Trakia Journal of Sciences, Vol. 7, No. 2, pp 8-17, 2009

Available online at:
http://www.uni-sz.bg
ISSN 1313-7050 (print)
ISSN 1313-3551 (online)

Original Contribution

ADAPTATION AND STABILITY ANALYSIS OF HULLESS BARLEY (*HORDEUM VULGARE L.*) GENOTYPES IN TEMPERATE REGIONS OF IRAN

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ABSTRACT

Different genotypes show various responses in different conditions (including low and high- input agriculture). Therefore, there is interaction between genotype and environment. There are several methods for determining the genotype-environment interaction. In order to analyze this interaction, 20 genotypes were studied in six locations for two years (2002-2004) in Iran. In order to evaluate the interaction and determine the stable genotypes, the stability analysis was done using regression analysis, Non-parametric and AMMI methods. Sum of the value of the IPC scores (SIPC) and Eigenvector value (EV) were used for determining the stability of parameters in the AMMI method. Also the Biplot method was used for recognizing those genotypes that are adapted to special environments. The results showed that ICNB93-369, Aleli/4/ mola 3 and SB91925 with the least interaction in both parameters were the most stable genotypes which were suitable for low-input locations. ICNBF8-653, Condor-BAR/4 and EHYTM80-1 with the most interaction in SIPC4 parameter were the least stable genotype and ICNB93-328, Condor-BAR/4 and Gloria with the most interaction in EV4 parameter were the least stable genotypes. Based on Biplot method, ICNBF8-582, Gloria and SB91925 genotypes were distinguished for Karaj location and Aleli/4/mola3 and SB91488 genotypes were determined for Esfahan location.

Key Words: Hulless Barley, Genotype×Environment Interaction, Stability, AMMI, Biplot

INTRODUCTION

Multi Environment Trials (METs) are important in plant breeding and agronomy for studying yield stability and predicting yield performance of genotypes across environments The differential response of genotypes to environment changes is a Genotype by Environment (G × E) interaction (1). Understanding of the causes of G × E interaction can be used to establish breeding objectives, identify ideal test conditions and formulate recommendations for areas of optional genotype adaptation (2). The term G × E interaction commonly refers to yield variation that cannot be explained by the genotype main effects (G). For genotype evaluation, however, both G and G × E must be considered simultaneously. Eberhart and Russell used yield mean, regression coefficient and root mean square error to identify stable varieties (3). Also, Perkins and Jinks determined two parameters such as regression coefficient and deviation from regression line as stable parameters (4). A number of distribution free methods were suggested to identify stable genotypes. In the method, in which the response and reflection of genotype to environment considered in the form of one-variable relation, such as equivalence of Wrick stability variance of Shukla, Finlay and Wilkinson's regression coefficient and also Perkins and Jinks's regression coefficient, it is now attempted to declare the genotype response to environment by calculation of a stability index (4, 5, 6, 7). For this reason, a special genotype may be estimated to be stable and in another method to be unstable, without coming to a similar result. But in multi-variable analysis, the response and reflection of a genotype in some

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different environments may be declared in a multi-dimensional space. Therefore, these methods can facilitate the interpretation of monotonous experiments of the yield and declare exactly the compound and complicated correlations among places, genotypes and/or between both of them by means of division diagram (8). Also using an environment regression model (SREG), Yan et al. combined G and G × E, denoted as G + GE or GGE and repartitioned this into non-crossover G × E interaction and crossover G × E interaction (9). The term G × E interaction will be hereafter used to denote this combination. Understanding the causes of non-crossover and crossover G × E interaction would help develop an understanding of the genotypic characteristics that contribute to a superior genotype and the environmental factors that can be manipulated to facilitate selection for such genotypes (9). Numerous methods have been used for an understanding of the causes of G × E interaction (10). These methods can be categorized into two major strategies. The first strategy involves factorial regression analysis of the G × E matrix (i.e., the yield matrix after the environment and genotype main effects are removed) against environmental factors, genotypic traits, or combinations thereof (11). The second strategy is associated with the use of the Additive Main Effects and Multiplicative Interaction (AMMI) model in MET data analysis. The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. AMMI is the only model that distinguishes clearly between the main and interaction effects and this is usually describable in order to make reliable yield estimations (12). AMMI biplot analysis is considered to be an effective tool to diagnose G × E interaction patterns graphically. The AMMI model describes the G × E interaction in more than one dimension and it offers better opportunities for studying and interpreting G × E interaction than analysis of variance (ANOVA) and regression of the mean (1). In AMMI, the additive portion is separated from interaction by ANOVA. Then the interaction principle components analysis (IPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of IPCA scores plotted against each other provides visual inspection and interpretation of the G × E interactions. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (13).

