

### **MODEL SELECTION IN ADDITIVE MAIN EFFECT AND MULTIPLICATIVE INTERACTION MODEL IN DURUM WHEAT**

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The study included data set of 20 durum wheat genotype across 15 rain-fed environments. A combined analysis of variance showed that the genotypes differed significantly for seed yield and GE (year × location) interaction. Cross validations procedure and four various F-tests including  $F_{Gollob}$ ,  $F_{Ratio}$ ,  $F_{GH1}$  and  $F_{GH2}$  are used for testing the GE interaction principal component analysis (IPCA) axes and indicated that two, four, six or seven axes could be significant. According to EV1, D1, AMGE1 and SIPC1 parameters, genotypes G3, G7 and G17 were the most stable genotypes while based on EV4, D4, SIPC4 and AMGE4 parameters, genotype G13 was the most stable genotype. The hierarchical clustering showed that the twenty one studied the

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AMMI stability parameters and mean yield could be divided into four distinct groups. Group III contains mean yield, SIPC4, SIPC6 and SIPC8 which were computed from four, six or eight IPCAs. In conclusion, G13 (DON-MD 81-36) was found to be the most stable genotype as well as high mean yield performance (2592.45 kg ha<sup>-1</sup>) and so is recommended for commercial release in semi-arid areas of Iran. Also, the SIPC-based stability parameters of the AMMI model was found to be useful in detecting the yield stability of the genotypes studied.

*Key words:* genotype × environment interaction, multi-environment trials, principal component analysis

#### INTRODUCTION

The multi-environment trials of new genotypes results in significant genotype × environment (GE) interaction in most situations. Knowledge of GE interaction can aid breeders to reduce the cost of genotype evaluation by eliminating unnecessary testing locations (GAUCH *et al.*, 2008). Sufficient understanding of GE interaction and its exploitation can contribute significantly to genotypic improvement for yield. The large magnitude of GE interaction may necessitate the performing of additional multi-environment trials. If genotypes are being selected for many locations, stability and mean yield across all environments are more important than yield for specific environments (PIEPHO, 1996). Most plant breeders explore for genotypes that show a stable property as well as high mean yield over environments and generally a genotype is known as the most stable when its yield performance across environments does not deviate from the average yield of the studied genotypes.

Several statistical methods such as ANOVA, joint linear regression model, principal component analysis can be used to evaluate GE interaction, which the advantages and disadvantages of these statistical methods have been discussed in literature (LIN *et al.*, 1986; BECKER and LEON, 1988; FLORES *et al.*, 1998). As a result, an alternative model has been suggested, including the application of additive main effects and multiplicative effects (AMMI) model. The AMMI model is a combination of ANOVA and multiplicative GE interaction obtained from a singular value decomposition of the matrix of residues (ZOBEL *et al.*, 1988). This model has been proclaimed as superior to both joint linear regression model and principal components analysis separately (CROSSA *et al.*, 1988). The AMMI model was introduced and has been applied for detailed understanding of both main effects (genotypes and environments) and GE interaction in multi-environment trials (ZOBEL, 1990).

An important step in the AMMI analysis is the determination of the portion of GE interaction indicating real responses to genotypes and environments, and the random variation affecting GE interaction (noise). At first time, GOLLOB (1968) introduced an especial F test for the assessment of GE interaction principal component analysis (IPCA) axes but this F test proved too liberal both on theoretical grounds and following simulation results (CORNELIUS, 1993). Also, the other F tests

including  $F_{\text{Ratio}}$ ,  $F_{\text{GH1}}$  and  $F_{\text{GH2}}$  tests have been proposed that permit a better control of Type-I error rates (CORNELIUS *et al.*, 1992; CORNELIUS, 1993). An alternative criterion is according to cross validation method and random splitting the observations of GE combination into modeling and validation data (GAUCH, 2006). In cross validation method of the AMMI models, including from AMMI0 to AMMIN (zero to N) IPCA axes, are compared in terms of predictive accuracy. These AMMI models are compared via root mean square prediction difference (RMSPD) between expected and validation models.

Yield stability can be assessed by AMMI analysis as the different statistical stability parameters. ZOBEL (1994) introduced averages of the squared eigenvector (EV) values as the AMMI stability parameter. SNELLER *et al.* (1997) suggested AMGE and SIPC stability parameters of AMMI model to describe the contribution of environments to GE interaction. The AMMI stability value (ASV) benefits from the first two IPCA of AMMI model (PURCHASE, 1997). The Euclidean distance from the origin of significant interaction IPCA axes as D parameter was suggested by ANNICCHIARICO (1997). The use of the AMMI stability parameters permits to evaluate yield stability after reduction of the noise from the GE interaction effects. Any of these parameters may also be of interest for breeding programs as an alternative to the conventional stability methods such as joint linear regression model. This investigation was carried out to evaluate the effect of GE interaction on the yield performance of cultivars and improved genotypes of durum wheat in semiarid areas of Iran. For this objective, the definition of stability parameters for the assessment of GE interaction PCA axes based on cross validation and the use of four other tests was envisaged.

