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## THE EVALUATION OF GENOTYPE × ENVIRONMENT INTERACTIONS OF DURUM WHEAT'S YIELD USING OF THE AMMI MODEL

#### **SUMMARY**

In order to study GE interaction and determine winning durum wheat genotypes, field experiments were conducted with 20 genotypes for 3 vears (2007-2009) in Iran. Highly significant differences were found for the GE interaction, indicating the possibility of selection for the most stable genotypes. F-test Gollob determined the first five axes and FGH1 and FGH2 tests identified the first three axes as significant AMMI (additive main effect and multiplicative interaction) components. According to the test F Ratio and cross validation results, the first two axes were significant. The illustrated yearly AMMI2 biplots showed that mega-environments patterns varied across years. This could be summarized as indicating that the test locations Gachsaran (with winning G15). Khoramabad (with winning G4) and Gonbad (with winning G19) can be considered as the individual mega-environments but the behaviour of the other test locations (Moghan and Ilam) was variable across years. In any case, it seems that, regarding both mega-environments, the winning genotypes G3 and G5 could be suitable for these test locations. The AMMI stability parameters (EV, AMGE, SIPC and D) according to the first two numbers of the IPCs indicated that genotype G15, followed by genotype G4, were as the most stable genotypes, but none of these genotypes were grouped as the winning genotypes. Therefore, evaluation of genotypes based on graphic presentation of AMMI biplot appears to be superior to the AMMI stability parameters.

**Keywords:** AMMI stability value, genotype × environment interaction, yield stability

#### **INTRODUCTION**

Durum wheat (*Triticum turgidum* spp. durum) is a species of great economical interest owing to the nutritional quality of its grain, as well as its high grain yield. The selection of genotypes with high productivity and adaptation ability to a wide range of environments which is referred to yield stability is a important issue in durum wheat breeding programs (Rharrabti et al., 2003).

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Considering the genetic background and unpredictable environmental factors which prevailing at the different locations and over years, differential responses are observed from the improved genotypes which tested in multi-environment trials (MET). These various genotypic responses in different environments are called genotype  $\times$  environment (GE) interaction (Allard and Bradshaw, 1964). The GE interaction that results in inconsistent genotype ranking across test environments is usually too large to be ignored. These effects tend to be large when there is wide variation among genotypes for abiotic stress tolerance such as soil salinity or drought and, concurrently, wide variation among test environments (Kang, 1998; Annicchiarico et al., 2011). The remarkable GE interaction for most quantitative traits such as grain yield can limit the genetic gain under selection and cultivar recommendation.

In every plant breeding program, GE interaction effects are of special interest for identifying the most favorable genotypes, mega-environments, representative locations and other adaptation targets. The GE interaction effects, usually having relatively low repeatability over years, must be investigated on a multiyear basis in annual crops (Annicchiarico, 2002). Several procedures of yield stability analysis are according to the basis of GE interaction existence, which differ in the concepts of stability or statistical principles. The linear regression strategy (Finlay and Wilkinson, 1963) has been a commonly used method for studying phenotypic stability. The use of multivariate statistical procedures to study GE interaction has been proposed to eliminate the problems of univariate methods.

The introduction of the additive main effects and multiplicative interaction (AMMI) model by Zobel et al., (1988) has increased the interest on the principal component analysis (PCA) method to explore GE interaction. The AMMI model uses an additive linear model to analyze a multivariate dataset and combines the additive analysis of variance for main effects with the multiplicative PCA for the GE interaction. According to Gauch and Zobel (1996) the first interaction PCA (IPCA1) is superior to linear regression in accounting for the GE variations. It seems that yield stability estimated by AMMI model could be more repeatable than other stability statistics because AMMI is effective and more useful in exploring complex GE interaction patterns. Gauch (2006) and Gauch et al. (2008) claimed that AMMI model always does as well as, but frequently much better than conventional univariate stability methods such as linear regression model and some multivariate procedures such as genotype plus GE interaction (GGE) biplot (Yan et al., 2000) in the sum of square recovery.