Concerning the use of AMMI in METs data analysis, which partitions the G × E interaction matrix into individual genotypic and environmental scores, an example was provided by Zobel et al., who studied the G × E interaction of a soybean MET. Other examples were provided by Annicchiarico and Perenzin, Yan et al., Vargas et al., Yan and Hunt, Kaya et al., Lafitte and Courtois, Brancour-Hulmel and Lecomte and Tarakanovas and Ruzgas (2, 9, 14, 15, 16, 17, 18, 19, 20). Among multivariate methods, AMMI analysis is widely used for G × E interaction investigation. This method has been shown to be effective because it captures a large portion of the G × E interaction sum of square; it clearly separates main and interaction effects that present agricultural researchers with different kinds of opportunities and the model often provides agronomically meaningful interpretation of the data (21). The results of AMMI analysis are useful in supporting breeding programme decisions such as specific adaptation and selection of environment (22). Usually, the results of AMMI analysis shown in common graphs are called biplot. The biplot shows both the genotypes and the environments value and relationship using singulars vectors technique (18). This study was undertaken to interpret G × E interaction obtained by regression analysis, Non-parametric analysis and AMMI analysis of performances of 20 hulless barley genotypes over 6 environments, visually assess how to vary yield performances across environments based on the biplot and group the genotypes having similar response pattern across environment.

MATERIAL AND METHODS

In order to do the research, 20 hulless barley genotypes (**Table 1**) were used in advanced lines from the hulless barley breeding programme of Iran and ICARDA/CIMMYT during two seasons (2002-2004) in six stations of Iran. Research stations were in Birjand, Esfahan, Karaj, Neyshabour, Yazd and Zarghan. Genotypes were sown in a randomized complete block with three replications.

***Table1**. Genotype and origin of genotypes*

	Genotype	Origin		Genotype	Origin
1	EHBYTM80-1	IRAN	11	ICNBF 8-582	ICARDA /CIMMYT
2	ALELI/4/MOLA/2…	ICARDA/ CIMMYT	12	ICNB 93-328	ICARDA /CIMMYT
3	ALELI/4/MOLA/3…	ICARDA/ CIMMYT	13	SB91925(13)	ICARDA /CIMMYT
4	CONDOR-BAR/4/…	ICARDA/ CIMMYT	14	BF 891M-592	ICARDA /CIMMYT
5	BF 891M-609	ICARDA/ CIMMYT	15	GLORIA	ICARDA /CIMMYT
6	SB 91488	ICARDA/ CIMMYT	16	ICNBF 8-617	ICARDA /CIMMYT
7	SB 91915	ICARDA/ CIMMYT	17	ICNBF 8-653	ICARDA /CIMMYT
8	ICNBF 8-611	ICARDA/ CIMMYT	18	SB 91925(18)	ICARDA /CIMMYT
9	CENTENO/CAM/…	ICARDA/ CIMMYT	19	ICNB 93-369	ICARDA /CIMMYT
10	LINO(CMB92.392-A-…)	ICARDA/ CIMMYT	20	EHBYTM 80-20	IRAN

