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Evaluation of Genotype×Environment Interaction in Barley (*Hordeum Vulgare* L.) Based on AMMI model Using Developed SAS Program

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ABSTRACT

Understanding the implication of genotype-by-environment interaction (GEI) and improving stability of crop yield in a target production environment is important in plant breeding. In this research, we used the AMMI (Additive Main Effects and Multiplicative Interaction) model to identify the stable genotype(s) by predictive accuracy of yield data. Results of this study indicated that the F_{GH} tests were useful to identify the best truncated AMMI model. In general, F_{GH1} and F_{GH2} tests had similar results. The findings of this study confirmed that the AMMI-4 was the best truncated AMMI model to distinguish the general and specific stability of genotypes across environments for recommending them to farmers. Based on AMMI-4 yield prediction, G15 and G17 were identified as useful genotypes for some environments, while G14 was found as a stable genotype in all environments.

Keywords: *F*-test, Stability, Truncated AMMI model, Yield prediction.

INTRODUCTION

Agricultural production is strongly influenced by environmental conditions that generally lead to wide variations in yield, both between years in one location and among locations in a single year or, even further, among locations and years (Pacheco *et al.,* 2005). Genotype-by-environment interaction (GEI) changes significantly by the magnitude of the differences in yield among the genotypes or changes in relative ranking of the genotypes in a series of environments (Allard and Bradshaw, 1964). The key to doubling agricultural production is increased efficiency in the utilization of resources i.e. increased productivity per hectare and per dollar, and this includes a better understanding of GEI and ways of exploiting it (Kang, 2002).

Various statistical techniques including univariate methods, nonparametric methods, and multivariate methods are used for estimating GEI in plant breeding (Flores *et al.,* 1998). Most of researchers agree that the use of AMMI model is an effective way to depict the adaptive responses of genotypes over environments (Crossa, 1990; Annicchiarico, 1997, Gauch, 2006a, Gauch, 2007). The AMMI model is used for initial statistical analysis of yield trials, clarifying GEI, and summarizing the patterns and relationships of genotypes and environments. It also improves the accuracy of yield estimates that are equivalent to raising the number of replications by a factor of two to five. Such advantages may reduce the costs of experimental agriculture by reducing the number of replications (Crossa, 1990). Imputing the missing data, increasing the

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flexibility and efficiency of experimental designs are the other advantages of AMMI approach (Gauch, 1992; Gauch and Zobel 1996).

Principal Component Analysis (PCA) in AMMI model or similar linear-bilinear models such as GGE-biplot or SHMM (Shifted multiplicative model) refers to partitioning of residual matrix from additive effects (environment and genotype effects). The additive nature of the ordinary ANOVA model allows adequate description of main effects; however, the interaction (residual from the additive model) is non-additive and requires other techniques to identify interaction relationships (Shafii and Price, 1998). Multiplicative interaction terms are estimated from the SVD of the *Z* matrix (Z= GEI). Thus λ_k is estimated by the k_{th} singular value of *Z*, γ_{ik} is estimated by the i_{th} element of the left singular vector, and δ_{jk} is estimated by the *j*th element of the right singular vector associated with λ_k (Mandel, 1971).The matrix of *Z* or bilinear term of AMMI model is the deviation from the additive part of the ANOVA model. In the SHMM model, the bilinear term absorbs the main effects of environment and genotype plus the GEI, whereas in the SREG (GGE biplot) model, only the main effects of genotype plus the GEI are absorbed into the bilinear terms (Crossa *et al.,* 2002).

On the other hand, the question of whether *F*-tests are applied for testing of multiplicative components has not been answered for researchers.

For all models that include singular value decomposition (SVD) matrix, the main question that researchers do not yet have an answer to is which test to apply for testing multiplicative components.

Cross-validation method is the one of the solutions that has been offered to select an optimal multiplicative term (Gauch, 1998). Random partitioning of the data set into *K* groups is the basic idea for cross-validation procedures. Then, the reduced data set is formed by deleting the first group and estimating the parameters of the model on the basis of the reduced data set. By using these parameters, the model values are calculated for the objects in the deleted group. Then, the sum of squares of prediction errors is calculated from the predicted values and observed values of the deleted objects. The procedure is repeated for the new reduced data set several times (Wold, 1978). Then, the Root Mean Square Predictive Difference (RMSPD) between the model and the validation observations (deleted group) is calculated as the square root of the quantity of the sum of square differences between the estimated model and the validation observations which is divided by the number of validation observations (Ebdon and Gauch, 2002). The advantage of cross-validation application is that the predictive accuracy of gain factor (statistical efficiency) associated with the AMMI model is increased, which is equivalent to increasing the number of replications in the data set (Ebdon and Gauch, 2002; Gouch, 2006b). Thus, estimates from two adjusted replicates are more accurate than the unadjusted means of the same replicates. By using the cross-validation procedure, noise is typically filtered from the data pattern. Therefore, the predictive accuracy is more interpretable and it provides a simple guide for model diagnosis by keeping the early axes that are mostly patterned than to discarded residual (Gauch, 1988).

