Targeting Promising Bread Wheat (*Triticum aestivum* L.) Lines for Cold Climate Growing Environments Using AMMI and SREG GGE Biplot Analyses

J. Ahmadi[1*], A. Mohammadi[2], and T. Najafi Mirak[3]

ABSTRACT

Genotype×environment interactions (GEIs) can affect breeding programs because they often complicate the evaluation and selection of superior genotypes. This drawback can be reduced by gaining insights into GEI processes and genotype adaptation. The objectives of this research were to evaluate: (1) the yield stability of promising wheat lines across locations and (2) the relationship among the test environments for selecting superior lines within the cold climate mega-environments of Iran. A total of 35 wheat promising lines were grown at 7 locations during the 2008-2009 cropping season. Combined analysis of variance showed that the environment (E) accounted for 75.7% of the model sum of squares. The magnitude of the GEI sum of squares was about three times larger than that for genotypes. To determine the effects of GEI on yields, the data were subjected to the additive main effects and multiplicative interaction (AMMI) and *genotype+(genotype×environment)* interaction (GGE) biplot analysis. The AMMI1 model was found to explain up to 88% of the main and interaction effects. According to the AMMI1 and GGE biplots, the lines G5 and G4 were found to produce high and stable yields across environments. There were three mega-environments (Euromieh and Ardebil as mega-environment I, Mashhad, Arak, Hamedan and Jolgerokh as mega-environment II, and Karaj as mega-environment III) according to the site regression genotype (SREG) GGE model. Application of AMMI and GGE biplots facilitated visual comparison and identification of superior genotypes for each target set of environments.

Keywords: AMMI, GEI, GGE biplot, Wheat, Yield stability.

INTRODUCTION

Genotype by environment interaction (GEI) is commonly observed by breeders as a differential ranking of genotype yields among locations and years. In yield trials, when a significant GEI exists, selection should not be based solely on the genotype (G) effect or on the GE effect; rather it should be based on both G and GE. Plant breeders conduct multi-environment yield trials (MEYTs) primarily to determine whether the target region is homogeneous or should be divided into different mega-environments, and, secondly, to select superior cultivars for a given mega-environment on the basis of multiple traits in addition to yield per se (Yan, 1999). The fulfillment of both tasks depends on an understanding of (i) the GE interaction pattern of the MEYTs, which has been the focus of numerous studies (Kang, 1990; Kang and Gauch, 1996; Cooper and Hammer, 1996), and (ii) the interrelations among the breeding objectives (Yan and Wallace, 1995).

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[1] Department of Genetic and Plant Breeding, International University of Imam Khomeini, Qazvin, Islamic Republic of Iran.
[*] Corresponding author; e-mail: njahmadi910@yahoo.com
[2] Islamic Azad University, Karaj Branch, Islamic Republic of Iran.
[3] Seed and Plant Improvement Institute, Karaj, Islamic Republic of Iran.

GEI analysis is particularly important when the rank of lines selected for breeding changes in different environments (crossover GEI). Indeed, high yielding genotypes in favorable environments can have inferior performances under poor growing conditions (Ceccarelli, 1996). Thus, understanding the causes of GEI would help in developing genotypes that show satisfactory performances in one to several environments. Therefore, experimental research needs to be carried out over multiple environment trials in order to identify and analyze the major factors that are responsible for genotype adaptation (De Lacy *et al*., 1996). Multi-environment yield trials (MEYTs) are used in the final selection cycles to identify superior genotypes in plant breeding programs. Several statistical models have been proposed for studying the GEI effect and exploiting its positive part in the variety development process. The additive main effects and multiplicative interactions (AMMI) and site regression (SREG) genotype plus genotype by environment interaction (GGE) biplot models can be 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). AMMI model analysis combines the additive parameters of traditional analysis of variance (ANOVA) with multiplicative parameters of principal component analysis (PCA). It has both linear and bilinear component of GEI and, hence, is very useful in visualizing multi-environment data and gaining accuracy (Gauch, 2006). Using a site regression (SREG) model, Yan (2001) combined genotype (G) with GEI and provided an excellent scientific method of visual analysis, called 'GGE biplot analysis' and developed a sophisticated Windows-based software called 'GGEbiplot'(see www.ggebiplot.com) 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). 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. The GGE-biplot clearly shows which genotype won in which environments, and thus facilitates mega-environments (MEs) identification (Yan *et al*., 2000). The AMMI and GGE biplot have been used to identify high yielding and adapted cultivars by many researchers and the effectiveness of this methods in analyzing multi-environment trials data have been well documented (Gauch, 2006; Fan *et al*., 2007; Setimela *et al*., 2007; Yan *et al*., 2000, 2007; Morris *et al*., 2004; Samonte *et al*., 2005; Dehghani *et al*., 2006; Yan and Tinker, 2005; Sabaghnia *et al*., 2006, 2008; Kang *et al*., 2006; Mohammadi *et al*., 2007, Asrat *et al*., 2009).

