



## RESEARCH PAPER

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## Additive main effect and multiplication interaction analysis of grain yield in bread wheat genotypes across environments

Mohammad Motamedi<sup>1\*</sup>, Parviz Safari<sup>2</sup>, Ghalamabbas Mohammadi<sup>3</sup>

<sup>1</sup>*Department of Agronomy and Plant Breeding, Shoushtar Branch, Islamic Azad University, Shoushtar, Iran*

<sup>2</sup>*Department of Plant Breeding and Biotechnology, University of Tabriz, Iran*

<sup>3</sup>*Department of Agronomy and Plant Breeding, Jiroft Branch, Islamic Azad University, Jiroft, Iran*

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### Abstract

Selection of wheat cultivars with wide adaptability across diverse farming environments is important before recommending them to achieve a high rate of cultivar adoption. Multi-environment trials including 3 locations for 20 genotypes of wheat were carried out in Iran. The results of combined analysis of variance for yield showed significant difference for genotype, locations and G×E interaction effect. Additive main effects and multiplicative interactions analysis (AMMI) indicated that the yield performances of genotypes were under the major environmental effects. Analysis of AMMI was employed and the biplot of the Interaction Principal Components (IPC) were evaluated for stability and adaptation relationships among genotypes and locations. Based on AMMI method, genotypes no. 12, 6 and 20 varieties showed general adaptability and genotypes 14 and 15 recognized to have specific adaptability to varamin and genotypes no. 4, 7, 8, 9 and 11 had specific adaptability to Kermanshah. Overall, based on stability analysis on yield genotypes no. 6, 20 and 12 with having good adaptability were determined as desirable genotypes.

\* **Corresponding Author:** Mohammad Motamedi ✉ [motamedi55@yahoo.com](mailto:motamedi55@yahoo.com)

## Introduction

Wheat (*Triticum aestivum* L.) is a major food crop for more than one third of the world population and is the main food of Asia (Shirazi *et al.*, 2001). It is estimated that out of 12 million hectares of arable lands in Iran, about 50% are located to wheat production. Wheat production in Iran reached 13.4 million tons in 2002-2003 growing season. This was harvested from 6.4 million hectares of area under wheat from which 2.4 million hectares were under irrigation producing 8.7 million tons (Najafian *et al.*, 2010).

The main task in access to a stable wheat variety is to account for environmental effects and a definition of interaction. The improved wheat genotypes are evaluated in multi-environment trials to test their performance across different environments and to select the best genotypes in specific environments. When imprecise analysis of the genotype  $\times$  environment interaction (GEI) is performed, several problems arise, mainly the reduction in the accuracy of genotype selection (Lavoranti, 2003). The  $G \times E$  interaction structure is an important aspect of both plant breeding programs and the introductions of new crop cultivars. Significant GEI results from the changes in the magnitude of differences between genotypes in different environments for changes in the relative ranking of the genotypes (Gorge and Fernandez, 1991).

Several methods have been proposed for analysis of GE interaction with the aim of explaining the information contained in the GE interaction data matrix (Eberhart and Russell, 1966; Lin *et al.*, 1986; Huhn, 1979; Kang and Pham, 1991; Hernandez *et al.*, 1993). They each reflected different aspects of stability and no single method can adequately explain cultivar performance across environments. An alternative and complementary method of evaluating cultivars is through multivariate analysis of GE interactions (Lin *et al.*, 1986; Crossa, 1990). A comprehensive description of GE interaction requires more sophisticated statistical methods than standard analysis of variance (ANOVA).

A popular extension of ANOVA for studying GE interaction is the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992). The additive main effect and multiplicative interaction (AMMI) method proposed by Gauch (1992) was a significant advance in the analysis and interpretation of  $G \times E$  interaction. The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. The model separates the additive variance from the multiplicative variance and then applies principal component analysis (PCA) to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern and the estimation accomplished using the least squares principle (Thillainathan and Fernandez, 2001). Purchase (1997) developed the AMMI Stability Value (ASV) based on the AMMI model's PCA1 and PCA2 (Principal Components Axis 1 and 2 respectively) scores for each cultivar.