The criteria for determining the optimal number of multiplicative terms that should be retained in the multiplicative model include sequential tests of the null hypothesis and random splitting of the data or cross-validation procedure that determine what multiplicative terms should be negligible (Moreno-Gonza´ lez, *et al.,* 2003). Gollob's *F*-test (Gollob, 1968) is one of the sequential tests that is generally used for determining the optimal truncated model. But, one of the major problems in using this method is its high type I error rate. In other words, by using this method, because of liberality, too many components are been significant (Cornelius, 1993).

The other criteria include F_{GH1}, F_{GH2}, and F_R tests proposed by Cornelius *et al.* (1992) for sequential testing of AMMI model. The F_{GH1}

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and F_{GH2} tests compared with *F*-Gollob in terms of controlling Type I error rates which eventually the superiority of F_{GH1} and F_{GH2} than to Gollob's test recognized (Cornelius, 1993). Cornelius (1993) also explained how many components must be interpreted for AMMI model. To verify the mentioned sequential tests, Annicchiarico (1997) evaluated four data sets of different cereals and proposed that the Gollob's test would be tended to the further flexibility, while the F_{GH2} test appeared somewhat more liberal than the F_R test.

The objectives of this research were: (1) to study genotype stability in the target environments by the selected AMMI model using many fitting approaches, (2) to compare all F-tests associated with AMMI model and cross-validation procedure to predict superior genotype and identify stable barley genotype(s), and (3) to provide a unique SAS code to calculate AMMI model and all of the reliable *F*-tests associated with it, since, currently, there is no unique special code in SAS to calculate the AMMI model, IPC axes, and all of the *F*-tests related to it.

MATERIALS AND METHODS

Field Trials

This study was carried out to determine the yield performances (kg ha^{-1}) of 20 promising barley varieties which were grown in fourteen environments during the two growing-seasons of 2006-2008. All research stations of this study were located in the cold regions of Iran and under the management of Seed and Plant Improvement Institute (SPII), Karaj, Iran. The characteristics of the locations and genotypes used in this research are presented in Tables 1 and 2, respectively. The G1 and G20 were the check cultivars. The experimental layout was a randomized complete block design with three replications. The area of the trial plots were 7.2 m^2, 1.2 m wide and 6 m long, consisting of 6 rows at 20 cm spacing. The experiments were sown and managed according to local practice. Appropriate pesticides were used to control insects, weeds, and diseases, and appropriate fertilizers were applied at usual recommended rates. For each environment and variety, grain yield was obtained from a sample area of 6 m^2 in the center of each plot.

Statistical Analysis

For genotypic yields in across-environment trials, prediction assessment was conducted using the AMMI method (Gabriel, 1978; Gauch, 1988).

The AMMI model used was as follows:

$$Y_{ij}= \mu+\alpha_i+\beta_j+\sum_{k=1}^{n} \lambda_k\gamma_{ik}\delta_{jk}+\varepsilon_{ij} \quad (1)$$

where, Y_{ij} is the yield of genotype i_{th} in environment j_{th} over all replicates, μ is the grand mean, α_i is the genotype i_{th} mean deviation (genotype mean minus grand mean), β_j is the environment j_{th} mean deviation, λ_k is the singular value for IPCA axis k, γ_{ik} is the genotype i_{th} eigenvector

Table 1. Locations characteristic and environment codes.

Location	latitude	longitude	altitude	Environmental code	
				First year	Second year
Arak	34˚06′N	49˚46′E	1708	E4[a]	E12
Jolgherokh	35˚50'N	58˚13'E	1650	E5	E13
Hamadan	35˚12′N	48˚41′E	1679.7	E1	E9
Karaj	35˚56′N	50˚54′E	1312.5	E3	E11
Mashhad	36˚16′N	59˚38E	990	E6	E14
Miandoab	36˚58′N	43˚03′E	1300	E2	E10
Ardabil	38˚15′N	48˚17′E	1350	E7	-
Tabriz	38˚05′N	46˚17′E	1361	E8	-

[a] Environmental code

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Table 2. Barley Genotype codes and their pedigrees.