#### MATERIALS AND METHODS

Statistical analysis was performed on grain yield data of 19 improved durum wheat genotypes and cultivar Seimareh collected from 5 different locations during years 2007-2009 (15 environments). The test locations were selected to sample climatic and edaphic conditions vary in latitude, rainfall, soil types, temperature and other agro-climatic factors. The descriptions of some properties of the locations are given in Table 1. These genotypes were developed by various plant breeders at different stations of International maize and wheat improvement center (CIMMYT) and International Center for Agricultural Research in the Dry Areas (ICARDA). The most widely grown durum wheat genotype cultivar Seimareh was included as check genotype at each environment. The codes and pedigrees of these genotypes are provided in Table 2.

At each environment 20 genotypes were grown in a randomized complete block design with 4 replications. The experimental plots were sown by precise planting machine in optimal time for environments. The seed was sown in six rows, 7 m long; with a between-row spacing of 17.5 cm. Currently accepted optimal levels of crop management and cultural practices for durum wheat were applied each environment.

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).

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	2477.72
2	G2	GREEN-14//YAV-10/AUK	CIMMYT	2491.33
3	G3	GA//2xCHEN/ALTAR84	CIMMYT	2429.70
4	G4	BCR//MEMO/GOO/3/STJ7	ICARDA	2578.22
5	G5	SERRATOR-1//SRN-3/AJAIA-15	CIMMYT	2356.75
6	G6	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-4AP-0AP	ICARDA	2490.85
7	G7	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-6AP-0AP	ICARDA	2504.90
8	G8	GREEN-14//YAV-10/AUK	CIMMYT	2590.25
9	G9	Bisu-1//CHEN-1/TEZ/3/HUI//CIT71/CII	CIMMYT	2566.05
10	G10	BCR/3/CH1//GTA/STK/4/BCR/LKS4 ICD92-0150-CABL-11AP-0AP-8AP-0TR-4AP-0AP	ICARDA	2581.80
11	G11	GSB1-1-4/D68/1/93A-1A//RUFF/FG/3/MTL/5 ICD95-1174-C-2AP-0AP-2AP-0AP	ICARDA	2245.48
12	G12	ALTAR84/STN/WDZ-2 ICD92-MABL-0238-4AP-0AP-5AP-0TR-15AP-0AP	ICARDA	2475.72
13	G13	DON-MD 81-36	ICARDA	2592.45
14	G14	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-2AP-0AP	ICARDA	2694.22
15	G15	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-6AP-0AP	ICARDA	2575.43
16	G16	OUASERL-1 ICD96-0758-C-2AP-0AP-5AP-0AP	ICARDA	2531.67
17	G17	TRE97/4/GDOVZ5512/CIT/RUFF/FG/3/ENTE/MARIO//CA ICD97-1044-C-0AP-6AP-AP-5AP-0AP	ICARDA	2454.22
18	G18	MARSYR-6 ICD95-1127-T-0AP-9AP-0AP-7AP-0TR-5AP-AP	ICARDA	2313.38
19	G19	ETH-LRBRI-133/3*ALTER 84 CDSP91B31-A-1H-030Y-030M-3Y-0M-1Y-0B	CIMMYT	2587.27
20	G20	Seimareh	Iran	2536.53

Plots were harvested with small plot harvest combine, when genotypes reached the full maturity. Grain yield of each genotype in each environment was obtained by expressing plot grain yields and converting them on hectare basis.

Statistical analysis of variance for linear-bilinear AMMI model and  $F_{\text{Gollob}}$  (GOLLOB, 1968) were performed via the SAS codes developed by BURGUENO *et al.* (2001) and using the SAS release 6.12 (SAS, 1996). Also,  $F_{\text{Ratio}}$  (CORNELIUS *et al.*, 1992),  $F_{\text{GH1}}$  and  $F_{\text{GH2}}$  tests (CORNELIUS, 1993) were used to test the significance of IPCAs for the AMMI model. Finally as alternative strategy, 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).

