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GGE Biplot and AMMI Analysis of Yield Performance of Barley Genotypes across Different Environments in Iran

S. M. M. Mortazavian[1*], H. R. Nikkhah[2], F. A. Hassani[3], M. Sharif-al-Hosseini[4], M. Taheri[5], and M. Mahlooji[6]

ABSTRACT

Twenty promising barley lines were evaluated at seven research stations in Iran, during two cropping seasons. The analysis of variance on grain yield data showed mean squares of environments, genotypes and Genotype×Environment Interaction (GEI) as significant, respectively accounting accounted for 60.38, 4.52 and 35.09% of treatment combination sum of squares. To find out the effects of GEI on grain yield, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) and Sites Regression (SREG) GGE biplot analysis. Mega-environmental investigation is the most suitable way to utilize GEI. "Which-won-where" pattern was followed with three distinct mega-environments found in the barley assessment. Entries G5 and G6 showed general adaptability while G7 and G13 exhibited specific adaptation to Neishabour and Esfehan, respectively. Considering both techniques, genotype G1 revealed high grain yield along with yield stability. With regard to barley assessment, Esfehan was identified as a location with larger main effects interaction, making it a less predictable location for barley variety evaluation. The results finally indicated that AMMI and GGE biplot are informative methods to explore stability and adaptation pattern of genotypes in practical plant breeding and in subsequent variety recommendations. In addition, finding mega-environments help to identify the must suitable barley cultivars that can be recommended for areas within the mega-environment in either one or more test locations.

Keywords: Adaptation, Bi-linear method, SREG, Stability analysis.

INTRODUCTION

The considerable variation in crop circumstances, because of climatic conditions and different soil constituents, cause large annual variations in yield performance of crops. This is mainly because of low heritability of yield as a typical quantitative trait. Thus, grain yield could be affected by not only genotype, but also by environment as well by and genotype×environment interactions. In this context, Multi Environment Trials (METs) are important for studying yield stability, adaptation and as well for a prediction of yield performance of genotypes across environments. Typically, environment expresses most of the total yield variations, while genotype and Genotype×Environment Interaction (GEI) are usually less effective (Yan and Kang, 2003; Dehghani *et al.*, 2009). A large GEI variation usually hinders

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[1] Department of Agronomy and Plant Breeding Sciences, College of Abouraihan, University of Tehran, P. O. Box: 4117, Islamic Republic of Iran.

[*] Corresponding author; email: mortazavian@ut.ac.ir

[2] Seed and Plant Improvement Institute (SPII) of Iran, Karaj, Islamic Republic of Iran.

[3] Agriculture and Natural Resources Research Center of Fars, Shiraz, Islamic Republic of Iran.

[4] Agriculture and Natural Resources Research Center of Khorasan Razavi, Mashhad, Islamic Republic of Iran.

[5] Agriculture and Natural Resources Research Center of Tehran, Varamin, Islamic Republic of Iran.

[6] Agriculture and Natural Resources Research Center of Isfahan, Isfahan, Islamic Republic of Iran.

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the accuracy of yield estimation and reduces the correlation between genotypic and phenotypic values. GEI is a universal phenomenon when different genotypes are tested in a number of environments, and is an important issue for plant breeders and agronomists to predict cultivar behavior in different locations across different years prior to any cultivar recommendation. Cultivars can be selected as based upon rank differences or difference in amount. Depending upon a researcher's aim, specific or general adaptability may be considered as a main selection factor. Various methods have been introduced in trying to deduce cultivar reaction in different situations. Additive Main Effects and Multiplicative Interaction (AMMI) analysis is one of the popular parametric but multivariate methods to predict adaptation and stability of cultivars. The usefulness of the method to be applied to some different crops has been noted by many researchers (Abay and Bjørnstad, 2009; Alwala *et al.*, 2010; Annicchiarico *et al.*, 2010). Zobel *et al.* (1988) proposed the name AMMI first, but the actual statistical method itself goes back to work by Pike and Silverberg (1952) and Williams (1952). AMMI analysis uses Analysis of Variance (ANOVA), followed by Principal Component Analysis (PCA) applied to the sums of squares allocated through ANOVA to G×E interaction. This method leads to identification of stable and adapted genotypes whether specific or general. AMMI is useful in delineating mega-environments by determining the which-wins-where pattern, that is, which genotype wins in which environments (Gauch, 1992; Gauch and Zobel, 1997). AMMI is successfully employed to estimate stability, adaptation and G×E explanation of different crops. Because of multivariate nature of environment and effect on GEI, many scientists believe this method to be useful in exploiting and judging about variations (Sarial *et al.*, 2008; Adugna, 2010; Annicchiarico *et al.*, 2010; Hassanpanah, 2011). Some researchers have employed pattern analysis to identify genotype and environments with the same reaction. In this method, ordering and clustering methods are simultaneously applied (Chapman *et al.*, 1997; Kaya, *et al.* 2006; Mortazavian *et al.*, 2009; DeLacy *et al.*, 2010). Chapman *et al.* (1997) used this method and applied cluster analysis through Ward method based on squared Euclidean distance. Similar results have been reported between AMMI and GGE biplot analysis (Ilker *et al.*, 2009). GGE biplot methodology was initially developed for Multi-Environment variety Trials (MET) data analysis (Yan and Kang, 2003). Ilker *et al.* (2009) offered these two as reliable methods to evaluate maize experimental hybrids and as well identify proper test environments. AMMI analysis technique uses double centered data while in GGE biplot environment, centered data is made used of.