The objectives of this research were (i) to apply AMMI and GGE biplot models to evaluate the significance and magnitude of GE interaction effect on grain yield of 35 wheat lines tested across 7 locations, and (ii) to evaluate the relationship among the test environments for selecting superior genotypes within the mega-environment for wheat production in the cold regions of Iran.

MATERIALS AND METHODS

The experimental materials consisted of 35 bread wheat genotypes, which included 32 advanced lines developed by the SPII (Seed and Plant Improvement Institute) crossing program and three released cultivars as checks. This study was carried out to determine the yield performances of wheat advanced lines under irrigated conditions across seven different research stations in Iran, during the 2008-2009 cropping season. The research stations were located in cold regions of Iran, including Mashhad and Jolgerokh Stations in the northeast; Ardabil and Euromieh Stations in the northwest; Hamedan and Arak Stations in the west, and Karaj Station in the north-central part of Iran. These sites widely differ in terms of

geographic position, altitude, and rainfalls (Table 1). The code of 35 wheat advanced lines and their pedigrees are given in Table 2. The experimental layout was a randomized complete block design with three replications at each station. Sowing was done in 1.2 m×6 m plots, consisting of 6 rows. Following harvest, grain yield was determined for each line in each test environment, and mean yield average was computed in accordance with the experimental design. The PROC GLM procedure available in SAS (Ver. 6, SAS Institute, 1996) was used to partition yield variation into environments, genotypes, and genotypes × environment interaction. The grain yield data were subjected to AMMI and GGE biplots analysis. The results of the AMMI model analysis were interpreted from the AMMI1 graph that showed the main and first multiplicative axis term (PC1) of both genotypes and environments. The GGE biplots were constructed from the first two principal components (PC1 and PC2) derived by subjecting the environment-centered yield data (which contains G and GE) to singular valued composition (SVD) (Yan *et al*., 2000; Yan, 2002). The GGE biplot 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, and (iii) correlation vectors among environments. Angles between environment vectors were used to judge correlations (similarities/dissimilarities) between pairs of environments (Yan and Kang, 2003).

RESULTS

Analysis of Variance

The combined analysis of variance and AMMI for grain yield (t ha^{-1}) is presented in Table 3. The analysis of variance for grain yield showed that mean squares of environments, genotypes and *genotype×environment* interaction were highly significant (P< 0.01) (Table 3) and accounted for 75.7%, 6.5% and 17.9% of model sum of squares, respectively. This case, along with a highly significant GEI, required using of stability analysis. The environment was the main cause of variation in grain yield, explaining 75.7% of the model (G + E + GEI) sum of squares (Table 3). A large yield variation explained by the environments indicated that the locations were diverse, with large differences among environmental means causing most of the variation in grain yield. The location yield means (averaged across genotypes) varied from 4.95 t ha^{-1} at Arak to 9.34 t ha^{-1} at Jolgerokh. Only a small portion (6.5%) of the total sum of squares was attributed to genotypic effects. The yield means of the advanced lines (averaged across environments) varied from 6.891 t ha^{-1} for G27 to 8.376 t ha^{-1} for G11 followed by G5, G4, and G20 with 8.328, 8.277 and 7.932 t ha^{-1}, respectively. Control genotypes (G1, G2, and G3 with 7.624, 7.505 and 7.290 t ha^{-1}, respectively) had grain yields near the median of all the tested genotypes. GEI

Table 1. Site description and rainfall data of the experimental sites in Iran.

Stations	Coordinate		Altitude (m)	Rainfall (mm)	Rainfall (mm)
	Longitude (E)	Latitude (N)		Yearly mean	2008-2009
Arak	49.40	34.6	1700	341.7	300
Ardebil	48.18	38.15	1311	303.9	303.5
Hamedan	49.27	34.35	1800	316.6	323
Jolgehrokh	58.60	35.50	1600	247.8	225
Karaj	59.15	35.43	1300	243.8	250
Mashhad	59.36	36.17	970	255.2	250
Euromieh	45.20	37.60	1332	341	239.2

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Table 2. Genotype codes and pedigree of 35 wheat advanced lines used in the study.