Genotypic Code	Pedigree
G1	(Bahman) (check cultivar)
G2	Radical/Star
G3	Boyer (F356J126/Com)/4/Productive/3/
G4	F2//Radical/Karat/3/Radical/4/Xemus
G5	Bereke-54
G6	Narcis//K-281/Skorohod/1
G7	Narcis//K-281/Skorohod/2
G8	Bugar/4/Hma-02//11012-2/CM67/3/Marageh
G9	Robur/J126//OWB753431D/SL3/3/Radical
G10	Kny/K-273
G11	Pamir-010/Bulbul
G12	Xemus/Rhn-03
G13	Productiv/3/Roho//Alger/Ceres362-1-1
G14	CWB117-77-9-7/Victoria
G15	Belt67-1608/Slr/3/Dicktoo/Cascade//Hip/4/Victoria
G16	Robur/J126//OWB753431D/SL3/3/Radical
G17	Belt67-1608/Slr/3/Dicktoo/Cascade-/Hip/4/Antares/Ky63-1294
G18	Reaserch/Ashar//Bahman
G19	Alpha/Badia
G20	(MAKOUEE//ZARJOW/80- 5151) (check cultivar)

value for IPCA axis *k*, δ_{jk} is the environment j_{th} eigenvector value for IPC axis *k* and ε_{ij} is the error term.

At the first step, to identify which model is appropriate in AMMI analysis, the method of p was defined for cross-validation by MATMODEL 3.0 (Gauch, 2007).

In this research, beside cross validation method, the resultant of robustness tests including Gollob (1968) F-test, F_{GH1}, F_{GH2}, F_R were compared. The Gollob's F-test assumes that $n\hat{\lambda}_k / s^2$ is distributed as chi-square, where, n is the number of replications and s^2 is the pooled error mean square on cell means. However, this judgment was evaluated via computer simulation by Cornelius (1993). But, the frequently optimum results by using this *F*-test have been obtained (Zobel *et al.,* 1988). The other statistical tests of IPC axes which have mainly been investigated for analysis of GEI data including F_{GH1} and F_{GH2} (Cornelius, 1993) and F_R (Cornelius *et al.,* 1992) were used here. The F_{GH1} and F_{GH2} tests require values for the expectation and standard deviation (u_1 and u_2) of the largest eigenvalues of a central Wishart matrix with specified dimension and *df* (p and n for the first eigenvalue to be tested, *p-1* and *n-1* for the second eigenvalue and so on). For equations with $p \leq 19$ and $n \leq 99$, these may be obtained from tables which Mandel (1971) presented by Mont Carlo simulation (Cornelius, 1993). Practicable Cornelius's (1980) formulas that were approximated by regression analysis were similar to the results of Mandel (1971) simulation. However, the F_{GH1} test requires more extensive calculation than F_{GH2}, but the outcomes of both approaches are identical. The steps that need to estimate F_{GH1} and F_{GH2} are as follows:

$$v_1 = u_2^2 + u_1^2 + (f - 4)u_1 \quad (2)$$

$$v_2 = (f-2)u_2^2 + 2u_1^2 \quad (3)$$

$$h_1 = 2v_1u_1 / v_2 \quad (4)$$

$$g = 2 + 2(f-2)v_1 / v_2 \quad (5)$$

$$F_{GH1} = g\hat{\lambda}^2 / h_1 f s^2 \quad (6)$$

$$F_{GH2} = \hat{\lambda}^2 / u_1 s^2 \quad (7)$$

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Where, $\hat{\lambda}^2$ is the particular eigenvalue being tested, s^2 is the pooled error mean square on a cell means. F_{GH1} and F_{GH2} both are distributed approximately as *F*-test. The numerator and denominator *df* for F_{GH1} are h_1 and *g*; the numerator and denominator *df* of F_{GH2} are h_2 and *f*, where $h_2 = 2u_1^2 / u_2^2$.

The F_R is alternative F-test that was used in this research; this type of *F*-test was also described by Cornelius *et al.* (1992). The F_R test is more robust in the presence of heterogeneous within site experimental errors than the F_{GH2} test (Piepho, 1995). Nonetheless, Cornelius *et al.* (1992) stated that the significance of F_R test for each model implies that the t-term model is an inadequate model, but this test does not have high power for detecting the need for another multiplicative term. The F statistic for F_R is:

$$F_R = (SS\ (GEI) - \sum_{k=1}^{n} \hat{\lambda}^2)/fs^2 \qquad (8)$$

As mentioned earlier, we developed consecutive codes in SAS IML and DATA-step to calculate the AMMI model and all of the criteria for selecting the best truncated AMMI model. This program can be accessed by sending an E-mail request to the corresponding author of this paper.

RESULTS AND DISCUSSION

Results of variance analysis for yield of barley cultivars in AMMI model and related Gollob's *F*-test are reported in Table 3. The GEI was statistically significant ($P \leq 0.001$). The results showed that 79% of the total sum of squares was attributable to environmental effects; only 1% to genotype effects, and 20% to genotype×environment interaction effects. All of the source additive effects, except the genotypic effects, were highly significant ($P < 0.01$). In multi-environmental trials (MET), environment explains 80% or higher of the total yield variation (Yan, 2002). More pronounced influence of environment on the grain yield compared to the genotype or the GEI effects has been documented in many crops

Table 3. ANOVA table for AMMI7 model and F-test approximated by Gollob's tests and average root mean square predictive difference (RMS PD) for barley experiment.