The most accurate model for AMMI can be predicted by using the first two PCA (Gauch and Zobel, 1997; Yan, 2002). Sabaghnia *et al.*, 2008 used AMMI model to study of adaptation and analyze yield stability in multi-environment trials on lentil genotype. Najafian (2005) was used AMMI analysis of grain yield to determine stability and adaptation status of 20 hexaploid wheat genotypes grown over 4 locations under late season moisture stress conditions. The results of that study showed specific adaptation for several genotypes toward one of the stations which was affected by frost damage.

Smith *et al.*, (2001) and Resende and Thompson (2003) presented the factor analytic multiplicative mixed model for GE analysis considering G and GE as random effects. Deghani (2006) was used Biplot Analysis of Genotype by Environment Interaction for Barley Yield in Iran. The results of that study indicate the possibility of improving progress from selections under diverse location conditions by applying the

GGL biplot (genotype plus genotype×location) methodology. Tian *et al.*, (2007) were analyzed Variation and Stability of Wheat genotype.

The objectives of this study are to (i) interpret Genotype main effect and GE interaction obtained by AMMI analysis, (ii) group the varieties having similar response pattern over all environments.

## Materials and methods

### Plant materials

Field experiments were conducted at 3 different research stations in Iran, which include Esfahan, Kermanshah and Varamin. The nursery was evaluated in 2007 as a yield trial. The names, codes, and origin of the genotypes are provided in Table 1. The experiments were carried out in a randomized complete block design (RCBD) with three replications over all environments. The experimental plots consisted of 6 rows of 6m length each. Row-to-row and plant-to-plant distances were kept at 20 cm and 120 cm, respectively at all the environments. Data on seed yield were taken from the middle 4 rows of each plot, leaving aside the guard rows on either side of a plot.

### Yield stability and AMMI model

Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA on the data. Pooled analysis of variance for G×E interaction on grain yield was done according to multivariate additive main effects and multiplicative interaction (AMMI) effects (Gauch, 1988) were computed for classification of genotypes and environments.

Different methods of data analysis were used to investigate G×E interactions for total grain yield. AMMI combines ANOVA into a single model with additive and multiplicative parameters. The model equation is:

$$Y_{ijk} = \mu + g_i + e_j + \sum^n \lambda_n g_{in} d_{jn} + \theta_{ij} + \varepsilon_{ijk}$$

where  $Y_{ij}$  is the yield of the  $i$ th genotype in the  $j$ th environment;  $\mu$  is the grand mean;  $g_i$  and  $e_j$  are the genotype and environment deviations from the grand mean, respectively;

$\lambda_n$  is the eigen value of the PC analysis axis  $n$ ;  $g_{in}$  and  $d_{jn}$  are the genotype and environment principal component scores (eigenvectors) for axis  $n$ ;  $n$  is the number of principal components retained in the model and  $\theta_{ij}$  is the residual and  $\varepsilon_{ijk}$  is the Error.

As mentioned above, the AMMI stability value (ASV) is the distance from the coordinate point to the origin in a two dimensional scattergram of PCA1 scores against PCA2 scores. Because the PCA1 score contributes more to the G x E sum of squares, a weighted value is needed. This weight is calculated according to the relative contribution of PCA1 to PCA2 to the interaction SS (Ferney *et al.* 2006).

The data were subjected to statistical analysis using AGROBASE 20 (Agrobases, 1999) computer software.

## Results

### Combined analysis

Bartlett's test suggested ( $P < 0.05$ ) that error variances were homogeneous. Results of the combined analysis of grain yield of wheat genotypes are given in table 2. The differences among genotypes for grain yield were significant ( $P < 0.01$ ). The effects were significant at  $P < 0.01$ . Mean squares associated with the GE interaction were also significant at  $P < 0.01$ . The significant GE interaction for yield confirms the differential rankings of cultivars to environments. The grain yield of the genotypes across environments ranged from 6.95 to 4.340 t·ha<sup>-1</sup> and grand mean grain yield was 5.97 t·ha<sup>-1</sup> (Table 3).

