Assessment of yield stability of spring bread wheat genotypes in multi-environment trials under rainfed conditions of Iran using the AMMI model

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ABSTRACT

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Selecting bread wheat (*Triticum aestivum* L.) genotypes with wide adaptation across various test environments is important for enhancing the adoption rate of newly released wheat cultivars for rainfed spring wheat growing areas of Iran. This study analyzed the grain yield of 18 bread wheat genotypes at four dryland locations in Iran during the 2010-11, 2011-12, and 2012-2013 cropping cycles using the AMMI (additive main effects and multiplicative interaction) model. The biplot of AMMI-1 and AMMI-2 models facilitated the visual evaluation and identification of suitable genotypes, which is useful for genotype recommendation and mega-environment determination. Combined analysis of variance (ANOVA) revealed significant genotype × environment interaction for bread wheat yield. According to the AMMI-2 biplot, there were six best genotypes and five best mega-environments. The AMMI-1 model indicated that genotypes G2, G5, G9, G13, G14, G16, and G17 were superior, with moderate yield and yield stability, based on the lowest genotype × environment interactions. Genotypes G1 and G15 performed successfully in Khorramabad and Gonbad (two distinct mega-environments), respectively. The AMMI model was a useful tool for identifying yield stability of spring bread wheat genotypes for rainfed spring wheat growing areas of Iran. The significant genotype × environment interaction suggested that breeding strategies for specific adaption genotypes in homogeneously grouped environments should be considered in the national rainfed spring bread wheat breeding program in Iran.

Keywords: adaptability, biplot, drought, dryland, grain yield

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an important crop worldwide, including in Iran, due to its high levels of production and consumption. It was estimated that global wheat production must increase by 40% by 2020 in order to meet the rising demand for wheat (Borlaug and Dowswell, 1997). Wheat breeders should therefore develop new wheat genotypes and test them for yield performance and stability in different environments; the success of a new wheat genotype depends upon its adaptation in those environments (Romagosa *et al.,* 1996; Sabaghnia *et al.,* 2012). Breeding and statistical methods during the last decades have contributed to a decrease in genotype × environment (GE) interactions and have facilitated the selection of genotypes with better yield stability across a wide range of environments.

GE interaction refers to differential responses of genotypes across a range of test environments in multi-environment trials (METs) and is an important issue for plant breeders. Plant breeders look for a non-crossover type of GE interaction, or preferably the absence of GE interaction, for wide adaptation in yield stability analysis (Matus-Cadiz *et al.,* 2003). Variation in soil and climate is reflected in variation in yield performance and yield stability of genotypes. Evaluating genotypic performance across

a number of environments provides useful information for identifying adaptation and yield stability (Kang, 2004). The GE interaction is universal phenomenon and usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Nachit *et al.,* 1992). Numerous statistical models for MET data analysis have been developed to expose patterns of GE interaction, such as joint linear regression (Finlay and Wilkinson, 1963), AMMI (additive main effects and multiplicative interaction) model (Gauch, 2006), and the GGE (genotype main effect plus GE interaction) biplot (Yan *et al.,* 2007).

While several methods for stability analysis have been introduced, each indicates different aspects of stability and GE interaction structure, andno single model sufficiently explains genotype performance across environments (Sabaghnia *et al.,* 2006). The AMMI model integrates combined analysis of variance (ANOVA) with principal component analysis (PCA) of the GE interaction in a unified approach. Gabriel (1971) proposed that the graphic analysis model via biplots allows visual examination of the relationships among the test environments, genotypes, and the GE interaction (Ortiz *et al.,* 2001; Gauch *et al.,* 2008).

Kempton (1984) claimed that the AMMI model refers to double centered PCA and is based on singular value decomposition (SVD) and considered to be effective tool ingraphically diagnosing GE interaction structures (Gauch *et al.,* 2008). Some researchers (van Eeuwijk *et al.,* 1996; Sabaghnia *et al.,* 2008) reported that this method can be used to identify superior genotypes, in addition to selecting favorable environments in the genotype evaluation process. The AMMI model is a useful tool for identifying environments that optimize genotypic performance, therefore, making better use of limited available resources inbreeding programs. It is particularly useful for depicting adaptive responses of small grain cereals (Romagosa *et al.,* 1996; Annicchiarico, 1997) and has been successfully used to interpret GE interaction in wheat (Oikeh *et al.,* 2004; Petrovic *et al.,* 2010; Mahmoodi *et al.,* 2011; Mohammadi *et al.,* 2012; Sabaghnia *et al.,* 2013).