Genotype code	Pedigree	Genotype code	Pedigree
G1	Shahryar	G19	ADYR
G2	Alvand	G20	1-72-92/Gascogne//Almt
G3	C-80-4	G21	Ymh /Tob //Mcd /3/Lira /4/Gascogne /5/Zarrin
G4	Owl/3/Alvd/Aldan/las58	G22	Gds/4/Anza/3/Pi/Nar//Hys/5/Vee/Nac/6/Gascogne /7/Zarrin
G5	Owl/4/Alvd/Aldan/las58	G23	Gds/4/Anza/3/Pi/Nar//Hys/5/Vee/Nac/6/Gascogne
G6	Omid/H7/4P839/3/Omid/Tdo/4/ICWHA811473/5/90Zhong87/6/Alamoot	G24	Gds/4/Anza/3/Pi/Nar//Hys/5/Vee/Nac/4/Gascogne /5/Zarrin
G7	Gascogne/Col No.3625//Alamoot	G25	Hys//Drc*2/7c/3/2*Rsh/4/Zagros
G8	Spb ″s″ //K134(60)/Vee ″s″ /3/ Gascogne /4/Alamoot	G26	1-72-92/Col/No.3617//Owl
G9	Alvad/Aldan/las58/3/MV17/5/Kal/Bb//Cj″s″/3/Hork″s″/4/Mv17	G27	Bhr*5/Aga//Sni/3/Trk13/4/MV 17/5/Alvd
G10	Rsh*2/10120/Zagros	G28	Gascogne/4/Kal/Bb//Cj/3/Hork ″s″
G11	1-72-2/Vratza//Almt	G29	Ymh/Tob/Mcd/3/Lira/4/ Catbird
G12	T X62A4793 / CB809 /5/ Gds /4/ Anza /3/ Pi/Nar// H ys /6/ Passarinho /7/Alamoot	G30	Nwt/3/Tast/Sprw//Taw12399.75/4/Sultan
G13	Bez/90zhong87/3/Alvd//Aldan/las	G31	H90005//Attila/3*Bcn
G14	Owl/ Azar#2	G32	Tirchmir1/Lco//Bez/ Sdv1
G15	Owl/4/Gv/D630//Ald″s″/3/ Azd	G33	Agri/Bjy//Vee/3/Tnmu/4/Ks82142/Cupe
G16	Alvd//Aldan ″s″ /las58/3/Bez	G34	Vorona/Hd2402/5/Jup/4/Cllf/3/II14.53/Odin//CI134431/SEL6425/WA00477
G17	Jup/4/Cllf/3/II14.53/Odin//CI13431/W00477/5/90ZHONG657/6/Tjb368.251/Buc//Anb/Buc	G35	Madsen/Tem-202/Tx89V4138
G18	Agri/Bjy//Vee/6/Sn64//Ske/2*Ane/3/SX/4/Bez/5/Seri/7/F10s1		

Table 3. AMMI analysis of variance and Partitioning of the sum of squares (SS) for grain yield (t ha^{-1}) of 35 wheat advanced lines evaluated across 7 locations.

| Source of variation	DF	SS	MS	Explained percentage of model SS	Explained percentage of GEI SS
Model	244	583.6			
Genotypes (G)	34	37.9	1.11**	6.5	
Location (E)	6	441.6	73.6**	75.7	
GEI	204	104.2	0.51**	17.9	
AMMI1	39	34.85	0.89**		33.5
AMMI2	37	25.81	0.69**		24.8
AMMI3	35	22.85	0.65**		21.9
AMMI4	33	14.7	0.65**		14.1
GE Residual	60	5.97	0.09^{ns}		
Pooled error	476	125.76	0.26		