Determination of appropriate and significant number of interaction PCAs in AMMI model is important for the exploring GE interaction nature. Due to essence of AMMI model, the conventional F-test is not correct for test of IPCAs. Gollob (1968), Cornelius et al. (1992) and (Cornelius 1993) introduced different F-test for AMMI model. It was demonstrated that the degrees of freedom in the conventional AMMI model are incorrect and the proposed tests require values for the expectation and standard deviation of the largest eigenvalue of a central

Wishart matrix of the specific dimension and degrees of freedom (Cornelius, 1980). A cross validation strategy was suggested for fitted AMMI model versus simulated AMMI model with considering the values of root mean square predicted difference (RMSPD) which determines the best AMMI model and proper number of significant interaction PCAs (Gauch and Zobel, 1997). Regarding AMMI1 and AMMI2 biplots, test environments are grouped into mega-environments and their winning genotype are identified. Several AMMI stability parameters were suggested; EV (Zobel, 1994), AMGE and SIPC (Sneller et al. (1997), ASV (Purchase 1997), and D parameter (Annicchiarico, 1997). Since the IPCs are orthogonal, they add pieces of information uncorrelated to each other and could be reflecting the different aspects of GE interaction and yield stability.

The objective of this study has been application AMMI model for exploration of the GE interaction, mega-environments identification and yield stability analysis in some durum wheat genotypes.

## **MATERIALS AND METHODS**

Twenty durum wheat genotypes were studied at five locations of Iran during three years (2007 to 2009), agricultural research stations except one location (Ilam) which evaluated during two years. At each environment (location  $\times$  year), the genotypes were planted using a randomized complete block design (RCBD) with four replications. The soil types were Regosols in Gachsaran, Gonbad, Khoramabad and Ilam, and Cambisols in Moghan. Some properties of the locations of the experimental environments are given in Table 1.

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
Gonbad	55° 12′E 37° 16′N	45	Silty Clay Loam	Regosols	367.5
Khoramabad	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

Table 1: Geographical properties of test locations

Each plot consisted of six rows spaced 17.5 cm apart. Row length was 7 m in all locations during all years. Seeding rate was adjusted to obtain  $\approx 20$  plants m<sup>-1</sup> row<sup>-1</sup>. Fertilizer application was 30 kg nitrogen ha<sup>-1</sup> and 70 kg P<sub>2</sub>O<sub>5</sub> ha<sup>-1</sup> at planting and 40 kg nitrogen ha<sup>-1</sup> at stem elongation stage. An area of 4.2 m<sup>2</sup> (4 rows with 6 m long) was harvested and yield (kg ha<sup>-1</sup>) was obtained by converting the seed yields obtained from plots to hectares.

A preliminary analysis was performed to distinguish homogeneity of error variances were homogeneous. Analyses variance was accomplished by the General Linear Model (GLM) procedure of SAS 9.1 software (SAS, 2004). A combined analysis of variance was done to determination of main effects of environments and genotypes as well as GE interactions. The model AMMI formula was:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

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 eigenvalue of the IPC analysis axis n;  $\gamma_{in}$  and  $\delta_{jn}$ are the genotype and environment eigenvectors for axis n; n is the number of principal components retained in the model and  $\rho_{ij}$  is the error term. Different Ftests including F-Gollob (1968),  $F_{Ratio}$  (Cornelius et al., 1992),  $F_{GH1}$  and  $F_{GH2}$  tests (Cornelius, 1993) were used to determine of significant numbers of IPCs in AMMI model. These statistical methods have been described in detail by the mentioned anthers. The RMSPD values of AMMI model for cross validation were computed by MATMODEL Version 3.0 (Gauch, 2007). For cross validation via MATMODEL, three replications for modeling and one replication for validation were used, and the 1000 numbers of different randomizations were averaged.