This study aimed to assess the grain yield stability of 18advanced spring bread wheat breeding lines in 11 rainfed test environments in Iran, as well as to interpret the GE interactions using AMMI biplots.

MATERIALS AND METHODS

A total of 18 advanced spring bread wheat breeding lines (Table 1) were evaluated at four locations (Gachsaran, Gonbad, Khoramabad, and Moghan) during the 2010-11, 2011-12, and 2012-13 cropping cycles. Details of each location (geographic position, altitude, soil, temperature, precipitation) are shown in tables 2 and 3. Data from Moghan during the 2010-11 cropping cycle was excluded due to severe drought stress, leaving data from 11 environments (location × year combinations) available for analysis. The experimental layout of all the trials was a randomized complete block design with four replications.

Table 1. Name and pedigree of the 18 bread wheat genotypes.

Genotype No.	Name/Pedigree
1	PASTOR/TILHI CMSS00Y01316S-030Y-030M-030WGY-16M-0Y
2	FRET2/TUKURU//FRET2 CGSS00B00158T-099TOPY-099M-099Y-099M- 9CEL-0B
3	RL6043/4*NAC//PASTOR/3/CROC_1/AE.SQUARROSA (224)// OPATA CMS S97 M03174T-040Y-020Y-030M-040SY-020M-2Y-010M-0Y-0SY
4	PASTOR/BAV92/3/BJY/COC//PRL/BOW CMSS97M03293T-040Y-020Y-030M-040SY-020M-11Y-010M-0Y-0SY
5	BABAX//IRENA/KAUZ/3/HUITES CMSS99M01622T-040Y-040M-040Y-15M-3CVLFY-3M-0Y
6	CROC_1/AE.SQUARROSA(224)//OPATA/3/PASTOR/4/ PASTOR *2/ OPATA CMSS 98Y03432T- 040M-0100M-040Y-020M-040SY-23M-0Y-0SY
7	CROC_1/AE.SQUARROSA (224)//OPATA/3/ ALTAR 84/ AEGILOPS SQUARROSA (TAUS)// OPATA/4/PASTOR CMS S98Y03433T-040M-0100M-040Y-020M-040SY-12M-0Y-0SY
8	SCA/AE.SQUARROSA (409)//PASTOR/3/PASTOR CMS S99 Y03439T-040M-040Y-040M-040SY-040M-23Y-010M-0ZTB-0SY
9	MILAN/SHA7/3/CROC_1/AE.SQUARROSA (224)//OPATA CMS S99Y00339S- 040Y-040M-040SY-040M-4Y-010M-0ZTB-0SY
10	MILAN/SHA7/3/CROC_1/AE.SQUARROSA (224)//OPATA CMS S99Y 00339S-040Y-040M-040SY-040M-14Y-010M-0ZTB-0SY
11	SUNCO/2*PASTOR CMSS99Y05530T-10M-040Y-040M-040SY-040M-6Y-010M-0ZTB-0SY
12	SUNCO/2*PASTOR CMSS99Y05530T-10M-040Y-040M-040SY-040M-7Y-010M-0ZTB-0SY
13	TIECHUAN 1*2/3/HE1/3*CNO79//2*SERI CMSS99 M01648F-040Y-040M-040SY-040M-040SY-15M-0ZTB-0SY
14	THELIN#2//ATTILA*2/PASTOR/3/PRL/2*PASTOR CGSS02Y00096T-099B-099M-099Y-099M-42Y-0B
15	THELIN/3/BABAX/LR42//BABAX/4/BABAX/LR42//BABAX CGSS02Y00083T-099B-099B-099Y-099M-48Y-0B
16	BABAX/LR42//BABAX*2/3/TUKURU CGSS01B00050T-099Y-099M-099M-099Y-099M-64Y-0B
17	WBLL1*2/BRAMBLING CGSS01B00066T-099Y-099M-099M-099Y-099M-8Y-0B
18	KOUHDASHT

Experiments were sown from 10 December to 10 January in different locations using a Winter Steiger planter with seeding density of 300 seed m^{-2}. Experimental plots consisted of six rows of 7 m long with 17.5 cm row spacing. Chemical fertilizers were used based on soil tests and recommendations for each location. Weeds were also controlled using appropriate herbicides.

