



## Graphic analysis of the genotype $\times$ environment interaction in durum wheat (*Triticum turgidum* L.) using AMMI model

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### Abstract

Selection of durum wheat (*Triticum turgidum* L.) genotypes with wide adaptability across different environments is important before their commercial recommendation to achieve a high rate of cultivar genotype. Multi-environment trials including three years and five locations for twenty durum wheat genotypes in randomized complete block design layout with four replications were carried out in Iran. The obtained data were analyzed with additive main effect and multiplicative interaction (AMMI) model to understand the GE interaction pattern. Combined analysis of variance showed the effect of year (Y) and genotype (G) were significant while the location (L) effect was not significant. The YL and GYL interaction were highly significant. ANOVA of grain yield showed that 92% of the total sum of squares was attributable to environmental effects, only 1% to genotypic effects and 7% to GE interaction effects. The first two interaction principal components analysis (IPCA1 and IPCA2) were used to create a 2-dimensional AMMI-2 model biplot and explained 24% and 15% of AMMI sum of squares (SS), respectively. The AMMI-2 biplot suggests three practical durum wheat mega-environments in Iran: two minor mega-environments (northwestern Iran consisting of Moghan and southwestern Iran consisting of Gachsaran), and a major one (western Iran consisting of Kouhdasht and Ilam). As a result, the findings from this investigation are as follows: (1) genotype G3 was the most stable and is thus recommended for commercial release in most test environments of Iran as broad adaptable genotype; (2) genotype G10 for Moghan, genotype G11 Gachsaran and G12 for both for Kouhdasht and Ilam, were the most stable and are thus recommended for commercial release in Iran as specific adaptability to these locations; (3) the AMMI model can be used to identify superior genotypes for target sites in Iran and regions in other parts of the world.

**Keywords:** multi-environmental trials; genotype  $\times$  environment interaction; principal component analysis.

### Introduction

The yield stability of durum wheat (*Triticum turgidum* L.) genotypes performance and quality traits is often difficult to accurately estimate due to genotype  $\times$  environment (GE) interaction. Environmental factors such as rainfall and temperatures in arid and semi-arid areas of Mediterranean regions indicate large and unpredictable fluctuations across different seasons (Annicchiarico et al. 2011; Karimizadeh et al. 2012a; Karimizadeh et al. 2012b). Much attention has been devoted to analyzing GE interaction to improve plant breeding efforts and favorable genotype selection as well as recommendation based on durum wheat yield multi-environmental trials could benefit from such analysis. Breeding of durum wheat in Iran is performed in collaboration of ICARDA (International Centre for Agricultural Research in the Dry Areas) and is aimed at developing genotypes adapted to the different test environments prevailing in Iran (Karimizadeh et al. 2012c).

The GE interaction analyses have the potential to reduce the number of test environments required to develop the confidence

necessary to recommend a special genotype across a range of environments, thereby reducing the adoption time for genotypes with superior yield potential (Annicchiarico et al. 2011). The improved durum wheat genotypes are evaluated in multi-environment trials to test their performance across environments and to select the best genotypes in specific environments or stable performing genotypes across a range of environments. Stability of genotype performance for high grain yield across different test environments and broad adaptation are the goals of most durum wheat breeding programs (Cooper et al. 2001). GE interaction often confounds the genetic differences that affect yield among durum wheat genotypes. The GE interaction is commonly encountered when different genotypes are evaluated in multi-environment trials, as suggested by many authors (Kang, 1998).

Most of the GE interaction analysis has been limited to ANOVA and mean comparison across environments. The ANOVA enables one to partition the total variation into the main components (environment, genotype and GE interaction) but it leaves out some of the valuable information on their structure (Zobel et al. 1988). Understanding of GE interaction

can lead to efficient progress in plant breeding program. The GE interaction expressed as the linear regression coefficient of the genotype on the location mean was first proposed by Finlay and Wilkinson (1963). Gauch (1988) and Zobel et al. (1988) were the first to link the GE component of the ANOVA model with the principal components analysis (PCA) in multi-environmental trials and called it as additive main effects and multiplicative interaction (AMMI) model.