S.O.V	*df*	*SS*	*MS*	Proportion	Noise	Model	*RMS* PD[a]	*RMS* PD[b]
GEN	19	16.96	0.893	0.01[d]	0.70[f]			
ENV	13	1410.93	108.533***	0.79[d]	0.01[f]			
ENV×GEN	247	360.19	1.458***	0.2[d]	0.43[f]	AMMI0	0.95197	0.95195
Component1	31	84.69	2.732***	0.24[b]	-	AMMI1	0.95021*	0.95034[c]
Component2	29	63.24	2.181***	0.18[e]	-	AMMI2	0.95255	0.95392
Component3	27	46.47	1.721***	0.13[e]	-	AMMI3	0.96041	0.96052
Component4	25	41.66	1.666***	0.12[e]	-	AMMI4	0.96326	0.96353
Component5	23	31.07	1.351***	0.09[e]	-	AMMI5	0.96661	0.96692
Component6	21	25.97	1.237**	0.07[e]	-	AMMI6	0.96822	0.9684
Component7	19	20.64	1.087*	0.06[e]	-	AMMI7	0.96844	0.9679
Residual	72	46.44	0.645	0.13[e]	0.13[g]	AMMIF	0.96942	0.96874
Error	560	350.32	0.626					

*, ** and ***; significant at 0.05, 0.01 and 0.001, respectively.

[a] Predicted by our SAS program with repeating 1,000 times splitting data; [b] Predicted by MATMODEL software with repeating 1000 times splitting data; [c] The selected model with a minimum root mean square predictive difference; [d] Calculated by dividing on sum of (GEN, ENV, and GEN×ENV) *SS*; [e] Calculated by dividing on ENV×GEN interaction *SS*; [f] Calculated by [*(df×MS Error)/SS*], [g] The portion of residual *SS* from total *GEN×ENV* Calculated as *SSE/(ENV×GEN SS).*

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(Solomon *et al.,* 2008; Kaya *et al.,* 2003).

By cross-validation procedure, the model of AMMI-1 was selected as the optimal model for predictive accuracy and analysis of GE interaction. By this procedure, the lowest assessment of deviation from validation data (0.9503) was dedicated to AMMI-1 model (Table 3). About 76% of the sum of squares of GEI would be loosed if we only judged based on cross-validation procedure. In other words, this proportion of GEI was not playing any role in interpreting GEI. Cornelius (1993) expressed that one of the plant breeder's objectives is to obtain from the entire data set the best estimates of the true performance levels of the cultivars in the environments where they were evaluated, not to predict a subset from another subset. Since the cross-validation might retain fewer terms than the optimum for the breeder's objective, selection of optimal model based on cross-validation seems to be more conservative than the other *F*-tests. Annicchiarico (1997) and Cornelius (1993) also stated that selecting AMMI model by cross-validation tend to be conservative and this issue refers to elimination of one or half replications of full data set for calculating the modeling data. To overcome on this problem and to use the full data set for modeling data Moreno-Gonza´lez *et al.* (2003) declared the theory of partitioning eigenvalue method. Cornelius and Crossa (1999) indicated that there was a little loss in efficiency (and sometimes a gain) if *a* truncated model was selected on the basis of F_{GH1} or F_{GH2} tests applied to the complete data set rather than by randomly splitting data and performing cross-validation.

The first seven IPC axes were significant by way of Gollob's test, as the first six IPC axes were significant at 1% probability level and the last IPC axis was significant at 5% probability level. This test revealed a more liberal property than the other tests and, therefore, it was relatively unreliable. The indiscrimination of noise and pattern, which can mislead the predictive accuracy, is one of the main factors that decreased the reliability of Gollob's *F*-test. The significant IPC axes through F-testes indicated that the GEI was very complex in this data, therefore, it can be expressed that each data with the same construction can be encompassed the more noise. Gauch (1988) explained that the noise is inherently stochastic, uncontrolled, and usually unexplainable variability among replicates and, as we move from the early *df* toward the late *df* or full data set, the amount of noise is added. Thus, it is suggested that when a researcher is faced with the same data structure, Gollob's test method to select optimal model can be ignored. In this research, the Gollob's test was applied as a non-optimal test for model selection in AMMI model.

The results of Gollob's test and F_R were relatively similar, showing significant IPC axes; also, the F_{GH1} and F_{GH2} tests were in agreement (Table 4). But, none of these tests were in accord with the results obtained by cross-validation procedure. Therefore, the question that comes to mind is which model is the best model and what type of *F*-test or procedure can identify the best agronomical outcome? However, the recommendation of a valuable criterion for selecting the best AMMI model needs more practice and more data sets as well as more discussion and statistical research, but, in the next paragraphs, we attempt to discuss the issue in more details with regard to the expressed question.