Statistical analysis

We used some parameters to determine stable genotypes such as Eberhart and Russell's regression method, Finlay and Wilkinson's regression method, Perkins and Jinks's regression method, equivalence of Wrick, stability variance of Shukla, the average and deviation from rank and yield index ratio of non-parametric method and AMMI method. Genotype × environment interaction for gain yield was analyzed according to a classical multiplicative model or AMMI (8, 23). It is written as follows:

$$X_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

In this formula, μ is the mean of the total experiment, and β_e are the genotype and environment main respectively, $\sum \lambda_n \gamma_{gn} \delta_{en}$ genotype × environment interaction, λ_n is the individual amount for n^{th} main component axle, γ_{gn} (IPC) genotype eigenvector for n^{th} axle, δ_{en} is the environment special vector for the n^{th} axle, P_{ge} is the rest amount resulted from multiplicative effects, and finally ε_{ger} which means Noise. Biplot derived by plotting the genotypes and environments markers (scores) of the first two multiplicative terms of the AMMI model are also useful for summarizing GE interaction patterns (1, 24).

RESULTS

Regression and Nonparametric analysis

In order to do compound varieties analysis of yield the difference between genotypes and the interaction of genotype, year and environment were signified, that indicated the difference between genotypes in different environments. The results of stability analysis based on Eberhart and Rusell that the effects of genotypes were also signified, that is, there is significant difference between them (3). Also the effects of environments have been signified meaning that they also have very significant difference. The interaction of genotype and environment has been signified, that means varieties react differently in response to environmental conditions (**Table 2**). Therefore, relationship between the regression coefficients and mean yield for 20 hulless barley genotypes are shown graphically in **Figure 1**. The regression coefficients of ICNBF 8-582, LINO, CONDOR-BAR/4, and ICNB 93-328 genotypes were close to 1. ALELI/4/MOLA/2 and ICNB 93-328 had the highest yield at confidence limits for yield and their regression coefficients were close to 1 at confidence limits for regression. These two genotypes, therefore, were the group of the best adaptation to all environments. Also, the other stability parameters for ALELI/4/MOLA/2 and ICNB 93-328 genotypes were parallel to the results of graph. When the other genotypes were evaluated in **Fig.1**, EHBYTM80-1, CONDOR-BAR/4, BF 891M-609, SB 91488, ICNBF 8-611, CENTENO/CAM , LINO, ICNBF 8-582, BF 891M-592, ICNB 93-369 and EHBYTM 80-20 were defined as mid-adaptation to all environments while GLORIA and ICNBF 8-617 had bad adaptation. Other genotypes were found to be outside of confidence limits (**Table 3**). Examining genotypes with equivalence of Wrick and stability variance of Shukla methods, showed that CENTENO, ICNBF 8-611, ALELI/4/MOLA/2 and SB91925 (13) had high stability and GLORIA and EHBYTM80-1 had low stability among the other genotypes (**Table 4**). The ICNB 93-328 and CONDOR-BAR/4 Genotypes had the highest stability and yield if we checked them with Perkins and Jinks's regression method;

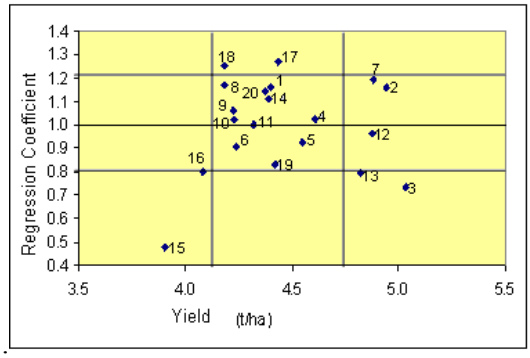
also in this method GLORIA genotype was recognized as an unstable one (**Table 4**). Based on Finlay and Wilkinson's regression method, the ICNB 93-328, followed by CONDOR-BAR/4 and BF 891M-609, were identified as stable genotypes. The ALELI/4/MOLA/2 had the lowest amount of average and standard deviation, so that we determined it as a stable genotype with this method. Following this were some genotypes, such as ALELI/4/MOLA/3, ICNB 93-328, SB91925 (13) and SB 91915 that were distinguished as stable ones. This method showed that ICNBF 8-617 and GLORIA were unstable (**Table 4**).