### AMMI analysis

Results of AMMI analysis of mean grain yield for the three locations showed significant differences ( $P < 0.01$ ) among the genotypes, the environments and G × E interaction (table 4) and this results also showed that 69.73% of the total sum of squares was attributable to environmental effects, only 11.68% to genotypic effects, and 7.78% to GEI effects (Table 4). Results from AMMI analysis (Table 4) also showed that the first principal component axis (PCA 1) of the interaction captured 65.99% of the interaction sum of squares in 52.6% of the interaction degrees of freedom.

The first two axes; IPC1 and IPC2 accumulatively defining 99% of G×E interaction variations were significant for grain yield. IPCAI value of variety was near to zero point according to ordinate picture, which showed there were small interactions between the cultivars and the environments, and their stability appeared stable.

**Biplot analysis**

The biplot analysis revealed that genotypes 20 and 12 exhibited IPCA scores close to zero and high mean yield, which indicated that they were insensitive to the environments, thus found to be stable.

The biplot of IPCA1 against IPCA2 compares relative magnitude and sign of the GE interaction controlled by each genotype and each environment. Genotypes with large IPCA1 or IPCA2, or both, have high interactions, whereas genotypes with IPCA1 or IPCA2 scores near zero have small interactions for the corresponding axis. In the Figure 1, the locations showed into three sectors and genotype exhibited into four groups: the best genotype with respect to site Varamin was genotype 14. Genotype 8 was best for site Kermanshah; genotypes 13, Azar2 and 10 were best for sites Esfahan. Genotypes located near the plot origin were less responsive than the other genotypes. Genotypes 20 and 12 were high production since their yield mean and they located, near the plot origin, thus they were found to be adapted.

Biplot also showed genotype 14, 13 high yielding environments but they had negative and great IPCA1 scores, thus these genotypes were unstable to the environments. Genotypes 16, 20 and 12 had high grain yield into environments with IPCA score near zero. The results of this study confirm the importance of testing genotypes under representative environmental conditions to identify the best, stable and high yielding genotypes. The IPCA of locations Esfahan was near to zero point line, which showed their stability was stable. In contrary, the IPCA of location Kermanshah and Varamin was far away from the zero line, which showed their stability was changeable.

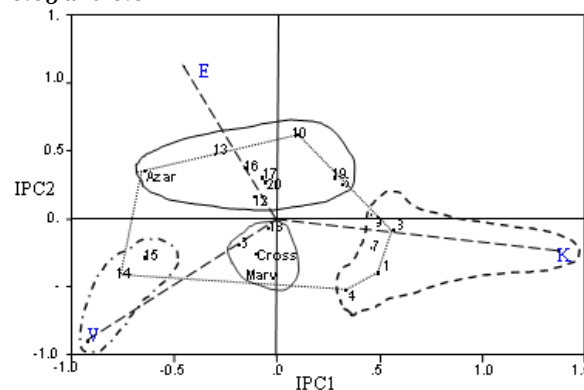
**Table 1.** Origin and pedigree of genotypes.