The results of F_{GH1} and F_{GH2} tests were practically alike. The first four IPC axes were significant at 1% probability levels and the fourth IPC at 5% probability level (Table 4). Approximately, 67% of GEI were allocated to the first four components (Table 3). It seems that the F_{GH} tests were moderated for this aspect of optimal model selection than both Gollob's test and cross-validation procedure. The feature of parsimony for AMMI model was more prominent when the F_{GH} tests were chosen to detect the optimal AMMI model relative to Gollob's test. The reported simulation test compared with Gollob's test and F_{GH} tests

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Table 4. F_{GH1}, F_{GH2} and F_R tests for components of genotype×environment interaction in barley yield.

Component	V_1[a]	V_2[a]	H_1[b]	GF[c]	F_{GH1}[d]	Pr. F_{GH1}	U_1[e]	U_2[e]	H_2[g]	F_{GH2}[h]	Pr. F_{GH2}	df[i]	SS F_R[j]	MS F_R	Pr. F_R
1	33137.9	35978.1	99.873	1029.90	2.49	0.000	54.217	7.344	108.98	2.497	0.000	247	360.19	1.458	0.000
2	30585.6	33657.7	91.521	1016.14	2.01	0.000	50.357	7.157	98.99	2.008	0.000	216	275.50	1.275	0.000
3	28065.1	31381.1	83.174	1000.07	1.59	0.000	46.501	6.963	89.19	1.597	0.000	187	212.26	1.135	0.000
4	25575.5	29139.9	74.859	981.49	1.56	0.002	42.646	6.760	79.59	1.562	0.002	160	165.79	1.036	0.000
5	23115.9	26924.9	66.608	960.12	1.28	0.070	38.792	6.547	70.22	1.280	0.071	135	124.13	0.919	0.001
6	20685.2	24725.7	58.455	935.63	1.186	0.165	34.936	6.319	61.13	1.188	0.164	112	93.05	0.831	0.021
7	18281.7	22529.7	50.435	907.58	1.06	0.363	31.077	6.076	52.33	1.062	0.362	91	67.08	0.737	0.139

[a] Calculated from U_1 and U_2 and then used for calculating H_1; [b] Numerator degrees of freedom for calculating F_{GH1}; [c] Denominator degrees of freedom for calculating F_{GH1}; [d] Approximately distributed as F distribution with H_1 and GF degrees of freedom; [e] Computed by approximations given by Cornelius (1980) for mean and standard deviation of largest p-variate Wishart matrix with q df, p= Min (row df, column df) and q= Max (row df, column df); [g] Numerator degrees of freedom for calculating F_{GH2}; [h] F_{GH2} is approximately distributed as F distribution with H_2 and f degrees of freedom; [i] Calculated by (G-i[th] component×E-i[th] component) where G and E is number of Genotypes and environments respectively, [j] F_R is computed sum of square residuals after fitting all previous terms.

by Cornelius (1993) showed that the F_{GH} tests give a predictive model with only a small loss in accuracy, and sometimes a gain, as compared to the expected model chosen by cross-validation with half of the data used for modeling and the other half for validation. Cornelius *et al.* (1996) also suggested that non-significant components have too small value that their predicted value can be assumed trivial. Therefore, they probably are the best omitted components from the model if a truncated AMMI model is to be chosen as the working model for estimation and prediction. Apparently, the F_{GH1} and F_{GH2} are the suitable tests to estimate the significance of consecutive IPC axes in AMMI model. Therefore, we only used both F_{GH} tests here to choose AMMI model.

Also, the results of F_R test as an alternative way of selecting model are given in Table 4. By this criterion, the first six IPC axes remained in AMMI model. Unlike the Annicchiarico (1997) who stated that the F_R test was a more conservative test than the others, in this paper, the obtained results demonstrated that the F_R test was more liberal than F_{GH} tests. The discrepancy of this result with the results obtained by Annicchiarico (1997) may be explained by the argument that a good predictive model generally has fewer terms relative to significant-components by the statistical tests (Piepho, 1995). Simulation studies performed by Piepho (1995) for AMMI analysis under normality and homogenous variance assumptions demonstrated that Type I error rates for F_R were very similar to Type I error rates for F_{GH} tests. But F_R test generally have a lower power to detect the last non-null terms. The F_R test has been mainly preferred for those data whose error variances are heterogeneous among environments.

As previously mentioned, the F_{GH} tests identified that AMMI-4 was the best model for predictive accuracy. According to the statistical theory suggestion (Gauch, 1992), the interaction GE for this model contained almost 43% noise (noise calculated as ([(*df*