Table 3. Equations of AMMI stability parameters

Parameters	Equation	Author(s)
EV	$\sum_{n=1}^N \gamma_{in}^2 / n$	Zoble (1994)
AMGE	$\sum_{n=1}^N \sum_{g=1}^M \lambda_n \gamma_{in} \delta_{jn}$	Sneller <i>et al.</i> (1997)
SIPC	$\sum_{n=1}^n \lambda_n^{0.5} \gamma_{in}$	Sneller <i>et al.</i> (1997)
D	$\sqrt{\sum_{n=1}^N (\lambda_n \gamma_{in})^2}$	Annicchiarico (1997)
ASV	$\sqrt{\frac{SSIPC}{SSIPC} \frac{1}{2} (PC 1)^2 + (PC 2)^2}$	Purchase (1997)

SSIPC1 and SSIPC2, sum of squares of interaction PC1 and IPC2, respectively

According to different results of significant numbers of IPCAs through F-test and cross validation, various AMMI parameters were computed. Five types of EV (ZOBEL, 1994), AMGEF and SIPC (SNELLER *et al.*, 1997), D parameter (ANNICCHIARICO, 1997) were calculated. Also, using two first numbers of IPCAs, the AMMI's stability value (ASV) was calculated (PURCHASE, 1997). The formulae for computing these AMMI stability parameters are summarized in Table 3. In these formulas,  $\lambda_n$  is the eigenvalue of the IPCA axes  $n$ ;  $\gamma_{in}$  and  $\delta_{jn}$  are the genotype and environment eigenvectors for axes  $n$  and  $n$  is the number of IPCA retained in the model. All parameters were computed using the statistical package Genstat release 12.0 (GENSTAT, 2010). The AMMI stability parameters were compared using their

ranks for each genotype via calculating Spearman's rank correlation and grouped through hierarchical clustering procedure.

#### RESULTS AND DISCUSSION

Analysis of variance was conducted to determine the effects of year, location, genotype, and their interactions; on grain yield of durum wheat genotypes. The effects of years (Y) were significant ( $P < 0.05$ ), the locations (L) effects were not significant ( $P > 0.05$ ) and their interactions (YL) were highly significant (Table 4). The main effect of genotype and the genotype by year interaction (GY) were significant but the genotype by location interaction (GL) was not significant. Also, three way interactions (GYL) were highly significant ( $P < 0.01$ ). The high significance of GE interactions is indicating the studied genotypes exhibited complicated GE interaction (both crossover and non-crossover types). The expression of grain yield as a quantitative trait is the result of genotype, environment and GE interaction. Complexity of these traits is a result of diverse processes that occur during plant development. The relative magnitude of GE interaction for grain yield found in this investigation are similar to those found in other yield stability analysis of crops in rain-fed environments (MOHEBODINI *et al.*, 2006; SABAGHNI *et al.*, 2008a). The presence of GE interaction reduces the progress from selection in any one environment (YAU, 1995).

Table 4. 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 × L	8	34610128.9**	23.98
Replication/ YL	45	618760.2	
Genotype (G)	19	680166.4*	1.12
G × Y	76	341113.3*	2.25
G × L	38	314535.9 <sup>ns</sup>	1.04
G × Y × L	152	248317.9**	3.27
R × G / YL	855	102927.8	

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

According to F-test GOLLOB (1968), the first eight IPCA axes of AMMI model were significant (Table 5). Also,  $F_{Ratio}$  (CORNELIUS *et al.*, 1992) indicated significance of the first four IPCA axes while both  $F_{GH1}$  and  $F_{GH2}$  tests (CORNELIUS, 1993) showed significance of the first six IPCA axes in the AMMI model (Table 5). In contrast, the RMSPD values between AMMI model's estimates and their respective validation observations indicated only first two IPCA axes of AMMI model were adequate for GE interaction interpretation (Table 5). Like to the results obtained from AMMI models used in soybean (ZOBEL *et al.*, 1988), lentil (SABAGHNI *et al.* 2008b), and chickpea (DEHGAHNI *et al.*, 2010), the AMMI model

used in the present investigation exhibited a more complex interaction which needed as many as two, four, six or eight IPCAs for description of variation in the GE interaction. This problem could be related with the nature of the crop, environmental conditions or diverse genetic background obtained from different sources.

Table 5. Amounts of different *F*-tests and cross validation for IPCAs of AMMI model