** Significant at the 0.01 probability level, ns: Non significant.

significantly explained 17.9% of the model variation in grain yield. The magnitude of the GEI sum of squares was about three times larger than that of genotypes. Gauch and Zobel (1997) reported that environment (E) accounts for about 80% of the total variation, while genotype (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 GE interaction effects has been documented in many crops (Kaya *et al.*, 2003; Akcura *et al.*, 2005). Similar results were found in our study since the E effect was about three times higher than *G+GE* effects. The AMMI analysis partitioned the GEI sum of squares into four significant interaction principal components axes (IPCA) (Table 3). The first principal axis (AMMI1) captured 34.85% of the GEI SS, the second 25.81%, the third 22.85%, and the fourth 14.7%. The adequacy of the multiplicative terms containing the real structure of GEI could be inspected by estimating the amount of noise present in the interaction from the pooled error and comparing it with the sum of squares retained in consecutive AMMIn models

(Voltas *et al.*, 2002). However, Admassu *et al.* (2008) proposed that two interactions PCA for AMMI model was sufficient for predictive model. Therefore, the approximation of factual interaction pattern of the 35 wheat advanced lines across 7 locations was best cross-validated with the first two multiplicative terms of genotypes and environments that easily visualized with the aid of a biplot.

AMMI Biplot Analysis

To visualize yield stability by line, the main and IPCA1 effects of both G and E on grain yield were shown in Figure 1. The AMMI biplot based on AMMI1 model (Figure 1) explained 88.1% of treatment SS, with 6.49% due to genotype SS, 75.66% due to environment SS, and 6% due to IPC1 SS. Since IPCA1 SS is 92% of that of the genotype SS, this emphasizes the importance of taking GEI into consideration when estimating cultivar yield at different locations or when targeting wheat lines onto specific locations. Displacement along the vertical axis indicated interaction differences between lines
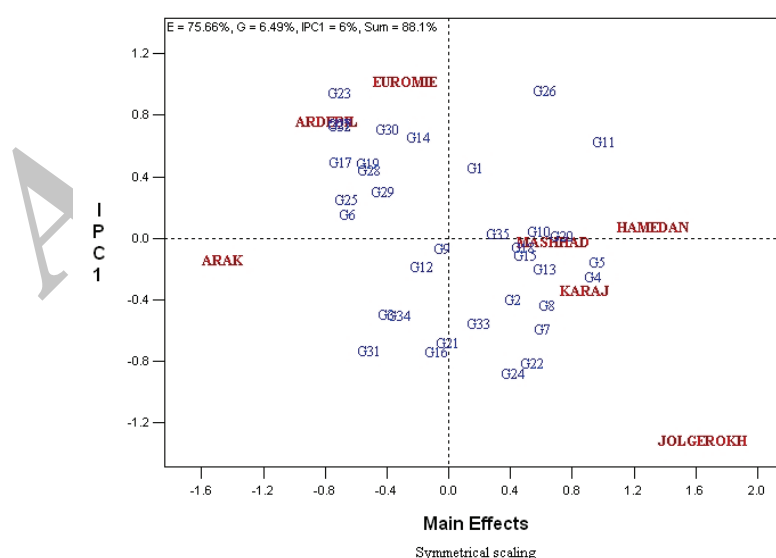

Figure 1. AMMI1 biplot showing IPCA1 *vs.* main effect, to show genotype performance in relation to stability of wheat advanced lines evaluated across 7 locations.

and between environments, and displacement along the horizontal axis indicated difference in genotype and environment main effects. 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). The differences among genotypes in terms of direction and magnitude along the *x* axis (yield) and *y* axis (IPCA1 scores) were also important to understand the response pattern of genotypes across environments. The best cultivar should be high-yielding and stable across environments. Therefore, the four high yielding (averaged over environments) lines G11, G5, G4 and G20 (with 8.376, 8.328, 8.277 and 7.932 t ha^{-1}, respectively) could be judged as the best genotypes based on their stability. G4, G5, and G20 combined low absolute PC1 score and high yield would be the best overall winners with relatively less variable yield across environments.