Table 2. Geographical characteristics of the four test locations.

Location	Longitude Latitude	Altitude (m)	Soil texture	Soil type
Gachsaran	50º 50´ E 30º 20´ N	710	Silty Clay Loam	Regosols
Gonbad	55º 12´ E 37º 16´ N	45	Silty Clay Loam	Regosols
Khorramabad	48º 35´ E 33º 46´ N	1148	Silt-Loam	Regosols
Moghan	47° 58´E 39° 39´N	32	Sandy-loam	Cambisols

Table 3. Average rainfall and temperature for the four test locations during the 2010-11, 2011-12, and 2012-13 wheat cropping cycles.

Station	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	June
					Rainfall (mm)				
					2010-11				
Gachsaran	0.0	31.3	133.1	64.4	84.1	29.0	167.3	2.0	0.0
Gonbad	30.0	63.9	63.2	10.6	35.7	148.1	65.2	25.0	15.1
Khorramabad	52.5	135.8	48.5	48.8	82.7	32.5	196.8	58.6	1.9
Moghan	21.2	16.0	12.2	7.1	8.5	22.3	41.3	15.1	30.0
					2011-12				
Gachsaran	0.0	0.0	53.7	105.4	23.0	1.1	0.8	0.0	0.0
Gonbad	13.3	2.4	68.2	21.8	42.8	40.8	9.8	8.9	14.3
Khorramabad	0.0	10.4	101.0	45.9	22.6	30.7	14.2	26.2	0.0
Moghan	19.5	33.7	63.1	15.1	23.5	10.6	9.5	36.9	9.0
					2012-13				
Gachsaran	0.0	41.6	25.9	12.0	44.1	5.9	77.4	0.0	0.0
Gonbad	19.0	33.1	53.8	20.3	112.2	18.5	80.7	27.3	15.8
Khorramabad	0.0	85.2	99.0	17.9	32.1	9.8	73.2	26.8	3.7
Moghan	47.2	19.9	15.5	19.5	4.2	17.6	21.2	12.4	15.1
					Temperature (ºC)				
					2010-11				
Gachsaran	26.2	20.5	10.7	9.1	13.3	14.2	18.4	25.4	30.0
Gonbad	23.4	17.5	7.9	9.6	9.1	10.5	14.8	22.1	26.7
Khorramabad	20.8	13.4	5.8	3.2	6.4	9.0	11.4	18.9	25.1
Moghan	19.1	12.7	5.2	3.7	7.1	6.4	10.2	16.3	25.4
					2011-12				
Gachsaran	26.5	17.8	14.3	8.9	10.9	15.8	21.2	26.4	30.6
Gonbad	21.6	16.5	11.2	2.7	4.9	12.9	17.7	21.4	25.0
Khorramabad	21.3	14.8	8.2	2.1	5.5	10.7	16.7	20.3	26.6
Moghan	18.1	12.0	5.3	-0.4	1.8	9.4	16.5	18.1	22.7
					2012-13				
Gachsaran	26.3	19.4	12.9	10.9	12.2	17.4	18.3	26.2	31.4
Gonbad	22.5	13.9	11.6	11.7	11.0	12.9	12.8	19.1	25.2
Khorramabad	21.3	13.0	6.9	5.1	7.7	10.1	11.6	17.9	25.2
Moghan	18.4	11.3	6.7	2.3	6.4	8.4	11.2	17.0	22.6

Environments were considered as random variables while the genotypes were treated as fixed variables. Analysis of variance was conducted using SAS (SAS/STAT User's Guide, 2004) to determine the effects of genotype, environment, and GE interactions on grain yield. The AMMI model was used to investigate GE interactions using the following equation:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n X_{in} U_{jn} + \varepsilon_{ij}$$

where Y_{ij} is the yield of the ith genotype in the jth environment; μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; λ_n is the eigenvalue of the interaction PCA (IPCA) axis n; X_{in} and U_{jn} are the genotype and environment eigenvectors for axis n; n is the number of principal components retained in the model; and ε_{ij} is the error term.