Components	$U_1$	$U_2$	$V_1$	$V_2$	$F_{GH1}$	$F_{GH2}$	$F_{Ratio}$	$F_{Gollub}$	RMSPD	% of GE
IPC1	56.32	7.44	51155.39	53515.83	3.140**	3.147**	2.382**	4.516**	411.65	24.13
IPC2	52.47	7.25	47457.68	50374.58	2.142**	2.147**	2.180**	3.062**	411.20	15.33
IPC3	48.63	7.06	43794.79	47275.41	2.040**	2.044**	1.962**	2.894**	413.41	13.53
IPC4	44.79	6.86	40166.01	44206.76	1.739**	1.743**	1.782*	2.448**	415.96	10.63
IPC5	40.95	6.66	36570.64	41155.97	1.635*	1.639*	1.589 <sup>ns</sup>	2.280**	416.79	9.13
IPC6	37.12	6.44	33007.92	38108.79	1.426*	1.430*	0.629 <sup>ns</sup>	1.967**	417.04	7.22
IPC7	33.29	6.20	29477.04	35048.78	1.335 <sup>ns</sup>	1.338 <sup>ns</sup>	0.503 <sup>ns</sup>	1.815*	417.28	6.06
IPC8	29.46	5.95	25976.98	31956.32	1.363 <sup>ns</sup>	1.366 <sup>ns</sup>	0.354 <sup>ns</sup>	1.823*	414.75	5.48

$U_1$ ,  $U_2$ ,  $V_1$  and  $V_2$  are computed by approximations for calculating  $F_{GH1}$  and  $F_{GH2}$  according to Cornelius (1980) and Cornelius (1993).

RMSPD, the root mean square prediction differences in cross validation

However, five types of AMMI parameters were calculated as EV1, AMGE1, SIPC1 and D1 parameters (using only one IPCA), EV2, AMGE2, SIPC2 and D2 parameters (based on RMSPD results and using IPCA1 and IPCA2), EV4, AMGE4, SIPC4 and D4 parameters (using the first four IPCAs), EV6, AMGE6, SIPC6 and D6 parameters (using the first six IPCAs), and EV8, AMGE8, SIPC8 and D8 parameters (using the first eight IPCAs). Considering explained variation due to each IPCAs, type 1-based parameters benefits 24.13%, RMSPD-based parameters benefits 39.46%, type 3-based parameters benefits 63.62%, type 4-based parameters benefits 79.97%, and type 4-based parameters benefits 91.51% of GE interaction variations (Table 5). It is clear that calculating AMMI stability parameters based on the larger numbers of IPCAs results in the most usage of GE interaction variations.

According to minimum values EV1 and D1 parameters, and minimum absolute values of AMGE1 and SIPC1 parameters, genotypes G3, G7 and G17 were the most stable genotypes (Tables 6 and 7). These stable genotypes indicated low mean yield across test environments and so could not be considered as the most favorable genotypes. It can be stated that, these genotypes had static concept of stability which equal to homeostasis phenomenon of quantitative genetics. Anyhow, most plant breeders have used the stability similar to the above targets and to determine a genotype which shows a relatively constant yield in various environmental (BECKER, 1981). Also, stable genotypes with static concept do not necessarily respond to improved growing conditions with increased yield (BECKER and LEON, 1988).

Genotypes G3, G7 and G13 were the most stable genotypes based on EV2 and D2 parameters, genotypes G4, G12 and G19 were the most stable genotypes

based on SIPC2 parameter, and genotypes G3, G7 and G19 were the most stable genotypes based on AMGE2 parameter (Tables 6 and 7). Although, most of these genotypes had not the high mean yield performance, but some genotypes (G13, G19 following to G14) showed relatively high mean yield. In recent decades, most plant breeders would prefer an agronomic concept of stability instead of static concept of stability (BECKER and LEON 1988). In agronomic or dynamic concept of stability it is not required that the genotypic response to environmental conditions should be equal for all genotypes. It seems that using first two IPCAs in stability analysis could benefits dynamic concept of stability in identification of the most stable genotypes and high mean yield.

Table 6. The EV and D parameters of AMMI model for durum wheat yields of 20 genotypes tested in 15 environments