×MSE)÷SS]×100). The first four components allocated 45% of the interaction *df*. In general, based on AMMI-F or full model, 11 genotypes won in all environments. But, seven genotypes won by AMMI-4. Naturally, the more components are used for judgment, the more genotypes are won in at least one environment (Ebdon and Gauch, 2002). As a result, three genotypes won by AMMI-1, the G3 won in 6 environments (E1, E3 and E8-E11), G17, individually, won in six other environments (E2, E4, E5 and E12-E14), and the G14 won in E6 and E7 (Table 5). But, G3 only won in E3 by AMMI-F and E3 and E9 by AMMI-4, respectively (Table 5). As already seen, the G3 showed a good superiority in E3 by AMMI-1, AMMI-4 and AMMI-F, respectively. Accordingly, the G3 had a specific stability to E3. On the other hand, choosing the cross-validation procedure to predict accuracy was equivalent to reminding the ruler of first component of AMMI model, and, consequently, it was the same as choosing the unstable G3 as stable genotype. This can be indicated as a reason to reject some of statistical confirmations, especially for agronomical objects and one of these statistical approaches can be cross-validation. By predicting based on AMMI-4, G15 in 10 environments showed a positive rank predictive yield and only in four environments showed a decreasing in predictive yield ranking (Table5). Considering the complexity of the data, recommending just one genotype for all environments was very difficult. Approximately, G15 had a good response to most environments, but not all the studied environments (Table 5). This genotype had a negative predictive yield in E2 and E10 environments, which were two consecutive years in the Miandoab location. Evidently, this genotype exhibited a negative response to the mentioned location. Lodging was one of the factors that reduced efficiency of this genotype in this location. Actually, the phenomenon of hyper-performance occurred there. Furthermore, G15 showed a loss in yield ranking from 10, based on data, to 19, based on AMMI-4 in E8; and lost its predictive yield ranking from 15, based on AMMI-F, to 17 based on AMMI-4 in E12 (Table 5). G15 had the first yield ranking predictive for both years of Jolgherokh. Therefore, G15 had a specific stability for Jolgherokh location. Despite poor predictive yield ranking for G7 in the majority of environments, it had a great response in both years in Mashhad location (E6 and E14) based on AMMI4 (Table 5). Lower status for G17 in yield ranking from AMMI-1 to AMMI-F indicated that GE interaction of this genotype was small. The high correlation existed among the predicted yield ranking by difference AMMI model in G17. In several environments, G17 displayed a relatively good predictive yield ranking by AMMI-4. The results demonstrated that G17 had high special stability in all of the studied environments, except for E3, E11, E1, E9, E8, and E10. The E3 and E11 were two consecutive years in Karaj location. The E1 and E9 were two consecutive years in Hamadan location. Predictive yield ranking of G14 was close to middle rank in all environments. This genotype presented a general stability in all environments by AMMI-4.

In this paper, the MATMODEL 3.0 (Gauch, 2007) was used for calculation of cross-validation method. But, this software is unable to compute the F_{GH} and F_R tests. On the other hand, manipulating the written-codes in this software for personal purposes is difficult and needs a lot of proficiency for users in FORTRAN program. As mentioned before, another objective of this study was to provide a unit program executable in SAS (2004) that is capable to calculate the AMMI model and all *F*-tests related to it. A few programs have been presented to display the two AMMI graphs including yield *vs.* IPC1 and IPC2 v*s.* IPC1; therefore, we also decided to bring a SAS code for presenting these graphs (Figures 1 and 2). Simultaneously, SAS data-step and SAS/IML were used in this program. Authors have attempted to write this program in a simple format so that those who require this program can use it for

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Table 5. Ranking of predictive yield, in each cell from left to right, by AMMI-1, AMMI-4, and AMMI-F, respectively, for each genotype in each environment.