In multi-environmental trials, usually a large number of genotypes are tested across a number of test environments, and it is often difficult to determine the structure of genotypic response across test environments without the help of graphical display of the data. Biplot introduced by Gabriel (1971) to allow simultaneous display of both samples and variables from a two-way data matrix. Biplot displays the two-way data and allows visualization of the interrelationship among environments, genotypes, and GE interaction. Two types of biplots, the AMMI biplot (Gauch, 1988) and the GGE biplot

(Yan et al. 2000) have been used widely to visualize GE interaction. According to Gower and Hand (1996) biplot can be considered multivariate analogues to a scatter plot. In AMMI model, several biplots could be generated based on significance of different AMMI model components; AMMI-1, AMMI-2 and etc.

Therefore to identify genotypes with stable grain yield and to evaluate GE interaction needs more sophisticated statistical tool as AMMI model. It was observed that AMMI model uniquely separates genotype, environment, and GE as needs for most breeding research purposes, and also separates variation pattern from noise as well as any other method for the purpose of gaining accuracy (Gauch et al. 2008; Anandan et al. 2009; Sabaghnia et al. 2013a). The objective of this study is (i) to determine the basis of adaptive response for grain yield in range of environments using the AMMI model, and (ii) to find association between genotype and environment using biplot method.

**Table 1. Agro-climatic properties of the location tested in Iran**

Location	Longitude Latitude	Altitude (m)	Soil Texture	Soil Type¶	Rainfall (mm)
Gachsaran	50° 50' E 30° 20' N	710	Silty Clay Loam	Regosols	460.8
Gonabad	55° 12' E 37° 16' N	45	Silty Clay Loam	Regosols	367.5
Kouhdasht	23° 26' E 48° 17' N	1148	Silt-Loam	Regosols	433.1
Ilam	46° 36' E 33° 47' N	975	Clay-Loam	Regosols	502.6
Moghan	48° 03' E 39° 01' N	1100	Sandy-Loam	Cambisols	271.2

¶ Based on the FAO soil classification system (FAO, 1990).

## Materials and Methods

The dataset of durum wheat yield multi-environmental trials including 19 new improved genotypes and one local check cultivar (Seimareh) which are grown for three years (2005-2007) at five test locations Gachsaran, Ilam, Kermanshah, Gonabad and Shirvan were used in this investigation. The test locations were selected to sample climatic and edaphic conditions likely to be encountered in rain-fed durum wheat growing throughout Iran and to vary in some properties such as latitude, rainfall, soil types, temperature and other agro-climatic factors. The characteristics of the mentioned experimental locations are given in Table 1. Shirvan and Gonabad in the north-east of Iran, are characterized by semi-arid conditions and have sandy loam soil. Kermanshah and Ilam, in western Iran, have moderate rainfall and have silt loam soil. Gachsaran, in southern Iran, is relatively arid and has silt loam soil.

The plant materials were from national durum wheat improvement program for rain-fed areas and ICARDA (International Centre for Agricultural Research in the Dry Areas) durum wheat breeding programs. The plant materials' name, pedigree and origin are given in Table 2. The experimental design of trials was a randomized complete block with four replicates. The experiment trials were sown and managed according to local practice which appropriate pesticides were used to control insects, diseases and weeds. Plot size was 7.35 m<sup>2</sup>, 7 m long, 6 rows, and 17.5 cm between rows. Appropriate fertilizers were applied at recommended rates usual for the each environment according to local practices. An area of 4.2 m<sup>2</sup> (4 rows with 6 m long) was harvested to estimate grain per plot and then converted to kg ha<sup>-1</sup>.