Genotype	Pedigree	Origin
marvdasht		
Cross		
alborz		
azar-2		
4	Ghod s *3/karko/Ghod...	Mashhad
5	Ghod s *3/karko/Ghod...	Mashhad
6	URES/3/FURY//SLN/...	WON-D(2000-01)
7	M-70-4/5/vres/3/Gov....	Kermanshah
8	M-70-4/Tvi s	Kermanshah
9	M-70-4/Tvi s	Kermanshah
10	Azd/HD2172//1-67-78	Mashhad
11	Bloyka lcw 84-0008....	int.nersury
12	Azd/HD2172//V-kawr s	Karaji
13	TEVEE s /sHvHA s	RWYT-MR(2000-01)
14	T.AEST/SPRW...	WON-D(2000-01)
15	ZIDNE 89/PERW/...	WON-D(2000-01)
16	cHAM-4/kAsGLE...	WON-D(2000-01)
17	GMU s /T/ b 84//...	Kermanshah
18	seri 82 /Rsh 2	Zarghan
19	shahi / kv2 /5 /shahi/4/...	D
20	Azd/ HD2172//pitoma/...	Mashhad

**Table 2.** Results of combined ANOVA of grain yield for 3 locations.

SOV	df	SS	MS
Model	65	456.33	6.02**
Environment	2	353.74	176.8**
Rep. in Env.	6	3.83	0.63
Genotype	19	59.4	3.12**
G×E	38	39.35	1.03**
Error	114	50.33	0.44

\*and\*\* Significant at probability level of less than 0.05 and 0.01



**Fig .1.** Biplot of G×E interaction for 20 genotypes and 3 locations as per their IPC1 and IPC2.

\* E= Esfahan, K= Kermanshah, V=Varamin

**Table 3.** Means of genotype to environments.

Genotype	Esfahan	Kermanshah	Varamin	Mean
<b>Mravdasht</b>	4.63	8.13	5.42	6.06
<b>Crossalborz</b>	4.61	7.73	5.14	5.83
<b>Azar2</b>	4.06	5.35	3.61	4.34
4	4.03	8.37	5.00	5.8
5	6.12	9.31	5.42	6.95
6	5.32	8.16	5.76	6.42
7	4.96	9.05	5.14	6.38
8	4.74	8.81	4.51	6.02
9	4.79	8.61	4.31	5.9
10	5.63	9.42	4.31	5.96
11	5.06	7.94	5.69	6.72
12	5.8	8.33	5.49	6.54
13	5.4	7.74	5.42	6.18
14	5.00	7.12	6.18	6.1
15	4.99	7.16	5.83	5.99
16	5.59	7.74	4.86	6.06
17	4.91	7.33	4.31	5.51
18	4.46	7.42	4.58	5.48
19	4.19	7.24	3.4	4.94
20	5.56	8.05	5.00	6.2
<b>mean</b>	4.99	7.95	4.97	5.97

\*\*, Significant at probability level of less than 0.01

**Table 4.** Results of combined ANOVA and AMMI analysis of grain yield for 3 locations.

SOV	df	SS	MS	F
Genotype	19	59.19	3.11	3.01**
Env.	2	353.26	176.63	171.48**
G×E	38	39.44	1.03	2.34**
IPC1	20	26.03	1.3	2.93**
IPC2	18	13.4	0.74	1.68**
Error	114	50.67	0.44	
<b>Total</b>	179	506.59		

\*and\*\* Significant at probability level of less than 0.05 and 0.01

## Discussion

### Combined analysis

In this study Genotype by environment (G×E) interactions were significant ( $P < 0.01$ ). These results were similar of other researcher on wheat in Iran. Dehghani *et al.*, (2006) and Najafian *et al.*, (2010) applied stability parameters and results of this study indicate the L and G effects were significant at  $P < 0.05$  and  $P < 0.01$ , respectively. The significance of G×E interaction effects demonstrated that genotypes

responded differently to variations in environmental conditions.