Table 2- *Yield Stability analysis of hulles barley genotypes in different environments*

S.O.V	DF	SS	MS
(E×G)+ E	220	272.609	1.239**
Genotype(G)	19	22.45	1.18**
Environment(E)	11	181.19	16.47**
E× G	209	71.34	0.34**
Linear Environment	1	181.19	181.19**
Genotype in linear Environment	19	6.95	0.37^{ns}
Deviation of regression	200	64	0.32
Pooled error	456	172.017	0.377

*ns: non significant, * significant, ** Highly significant*

Figure 1. *The diagram of hulless barley genotypes diffusion in terms of yield and regression coefficient*



Examining genotypes with Average of Rank and Deviation from rank of Non-parametric methods showed that ALELI/4/MOLA/2, ALELI/4/MOLA/3, ICNB 93-328 and SB91925 (13) had high stability and ICNBF 8-617 and GLORIA had low stability among the other genotypes (**Table 4**). Also, examining genotypes with yield index ratio revealed ALELI/4/MOLA/3 and genotype No ALELI/4/MOLA/2, SB 91915, ICNB 93-328, and SB91925 (13) had most stability among the other genotypes. Genotypes No 15 with this method was introduced as an unstable one (**Table 4**).

AMMI analysis

The AMMI analysis of variance (Additive main effects) showed significant effects for genotype, environment and G × E interaction (**Table 5**).These results showed that 65.76% of the total sum of square (SS) was attributable to environment effect; only 8.15% and 21.19% to genotype and G × E interaction effects, respectively. A large SS for environment indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. The magnitude of the G × E interaction SS was 3.18 times larger than that for genotypes, indicating that there were sustainable differences in genotypic response across environment. Results from AMMI analysis (Multiplicative effect) also showed that the first Interaction Principle Component Axis (IPCA1) captured 25.12% of the interaction SS in 13.87% of the interaction Degrees of Freedom (df). Similarity in the IPCA2 and IPCA3 explained a further 19.83% and 15.56% of the G × E interaction SS, respectively. The mean squares for IPCA1 and IPCA2 were significant ($p<0.01$) and cumulatively contributed to 44.95% of the total G × E interaction. Therefore, the post-dictive evaluation using an F-test at P=0.01 suggested that two IPCA1 and IPCA2 were significant for the model with 20 df.

Table 3*.Different Eberhart and Russell's parameter for Hulless Barley genotypes*

Genotype	Yield (t/ha)	Eberhart and Russell's regression coefficient (b_i)	Deviation of regression line (S_i^2)	R-square (R_i^2)
1	4.403	1.159^{ns}	0.482	66.7
2	4.945	1.159^{ns}	0.049	87.4
3	5.034	0.732^{ns}	0.165	62.5
4	4.608	1.023^{ns}	0.371	65.7
5	4.547	0.923^{ns}	0.315	63.7
6	4.239	0.906^{ns}	0.333	61.8
7	4.881	1.193^{ns}	0.110	84.5
8	4.184	1.171^{ns}	0.015	89.8
9	4.223	1.063^{ns}	-0.059	93.8
10	4.230	1.025^{ns}	0.195	74.7
11	4.321	1.002^{ns}	0.257	70.5
12	4.875	0.965^{ns}	0.355	63.6
13	4.821	0.793^{ns}	0.046	77
14	4.391	1.112^{ns}	0.164	79.3
15	3.904	0.476^{ns}	0.548	23.4
16	4.082	0.799^{ns}	0.121	70
17	4.438	1.271^{ns}	0.078	87.7
18	4.185	1.253^{ns}	0.170	82.9
19	4.420	1.832^{ns}	0.080	75.4
20	4.378	1.141^{ns}	0.125	82.5

From **Figure 2**, the locations' icons (designated Ny, Zr, Br, Kr, Sf and Yz) appeared much more dispersed than genotypes' icons (indicated 1-20) according to picture, which indicated the locations were far greater than that of the genotypes. The stability was analyzed from low to high by the genotypes icons from left to right. The genotypes GLORIA and ICNBF 8-617 had short stability, while ALELI/4/MOLA/3, ALELI/4/MOLA/2 and ICNB 93-328 genotypes had very long stability, and other genotypes had medium stability.