The EV parameter of AMMI (Zobel, 1994), the AMGE and SIPC parameters (Sneller et al., 1997), the D parameter of AMMI model (Annicchiarico, 1997), and AMMI's stability value (ASV) of Purchase (1997) were calculated.

### **RESULTS AND DISCUSSION**

The grain yield of dueum wheat genotypes varied from 154.5 kg ha<sup>-1</sup> in genotype G16 grown at Moghan in 2007 to 6330.0 kg ha<sup>-1</sup> at Gachsaran in genotype G15 grown in 2007. Maximum mean yields varied from 6330.0 kg ha<sup>-1</sup> in G15 to 4529.3 kg ha<sup>-1</sup> in G4, while minimum mean yield varied from 154.5 kg ha<sup>-1</sup> in genotype G16 to 475.0 kg ha<sup>-1</sup> in G6 (Table 2). Average yield was positively correlated with minimum mean yield but no with maximum. Yield amplitudes were very large, from 4093.0 kg ha<sup>-1</sup> to 6002.5 kg ha<sup>-1</sup> and were correlated with maximum yield, but not with minimum and average mean yield. The combined analysis of variance was conducted to determine the effects of environment (location × year combination), genotype, and their interactions on grain yield of durum wheat genotypes (Table 3). The main effect of environment (E) was highly significant (P < 0.01), while the main effect of genotypes (G) was only significant at 1% probability level (P < 0.01). Environments had the

largest effect, as explained 96.43 % of E+G+GE variations while genotypes explained 0.43, GE interaction signal explained 1.57%, and GE interaction noise explained 1.38%. 3.14% of total E+G+GE sum of squares, respectively (Table 3). From Table 3 it implies that the GE interaction is comprised of 44% noise and 56% signal. It is known that GE signal increases the number of useful mega-environments whereas GE noise decreases the number of useful mega-environments (Annicchiarico, 1997; 2002).

	Average	Minimum	Maximum	Amplitude
G1	2520.79	366.75	5158.50	4791.75
G2	2697.18	456.00	5495.75	5039.75
G3	2452.93	344.75	4860.25	4515.50
G4	2635.18	436.25	4529.25	4093.00
G5	2509.20	442.25	4913.00	4470.75
G6	2528.38	475.00	5288.00	4813.00
G7	2644.70	454.75	5179.75	4725.00
G8	2580.16	206.25	4930.25	4724.00
G9	2564.50	473.00	5236.50	4763.50
G10	2637.43	330.50	5445.75	5115.25
G11	2513.63	361.25	5463.00	5101.75
G12	2493.38	306.75	4921.00	4614.25
G13	2397.30	331.50	5040.50	4709.00
G14	2562.68	391.25	5455.25	5064.00
G15	2680.38	327.50	6330.00	6002.50
G16	2376.07	154.50	5056.00	4901.50
G17	2564.14	320.25	5127.25	4807.00
G18	2641.20	400.75	4991.75	4591.00
G19	2745.07	466.50	4777.00	4310.50
G20	2470.54	299.00	4621.50	4322.50

Table 2: Average, maximum and minimum grain yields and yield amplitude in 20 durum wheat genotypes

The results of different F-test indicated that, according to F-Gollob (1968), first five IPCs were significant. Also, based on  $F_{Ratio}$  (Cornelius et al., 1992), the first two components were significant while according to  $F_{GH1}$  and  $F_{GH2}$  tests (Cornelius, 1993), three IPCs were meaningful (results are not shown). Most of F-test results verified the complex GE interaction which could be associated with the nature of the crop, environmental conditions or diverse genetic background obtained from different sources. Applying cross validation procedure for the fitted AMMI model of durum wheat dataset, indicated similar to  $F_{Ratio}$ , only the first two components were sufficient for interpreting this dataset. This implies that the GE is comprised of 44% noise and 56% signal (Table 3). This signal portion is relatively close to the account of the both first two IPCs and so verifies

diagnosing the AMMI2 member of this model family. The AMMI gain factor is 1.54 and so given 3 replications this amounts to 1.62 free replications.