The present research was carried out to interpret Genotype-Environment (G×E) interaction effects on barley grain yield *via* AMMI analysis, find out stability and adaptation pattern of genotypes using visual assessment technique of GGE biplot, and determine the most suitable genotypes while combining a high level of grain yield with yield stability.

MATERIALS AND METHODS

Twenty diploid barley genotypes (Coded G1 to G20) were grown in national advanced regional yield trials. Pedigrees of investigated genotypes are presented in Table 1. The experiments were conducted across 14 environments, throughout two crop seasons, 2009-2010, over seven research stations namely:: Karaj, Neishabour, Esfehan, Zarghan, Varamin, Birjand, and Kerman. The characteristics of these sites are listed in Table 2. The experimental design employed, was a Randomized Complete Block Design (RCBD) of three replications. The experimental plots were 6 m in length with 1.2 m of width. All the cultural practices were carried out as recommended. The

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Table 1. Pedigree of the investigated genotypes.

	Genotypes	
Entry Code	Pedigree	Overall mean in all environments
G1	Check -1 (Nosrat)	6.098
G2	LB.Moghan//Gloria"S"/Copla"s"/3/Arar/L.527	5.409
G3	L.527/NK1272//Alanda/3/Alanda-01*2	5.838
G4	24569/3/L.640/Bgs//Cel	6.018
G5	Np106/Minn14133//Gva/Doluis/3/Numar	5.523
G6	Comp-74-K	5.630
G7	ZARJOU/80-5151//K-332/1	5.157
G8	Gloria"s"/Copal"S"//Alger	5.731
G9	TOCTE	5.394
G10	Hma-02//11012-2/CM67/3/Alanda	5.162
G11	Eldorado//Alanda/Zafraa	5.369
G12	Kitchin/SLB60-35	5.895
G13	TOCTE/ESPERANZA//QUINA	5.385
G14	Lignee 527/NK1272//JLB 70-63	6.103
G15	Mammut//Gloria'S'/Come'S'	5.491
G16	Kavir *2/Zdm 938	5.797
G17	Kavir /3/Roho//Alger/4/Kavir/Zdm 938	5.637
G18	Avt/Emir/Espe//SV.Mari/3/Rihane	5.520
G19	Reaserch/Kavir	5.487
G20	Check-2 (3rd EBYTM81-8(Deir Alla106//Hem/Bc/3/Rihane"S"))	5.683
	Mean	5.616

Table 2. Stations, geographical locations and overall mean of grain yield in each location.

Locations	Year	Location code	Latitude	Longitude	Altitude (m)	Annual rainfall (mm)	Min temp (C)	Max temp (C)	Mean grain yield (t ha^{-1})
Karaj	1st	Krj1	35 49 N	50 58 E	1300	309.9	8.8	21.4	4.98
	2nd	Krj2				221.6	9.8	22.9	7.19
Neishabour	1st	Nei1	36 22 N	58 82 E	1250	261.1	7.2	21.5	3.65
	2nd	Nei2				181.8	7.5	23	5.37
Esfehan	1st	Esf1	32 39 N	51 40 E	1590	104.6	9.5	24	6.86
	2nd	Esf2				199.4	9.8	24.5	7.17
Zarghan	1st	Zar1	29 46 N	52 44 E	1590	398.3	8.2	24.8	4.57
	2nd	Zar2				317.7	8.4	25.6	6.12
Varamin	1st	Var1	35 32 N	51 65 E	918	161.7	11.1	24.6	5.68
	2nd	Var2				129.2	11.4	25.9	5.72
Birjand	1st	Bir1	32 88 N	59 22 E	1491	219.3	8.6	23.8	5.94
	2nd	Bir2				75.7	9.3	25.7	4.42
Kerman	1st	Ker1	30 17 N	57 04 E	1755	122.6	8.1	25	5.73
	2nd	Ker2				78.3	7.4	25.7	5.23

plots' crops were harvested mechanically. Data on seed yield were converted to t ha^{-1} and combined analysis of variance across the test environments of stations *vs*. years was undertaken. Adaptability and phenotypic stability analyses were performed through AMMI method as described in Zobel *et al.* (1988) using the following statistical model:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + r_{ij} + \varepsilon_{ij}$$

