean and stability of 18 barely genotypes for yield and GEI.

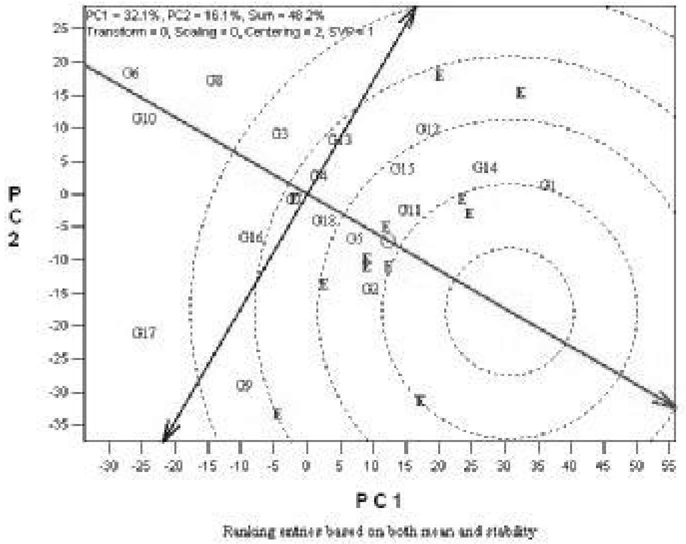

Figure 4. Comparison of 18 barely advanced lines against the 'ideal' genotype for grain yield and stability of performance across environments

An ideal environment should have more power to discriminate genotypes in terms of the genotypic main effect (large PC1 scores) and at the same time more representative of the overall environments (small absolute PC2 scores). 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 (Yan *et al.* 2000). In Figure 5, the environments are ranked based on both discriminating ability and representativeness. Thus, LOR4 was a relatively favorable test environment, followed by GAC5, with the highest yield, as a group. Overall, the poorest test environments relative to the ideal environment were GAC6, LOR5, MOG4 and MOG6.

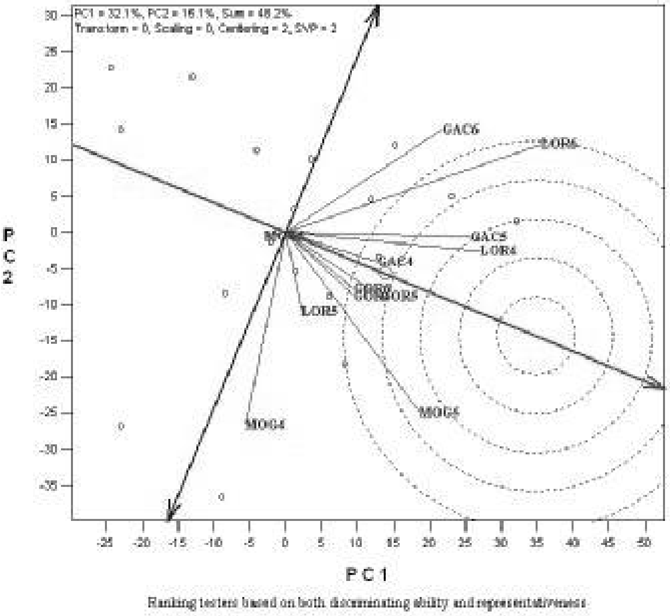

Figure 5. Comparison of 12 test environments against the 'ideal' environment based on discriminating ability and representativeness

Comparing performance of two genotypes at all environments

The performance of the top two high yielding and stable lines (G2 and G11) was compared in GGE biplot by a straight line connecting the markers of the two genotypes and a broken perpendicular line passing the plot origin (Figure 6). This perpendicular line divided the environments into two groups; each of these genotypes would yield better than the other at environments with markers on its side of the perpendicular, and vice versa (Yan *et al.* 2000). Thus, G11 would yield better than G2 at GAC in all years (2004, 2005 and 2006) and at LOR in 2004 and 2006, whereas G2 would yield better than G11 at GOR in all years (2004, 2005 and 2006), MOG in all years (2004, 2005 and 2006) and LOR in 2005. Therefore, G11 is the ideal genotype for planting in Gachsaran and Lorestan and G2 is the best for Gorgan and Mogan.

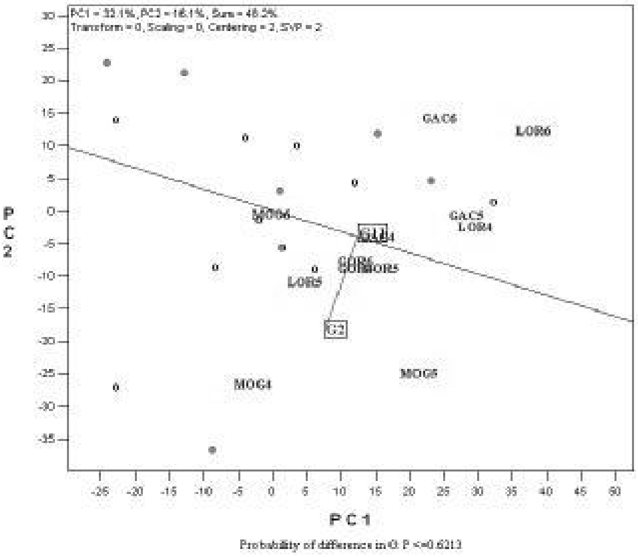

Figure 6. GGE biplot obtained from site regression (SREG) analysis that clusters the environments into those where G2 out-yields G11 (below the broken line) and where G11 out-yields G2 (above the broken line)

Conclusion

The AMMI and GGE biplot analyses revealed two highly adapted lines to several environments (G11 had the highest yield and durability in Gacsaran and Lorestan, followed by G2, with the highest yield and durability in Gorgan and Mogan). Thus, the lines G11 and G2 can be proposed for planting by the farmers under rain-fed conditions. Also, it was detected that only the test environments LOR4 and GAC5 can be sufficient for deciding about which genotypes are recommended. This information should be useful for plant breeders in performance trials by targeting appropriate barely genotypes to different regions and by identifying the best test environments to use economically limited resources such as time and money. The GGE biplot aided in comparison of the performance of lines at different environments, determination of the relative performance of lines at a specific environment and identification of lines suitable for groups of environments. In addition, it was concluded that there was no difference between the AMMI and GGE biplot analyses in evaluation of barely advanced lines under study and both methods were successful in determining suitable barely genotypes and locations under Iranian rain-fed climate conditions.

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