Source of Variation	DF	Mean Squares	% of G+E+GE	Eigenvalue	Proportion	Cumulative
Environment (E)	13	177747550.3**	96.43			
Replication within E	42	826660.4				
Genotype (G)	19	544937.2 <sup>*</sup>	0.43			
$G \times E$	247	304181.0**	3.14			
IPC1	31	750125.5†		$5.81\times10^{+6}$	31.0	31.0
IPC2	29	606528.3		$4.40\times10^{+6}$	23.4	54.4
IPC3	27	362863.5		$2.45\times10^{+6}$	13.0	67.4
IPC4	25	308436.9		$1.93\times 10^{+6}$	10.3	77.7
IPC5	23	287246.1		$1.65  imes 10^{+6}$	8.8	86.5
Noise	112	90844.6				
$\mathbf{R} \times \mathbf{G}$ within E	798	133065.7				

Table 3: Combined analysis of variance, eigen values and contributions of the first five principal components of durum wheat performance trial yield data

the significance of IPCs are given in table

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



Figure 1: AMMI2 biplot for 20 durum wheat genotypes grown at 5 locations in 2007. The genotype and environment scores are shown on the abscissa for IPC1, with a vertical line and the IPC2 scores are shown on the ordinate

In the biplot of the first year dataset (Figure 1), some corner genotypes can be visually determined as genotypes G15, G11, G3, G1, G19, G4, G6 and G10. These were the best genotypes at the related test locations which are determined as mega-environments. By connecting these corner genotypes a polygon is formed and the test locations are divided among several sectors (each one with a different corner genotype) by drawing perpendiculars to each side of the polygon passing through the plot origin. In Figure 1, the test locations are divided between eight sectors but only four mega-environments were identified. The first mega-environment contains test location Gachsaran with genotype G15 as the winner; the second mega-environment contains test location Moghan with genotype G1 as the winner; and the fourth mega-environment contains test locations Khoramabad and Ilam with genotype G3 as the winner.



Figure 2: AMMI2 biplot for 20 durum wheat genotypes grown at 5 locations in 2008. The genotype and environment scores are shown on the abscissa for IPC1, with a vertical line and the IPC2 scores are shown on the ordinate

In the biplot of the second year dataset (Figure 2), some corner genotypes can be visually determined as genotypes G1, G4, G19, G15 and G16. In Figure 2, the test locations are divided between five sectors but only three mega-environments were identified. The first mega-environment contains test location Khoramabad with genotype G1 as the winner; the second mega-environment contains test location Moghan with genotype G15 as the winner; the third mega-environment contains test locations fachsaran and Gonbad with genotype G16 as the winner.



Figure 3: AMMI2 biplot for 20 durum wheat genotypes grown at 5 locations in 2009. The genotype and environment scores are shown on the abscissa for IPC1, with a vertical line and the IPC2 scores are shown on the ordinate

In the biplot of the third year dataset (Figure 3), genotypes G6, G9, G5, G3, G4 and G19 were determined as corner genotypes and the test locations are divided between six sectors but five mega-environments were identified. In other word, each test location was a single mega-environment; Gachsaran with genotype G6 as the winner; Moghan with genotype G9 as the winner; Ilam with genotype G3 as the winner; Khoramabad with genotype G4 as the winner; Gonbad with genotype G19 as the winner. Although the illustrated yearly biplots showed clear crossover GE interactions among test locations but mega-environments patterns varied across years.