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 (Gauch and Zobel, 1997; Yan *et al*., 2000, 2001). 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 (Yan and Kang, 2003). 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; Yan and Rajcan, 2002). This polygon is formed by connecting the genotypes that are further away from the biplot origin in a way that all other genotypes are contained in the polygon. With the present data set (Figure 2), the wheat lines G11, G5, G4, G22, G24, G7, G3, G25, G23,
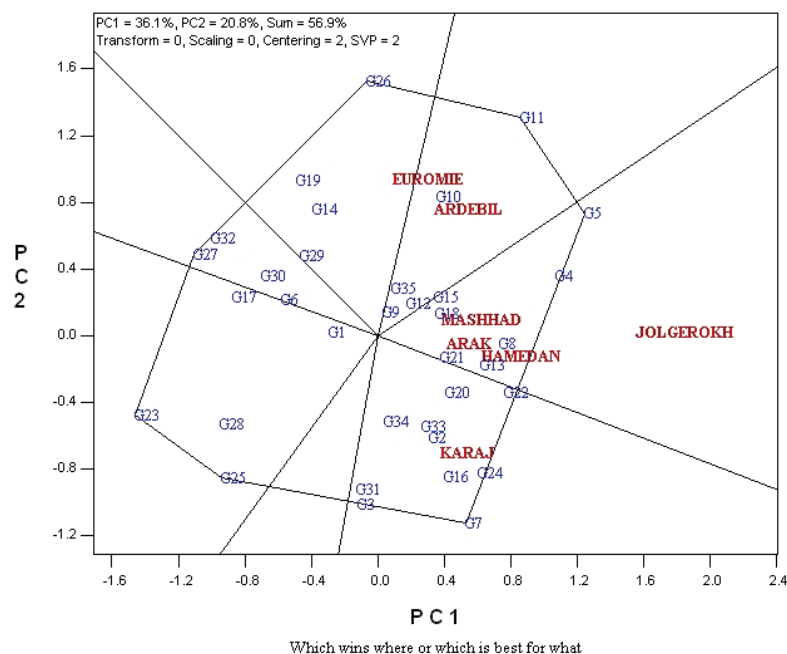
Figure 2. Polygon views of the GGE biplot based on symmetrical scaling for which won where pattern for 35 wheat genotypes and 7 locations.

G27, G32, and G26 expressed highly interactive behavior. Connecting the extreme genotypes on a GE biplot forms a polygon and the perpendiculars to the sides of the polygon form sectors of genotypes and sites (Hernandez and Crossa, 2000). The genotypes at vertex are the highest yielding at the sites included in that sector. Seven rays in Figure 2 divide the biplot into seven sectors and the environments fall into three of them. Two locations, namely, Euromieh and Ardebil, fell into the first sector and the vertex line with the highest yield for this sector and locations was line G11. Therefore, these locations could be considered as separate mega-environment for wheat variety evaluation and recommendation (mega-environment I). Four locations, namely, Mashhad, Arak, Hamedan and Jolgerokh, fell into second sector (mega-environment II). The vertex genotype for this sector was G5 and G4. Karaj fell into the third sector and the vertex genotype with the highest yield for this location was G7. The length of an environmental vector is an estimation of discriminating power of the environment (Yan *et al.*, 2007). Test environments with longer vectors (Jolgerokh in Figure 2) are more discriminating of the genotypes. If a test environment is close to the biplot origin (Mashhad and Arak in Figure 2), it means that it exhibited low interaction and all genotypes performed similarly and, therefore, it provided little or no information about the genotype differences. The nearly additive behavior of Mashhad and Arak indicated that genotypic yields in those environments were highly correlated with the overall genotypic means across environments. Therefore, Figure 2 suggests that there exist three possible cold continent wheat mega-environments in Iran. However, this mega-environment pattern needs verification through other multi-environment trials for this target region.

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) (Yan, 2001; Yan and Hunt, 2002; Yan, 2002). 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 that serves as the abscissa of the average environment coordinate (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 the 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 reduced 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. In this study, genotypes with above-average means i.e. G5, G4, G11, G8, G22, G13, G10, G15, G18, G21, G20, G1, G35, G26, G24, G16, G7, G2, G33, G35 and G9, were selected and the rest were discarded. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments or vice versa. For instance, genotypes G5, G4 and G8 were more stable and high yielding as well. Conversely, G26, G7, G24, G16 and G11 were more variable, but still 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

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.
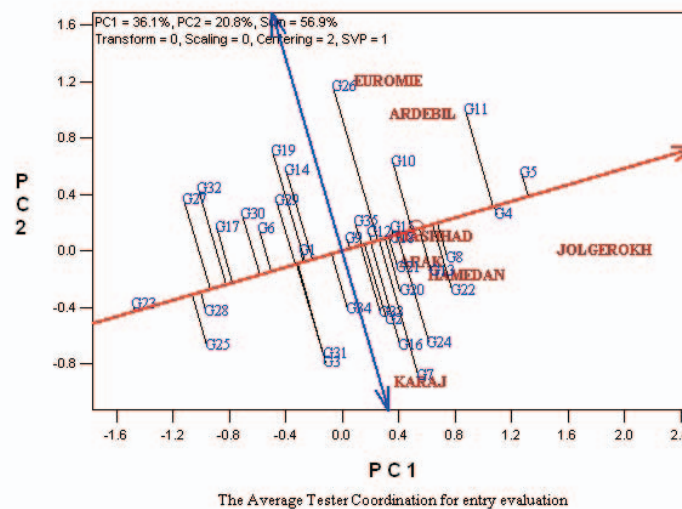
Figure 3. GGE biplot obtained from sites regression (SREG) analysis showing mean and stability of 35 wheat genotypes for yield and GEI across 7 locations.