	EV1	EV2	EV4	EV6	EV8	D1	D2	D4	D6	D8
G1	0.01781	0.12141	0.15915	0.27422	0.39627	285.0	617.7	691.4	797.2	873.6
G2	0.01021	0.04714	0.05644	0.08585	0.13736	215.8	391.9	416.7	472.9	528.7
G3	0.00037	0.00266	0.18082	0.35107	0.51121	41.3	91.2	617.2	812.9	918.3
G4	0.00828	0.03212	0.41823	0.44827	0.56319	194.4	327.0	1024.1	1046.9	1106.9
G5	0.01278	0.06075	0.07632	0.14991	0.17022	241.5	444.2	487.0	600.7	619.6
G6	0.01105	0.08722	0.11679	0.12408	0.21672	224.5	520.8	586.1	595.0	670.8
G7	0.00004	0.01002	0.10120	0.23859	0.28426	14.2	170.7	512.2	686.2	720.6
G8	0.00067	0.03544	0.13737	0.24058	0.27608	55.3	322.3	600.8	714.9	740.6
G9	0.04725	0.05235	0.09827	0.10847	0.11314	464.2	479.9	584.3	596.5	600.8
G10	0.34615	0.39375	0.50796	0.60820	0.73598	1256.5	1310.3	1395.1	1443.4	1493.2
G11	0.05961	0.10997	0.13105	0.32231	0.67871	521.4	646.4	683.6	883.2	1086.2
G12	0.19540	0.40594	0.43677	0.60725	0.68608	944.1	1225.4	1256.1	1346.1	1377.0
G13	0.00395	0.01635	0.06651	0.13900	0.30740	134.2	232.3	426.6	537.1	684.3
G14	0.04695	0.21397	0.46239	0.47313	0.50023	462.8	835.7	1099.3	1107.6	1120.2
G15	0.01590	0.03824	0.14764	0.16540	0.32118	269.3	370.5	639.2	662.7	783.8
G16	0.04057	0.04197	0.19677	0.23086	0.30230	430.2	434.9	724.6	760.7	808.4
G17	0.00013	0.07075	0.11420	0.14262	0.32035	24.4	453.1	562.2	603.5	740.8
G18	0.12190	0.16149	0.25550	0.63083	0.64023	745.6	819.0	933.1	1225.7	1230.1
G19	0.01481	0.04036	0.08088	0.31902	0.46470	259.9	376.3	494.9	779.1	872.6
G20	0.04615	0.05810	0.25572	0.34033	0.37436	458.8	495.1	808.1	876.7	898.4

According to minimum values EV4 and D4 parameters, genotypes G2, G5 and G13 were the most stable genotypes while based on minimum absolute values of SIPC4 parameter, genotypes G9, G10 and G13 were the most stable genotypes and According to minimum absolute values of AMGE4, genotypes G3, G9 and G13 were the most stable genotypes (Tables 6 and 7). Only genotype G13 had high mean yield and genotypes G9 and G10 had moderate mean yield while the other most stable genotypes had relatively low mean yield. Although the AMMI stability parameters

based on the first four IPCAs explain 63.62% of GE interaction variations instead of 39.46% of RMSPD-based parameters, but it seems that they can not interpret GE interaction in a good manner. Parsimony or simplicity is another important criterion in AMMI model analysis and says go with the simpler model because when higher-order AMMI models are most predictively accurate by a significant and substantial amount, then plant breeders need to consider two or more mega-environments, which is more complexity and more work (GAUCH *et al.*, 2008).

Table 7. The SIPC and AMGE stability parameters of AMMI model for durum wheat yields of 20 genotypes tested in 15 environments

	SIPC1	SIPC2	SIPC4	SIPC6	SIPC8	AMGE1	AMGE2	AMGE4	AMGE6	AMGE8	ASV
G1	6.17	19.45	11.61	-0.97	13.12	-26.01	-76.02	-47.41	-11.20	-52.48	15.37
G2	-4.67	-12.60	-7.51	-3.15	-2.77	-133.82	-336.70	-215.09	-220.41	-215.49	9.86
G3	0.89	2.87	-5.24	-25.14	-9.46	-3.77	-11.19	15.27	67.41	20.82	2.27
G4	4.21	-2.16	30.71	29.82	34.91	120.54	-42.48	756.94	938.98	1044.81	8.27
G5	5.23	14.26	19.30	25.16	19.36	-22.04	-56.06	-74.43	-64.16	-46.95	11.16
G6	-4.86	-16.25	-13.05	-11.77	-21.54	-139.23	-430.60	-347.03	-318.32	-511.66	12.92
G7	-0.31	-4.43	-16.46	-34.82	-44.17	1.30	16.82	60.73	90.73	118.22	4.14
G8	-1.20	-8.89	-24.31	-9.00	-0.88	-34.28	-231.14	-609.06	-435.20	-273.16	7.84
G9	10.05	7.10	3.76	8.35	5.23	-42.36	-31.27	-18.20	-36.75	-27.55	12.94
G10	27.19	18.19	5.14	14.92	4.51	779.14	548.78	243.62	355.07	143.19	35.27
G11	11.28	20.54	19.41	40.64	48.96	-47.58	-82.45	-77.60	-108.35	-133.83	16.91
G12	-20.43	-1.50	-5.34	6.39	-6.12	-585.40	-100.96	-200.18	119.67	-130.23	31.86
G13	2.90	7.50	-0.50	-13.50	-31.74	-12.24	-29.55	-0.18	22.09	75.71	5.86
G14	-10.01	-26.88	-14.54	-18.69	-13.19	-286.95	-718.43	-438.65	-281.92	-172.89	21.03
G15	-5.83	-11.99	-28.94	-33.77	-16.59	24.58	47.80	108.65	118.58	67.72	9.56
G16	-9.31	-7.77	-11.68	-20.88	-31.86	-266.75	-227.31	-306.35	-508.57	-727.45	11.78
G17	0.53	11.49	20.78	24.93	36.02	-2.23	-43.52	-77.19	-74.08	-106.19	10.99
G18	-16.13	-24.34	-28.91	-15.37	-17.78	-462.37	-672.43	-770.78	-1019.3	-1068.6	21.84
G19	-5.62	0.97	9.84	10.90	15.81	23.72	-1.12	-33.31	-74.54	-88.41	9.66
G20	9.93	14.44	35.95	25.93	18.17	284.48	399.92	910.28	845.64	689.36	13.24