The IPCA1 value of genotype was near to zero point according to ordinate picture, which showed there were small interactions between the genotypes and environment, and their stability appeared stable. The genotypes ALELI/4/MOLA/2, CENTENO and ICNB 93-328 were near to the line passing zero point, which indicated that they were insensitive to the environments. However, BF 891M-609 and CONDOR-BAR/4 genotypes were far away from this line, which showed that these two genotypes were unstable and sensitive to the environments. The IPCA1 of locations Kr, Br and Zr were near to zero point line, which showed their stability was changeable and had good ability to resolve the mutant.

Table 4. *Different Stability Parameters in Hulless barley Genotypes. And Yield Stability analysis of hulles barley genotypes with nonparametric methods.*

Genotype	Variance of Shukla	Equivalence of Wricke	Finlay and Wilkinson's regression	Perkins and Jinks's regression	Average of Rank $(\overline{R}_i)$	Deviation from rank $(STD-R)$	yield index ratio $(Y.I.R)$
1	0.618	6.307	0.159	0.159	11.25	6.57	98.83
2	0.181	1.976	0.159	0.159	5.17	4.26	111
3	0.24	3.557	0.732	-0.268	5.67	3.65	113
4	0.487	5.007	0.023	0.023	8.83	6.04	103.43
5	0.433	4.475	0.923	-0.077	10.25	6.06	102.06
6	0.454	4.68	0.906	-0.094	12.08	5.25	95.15
7	0.253	2.689	0.193	0.193	6.75	4.29	109.56
8	0.151	1.682	0.171	0.171	13.17	4.65	93
9	0.053	0.71	1.063	0.063	14.08	3.34	92
10	0.306	3.215	1.025	0.025	12.5	5.45	94.95
11	0.367	3.826	1.002	0.002	12.58	6.23	96.99
12	0.468	4.819	0.965	-0.035	6.5	6.01	109.43
13	0.193	2.103	0.793	-0.207	6.67	4.18	108.21
14	0.286	3.017	1.112	0.112	10.92	5.91	98.56
15	0.913	9.224	0.476	-0.524	13.83	6.82	87.63
16	0.268	2.842	0.799	-0.201	14.08	3.6	91.63
17	0.254	2.706	1.271	0.271	10.83	4.57	99.62
18	0.338	3.538	1.253	0.253	13.83	4.95	93.33
19	0.215	2.312	0.832	-0.16	10.08	5.77	99.21
20	0.252	2.682	1.14	0.14	10.92	4.54	98.27

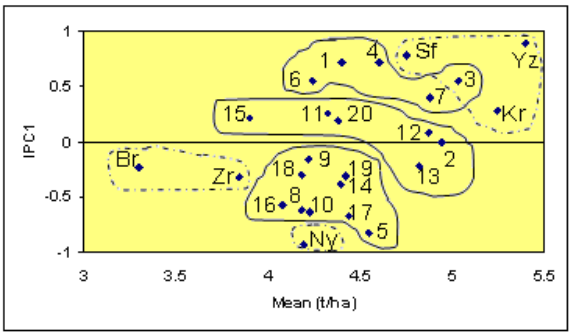


Figure 2*. Bipot of means of genotypes and locations on IPC1. Solid and dash lines show grouping of IPC1 genotypes and locations, respectively*

From **Figure 3**, the stability of the hulless barley genotypes can be assessed using the distance from the icons to the coordinate origin, for example, the ICNB 93-328 genotype appeared to be better stable than other genotypes, and GLORIA, CONDOR-BAR/4 and BF 891M-609 genotypes appeared unstable. In addition, the length between the location and the coordinate origin indicated the interaction effect of the genotypes and locations. The interactions' effect of the Ny (Neyshabour) appeared very large, while the Kr (Karaj) location was very small. In addition, the two genotypes ALELI/4/MOLA/3 and SB 91488 had interactions similar to the Esfahan location and the genotypes CONDOR-BAR/4, EHBYTM80-1 and SB 91915 showed similar interaction with the Yazd station. Also, Genotypes ICNB 93-369, ICNBF 8-617, BF 891M-609, BF 891M-592 and LINO were adapted to the Neyshabour location. The information obtained from **Figure 3** showed as well that the genotypes ICNBF 8-582, GLORIA and SB91925 (13) were adapted to the Karaj location.