Statistical analysis of variance for linear-bilinear AMMI model was performed via the SAS codes developed by Burgueno et al. (2001) and using the SAS package release 6.12 (SAS, 1996). The cross validation was used to determine the adequate number of interaction IPCAs to retain in the AMMI. This strategy used 1000 validation runs, each using three replications to build a model and one replication to validate the model and the related AMMI models produced the root mean square predicted difference (RMSPD; Gauch and Zobel, 1988). The minimum RMSPD was used as a model selection index selected and its calculations were done by software MATMODEL version 3.0 (Gauch, 2007). To investigate the stability pattern and GE interaction, AMMI-1 and AMMI-2 biplots were constructed for grain yield. AMMI-1 biplot of main effects are shown along the abscissa and the ordinate represents the first IPCA (interaction PCA).

The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it shows negligible GE interaction. When a genotype or environment has the same behavior on the IPCA axis, their interaction is positive; if different, their interaction is negative. The IPCA1 versus IPCA2 biplot (AMMI-2 biplot), describes the magnitude of GE interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors. The details of polygon view of AMMI-2 biplot are given in Sabaghnia et al. (2012a). All of the biplots of this research were generated via STATISTICA version 7.0 (StatSoft, 2001).

**Table 2. The characterization of 20 durum wheat genotypes studied in multi-environmental trials**

No	Code	Name / Pedigree	Origin	MY
1	G1	SRN-1/KILL//2*FOLTA-1	CIMMYT	2478
2	G2	GREEN-14//YAV-10/AUK	CIMMYT	2491
3	G3	GA//2×CHEN/ALTAR84	CIMMYT	2430
4	G4	BCR//MEMO/GOO/3/STJ7	ICARDA	2578
5	G5	SERRATOR-1//SRN-3/AJAIA-15	CIMMYT	2357
6	G6	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-4AP-0AP	ICARDA	2491
7	G7	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-6AP-0AP	ICARDA	2505
8	G8	GREEN-14//YAV-10/AUK	CIMMYT	2590
9	G9	Bisu-1//CHEN-1/TEZ/3/HUI//CIT71/CII	CIMMYT	2566
10	G10	BCR/3/CH1//GTA/STK/4/BCR/LKS4 ICD92-0150-CABL-11AP-0AP-8AP-0TR-4AP-0AP	ICARDA	2582
11	G11	GSB1-1-4/D68/1/93A-1A//RUFF/FG/3/MTL/5 ICD95-1174-C-2AP-0AP-2AP-0AP	ICARDA	2245
12	G12	ALTAR84/STN/WDZ-2 ICD92-MABL-0238-4AP-0AP-5AP-0TR-15AP-0AP	ICARDA	2476
13	G13	DON-MD 81-36	ICARDA	2592
14	G14	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-2AP-0AP	ICARDA	2694
15	G15	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-6AP-0AP	ICARDA	2575
16	G16	OUASERL-1 ICD96-0758-C-2AP-0AP-5AP-0AP	ICARDA	2532
17	G17	TRE97/4/GDOVZ5512/CIT/RUFF/FG/3/ENTE/MARIO//CA ICD97-1044-C-0AP-6AP-AP-5AP-0AP	ICARDA	2454
18	G18	MARSYR-6 ICD95-1127-T-0AP-9AP-0AP-7AP-0TR-5AP-AP	ICARDA	2313
19	G19	ETH-LRBRI-133/3*ALTER 84 CDSP91B31-A-1H-030Y-030M-3Y-0M-1Y-0B	CIMMYT	2587
20	G20	Seimareh	Iran	2537