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 genotypes G5 and G4 in the center of the concentric circles represented the ideal genotypes. The genotypes G8, G11, G22, G13, G18, G15 and G10 (in the second concentric circle) were the closest to the ideal genotypes and could be regarded as the desirable genotypes. Ranking of other genotypes based on the ideal genotypes is presented in Figure 4. On the other hand, the lower yielding genotypes, such as G23, G25, G28, G17, G27 and G32, are unfavorable because they are far away from the ideal genotypes. 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 such as rice (Samonte *et al*., 2005), wheat (Kaya *et al*., 2006), barley (Dehghani *et al*., 2006), and maize (Fan *et al*., 2007).

Correlation among Environments

The correlation coefficients among the 7 locations are presented in Table 4. Also, a GGE biplot which was based on environment-focused scaling was described to estimate the pattern of locations (Figure 5). The vector view of a GGE biplot provides a succinct summary of the interrelationships among the environments (Yan 2002). The cosine of the angle between two vectors represents the correlation between them. The linear map to the right of the graph (in degrees) helps indicate relationships between locations. Therefore, the most prominent relations were: (i) near-zero correlations (r= Cos90= 0) between Jolgerokh with Euromieh and between Hamedan with Euromieh as indicated by the near-perpendicular vectors. Also Figure 5 demonstrated that Hamedan and Mashhad were closely correlated locations, but an insignificant near-zero correlation coefficient (Table 4) was obtained between them. Others have found similar inconsistencies and implied that the biplot analysis did not explain 100% of the GGE variations (Kaya *et al*., 2006); and

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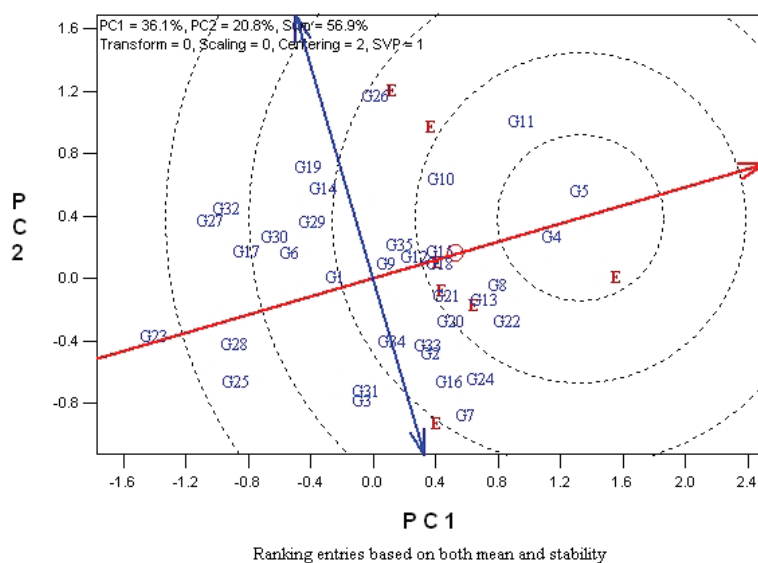
Figure 4. Comparison of 35 wheat advanced lines against the ideal genotype for grain yield and stability across locations.

Table 4. Mean comparison of grain yield at 7 locations and correlation coefficients among test locations.