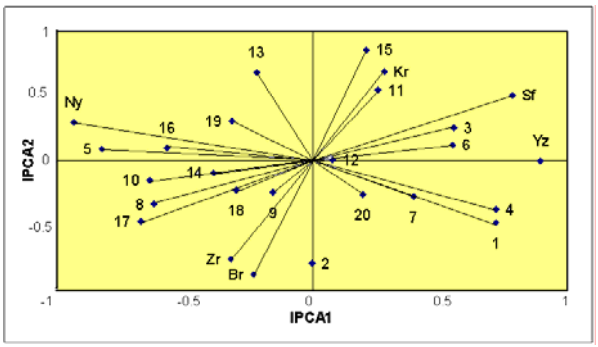
DISCUSSION

There are two strategies for developing genotypes with low G × E interactions. The first is subdivision or stratification of heterogeneous area into smaller, more homogeneous sub regions, with breeding programmes aimed at developing genotypes for specific sub regions. However, even with this refinement, the level of interaction can remain high, because breeding area does not reduce the interaction of genotypes with environments and years. The second strategy for reducing G × E interaction involves selecting genotypes with better stability across a wide range of environments in order to better predict behaviour (24, 25). Numerous methods have been used for understanding the causes of G × E interaction (10).

Table 5. *AMMI analysis of hulless barley genotypes in different environments*

S.O.V	DF	SS	MS
Treatment	239	825.141	3.452**
Model	241	826.707	3.43**
Genotype(G)	19	67.4	3.547**
Environment(E)	11	543.643	49.422**
G×E	209	214.098	1.024**
IPCA1	29	53.777	1.854**
IPCA2	27	42.469	1.573**
IPCA3	25	33.326	1.333**
IPCA4	23	22.01	0.957**
IPCA5	21	18.686	0.890**
IPCA6	19	13.954	0.734**
IPCA7	17	13.05	0.768**
Residual	33	16.826	0.510
Error	478	183.756	0.384
Pooled error	480	185.322	0.386
Total	719	1010.463	

Figure 3. *Bipot of the first and second IPC of genotypes and locations*



In this study, partitioning and interpretation of the G × E interaction was based on linear regression techniques and multivariate analysis (5, 20, 26). The former method had shown certain deficiencies for determining G × E interaction patterns and explains a small part of the sum of square of this interaction. This observation was encountered in this and other similar studies (14, 20, 27), because the regression technique confuses interaction and main effects (28), and is unable to predict non-linear genotypic response to the environments (26, 29). On the other hand, AMMI analysis appeared to be able to extract a large part of the interaction and is thus more efficient in analyzing G × E interaction pattern, as demonstrated by Zobel et al. (20). The AMMI model describes the G × E interaction in more than one dimension and it offers better opportunities for studying and interpreting G × E interaction than analysis of variance (ANOVA) and regression of the mean (1). In AMMI, the additive portion is separated from interaction by ANOVA. Then the interaction Principle Components Analysis (IPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of IPCA score plotted against each other provides visual inspection and interpretation of the G × E interactions. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance

across diverse environments (13).

In this study the results of AMMI analysis indicated that the AMMI model fits the data well. Therefore, this made it possible to construct the biplot and calculate genotypes and environments effects (2, 16, 19, 22). The Interaction Principle Component Axes (IPCA) scores of a genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA scores to zero, the more stable the genotypes are across their testing environments (30). In this study, number 3 genotype gave the highest average yield (Large IPCA1 score) but was relatively stable over the environments. In contrast the non-adapted genotypes of GLORIA and ICNBF 8-617 yielded low at all environments, as indicated by their small IPCA1. The genotypes ICNB 93-328 and ALELI/4/MOLA/2 had high yield and relatively highly stable. The most accurate model for AMMI can be predicted by using the first two IPCAs (2, 16, 22). Conversely, Sivapalan et al. recommended a predictive AMMI model with the first four IPCAs. These results indicate that the number of the terms to include in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment (31). In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (20, 24). Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observation. In this study, the interaction of the 20 genotypes with 6 environments during 2 seasons was best predicted by the first principle components of genotypes and environments.