## Results and Discussion

Combined analysis of variance was performed to determine the main effects of year, location, genotype as well as their interactions on grain yield of durum wheat genotypes. The main effect of year (Y) was significant, the location (L) main effect was not significant ( $P > 0.05$ ) while their interactions (YL) were highly significant (Table 3). The main effect of genotype and the genotype  $\times$  year interaction (GY) were significant but the genotype  $\times$  location interaction (GL) was not significant while three way interaction (GYL) or GE interaction was highly significant. The high significance of GE interactions is indicating the durum genotypes exhibited complicated GE interaction (non-additive type). The expression of quantitative traits such as grain yield is the result of genotype, environment and GE interaction and the complexity of grain yield character due to diverse processes which occur during plant development increases the GE interaction. The complex GE interaction found in this study in arid and semi-arid environments of Iran are similar to those found in other yield stability analysis of different crops in rain-fed condition of Iran (Mohebodini et al. 2006; Sabaghnia et al. 2008; Karimizadeh et al., 2012; Sabaghnia et al. 2012b). The presence of such complex GE interaction usually reduces the progress from selection in tested environments (Yau, 1995).

According to Gauch (2006) and Gauch et al. (2008), using RMSPD values for cross validation is more efficient from any other IPCA testing methods or different F-tests as F-test Gollob (1968), FRatio (Cornelius et al. 1992) and, FGH1 and FGH2 tests (Cornelius, 1993). The RMSPD values of different AMMI model's estimates their respective validation observations and show the adequate IPCAs numbers for GE interaction interpretation. According to cross validation results, only first two IPCA axes of AMMI model were sufficient for GE

interaction interpretation (Table 4). Like to the results obtained from some AMMI models used in common bean (Carbonell et al. 2004), chickpea (Farshadfar et al. 2011) and soybean (Amira et al. 2013), the AMMI model used in the present investigation exhibited a relatively simple GE interaction and needed only two IPCAs for description of variation in the GE interaction.

**Table 3. Combined analysis of variance of durum wheat performance trial yield data**

Source	DF	MS	% of (G, E, GE)
Year (Y)	2	206213572.0*	35.72
Location (L)	4	94220057.1 <sup>ns</sup>	32.64
Y $\times$ L	8	34610128.9**	23.98
Replication/ YL	45	618760.2	
Genotype (G)	19	680166.4*	1.12
G $\times$ Y	76	341113.3*	2.25
G $\times$ L	38	314535.9 <sup>ns</sup>	1.04
G $\times$ Y $\times$ L	152	248317.9**	3.27
R $\times$ G / YL	855	102927.8	

\*\* , \* and <sup>ns</sup> significant at the 0.01 and 0.05 probability level, respectively and non-significant.

In contrast, the results obtained from AMMI models used in soybean (Zobel et al. 1988), lentil (Sabaghnia et al. 2008), chickpea (Dehghani et al. 2010), and durum wheat (Sabaghnia et al. (2012a; 2013b), showed a more complex interaction which required as many as three to eight IPCAs for explanations of GE interaction variation. These differences among various studies could be related with the nature of the crop, environmental conditions or diverse genetic background of plant materials obtained from different sources and so on.

**Table 4. Cross validation for IPCAs of AMMI model**

Components	DF	SS	RMSPD	% of GE	% of GE
IPC1	32	18244330.82	411.65	24.13	24.13
IPC2	30	11595713.72	411.20	15.33	39.45
IPC3	28	10231566.27	413.41	13.53	52.98
IPC4	26	8035982.67	415.96	10.63	63.61
IPC5	24	6906996.60	416.79	9.13	72.74
Residuals	126	55014589.90			

RMSPD, the root mean square prediction differences in cross validation.

The AMMI1 biplot indicates that the genotypes G3, G7 and G8 stood out with the lowest IPCA1 scores (Fig. 1). This indicates that these genotypes were least involved with the GE interaction, and are the most stable ones. However, only the yield of genotypes G7 and G8 was above-average. The mean genotype yield performance, in decreasing order, ranked G14 first (most productive), G13 and G8 (Table 2). Thus, considering adaptability and stability in all test environments, the best genotypes is G8, since it ranked third in yield and was more stable than the highest-yielding genotypes (Fig. 1). According to IPCA1 scores, genotypes could be divided to two main groups: G2, G6, G8, G12, G14, G15, G16, G18 and G19 as the negative IPCA1 scores and the other remained genotypes as the positive IPCA1 scores (Fig. 1). Also, the test environments could be divided to two mega-environments (ME) as: ME-A including IL-06 (Ilam-2006), IL-07 (Ilam-2007), IL-08 (Ilam-2008), KO-06 (Kouhdasht-2006), KO-07 (Kouhdasht-2007), KO-08 (Kouhdasht-2008), MO-06 (Moghan-2006) and GO-06 (Gonabad-2006), and the other remained environments are grouped as ME-B (Fig. 1).