Location	Yield (t h^{-1})	Arak	Ardebil	Hamedan	Jolgerokh	Karaj	Mashhad	Euromieh
Arak	4.95 g[a]	1						
Ardebil	6.51 f	0.26[ns]	1					
Hamedan	8.69 b	0.33*	0.22[ns]	1				
Jolgerokh	9.34 a	0.67**	0.11[ns]	0.25[ns]	1			
Karaj	8.01 c	0.33*	-0.18[ns]	0.35*	0.20[ns]	1		
Mashhad	7.68 d	0.27[ns]	0.06[ns]	-0.02[ns]	0.56**	0.29[ns]	1	
Euromieh	7.25 e	-0.13[ns]	0.11[ns]	0.07[ns]	0.03[ns]	-0.23[ns]	0.31*	1

** Significant at the 0.01 probability level; * Significant at the 0.05 probability level, ns: Non significant.
[a] Mean followed by similar letters are not significantly different at the 0.01 probability level according to Duncan's multiple range test.

(ii) positive associations between Euromieh with Ardebil (mega-environment I), among Mashhad, Arak, Hamedan and Jolgerokh (mega-environment II) as indicated by acute angles. The vector view of a biplot can be used to identify different mega-environments; test environments from different mega-environments should have large angles or low or negative correlations. Another useful property of the vector view of the biplot is that the length of the environment vectors approximates the standard deviation within each environment and discriminating ability

(Yan and Kang, 2003), which is a measure of their discriminating ability. Thus, Jolgerokh was most discriminating in 2008-09 (Figure 5).

Comparing Performance of Two Best Genotypes at all locations

The performance of the top two high yielding and stable lines (G5 and G4) was compared in a GGE biplot by a straight line connecting the markers of the two genotypes
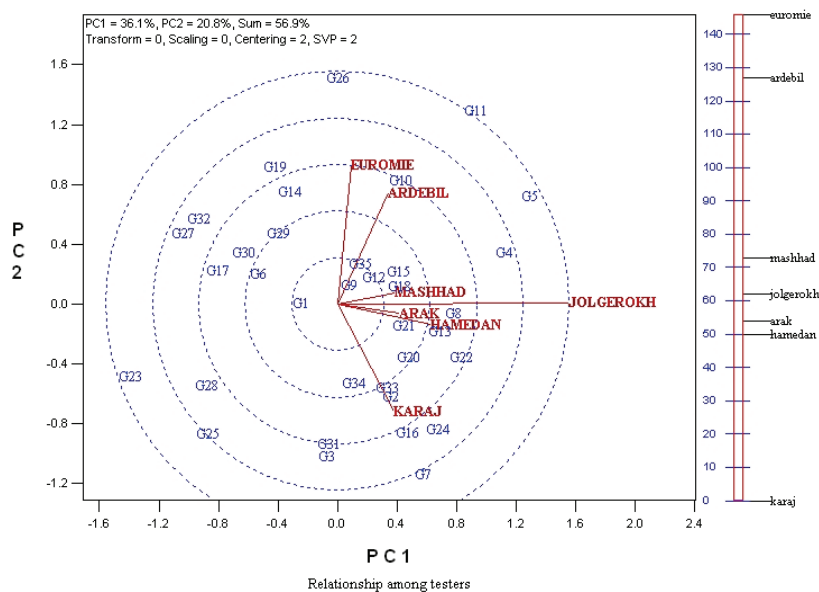
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Figure 5. GGE biplot showing relationships among 7 locations. The unit of the linear map to the right of the graph is in degrees. The smaller the angle between any two vectors, the greater the correlation between them (Yan and Kang, 2003).

and a broken perpendicular line passing plot origin (Figure 6). This perpendicular line divided the locations into two groups; each of these genotypes would yield better than the other at locations with markers on its side of the perpendicular, and vice versa (Yan *et al.*, 2000). Thus, both G5 and G4 would yield the best and are the most promising lines in all
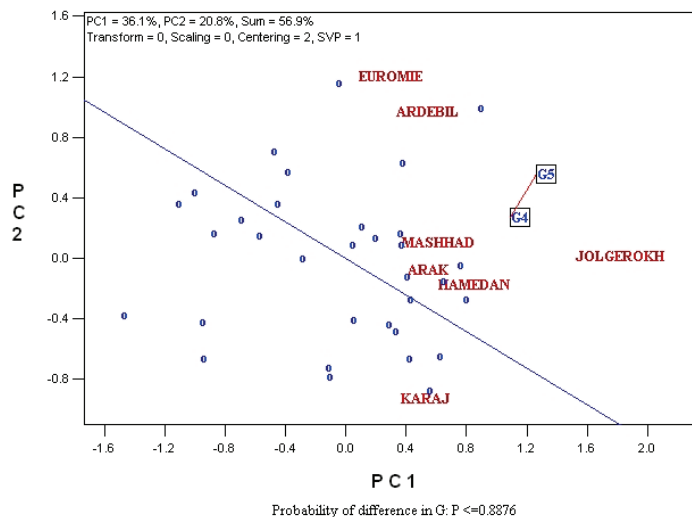

Figure 6. GGE biplot obtained from site regression (SREG) analysis that clusters the locations into those where G5 out-yields G4 and vice versa.

locations except Karaj.