In addition, IPCA axes were extracted and statistically tested using Gollob's (1968) F-test procedure. The first two components were used to obtain an AMMI biplot (Burgueno et al., 2001), which is used to interpret the AMMI model by relating genotypic means to the first two IPCA by

enabling the visual presentation of the GE interaction estimate. Biplots were drawn using Statistica 7.0 (StatSoft, 2004).

RESULTS AND DISCUSSION

Combined ANOVA for grain yield revealed significant GE interactions (Table 4). The main effects of environment (E) and genotype (G) were also significant. Grain yield was significantly affected by E, which accounted for about 96% of the sum of squares of E+G+GE, whereas G and GE interaction captured 1% and 3%, respectively. According to Yan *et al*. (2007), the large yield variation in most crops is due to environment and is the main source of variation.

While the combined ANOVA gives an overall

Table 4. Combined analysis of variance (ANOVA) and AMMI analysis for grain yield of advanced spring bread wheat lines.

S. O.V.	DF	Mean Squares	RMSPD¶	% of GE†	% of GE‡
Environment (E)	10	161572682.5**			
Replication/E	33	1271585.7			
Genotype (G)	17	609621.1**			
GE	170	302985.5**			
IPC1	26	559204.9**	506.7	28.2	28.2
IPC2	24	407300.2**	484.4	18.9	47.1
IPC3	22	406460.4**	509.1	17.4	64.6
IPC4	20	309634.9*	511.9	12.0	76.6
Residual	78	154592.9			
Error	561	140808.5			

¶ RMSPD, the root mean square prediction differences of cross validation
†Percentage of each IPC from GE interaction
‡ Cumulative percentage of each IPC from GE interaction
**, * and ns, respectively significant at the 0.01and 0.5 probability level and non-significant

picture of the relative magnitude of G, E, and GE interaction variance components, the AMMI model enables further analysis of the GE interaction. Gollob's (1968) F-test indicated that the first four IPCA were significant, while the RMSPD (root mean square prediction differences) values of the cross validation procedure demonstrated the AMMI-2 model as the appropriate statistical model for describing the GE interaction (Table 4). The AMMI-2 model, including IPC1 and IPC2, accounted for 47.1% of the GE variation of grain yield in advanced rainfed spring bread wheat genotypes. The AMMI model showed that there was a relatively simple interaction of GE, which could facilitate graphical visualization of the genotypes in low dimensions.

The abscissa of the AMMI-1biplot (Fig. 1) indicated differences in the main effects and ordinate differences in the GE interaction structures. According to the AMMI-1 biplot, genotypes G2, G5, G9, G13, G14, G16, and G17 had the lowest GE interaction (zero or near zero), as well as moderate mean yield (Fig. 1). All of these are favorable candidates for wide adaptation for most of the test environments.

According to Gauch (2006), genotypes with a flat response show high yield stability and are adapted (if they also possess high mean yield). In general, the IPC1 scores divided the genotypes into two distinct groups: group 1 (G3, G4, G5, G7, G8, G10, and G14) and group 2 (G1, G2, G6, G9, G11, G12,

G13, G16, G17, and G18). Genotypes in each group interact positively with the related test environment, and interact negatively with the test environments of the other group (Fig. 1). The IPC1 scores divided the test environments into two main mega-environments (ME): E2, E3, E6, E7, E9, and E10 (ME-1) with winner genotype G1, and E1, E5, E8, and E11 (ME-2) with winner genotypes G4 and G7. The AMMI-1 ME geometry is quite simple, involving a single horizontal line at an IPC1 score of 0.0. The performances of the winner genotypes of AMMI-1 biplot were relatively moderate.