Genotypes G2, G6 and G19 based on EV6, genotypes G2, G6 and G13 based on D6, genotypes G1, G2 and G12 based on SIPC6, and genotypes G1, G9 and G13 based on AMGE6, were the most stable genotypes (Tables 6 and 7). Among these stable genotypes, G13 and G19 following to G9 could be regarded as the high mean yielding genotypes. It seems that these AMMI parameters tend to select candidate genotypes based on static or biologic concept of stability. In higher AMMI models like as AMMI6, the magnitudes of noise are increasing and do not result in good conclusion about GE interaction and yield stability analysis. Also, according to EV8 and D8, genotypes G2, G5 and G9; based on SIPC8, genotypes G2, G8 and G10 and due to AMGE8 parameter, genotypes G3, G5 and G9 were identified as the most stable genotypes (Tables 6 and 7). Considering men yield performance,

genotypes, G8 and G10 following to G9 could be selected as the most favorable genotypes with high mean yield.

According to ASV parameter, genotypes G3, G7 and G13 were the most stable genotypes while genotypes G10, G12 and G18 were the most unstable genotypes (Table 6). Considering first two IPCAs in ASV parameter, 39.46% of GE interaction is used in GE interaction exploration. The two IPCAs have different values and meanings and the ASV parameter using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced parameter between the two IPCA scores (PURCHASE, 1997). Also, ASV parameter of this investigation used advantages of cross validation due to computation from first two IPCAs. The results of ASV parameter have many similarities with the other AMMI stability parameters which calculated from the first two IPCAs scores.

Finally according to the most of type 1 of AMMI parameters (EV1, AMGE1, SIPC1 and D1), genotypes G3, G7 and G13; based on the type 2 of AMMI parameters (EV2, AMGE2, SIPC2, D1 and ASV), genotypes G3, G7 and G19; due to type 3 of AMMI parameters (EV4, AMGE4, SIPC4 and D4), genotypes G9, G13 and G19; cording to the type 4 of AMMI parameters (EV6, AMGE6, SIPC6 and D6), genotypes G2, G9 and G13; and based on the type 5 of AMMI parameters (EV8, AMGE8, SIPC8 and D8), genotypes G2, G5 and G9 were detected as the most stable genotypes. Considering all of the AMMI stability parameters, genotypes G13, G7 and G3 following to genotypes G2 and G9 were the most stable genotypes. Among these stable genotypes, only genotype G13 (DON-MD 81-36) had the high mean yield performance ( $2592.45 \text{ kg ha}^{-1}$ ) while the yield performance of G7, G2 and G9 was moderate and G7 was low.

The Spearman's rank correlation among the AMMI stability parameters may indicate if more estimates should be obtained to improve confidence in the prediction of genotype behavior. The rank correlation between the mean yield (MY) and all AMMI stability parameters was not significant positively or negatively. Thus, selecting the most stable genotypes based on these stability statistics did not result in choosing high mean yielding genotypes (Table 8). The other results of rank correlation among the AMMI stability parameters are given in Table 8 and due to confusing of reporting all results, a PCA analysis was performed on the ranks matrix and plot of two first PCAs was shown (Figure 1). According to this figure which is explaining only 65% of total variation (48 and 17% by PC1 and PC2, respectively), the overall results of rank correlation can be seen as the mean yield did not indicate any association with the AMMI stability parameters. Also most of the AMMI stability parameters were correlated with each other.

To better reveal associations among the AMMI stability parameters and using all information of total variation, the dataset of was analyzed using Ward's hierarchical clustering procedure. The dendrogram of clustering showed that the twenty one studied the AMMI stability parameters and mean yield could be divided into four major groups (Figure 2). Group I contains EV1, EV2, D1, D2, SIPC1, SIPC2, AMGE1 and AMGE2 which were computed from the IPCA1 or both IPCA1 and IPCA2 scores. Group II contains EV4, EV6, EV8, D4, D6 and D8 which were

computed from four, six or eight IPCAs according to EV and D parameters. Group III contains mean yield, SIPC4, SIPC6 and SIPC8 which were computed from four, six or eight IPCAs according to SIPC parameter. Group IV contains AMGE4, AMGE6 and AMGE8 which were computed from four, six or eight IPCAs according to AMGE parameter. Although there was not any significant correlation between SIPC parameters and mean yield, but they grouped together. Also, the most stable genotypes based on these three parameters (SIPC4, SIPC6 and SIPC8) were moderate mean yielding genotypes.