In total, the study of genotypic stability revealed why some genotypes are grown in the Iran. In fact, from the advance genotypes of the ICARDA/CIMMYT hulless barley breeding programs ALELI/4/MOLA/2, ALELI/4/MOLA/3 and ICNB 93-328 genotypes demonstrated higher stability for grain yield. They not only appear to have a specific adaptation to some region but can also be grown successfully in all zones of Iran. Thus, this promising entry could be recommended to farmers dealing with the good yield. Therefore, genotypes could be used successfully in breeding programmes for the production of high grain yield hulless barley in the Iran.

Genotypes evaluation must be conducted in multiple locations for multiple years to fully sample the target environment (32). Genotype in the presence of unpredictable G × E interaction is a perennial problem in plant breeding (33). To select for superior genotypes, it seems that there is no easier way than to test widely (34), and select for both average yield and stability (35, 36).

CONCLUSIONS

AMMI analysis provided a better description of G × E interaction than other methods analysis, which was less effective in explaining this interaction. For genotypic stability, the ICARDA/CIMMYT advanced genotypes, ALELI/4/MOLA/2, ALELI/4/MOLA/3 and ICNB 93-328 showed high stability for yield and proved to be the best within the pool of the studied genotypes.

REFERENCES

1. Vargas, M., Crossa, J., van Eeuwijk, F., Sayre, K. D. and Reynolds, M. P., Interpreting treatment×environment interaction in agronomy trials. Agron. J. 93: 949-960, 2001.
2. Yan, W. and Hunt, L. A. Interpretation of genotype×environment interaction for winter wheat yield in Ontario. Crop Sci. 41: 19-25, 2001.
3. Eberhart, S. A. and Russell, W. A., Stability parameters for comparing varieties. Crop Sci. 6: 36–40, 1966.
4. Perkins, J. M. and Jinks, J. L., Environment and genotype-environmental components of variability. Heredity. 23: 339-356, 1968.
5. Finlay, K. W. and Wilkinson, G. N., The analysis of adaptation in a plant breeding programme. Aust. J. Agric. Res. 14: 742–754, 1963.
6. Shukla, G. K., Some statistical aspects of partitioning genotype-environmental components of variability. Heredity. 29: 237-245, 1972.
7. Wrick, G., Uber eine Method zur Refassung der Okologischen Streubreite in Feldversuchen. Flazenzuecht. 47: 92-96, 1962.
8. Shah Mohammadi, M., An Analysis of Genotype and Environment Interaction in Barley Varieties Based on AMMI Method and Comparison with Other Methods. MA thesis. Plant breeding. Tehran tarbiyat Modares university. P 132, 2003.
9. Yan, W., Hunt, L. A., Sheng, Q. and Szlavnics, Z., Genotype evaluation and