Table 4:	Genotype	(G),	location	(L),	and	genotype	$\times$	location	(GL)	variance
terms for	durum whe	eat m	ulti-envir	onme	ental	trials				

Source of	Year 2007					
Variation	df	MS	%†			
Location (L)	4	270437984.9**	96			
R / L	15	1293568.4				
Genotype (G)	19	301161.9 <sup>ns</sup>	1			
$G \times L$	76	410438.1**	3			
$R \times G  /  L$	285	168692.1				

Year 2008					
df	MS	%			
3	68348742.2**	95			
12	466329.1				
19	257918.5**	2			
57	99624.4**	3			
228	34087.1				

Year 2009					
df	MS	%			
4	53609794.8**	85			
15	648017.5				
19	494611.3 <sup>*</sup>	4			
76	376243.3**	11			
285	176622.1				

 $_{**}$ % of G+L+GL

 $^{**,\ *}$  and  $^{ns}$  significant at the 0.01 and 0.05 probability level and non-significant, respectively

This conclusion was supported by analysis of variance of the individual year's data involving 5 or 4 locations and 20 genotypes (Table 4). The location main effect accounted for 85 to 96% of the total yield variation due to G+L+GL; and the genotype × location interaction accounted for 3 to 11% of the total variation due to G+L+GL.

According to biplot of first two IPCs (Figure 4), some corner genotypes, which are the most responsive ones, can be visually determined. These vertex genotypes were G19, G6, G15, G5, G3 and G4. These are either the best or the poorest genotypes at some or all test environments and could be utilized to determine mega-environments. By connecting these corner genotypes a polygon is formed and the test environments are divided among several sectors (each one with a different corner genotype) by drawing perpendiculars to each side of the polygon passing through the plot origin.



Figure 4: AMMI2 biplot for 20 durum wheat genotypes grown at 14 environments. The genotype and environment scores are shown on the abscissa for IPC1, with a vertical line and the IPC2 scores are shown on the ordinate

In Figure 4, the test environments are divided between six sectors. The first sector (MG1; mega-environment 1) contains test environments E3 (Gonbad at 2007), E9 (Moghan at 2008) and E12 (Gonbad at 2009), with genotype G19 being the winner. The second sector (MG2; mega-environment 2) contains no test environments, with genotype G6 being the winner. The third sector (MG3; mega-environment 3) contains test environments E1 (Gachsaran at 2007), E6 (Gachsaran at 2008), E8 (Gonbad at 2008) and E10 (Gachsaran at 2009), with genotype G15 being the winner. The fourth sector (MG4; mega-environment 4)

contains test environments E4 (Moghan at 2007) and E5 (Ilam at 2007), with genotype G5 being the winner. The fifth sector (MG5; mega-environment 5) contains test environments E2 (Khoramabad at 2007), E13 (Moghan at 2009) and E14 (Ilam at 2009), with genotype G3 being the winner. The sixth sector (MG6; mega-environment 6) contains test environments E7 (Khoramabad at 2008) and E11 (Khoramabad at 2009), with genotype G4 being the winner.

It could be summarized that the test locations Gachsaran (G15 wins), Khoramabad (G4 wins) and Gonbad (G19 wins) can be considered as the individual mega-environments but the behavior of the other test locations (Moghan and Ilam) was variable across years. Although the illustrated biplot show clear crossover GE interactions among test environments representing the three single mega-environments, the pattern of the other location groupings varied across years. Thus, the western (Ilam) and northwestern (Moghan) durum wheat–growing regions cannot be further divided or grouped into meaningful mega-environments. In contrast, they should be considered as a unique mega-environment with unpredictable crossover GE interactions. However, the GE interaction (3.14%) is the basis for any mega-environments ME4 and ME5, the wining genotypes G3 and G5 could be suitable for these test locations (Moghan and Ilam).



Figure 5 indicates the AMMI1 biplot for the durum wheat MET.