DISCUSSION

GEI is a common phenomenon in variety trials and its presence usually complicates variety selection and release decision. We exploited the AMMI and GGE biplot analysis as the statistical methods for evaluating wheat promising lines using the grain yield data for cold regions of Iran. This paper demonstrated that the AMMI and SREG GGE models were very effective for studying the pattern of GEI and interpreting wheat grain yield data from multi-environment trials. It revealed that the GE interaction was an important source of wheat yield variation and its biplots were effective enough for visualizing the response patterns of genotypes and environments. The AMMI and GGE biplot analysis revealed similar results in identifying the ideal lines and in identifying the best test environments. Although the highest yielding line was G11, the mean grain yield between G11, G5 and G4 (as second and third ranks) was insignificant according to t-test result. AMMI and GGE biplot analysis revealed two lines, G5 and G4, to be highly adapted to several locations. The use of these wheat lines by farmers would assure them stable performance across various environments. These wheat lines could also be used in a breeding program to develop new consistent-performing varieties. This information should be useful for plant breeders in performance trials by targeting appropriate wheat genotypes to different regions and by identifying the best test environments to use economically limited resources such as time and money. Gauch *et al*. (2008) reviewed many articles comparing AMMI and GGE and concluded that it required clarification after controversial statements and contrasting conclusions appeared between these methods. According to the similar results of the AMMI and GGE biplot analyses obtained from our multi-environment trials data, both of these statistical methods can be used reliably by plant breeders. The GGE biplot aided in comparison of the performance of lines at different locations, determination of the relative performance of lines at a specific location and identification of lines suitable for groups of locations. Both methods can be used successfully in determining suitable wheat genotypes and locations for Iranian cold climate conditions.

ACKNOWLEDGEMENTS

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هدف گیری لاینهای امیدبخش گندم (.Triticum aestivum L) برای کشت در اقلیم سرد با استفاده از تجزیه AMMI و SREG GGE Biplot

ج. احمدی، ع. محمدی، ت. نجفی میرک

چکیده

اثرات متقابل ژنوتیپ × محیط بدلیل پیچیده کردن ارزیابی و گزینش ژنوتیپ های برتر برنامه های اصلاحی را تحت تاثیر قرار می‌دهند. این مشکل می‌تواند از طریق دانش فرآیند اثر متقابل و سازگاری ژنوتیپی کاهش یابد. موضوع این تحقیق ارزیابی پایداری عملکرد لاین‌های امید بخش گندم در مکان‌ها و روابط محیط‌های ارزیابی برای گزینش لاین‌های برتر در محیط‌های بزرگ در اقلیم سرد ایران بود. تعداد ۳۵ لاین امید بخش گندم در ۷ مکان در سال زراعی ۲۰۰۹-۲۰۰۸ کشت شدند. تجزیه واریانس مرکب نشان داد که عامل محیط درصد بالائی (۷۵/۷ درصد) از مجموع مربعات کل را توجیه می‌کند. مجموع مربعات اثر متقابل GE در حدود سه برابر بزرگتر از مجموع مربعات ژنوتیپ (G) بود. برای بررسی اثرات GE بر روی عملکرد، داده ها مورد تجزیه روشهای AMMI و GGE بای پلات قرار گرفتند. مدل AMMI1 ۸۸ درصد از اثرات اصلی و متقابل را توجیه نمود. بر اساس نتایج بای پلات‌های AMMI و GGE لاین‌های امید بخش G5 و G4 می‌توانند با اطمینان برای کشت توصیه شوند. بر اساس مدل SREG GGE سه محیط بزرگ (ارومیه و اردبیل به عنوان بزرگ محیط یک، مشهد، اراک، همدان و جلگه رخ به عنوان بزرگ محیط دو و کرج به عنوان بزرگ محیط سه) مشخص شد. در این آزمایش کاربرد بای‌پلات‌های AMMI و GGE مقایسه بصری و شناسائی ژنوتیپ های برتر را تسهیل نمود.

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