**Table 5.** IPCA1 and IPCA2 scores for genotype and environment.

Genotype	IPC1	IPC2
1	-0.001	-0.399
2	-0.098	-0.254
3	-0.645	0.359
4	0.335	-0.571
5	0.32	0.261
6	-0.184	-0.188
7	0.459	-0.203
8	0.579	-0.029
9	0.543	0.104
10	0.103	0.62
11	0.449	-0.429
12	-0.11	0.171
13	-0.301	0.484
14	-0.767	-0.42
15	-0.639	-0.281
16	-0.156	0.384
17	-0.069	0.305
18	-0.041	-0.066
19	0.281	0.311
20	-0.053	0.278
<b>Environment</b>	<b>IPC1</b>	<b>IPC2</b>
<b>Esfahan</b>	-0.454	1.123
<b>Kermanshah</b>	1.37	-0.228
<b>Varamin</b>	-0.921	-0.894

The difference in the rank of the genotypes in the various environments indicated the presence of G×E interactions. From Table 3, it is possible to see variation of genotypes in various environments and change of ranking, such as genotype 4 and 19. High yield stability usually refers to a genotype's ability to perform consistently, whether at high or low yield levels, across a wide range of environments (Ferney *et al.*, 2006).

#### *AMMI analysis*

The results of AMMI analysis of variance showed that 69.73% of the total sum of squares was attributable to environmental effects. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. In the present study, partitioning and interpretation of the G×E interaction was based on the AMMI stability technique (Zobel *et al.*, 1988) Multivariate statistical methods such as AMMI have been introduced to explore multidirectional aspects and attempt to extract more information from this component. In contrast, AMMI analysis appears to be able to extract a large portion of the G×E interaction and is thus more efficient in analyzing G×E interaction pattern in different crops such as cereals (wheat), legumes (lentil), and oilseeds (soybean), as demonstrated by Zobel *et al.* (1988).

Results from AMMI analysis (Table 4) also showed that the first principal component axis (PCA 1) of the interaction captured 65.99% of the interaction sum of squares in 52.6% of the interaction degrees of freedom. The first two axes; IPC1 and IPC2 accumulatively defining up to 99% of G×E interaction variations were significant for grain yield. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model. The AMMI analysis provides a graphical representation of summary information on main effects, and the first interaction axis in the form of a biplot of IPCA1 and G×E interaction to classify genotypes and environments. The means and IPCA scores of genotypes and environments for grain yield are given in Table 5.

IPCAI value of variety was near to zero point according to ordinate picture, which showed there were small interactions between the cultivars and the environments, and their stability appeared stable. Balestre *et al.*, (2009) were evaluated Yield stability and adaptability of maize hybrids based on GGE biplot analysis characteristics and indicated the genotypic values predicted for each environment were submitted to AMMI analysis obtaining genotypic adaptability and stability.

#### *Biplot analysis*

Based on biplot generated using genotypic and environmental scores of the first two AMMI components (Fig. 1) genotypes such as, 14 which had special adaptability for restriction environments, there were unstable, and unsuitable for cultivation in widely location. In fact, specific adaptation could be characterized as positive coincidence of plant phenology with such environmental reducing events as frost damage in winter and/or terminal drought. For example, in case of a dry season, during terminal stages of crop growth, early maturing drought tolerant genotypes may bring about a good performance which is detectable as specific adaptation in the AMMI plotting.

Kaya *et al.* (2002) was studied on stability Yield Performances Bread Wheat Genotypes by AMMI method And showed biplot generated using genotypic and environmental scores of the first two AMMI components also showed that genotypes with larger PCA 1 and lower PCA 2 scores gave high yields (stable genotypes), and genotypes with lower PCA 1 and larger PCA 2 scores had low yields (unstable genotypes), as in the sites tested.

The PCA scores of a genotype in the AMMI analysis are an indicator of the stability of a genotype over environments. The greater the PCA scores, either negative or positive, the more specifically adapted a genotypes are to certain environments. The more the PCA scores approximate zero (0), the more stable the genotype is over all environments sampled (Ferney *et al.*, 2006).



Consequently, biplots generated using genotypic and environmental scores of the AMMI components can help breeders have an overall picture of the behavior of the genotypes, the environments and G×E interaction. (Aminzadeh, 2010). Overall, genotypes no. 6, 20 and 12 showed small interactions; therefore they were selected for yield stability across locations. Thus, these genotypes may have broad adaptation and make good sources for breeding wheat cultivars.

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