Figure 5: AMMI1 model biplot for yield data from 20 durum wheat genotypes grown at 14 environments. The genotype and environment means are shown on the abscissa, with a vertical line and the IPC1 scores are shown on the ordinate

This biplot (mean yield versus IPC1) provide a good description of the patterns in the data, even though it misses some additional information in IPC2. According to this biplot, there are two mega-environments including ME-A as E1, E6, E8, E10 and E13 with wining genotype G2; and ME-B as the other remained test environments with wining genotype G19 (Figure 6). Although some of these findings were similar to AMMI2 biplot but most of them were different. This phenomenon maybe was owing to relatively small explanation of GE interaction due to IPC1 (31%). According to Gauch et al. (2008), IPC1 of AMMI1 often correlates highly with PC2 from GGE biplot model and so the above conclusion could be expected from GGE biplot methodology.

The AMMI stability parameters were calculated according to the first two numbers of IPCs which are detected as the important components through different  $F_{Ratio}$  and cross validation. In other word, in EV, AMGE, SIPC and D formulas, these parameters using two IPCs were calculated. According to EV2 (benefits from IPC1 and IPC1), genotypes G7, G8 and G20 were the most stable genotypes (Table 5). The stability which is disscused here is benefits from static or biological concept of yield stability (Sabaghnia et al., 2008). It is notice that in EV2 parameter only 34.4% of GE interaction variation is used in cultivar evaluation. According to SIPC2, genotypes G3, G4 and G5 were the most stable genotypes but most of these stable genotypes had low mean yield (Table 5).

	MY	EV2	D2	SIPC2	AMGE2	ASV
G1	2520.79	0.0636	606.33	-10.42	0.00047	14.18
G2	2697.18	0.0234	360.47	9.77	0.00040	8.36
G3	2452.93	0.1796	927.59	-27.46	0.00016	20.76
G4	2635.18	0.2115	1098.04	-15.70	0.00027	25.61
G5	2509.20	0.1896	914.20	-21.72	-0.00187	19.98
G6	2528.38	0.1508	858.08	25.58	0.00140	19.30
G7	2644.70	0.0044	155.74	4.32	0.00056	3.60
G8	2580.16	0.0138	261.75	0.48	0.00030	5.92
G9	2564.50	0.0944	653.80	-8.80	-0.00077	14.40
G10	2637.43	0.0379	446.42	13.03	0.00063	10.23
G11	2513.63	0.0958	726.85	20.02	0.00096	16.83
G12	2493.38	0.0274	352.31	-9.70	-0.00073	7.76
G13	2397.30	0.0603	517.87	-8.81	0.00088	11.35
G14	2562.68	0.0628	551.45	-2.64	0.00041	12.38
G15	2680.38	0.2731	1254.20	29.82	-0.00245	29.31
G16	2376.07	0.0243	350.56	10.44	-0.00016	7.96
G17	2564.14	0.0315	373.83	9.54	0.00075	8.19
G18	2641.20	0.0426	488.20	-13.07	-0.00105	11.34
G19	2745.07	0.3966	1401.26	3.16	0.00100	31.64
G20	2470.54	0.0165	305.38	-7.87	0.00019	7.11

Table 5: Mean yield and different AMMI stability parameters

MY, mean yield; EV2, AMMI stability parameter of Zobel (1994); D2, AMMI stability parameter of Annicchiarico (1997); SIPC2 and AMGE2, AMMI stability parameters of Sneller et al. (1997), ASV, AMMI's stability value of Purchase (1997).

Based on AMGE2 (benefits from IPC1 and IPC1), genotypes G5, G9 and G15 were the most stable genotypes (Table 8). The mean yield performance of genotype G15 was high and the genotype G4 relatively could be considered as the high mean yielding genotype. It is interesting that none of the most stable genotypes were grouped as the identified wining genotypes. Also, the ranks of the six wining genotypes according to the AMMI stability parameters were low but the mean yield of some of them (G15 and G19) was high. Therefore, it seems that evaluation of genotypes based on graphic presentation of AMMI biplot is more superior to the AMMI stability parameters.