The AMMI-1 biplot is simpler and easier to visualize, and according to Gauch *et al*. (2008), this biplot is comparable with the GGE biplot, as both capture GE interaction essentially on one IPCA, though the AMMI-1 biplot is simpler than the GGE biplot for ME identification, genotype response determination, and similarities among environments in GE interaction. The AMMI-1 model is also analogous to the joint linear regression model (Finlay and Wilkinson, 1963), except that environment IPC1 scores substitute for environment means along the abscissa, while the AMMI-1 model captures more GE interaction than the joint linear regression model.

A simple model such as AMMI-1 is sufficient when analyzing genotype × location interaction of METs that are repeated in time factor (Annicchiarico, 1997). Using simple statistical
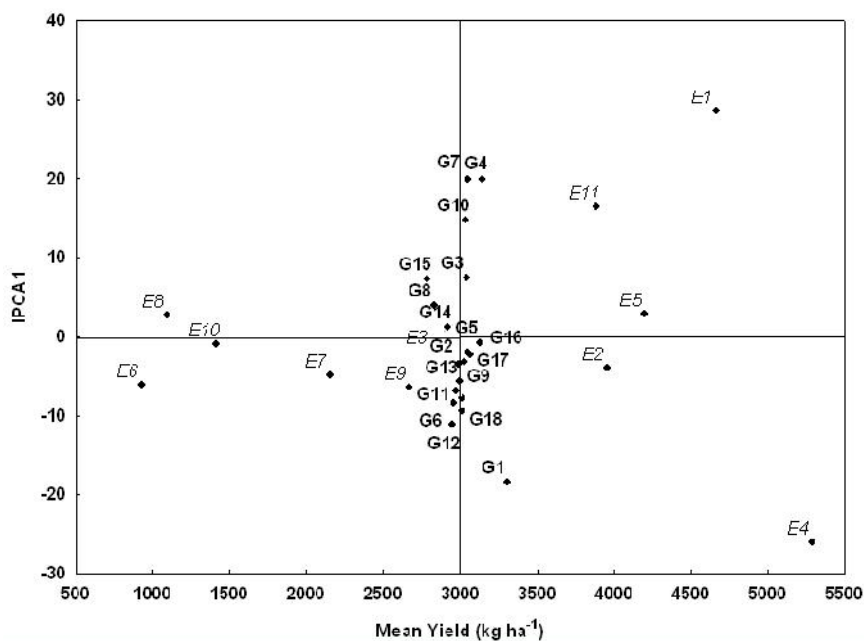
Fig. 1. AMMI-1 biplot for rainfed spring bread wheat multi-environmental trials. The genotype and environment means are shown on the abscissa, with a vertical line at the grand mean of 3000 kg ha^{-1}. Interaction principal component 1 (IPC 1) scores are shown on the ordinate, with a horizontal line at 0.

models and fewer ME may result in the benefit of greater gains from specific adaptation and the disadvantage of less data.

Some corner genotypes (i.e. the most responsive ones) can be visually identified on the AMMI-2 biplot. These are either the best or the poorest genotypes at some or all test environments and can be used for identifying ME. The corner genotypes for the rainfed spring bread wheat dataset were G4,

G7, G15, G12, G1, and G16 (Fig. 2). By connecting corner genotypes, a special polygon is generated; perpendiculars to each side of this polygon and the plot origin then divides the test environments into various sectors, each with a different vertex genotype.

In Figure. 2, the test environments are divided between five sectors. The first sector contains test environment E1 with genotype G4 the winner. The
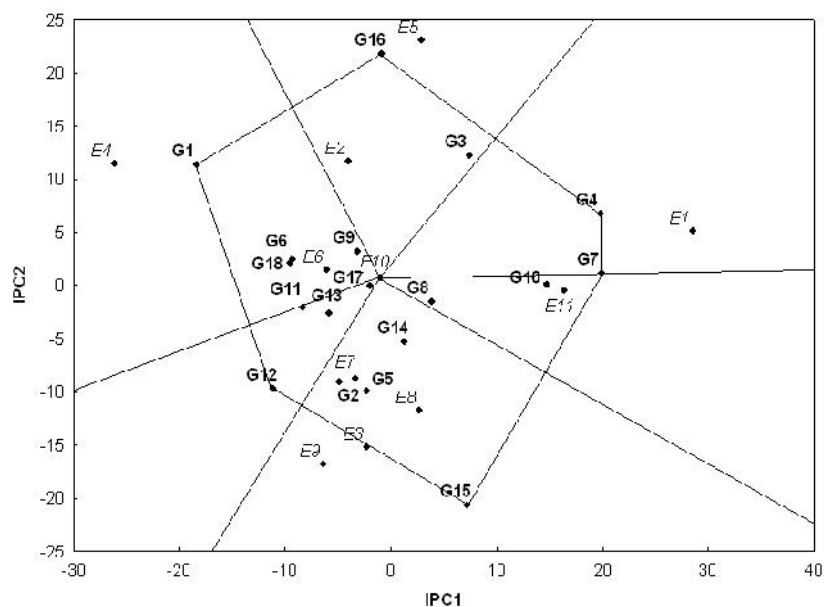