In the biplot of the first two IPCAs (IPCA1 versus IPCA2), genotypes G3 and G13 can be visually determined as the most stable genotypes in the plot center which have nearly zero IPCAs scores (Fig. 2). Also, test environments IL-06 and GA-07 were in the center of biplot and so indicated low GE interaction. Regarding the negative and positive scores of both IPCAs, four mega-environments are identified in this biplot: ME-I including MO-06, GO-06, IL-06 and IL-08; ME-II including GA-06, MO-07, MO-08 and GO-07; ME-III including GO-08, GA-08 and GA-07; and ME-IV including KO-06, KA-07, KA-08 and IL-07 (Fig. 2). These test environments interact positively with each other and interact negatively with the test environments of other mega-environments. Also, the genotypes of each mega-environment had good and positive interaction with the related test environments. For example, genotypes G1, G5, G11, G13, G17 and G20 had this positive interaction with the test environments of second mega-environment (ME-III) including GA-06, MO-07 and MO-08. Similar to test environments, the durum wheat genotypes could be divided into four distinct groups.

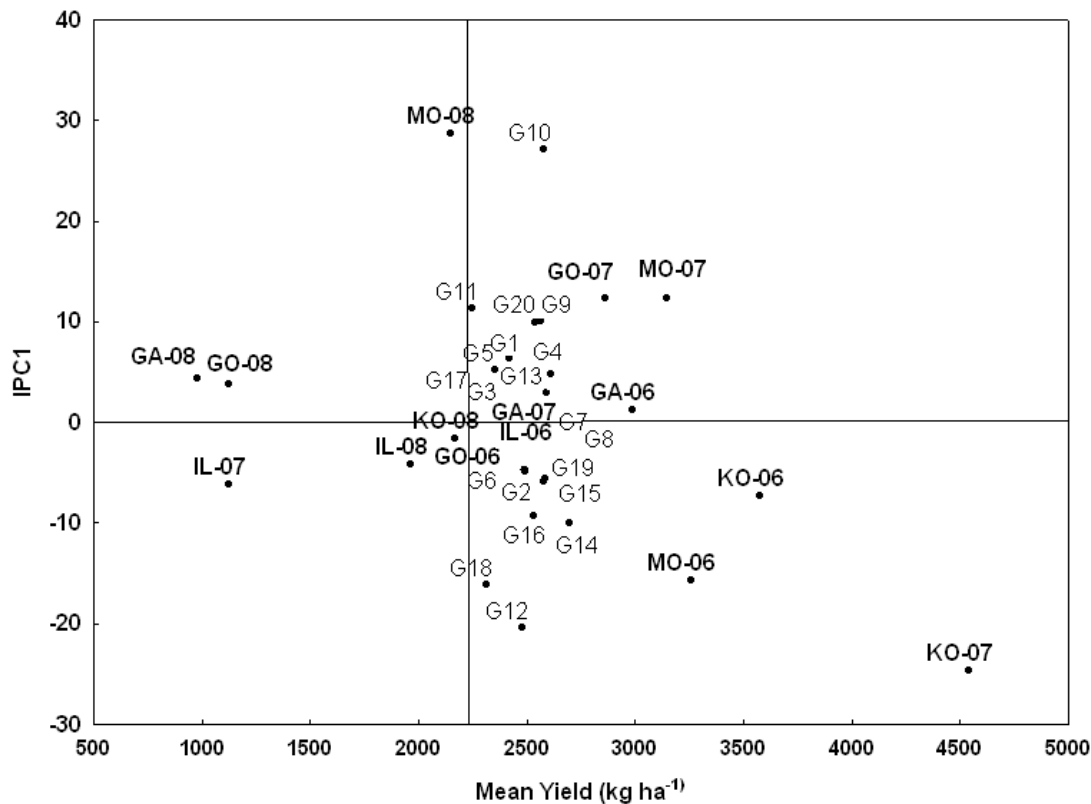


Fig. 1. AMMI-1 biplot for 20 durum wheat genotypes grown at 5 locations. The genotypes and environments scores are shown on the abscissa for IPC1, and the mean yield (kg ha<sup>-1</sup>) are shown on the ordinate

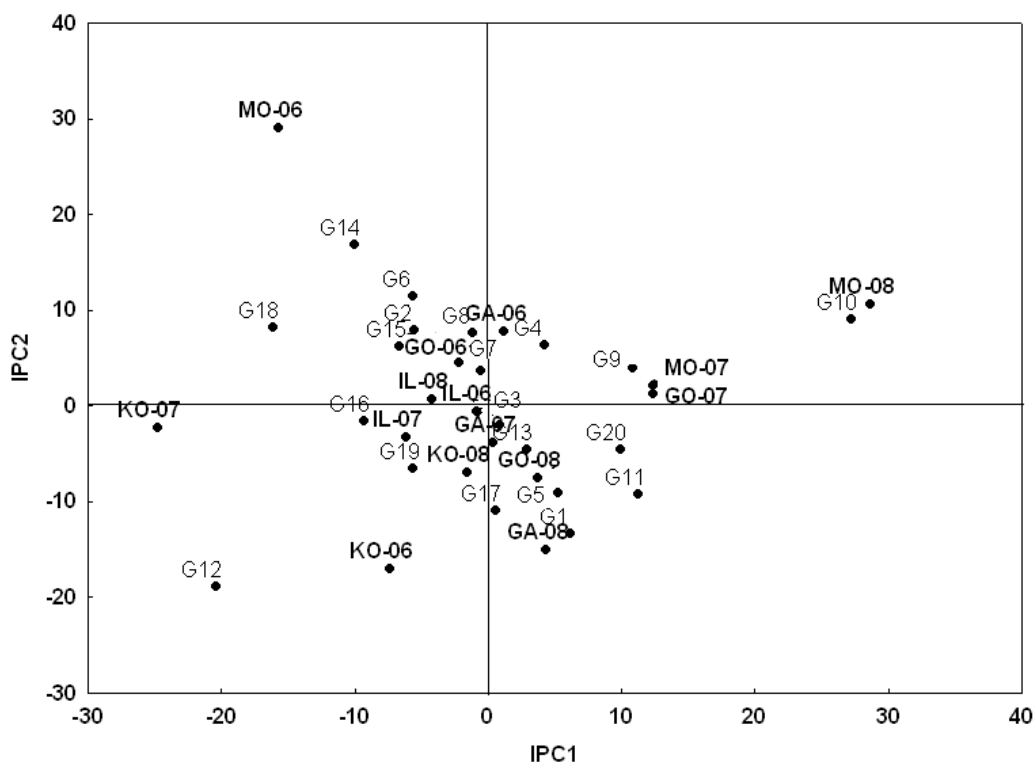


Fig. 2. AMMI-2 biplot for 20 durum wheat genotypes grown at 5 locations. The genotypes and environments scores are shown on the abscissa for IPC1, and IPC1 scores are shown on the ordinate

The groups are: the first group (G-I) consist on G2, G6, G7, G8, G14, G15 and G18; the second group (G-II) consist on G3, G4, G9 and G10; the third group (G-III) consist on G2, G1, G5, G11, G13, G17 and G20; and the fourth group (G-IV) consist on G12, G16 and G19 (Fig. 2).