mega-environment investigation based on the GGE biplot. Crop Sci. 40: 597-605, 2000.
10. Van Eeuwijk, F. A., Denis, J. B. and Kang, M. S., Incorporate Additional Information on Genotypes and Environments in Models for Two-way Genotype-by-environment Tables. In: Genotype-by-Environment Interaction, Kang, M.S. and H.G. Gauch(Eds.). CRC Press, Boca Raton, FL. PP:15-49, 1996.
11. Baril, C. P., Denis, J. B., Wustman, R. and van Eeuwijk, F. A., Analyzing genotype-by-environment interaction in Dutch potato variety trials using factorial regression. Euphtica. 82: 149-155, 1995.
12. Gauch, H. G., Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs. Elsevier, Amsterdam,. 1992.
13. Thillainathan, M. and Fernandez, G. C. J., SAS applications for Tai's stability analysis and AMMI model in genotype×environmental interaction effects. J. Heredity. 92: 367-371, 2001.
14. Annicchiarico, P. and Perenzin, M., Adaptation patterns and definition of macro-environments for selection and recommendation of common wheat genotypes in Italy. Plant Breed. 113: 197-205, 1994.
15. Brancourt-Hulmel, M. and Lecomte, C., Effect of environmental varieties on genotype × environment interaction of winter wheat. Crop Sci. 43: 608-617, 2003.
16. Kaya, Y., Palta, C. and Taner, S., Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turk. J. Agric. For. 26: 275-279, 2002.
17. Lafitte, H. R. and Courois, B., Interpreting genotype×environment interaction for yield in Upland Rice. Crop Sci. 42: 1409-1420, 2002.
18. Tarakanovas, P. and Ruzgas. V., Additive main effects and multiplicative interactions analysis of grain yield of wheat varieties in Lithuania. Agron. Res. 4: 91-98, 2006.
19. Vargas, M. and Crossa, J., The AMMI analysis and graphing the biplot. Biometrics and Statistics unit, CIMMYT, 2000.
20. Zoble, R. W., Wright, M. J. and Gauch, H. G., Statistical analysis of a yield trial. Agron. J. 80:388-393, 1988.
21. Ebdon, J. S. and Gauch, H. G., Additive main effects and multiplicative interaction analysis of National Turfgrass performance trials. II genotype recommendation. Crop Sci. 42: 497-506, 2002.
22. Gauch, H. G. and Zobel, R.W., AMMI Analysis of Yield Trials. In: Genotype by Environment Interaction, Kang, M.S. and H.G. Gauch (Eds.). Boca Raton, CRC Press. PP: 85-122. 1996.
23. Richard, M. J., Zobel, R.W. and Gauch, H. G., Statistical analysis of a yield trial. Agronomy Journal, 80: 388-393, 1988.
24. Mohammadi, R., Armion, M., Shabani, A. and Daryaei, A., Identification of Stability and Adaptability in Advanced Durum Genotypes Using AMMI Analysis. Asian Journal of Plant Sciences. 6: 1261-1268, 2007.
25. Tai, G. C. C., Genotypic stability analysis and its application to potato regional trials. Crop Sci. 11: 184-190, 1971.
26. Rharrabti, Y., Garcia del Moral, L. F., Villegas, D. and Royo, C., Durum wheat quality in Mediterranean environments III. Stability and comparative methods in analyzing G × E interaction. Field Crops Research. 80: 141-146, 2003.
27. Annicchiarico, P., Joint regression vs AMMI analysis of genotype–environment interactions for cereals in Italy. Euphytica. 94, 53–62, 1997.
28. Wright, A. J., The analysis and prediction of some two factor interactions in grass breeding. J. Agric. Sci. 76: 301–306, 1971.
29. Nachit, M. M., Nachit, G., Ketata, H., Gauch, H. G. and Zobel, R. W., Use of AMMI and linear regression models to analyse genotype–environment interaction in durum wheat. Theoret. Appl. Genet. 83: 597-601, 1992.
30. Carbonell, S. A., Filho, J. A., Dias, L. A., Garcia, A. A. and Morais, L, K., Common bean genotypes and lines interactions with environments. Sci. Agic. *(Piracicaba brax.)*, 61: 169-177, 2004.
31. Sivapalan, S., Brein, L. O., Ferrara, G. O., Hollamby, G. L., Barclay, I. and Martin, P. J., An adaptation analysis of Australian and CIMMYT/ICARDA wheat germplasm in Australian production environments Aust. J. Agric. Res. 51: 903-915, 2000.
32. Cooper, M., Stucker, R. E., Delacy, L. H. and Harch, B. D., Wheat breeding nurseries, target environments and

indirect selection for grain yield. Crop Sci. 37: 1168-1176, 1997.
33. Bramel-Cox, P. J., Breeding for Reliability of Performance Across Unpredictable environments. In: Genotype-by -Environment Interaction, Kang, M.S. and H.G Gauch (Eds.). CRC Press, Boca Raton, FL. PP: 309-339, 1996.
34. Troyer, A. F., Breeding for widely adapted popular maize hybrids. Euphytica. 92: 163-174, 1996.
35. Kang, M. S., Using genotype-by-environment interaction for crop genotype development. Adv. Agron. 62: 199-252, 1997.
36. Lin, C. S. and Binns, M. R., Concepts and methods for analysis regional trial data for genotype and location selection. Plant Breed. Rev. 11: 271-297, 1994.