Genotype	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	E14
G1	3,5,10	13,16,12	5,6,3	14,15,16	12,2,2	8,19,4	10,1,13.5	4,7,12.5	4,12,15	3,15,13	4,1,1	12,13,7	13,3,2	13,18,20
G2	12,11,3	15,12,15	7,9,8	15,14,9	16,4,11	12,20,20	14,2,1	8,8,14	8,13,13	13,19,14	7,5,11	16,11,9	15,9,15	15,20,19
G3	1,16,15	20,17,11	1,1,1	20,19,19	20,19,19	14.5,12,11	19,15,10	1,2,8	1,1,2	1,14,15	1,6,2	20,14,14	20,20,20	20,17,16
G4	5,9,14	19,20,20	2,2,11	19,20,20	19,18,10	20,13,12	20,18,19	3,5,2	3,7,3	10,6,2	2,4,6	19,19,13	19,18,16	19,16,17
G5	2,3,2	12,18,19	3,8,7	12,17,12	9,13,17	7,2,7	7,19,15	2,9,15	2,16,16	2,1,1	3,2,3	10,20,19	11,10,14	12,2,2
G6	10,6,12	18,19,18	6,10,15	18,18,18	18,10,9	16,15,18	18,14,12	6,11,5	6,19,9	12,5,4	6,3,4	18,18,20	18,11,11	18,15,15
G7	17,7,7	11,8,8	14,15,13	11,12,15	13,20,20	18,1,3	16,20,20	16,12,17	16,10,12	19,4,5	16,18,18	13,10,6	12,19,18	11,1,3
G8	13,2,4	9,7,3	11,16.5,16	9,8,10	8,15,4	9,4,1	9,17,8	11,3,1	12,9,14	11,17,18	11,12,13	8,4,12	9,15,19	9,13,9
G9	6,8,5	7,3,2	9,11,9	8,6,3	6,16,16	6,3,17	6,11,18	7,4,6.5	7,3,4	6.5,13,7	8,14,16.5	6,2,2	7,16,13	7,7,14
G10	15,19,18	14,15,16	12,7,2	13,11,5	15,14,15	17,14,16	17,12,16	14,16,6.5	15,6,17	15,7,10.5	13,15,20	15,16,16	14,13,10	14,9,7
G11	9,13,6	3,4,13	15,13,14	3,3,4	3,6,14	2,6,13	3,6,2	13,13,11	13,8,7	8,9,10.5	14,13,14	3,6,4	3,7,4	3,6,4
G12	20,10,11	8,10,7	19,20,19	7,9,14	10,9,8	19,16,5	13,16,13.5	19,15,16	20,20,20	20,12,19	19,16,9	9,12,18	8,8,9	8,10,5
G13	18,14,20	6,2,6	18,14,18	6,4,1	7,12,5	11,10,6	8,9,11	18,14,3	18,5,10	16,18,16	18,19,15	7,3,5	6,12,17	6,12,13
G14	8,20,16	2,6,5	13,3,6	2,2,6	2,7,3	1,5,10	1,5,7	12,18,20	11,2,1	4,3,6	12,17,19	2,8,11	2,4,6	2,3,1
G15	7,17,19	5,13,9	10,5,5	5,7,8	5,1,1	4,11,14	5,3,3	10,19,10	9,14,18	6.5,3,2	10,7,8	5,17,15	5,1,3	5,5,6
G16	16,15,13	10,14,14	17,12,12	10,10,11	11,8,7	13,18,15	12,8,9	17,17,18	17,18,11	18,8,9	17,11,12	11,15,17	10,6,5	10,11,11
G17	19,18,17	1,1,1	20,19,20	1,1,2	1,3,6	5,9,9	2,4,4	20,20,19	19,11,6	17,16,12	20,20,16.5	1,1,3	1,2,1	1,4,8
G18	11,4,8	4,5,4	16,16.5,10	4,5,7	4,5,13	3,7,8	4,7,5	15,10,12.5	14,15,19	9,11,8	15,10,8	4,5,1	4,5,7	4,8,12
G19	14,1,1	16,9,10	8,18,17	16,16,13	17,11,12	14.5,17,19	15,10,17	9,1,4	10,17,8	14,20,20	9,7,5	17,7,8	17,14,8	16,19,18
G20	4,12,9	17,11,17	4,4,4	17,13,17	14,17,18	10,8,2	11,13,6	5,6,9	5,4,5	5,10,17	5,9,10	14,9,10	16,17,12	17,14,10

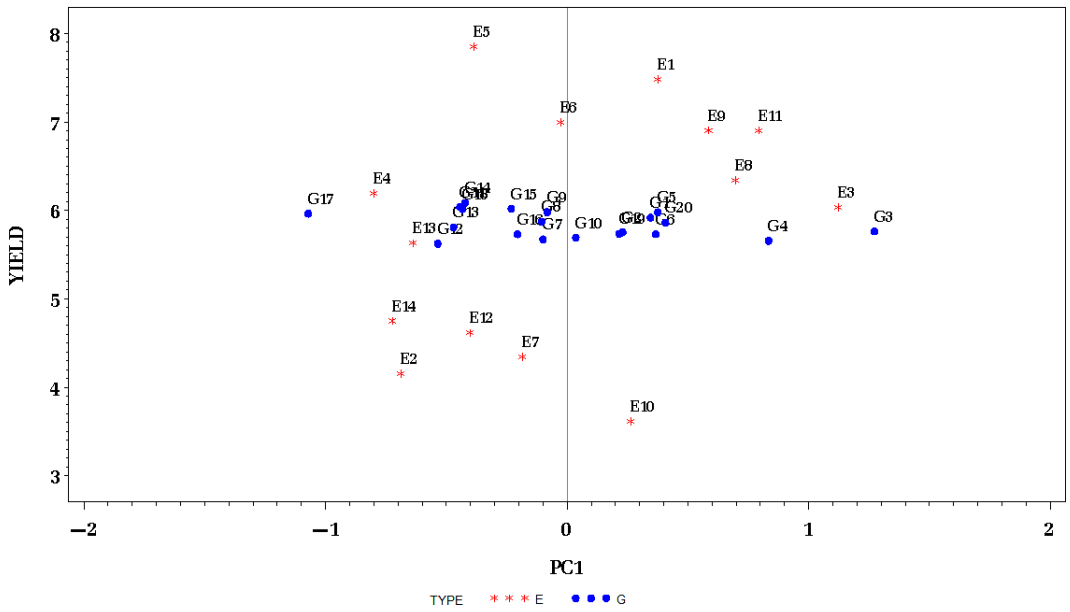

Figure 1. AMMI-1 model biplot for grain yield (t.ha^{-1}) of 20 barley cultivars in 14 environments.