### DISCUSSION

This study demonstrated that GE interaction was highly significant and had remarkable affect on genotypes performance is different environments. The GE signal magnitude was 3.6 times larger than genotype main effect and so must be explored effectively. Although, the grain yield is a result of G, E and GE interaction and E is responsible for about 80% of the yield grain variation but only G and GE interaction that are relevant to genotype evaluation in MET (Yan and Kang 2002). Therefore, it seems that GE interaction should be investigated for studied durum wheat genotypes using multivariate statistical approaches. The multivariate procedures such as AMMI model can display several aspects of multi-dimensions GE interaction phenomenon.

There is no doubt that the AMMI biplot is a useful tool for visualization of the complex GE interaction patterns (Gauch et al., 2008; Yang et al., 2009). However, AMMI2 biplot has been used to identify "which-wins-where" patterns and mega-environments identification. Although, there has been a debate on merits and demerits of AMMI2 versus G+GE (GGE) biplots for GE interaction investigation and stability analysis (Gauch, 2006; Gauch et al., 2008; Yang et al., 2009), but it seems that regarding cross validation benefits and exploration of only GE interaction instead of both G plus GE interaction.

The AMMI model seems to display a portion of the GE interaction variation that determines what is in fact caused by a standard portion (main effects of G and E) and a noise portion, which is an unpredictable and not interpretable (Crossa et al., 1990). To choose the proper AMMI model, the cutting point would be the number of significant IPCAs. The AMMI models may be considered as AMMI0 (with no interaction term), AMMI1 (with the first axis of the interaction) and so on. However, the results of the other F-tests were different from the F-test Gollob (1968), and identified first two and three principal components with significant differences according to  $F_{Ratio}$  (Cornelius et al., 1992) or  $F_{GH1}$  and  $F_{GH2}$  tests (Cornelius, 1993), respectively.

The cumulative percentage of description on each IPCA is important because there should be greater concentration of the GE interaction pattern on the first IPCA. When the number of selected IPCA axes increases, the noise percentage increases as well, reducing the predictive power of AMMI model (Gauch, 2006). Although, the values obtained from several IPCAs are relatively low, the first axis captures the greatest portion of the GE interaction, while the subsequent axes show pattern reduction and noise increase (Gauch, 1988). Thus, the evaluation GE interaction using the first two IPCs (AMMI2 model) is acceptable. These findings are verified through cross validation procedure and minimum RMSPD values and genotypes can be detected that contributed least to the GE interaction (most stable) as well as the desirable combinations of genotypes and environments in terms of specific adaptability.

According to AMMI biplot six winning genotypes (G19, G6, G15, G5, G3 and G4) and five mega-environments were identified. The test locations Gachsaran, Khoramabad and Gonbad can be considered as the individual megaenvironments but the behavior of the Moghan and Ilam locations was variable across years. The locations Moghan and Ilam should be considered as a unique mega-environment with unpredictable crossover GE interactions. There is no doubt that the AMMI biplot is a useful tool for visualization of the complex GE interaction patterns (Gauch et al., 2008; Yang et al., 2009). However, AMMI2 biplot has been used to identify "which-wins-where" patterns and megaenvironments identification. Although, there has been a debate on merits and demerits of AMMI2 versus G+GE (GGE) biplots for GE interaction investigation and stability analysis (Gauch, 2006; Gauch et al., 2008; Yang et al., 2009), but it seems that regarding cross validation benefits and exploration of only GE interaction instead of both G plus GE interaction, the AMMI procedure is better than GGE model.

The AMMI parameters based on EV, D, SIPC and AMGE formulas displayed genotypes G7, G8 and G20 as the most stable genotypes. The applied parameters of adaptability and stability presented some incongruence, since they identified the different genotypes as stable. The mean yield performance of genotype G7 was as the high mean yielding genotypes and so could be regarded as the most favorable durum wheat genotypes. But it was clear that most of the stable genotypes according to seventeen AMMI stability parameters had moderate or low mean yield. Our findings agree to the most understanding of adaptation, according to which least stable genotypes have the highest economic production in rein-fed conditions or dry land areas (Ceccarelli, 1996).