Polygon view of AMMI-2 biplot (Gauch, 1992) has been used to identify “which-wins-where” patterns in data analysis of durum wheat multi-environmental trials. In this biplot lines are drawn to connect the furthest genotypes and then a line is drawn perpendicular to that side of the polygon so as to pass through the origin. The furthest genotype is the best performer in the environments included in that sector. There were five rays in Fig. 3 which divide the biplot into five sectors, and the environments fall into all of them. An interesting property of the polygon view of biplot is that each vertex genotype has higher yield than the other genotypes in all environments that fall in the related sector. Thus, three environments (GO-07, MO-07 and MO-08) fell into sector 1 and the vertex genotype for this sector was G10, suggesting that high yielding genotype for these environments was G10. This genotype was better than the other genotypes which fell into sector 1 (genotypes G4, G9 and G20). Three other environments (GO-08, GA-07 and GA-08) fell into sector 2 and the vertex genotype for this sector was G11 which had high mean yield in these environments (Fig. 3). This genotype was better than the other genotypes which fell into sector 2 (genotypes G1 and G5). Environments KO-06, KO-07, KO-08, IL-06, IL-07 and IL-08 fell into sector 3 with the vertex genotype G12. Genotype G12 was better than genotypes G16, G17 and G19 which fell into sector 3 (Fig. 3). Also, one environment (GO-06) fell into sector 4 and the vertex genotype for this sector was G18, suggesting that high yielding genotype for this environment was G18 and it was better than genotype G15 which fell into sector 4. Finally, the test

environment GA-06 with vertex genotype G14 generated sector 5. The performance of genotype G14 was better than genotype G2, G6, G7 and G8 in environment GA-06 (Fig. 3).

This investigation shows the possibility of identifying the most stable genotypes under diverse environmental conditions by applying an AMMI model. Although, there are several methods to assess the GE interaction (the most commonly used are based on regression model), but multivariate procedures are preferred by most plant breeders. The regression models have some limitations including its attempts to explain the GE interaction variation in one dimension, when in fact it can be quite complex (Crossa, 2010). The application of multivariate procedures can be useful to better exploit the information contained in the data. The AMMI model as one of the most important multivariate procedures has also been used for environmental stratification, and it based on the favorable genotypes is more efficient than of other procedures (Oliveira et al. 2010). In this study, there is good correspondence between the results of AMMI-1 and AMMI-2 models of stability analysis as discrimination among tested genotypes in different environments is reasonable.

The AMMI model has both linear and bilinear component of GE interaction and hence very useful in visualizing multi-environmental trials dataset. It is useful for understanding complex GE interaction and determining which genotype won which environment and improves genotype recommendation and accelerating progress (Gauch, 2006). Successful genotypes of require to be adapted to a broad range of environmental conditions and in order to ensure their stability. The information on GE interaction is of paramount importance for durum wheat breeders (Sabaghnia et al. 2012b). It is clear that the AMMI model is suitable way to study GE interaction and yield stability analysis and it related biplots are excellent tools for visual multi-environmental trials data analysis.