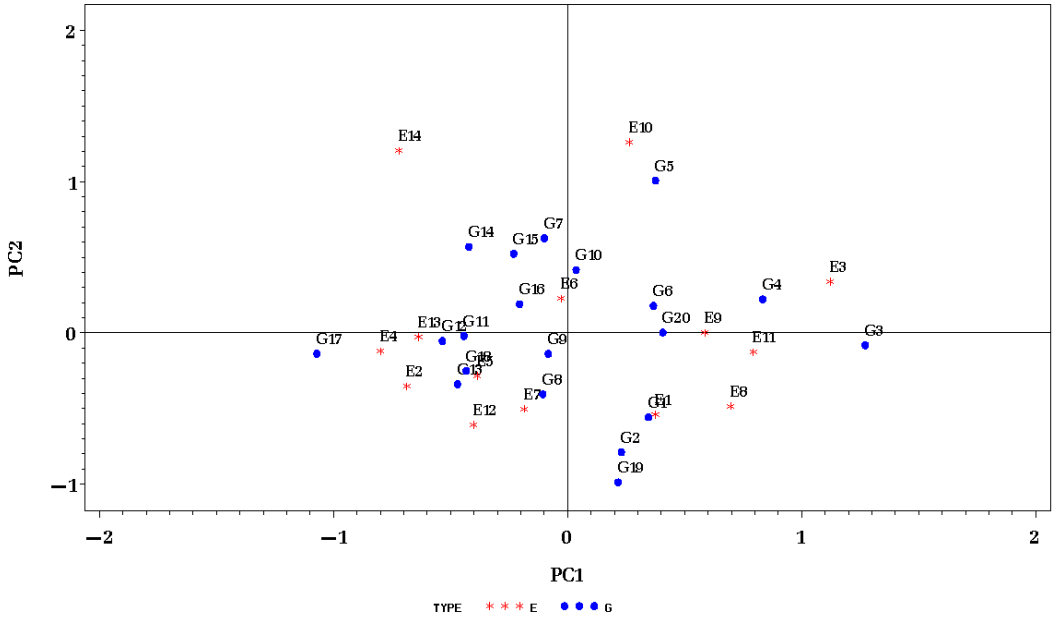

Figure 2. AMMI-2 model biplot for IPC1 vs IPC2 for 20 barley cultivars in 14 environments.

personal purposes. To verify the correct working and accuracy of this program, the published data by Cornelius (1993) and Cornelius *et al.* (1996) were recalculated and compared with the obtained results of F_{GH} and F_R tests as well as the data reported by Gauch (1992) used for the Gollob's test comparison.

Results of this study indicated that the F_{GH} tests were useful to identify the best truncated AMMI model. In general, F_{GH1} and F_{GH2} tests had similar conclusion. The achieved results from this study confirm that the AMMI-4 is the best truncated AMMI model to distinguish the general and specific stability of genotypes across environments

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for recommending them to farmers. Also, according to yield prediction based on AMMI-4, G15, G17 and G7 were identified as useful genotypes for some of the environments, while G14 was found as a stable genotype in all environments.

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تجزیه و تحلیل مدل امی برای بررسی اثر متقابل ژنوتیپ × محیط ژنوتیپ‌های جو (*Hordeum vulgare* L.)با استفاده از برنامه نوین طراحی شده درSAS

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چکیده

درک مفهوم ساختار اثر متقابل ژنوتیپ × محیط (GEI) و بهبود سازگاری عملکرد محصولات در محیط تولید هدف، یکی از مهمترین اهداف اصلاح نباتات است. در این تحقیق از مدل امی (AMMI) برای مشخص کردن ژنوتیپ‌های پایدار با استفاده از پیش‌بینی درست عملکرد استفاده گردید. همچنین علاوه بر روش اعتبار سنجی مدل‌های امی(Cross-validation)، معنی‌داری F تست‌های مربوط به تجزیه امی شامل F گلوب، FGH1، FGH2وFR به صورت مقایسه‌ای برای انتخاب بهترین مدل امی استفاده شدند. بر اساس تست‌های FGH که به عنوان بهترین F- تست‌ها انتخاب شده بودند، مدل امی-۴ به عنوان بهترین مدل در بین تمامی مدل‌های امی شناخته شد. بر اساس پیش‌بینی عملکرد بر اساس مدل امی-۴ ژنوتیپ‌های ۱۵ و۱۷ به عنوان ژنوتیپ‌های مفیدی برای برخی از محیط ها شناخته شدند و ژنوتیپ ۱۴ به عنوان یک ژنوتیپ با پایداری عمومی، برترین ژنوتیپ برای تمامی محیط‌ها شناخته شد.

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