Fig. 2. AMMI-2 biplot for rainfed spring bread wheat multi-environmental trials. Interaction principal component 1 (IPC 1) scores are shown on the abscissa. IPC 2 scores are shown on the ordinate, with a horizontal line at 0.

test environment E11 makes up the second sector with genotype G7 the winner (Fig. 2). The third sector contains test environments E3, E7, E8, and E9, with genotype G15 the winner. The fourth sector contains test environments E4, E6, and E10 with genotype G1 the winner. The other test environments (E2 and E5) make up the fifth sector, with genotype G16 the winner (Fig. 2). If the ME concept is explained by different winning genotypes (Gauch and Zobel, 1997), Fig. 2 would identify five ME for rainfed spring bread wheat in Iran. However, such a subdivision should be regarded a proposal as it is based solely on one MET dataset and must be further verified using other similar datasets.

Of the four locations, Khorramabad and Gonbad could be regarded as distinct ME, while Gachsaran and Moghan could not be regarded as such due to variable responses over different years. Genotype G1 was the best performing genotype for Khoramabad and genotype G15 was the best performing genotypeat Gonbad.

The gain factor of the AMMI-2 model for the rainfed spring bread wheat METs was 2.19, thoughit usually obtains a statistical efficiency of 1.5-4.0 (Gauch and Zobel, 1996). Ebdon and Gauch (2002) reported an exceptional statistical efficiency of 5.6 for the AMMI-2 model for rye grass METs. Winning genotypes and ME identified by the AMMI-2 model are also more reliable over years. The yield and its stability aspects are graphically depicted by the abscissa and ordinate of the biplot. Moreover, the biplot technique can be applied to balanced subsets extracted from multiple years of trials.

Newly improved genotypes require testing at multiple environments before they can be recommended for a given region and thus breeding programs have to manage recurring GE interactions. The GE interaction is as much a function of the environmental factors as a function of the morphological and physiological characters of the genotypes (Nachit *et al.,* 1992). New developments in plant physiology, statistics, and some integrated models have enabled the study of GE interaction. However, it seems that the AMMI model is more efficient than most statistical procedures. It is superior to conventional stability procedures and to avoid unnecessary analyses, there is no call for a mix-and-match strategy using AMMI model (Gauch *et al.,* 2008). Among singular value decomposition-based models, AMMI is the analysis that separates G, E, and GE interaction as needed for most breeding goals. The AMMI model also separates signal from noise as well as any other method for the purpose of gaining accuracy.

CONCLUSIONS

Selection of genotypes for high yield and yield stability is an important component of any wheat breeding program in arid and semi-arid environments, where the environment is variable and unpredictable. According to this study, the superior genotypes were G2, G5, G9, G13, G14, G16, and G17, which had moderate yield and high yield stability based on the lowest GE interaction. These genotypes were more suitable for use in crossing block for warm dryland regions. Six winning genotypes and five mega-environments were identified according to the AMMI-2 model biplot. Genotype G1 was the best performing genotype in Khorramabad (one ME), while genotype G15 was the superior genotype at Gonbad (another ME). The AMMI model was a useful tool for identifying the yield stability of rainfed spring bread wheat genotypes. The significant GE interaction suggested that a breeding strategy for specific adaption genotypes in homogeneously grouped environments should be considered in the national rainfed spring bread wheat breeding program in Iran.

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