- Farshadfar E, Zali H, Mohammadi R, 2011. Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot. *Annals of Biological Research*, 2: 282–292.
- Finlay KW, Wilkinson GN, 1963. The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, 14: 742–754.
- Gabriel KR, 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58: 453–467
- Gauch HG, 1992. *Statistical analysis of regional yield trials: AMMI analysis of factorial designs*. Amsterdam, Elsevier.
- Gauch HG 2006. *Statistical analysis of yield trials by AMMI and GGE*. *Crop Science*, 46: 1488–1500.
- Gauch HG, 2007. MATMODEL version 3.0: Open source software for AMMI and related analyses. Available at <http://www.css.cornell.edu/staff/gauch> (verified 17 Jan. 2013). *Crop and Soil Sciences*, Cornell Univ., Ithaca, NY.
- Gauch HG, Zobel RW, 1988. Predictive and postdictive success of statistical analyses of yield trials. *Theoretical and Applied Genetics*, 76: 1–10.
- Gauch HG, Piepho HP Annicchiarico P, 2008. *Statistical Analysis of Yield Trials by AMMI and GGE: Further Considerations* *Crop Science*, 48: 866–889.
- Gauch HG, 1988. Model selection and validation for yield trials with interaction. *Biometrics* 44: 705–707.
- Gollob HF, 1968. A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, 33: 73–115.
- Gower JC, Hand DJ, 1996. *Biplots*. Chapman & Hall, London, UK.
- Kang, M.S. 1998. Using genotype-by-environment interaction for crop cultivar development. *Advanced Agronomy*, 35: 199–240
- Karimizadeh R, Mohammadi M, Sabaghnia N, Shefazadeh MK, 2012a. The use of corrected and uncorrected nonparametric stability measurements in durum wheat multi-environmental trials. *Spanish Journal of Agricultural Research*, 10: 722–730.
- Karimizadeh R, Mohammadi M, Sabaghnia N, Shefazadeh MK, Pouralhossini J, 2012b. Univariate stability analysis methods for determining genotype  $\times$  environment interaction of durum wheat grain yield. *African Journal of Biotechnology*, 11: 2563–2573.
- Karimizadeh R, Mohammadi M, Sabaghnia N, Hosseinpour T, Shefazadeh MK, 2012c. Analysis of genotype and genotype  $\times$  environment interaction in durum wheat in warm rainfed areas of Iran. *Crop Breeding Journal* 2: 71–78.
- Mohebodini M, Dehghani H, Sabaghpour SH, 2006. Stability of performance in lentil (*Lens culinaris* Medik) genotypes in Iran. *Euphytica* 149: 343–352.
- Oliveira RL, Pinho RG, Balestre M, 2010. Ferreira. Evaluation of maize hybrids and environmental stratification by the methods AMMI and GGE biplot. *Crop Breeding and Applied Biotechnology*, 10:
- Sabaghnia N, Mohammadi M, Karimizadeh R, 2012a. The evaluation of genotype  $\times$  environment interactions of durum wheat's yield using of the AMMI model. *Agriculture and Forestry*, 55: 5–21.
- Sabaghnia N, Mohammadi M, Karimizadeh R, 2013a. Parameters of AMMI model for yield stability analysis in durum wheat. *Agriculturae Conspectus Scientificus*, 78(2): 119–124.
- Sabaghnia N, Karimizadeh R, Mohammadi M, 2012b. Grain yield stability analysis of lentil genotypes by additive main effects and multiplicative interactions model. *Yuzuncu Yil Universitesi Journal of Agricultural Sciences*, 22, 155–164.
- Sabaghnia N, Karimizadeh R, Mohammadi M, 2013b. GGL biplot analysis of durum wheat (*Triticum turgidum* spp. durum) yield in multi-environment trials. *Bulgarian Journal of Agricultural Science*, 19: 756–765.
- Sabaghnia N, Dehghani H, Sabaghpour SH, 2008. Graphic analysis of genotype by environment interaction for lentil yield in Iran. *Agronomy Journal*, 100: 760–764.
- SAS Institute, 2004. *SAS/STAT user's guide*. v. 9.1. SAS Inst., Cary, NC.
- Statsoft 2001. *STATISTICA for Windows version 7.0 ed*. Tulsa, StatSoft, Inc. USA.
- Yan W, Hunt LA, Sheng Q, Szlavnic Z, 2000. Cultivar evaluation and megaenvironment investigation based on the GGE biplot. *Crop Science*, 40: 597–605.
- Yau SK, 1995. Regression and AMMI analyses of genotype  $\times$  environment interactions: An empirical comparison. *Agronomy Journal*, 87: 121–126.
- Zobel RW, Gauch HG, 1988. *Statistical analysis of a yield trial*. *Agronomy Journal*, 80: 388–393.