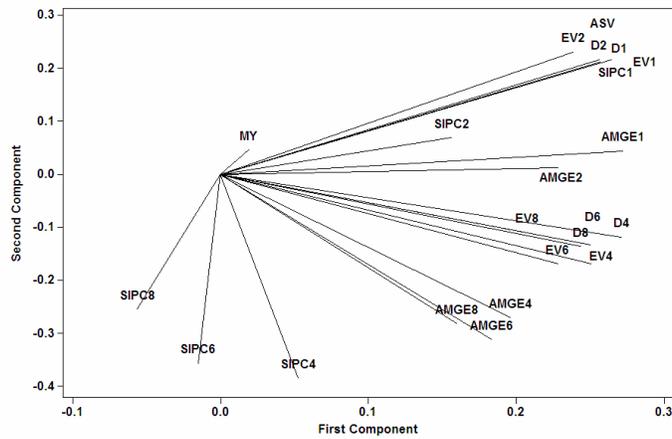


Figure 1. Plot of first two principal component analysis for mean yield and AMMI stability parameters

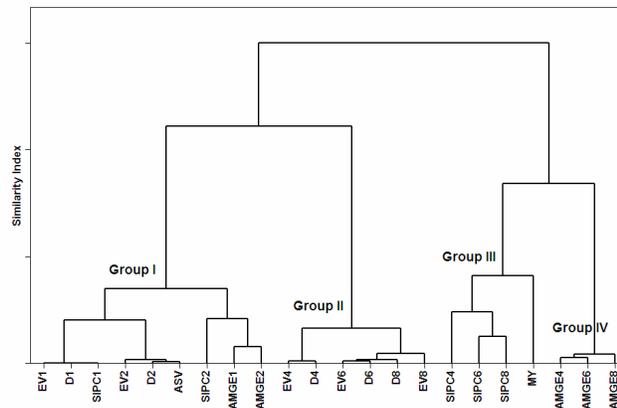


Figure 2. Hierarchical cluster analysis based on Ward's method using for mean yield and AMMI stability parameters.

Table 8. Spearman's rank correlation coefficients among ranks of 20 durum wheat genotypes at 15 environments based on AMMI stability parameters

	MY	EV1	EV2	EV4	EV6	EV8	D1	D2	D4	D6	D8	SIPC1	SIPC2	SIPC4	SIPC6	SIPC8	AMGE1	AMGE2	AMGE4	AMGE6	AMGE8	
EV1	0.07																					
EV2	0.27	0.76																				
EV4	-0.09	0.52	0.43																			
EV6	0.03	0.48	0.37	0.83																		
EV8	0.10	0.48	0.40	0.72	0.89																	
D1	0.07	1.00	0.76	0.52	0.48	0.48																
D2	0.22	0.84	0.98	0.49	0.41	0.43	0.84															
D4	-0.04	0.65	0.53	0.98	0.81	0.74	0.65	0.60														
D6	0.05	0.58	0.47	0.87	0.98	0.90	0.58	0.52	0.88													
D8	0.04	0.55	0.46	0.87	0.95	0.96	0.55	0.50	0.88	0.97												
SIPC1	0.07	1.00	0.76	0.52	0.48	0.48	1.00	0.84	0.65	0.58	0.55											
SIPC2	0.20	0.42	0.62	0.23	0.14	0.11	0.42	0.62	0.28	0.17	0.17	0.42										
SIPC4	0.14	-0.11	-0.03	0.23	0.20	0.07	-0.11	-0.04	0.21	0.18	0.14	-0.11	0.27									
SIPC6	0.18	-0.17	-0.29	0.14	0.18	0.19	-0.17	-0.25	0.10	0.16	0.17	-0.17	0.06	0.58								
SIPC8	0.27	-0.26	-0.17	-0.14	-0.10	0.03	-0.26	-0.16	-0.12	-0.09	-0.04	-0.26	0.01	0.41	0.70							
AMGE1	-0.08	0.79	0.68	0.67	0.49	0.40	0.79	0.75	0.73	0.37	0.54	0.79	0.40	0.03	-0.25	-0.32						
AMGE2	0.01	0.54	0.69	0.50	0.29	0.15	0.54	0.70	0.52	0.34	0.31	0.54	0.75	0.23	-0.18	-0.25	0.82					
AMGE4	-0.10	0.29	0.33	0.58	0.40	0.20	0.29	0.37	0.58	0.42	0.37	0.29	0.40	0.63	0.12	-0.02	0.71	0.78				
AMGE6	-0.14	0.27	0.17	0.59	0.45	0.27	0.27	0.23	0.57	0.46	0.42	0.27	0.21	0.52	0.17	0.00	0.70	0.65	0.94			
AMGE8	-0.10	0.19	0.20	0.43	0.32	0.18	0.19	0.25	0.44	0.33	0.31	0.19	0.27	0.48	0.07	0.16	0.65	0.66	0.90	0.93		
ASV	0.21	0.90	0.95	0.52	0.43	0.43	0.90	0.99	0.63	0.55	0.52	0.90	0.59	-0.04	-0.24	-0.18	0.78	0.69	0.38	0.26	0.27	