The AMMI stability parameters could be regarded from static or dynamic concept of stability. Most stability statistics relate to either of two concepts of stability as static (biological) or dynamic (agronomical) type of stability (Becker and Léon, 1988).. Static stability concept may be more useful than dynamic concept of stability in a wide range of environmental changes, especially in developing countries (Simmonds 1991). Sabaghnia et al. (2008) and Dehghani et al. (2010) reported static concept of stability for EV, SIPC and AMGE parameters which were calculated for significant numbers of the F-test Gollob (1968). In contrast there is not any report for the stability nature of AMMI

stability parameters based on the other F-tests. However, it seems that the AMMI stability parameters have static or biological concepts of stability and usually introduce low mean yielding genotypes as the most stable (Table 5). The AMMI model analysis was as an effective tool in understanding complex GE interactions in MET of durum wheat. Also, besides differences in crops and regions (climatic conditions, soil properties and etc), the observed GE interactions may be partly explained by the structure of the dataset that was considered and the selection of the genotypes.

### CONCLUSION

Genotype G15 can be considered as the most favourable genotype (2680 kg ha<sup>-1</sup>) for Gachsaran; Genotype G4 (2635 kg ha<sup>-1</sup>) was the winner at Khoramabad; Genotype G19 (2745 kg ha<sup>-1</sup>) was the winner at Gonbad. Genotypes G3 (2453 kg ha<sup>-1</sup>) and G5 (2509 kg ha<sup>-1</sup>) can also be considered as the most favourable genotypes for Moghan and Ilam. These genotypes are recommended for release as cultivars by the Dry Land Agricultural Research Institute of Iran.

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### OCJENA GENOTIP×OKOLINA INTERAKCIJE PRINOSA DURUM PŠENICE UPOTREBOM AMMI MODELA

## SAŽETAK

U cilju da studiraju GE interakcije i utvrde Vining genotipova durum pšenica, terenski eksperimenti su sprovedeni sa 20 genotipova za tri godine (2007-2009) u Iranu. Rezultati su pokazali visoko značajne razlike za GE interakcije ukazuje na mogućnost izbora za najstabilnijih genotipova. F-test Gollob određuje prvih pet osa i FGH1 i FGH2 testovi identifikovali prve tri ose kao značajne Ammi (aditivni i multiplikativni efekat glavna interakcija) komponenti. Prema testiraju FRatio i poprečnim rezultate validacije, prve dve ose bile značajne. Ilustrovane godišnji AMMI2 biplots pokazala da mega-okruženja obrasci varirao tokom godina. Može se sumirati da su lokacije test Gachsaran (sa osvajanja G15), Khoramabad (sa osvajanja G4) i Gonbad (sa osvajanja G19) smatra se pojedinac mega-okruženia, ali ponašanje drugih testova lokacijama (Moghan i Ilam) je promenljiva tokom godina. U svakom slučaju, izgleda da je u vezi sa obe mega-okruženia, može se Vining genotipovi G3 i G5 biti pogodna za ove test lokacija. U Ammi parametri stabilnosti (EV, Amge, SIPC i D) u skladu sa prva dva broja IPCs ukazuju da genotip G15 posle da genotip G4 su kao najstabilnijih genotipova, ali nijedan od ovih genotipova su grupisani kao Vining genotipova. Dakle, izgleda da procena genotipova na osnovu grafičkog predstavljanja Ammi biplot je superioran u odnosu Ammi stabilnosti parametara.

**Ključne riječi:** glavni efekat aditiva i multiplikativna interakcija, vreijdnost AMMI stabilnosti, interakcija genotip×okruženje, stabilnost prinosa