\* Critical values of correlation  $P < 0.05$  and  $P < 0.01$  (D.F. 18) are 0.44 and 0.56, respectively.

Each of the AMMI stability parameters relates to a different concept of yield stability and may be useful to plant breeders attempting to select genotypes with high, stable and predictable yield across environments. However, it seems that there is not a way to consider all of these parameters simultaneously, and some of them should be used in each investigation regarding number of significant IPCAs. In contrast to our results, ASV by SABAGHNI *et al.* (2008b) and F-test based parameters (EV, SIPC and AMGE) by DEGHANI *et al.* (2010) are reported as the good criteria for detecting stable genotypes based on dynamic stability. Anyhow, our most favorable genotype (G13) was the most stable genotype according to all AMMI stability parameters except type 5 parameters (EV8, AMGE8, SIPC8 and D8). In agreement with our results, SNELLER *et al.* (1997) reported some utilities for SIPC-based parameters in comprising to the other the AMMI stability parameters especially when selection is based on data from an expanded array of environment.

In this investigation, GE interaction was analyzed according to the AMMI model with several distinct significant multiplicative terms. Response levels of genotype in a given environment can be better predicted using multiplicative models the AMMI (GAUCH and ZOBEL, 1988). The AMMI model has demonstrated useful for exploring complex GE interaction, gaining accuracy, improving selections, and increasing experimental efficiency (GAUCH and ZOBEL, 1996). Also, several AMMI stability parameters were computed and used for durum wheat stability analysis and GE interaction exploration. These parameters represent different concepts of stability

and each may be suited for a different breeding application. In conclusion, the following results can be summarized from the this investigation: (i) G13 (DON-MD 81-36) was found to be the most stable genotype as well as high mean yield performance (2592.45 kg ha<sup>-1</sup>) and so is recommended for commercial release in semi-arid areas of Iran; (ii) the SIPC-based stability parameters of the AMMI model was found to be useful in detecting the yield stability of the genotypes studied; and (iii) the significant GE interactions and the changes in ranks of genotypes across environments suggest a breeding strategy of specifically adapted genotypes in homogeneously grouped environments.

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**MODEL SELEKCIJE TVRDE PŠENICE PREKO MODELA GLAVNOG  
ADITIVNOG EFEKTA I VIŠESTRUKO INTERAKCIJE**

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**I z v o d**

Prikazani su rezultati seta od 20 genotipova tvrde pšenice na 15 lokacija. Kombinovana analiza variance je pokazala da se ispitivani genotipovi značajno razlikuju u prinosu i GE (godina x lokacija) interakciji. Metode unakrsne validacije i četiri različita F- testa, uključujući  $F_{G_{\text{ollob}}}$ ,  $F_{\text{Ratio}}$ ,  $F_{GH1}$  and  $F_{GH2}$  su korišćena za testiranje interakcije G x E, IPCA (analiza glavnih komponenata prinosa) osovina i ukazal da dve, četiri, šest ili sedam osovina mogu da budu značajne. Prema EV1, D1, AMGE1 i SIPC1 parametima, genotipovi G3, G7 i G17 su najstabilniji dok je na osnovu EV4, D4, SIPC4 i AMGE4 parametara najstabilniji bio genotip G13. Hierarhijsko grupisanje u klastere je pokazalo da dvadeset jedan AMMI parameter stabilnosti i prosečan prinos mogu da budu podeljeni u četiri različite grupe. Grupa III sadrži prosečne prinose, koji su izračunate iz četiri, , šest ili osam IPCAs (SIPC4, SIPC6 i SIPC8). U zaključku, G13 (DON-MD 81-36) je utvrđen kao najstabilniji genotip sa najvišim prinosom (2592.45 kg ha<sup>-1</sup>) i preporučen je za komercijalno gajenje u semi'aridnim uslovima Irana. Takođe, parametri bazirani na SIPC parametrima stabilnosti AMMI modela je nađen kao koristan u utvrđivanju stabilnosti prinosa ispitivanih genotipova.

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