The employed GGE biplot as based on the Sites Regression (SREG) linear-bilinear

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(multiplicative) model (Cornelius *et al.*, 1996) can be written as:

$$Y_{ij} = \mu + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where Y_{ij} is the mean response of genotype *i* in the environment *j*; μ is the overall mean; g_i the fixed effect of genotype *i* (i= 1, 2, ... g); e_j is the random effect of environment *j* (j= 1, 2, ... e); ε_{ij} is the average experimental error; the G×E interaction is represented by the factors; λ_k, a unique value or singular value of the k^{th} Interaction Principal Component Analysis (IPCA), (k= 1, 2, ... t, where t stands for the maximum number of estimable main components), α_{ik} is a singular value for the i^{th} genotype in the k^{th} IPCA, y_{jk} is a unique value of the j^{th} environment in the k^{th} IPCA; r_{ij} the error for the G×E interaction or AMMI residue (noise present in the data); and *k* the characteristic non-zero roots, *k= [1, 2, ... min (G - 1, E - 1)]*.

Analysis of variance was performed using SAS software (SAS Institute, 1996). AMMI analysis of G×E interaction and calculation of Root Mean Square Prediction Differences (RMSPD) were processed using MATMODEL 3.0 (Gauch, 1997).GGE biplot was employed to analyze the Multi-Environment Trial (MET) data and find "which-won-where" pattern of MET data. The model used for the GGE interaction biplot analysis was an environment-centered model with no-scaling.

RESULTS AND DISCUSSION

The combined analysis of variance for grain yield data is given in Table 3. All the sources except entry×year were significant. Significant interactions were resulted from the changes in the relative ranking of the genotypes or changes in the magnitudes of differences between genotypes from one environment to another. Significant difference between two years suggests the different reactions of genotypes from a year to another. The same interpretation can be expressed for locations. The significant G×L effect demonstrated different responses of genotypes to the variation in environmental conditions of location indicating the necessity of testing barley varieties at multiple locations. Analysis of variance

Table 3. Combined and AMMI analysis of variance for barley grain yield (t ha^{-1}) genotypes across environments.

SOV	*df*	*SS*	*MS*	*F* Value	Explained % of E SS
Replication (R)	2	0.854	0.427	ns 0.46	
Environment (E)	13	830.956	63.919	** 63.60	
Year (Y)	1	62.07	62.07	71.59 **	7.46
Location (L)	6	444.83	74.14	85.51 **	53.53
Y×L	6	324.06	54.01	62.29 **	38.99
Entry (G)	19	62.286	3.278	** 3.26	
G×L	114	265.80	2.33	2.69 **	
G×Y	19	12.39	0.65	0.75 ns	
G×L×Y	114	204.81	1.80	2.07 **	
G×E	247	482.99	1.96	1.95 **	Explained % of GEI SS
IPCA 1	31	138.222	4.45	4.42**	28.61
IPCA 2	29	119.737	4.128	4.10**	24.79
IPCA 3	27	66.891	2.47	2.45**	13.84
IPCA 4	25	49.135	1.965	1.95 **	10.17
Noise	135	110.402	0.817	0.81ns	22.85
Error	560	563.212	1.005	-	
Total	839	1890.59	-	-	
CV= 16.58%					

* and **: Significant difference at 0.05 and 0.01 probability level, respectively.

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revealed that the effects of Environments (E), Genotypes (G) and Genotype×Environment Interaction (GEI) are highly significant. Mean of Squares (MS) revealed genotypic differences towards adaptation to different environments, so genotypes may be selected for adaptation to specific environments. Environment significantly explained about 60.38% of the total sum of squares due to treatments (G + E+ GEI). A large yield variation, explained by environments, indicated that the environments were diverse and a major part of variation in grain yield can be resulted from environmental changes (Table 2). GEI significantly explained 35.09% of the treatments' variation in grain yield. Environment grain yield ranged from 3.65 t ha^{-1} in Neishabour during the first year to 7.19 t ha^{-1} in Karaj during the second year (Table 2). Among locations, Esfehan with grain yield of 7.02 t ha^{-1} ranked first and Neishabour with 4.51 t ha^{-1} yielded the lowest grain. Genotype grain yield ranged from 5.157 (G7) to 6.103 t ha^{-1} (G14) (Table 1). Only a small portion (4.52%) of the total sum of squares due to treatments was attributed to genotypic effects. High percentage of E and G×E interaction out of total variations of barley grain yield, implicates the low efficiency of indirect selection to improve potential yield, ignoring the GEI effect. Table 4 gives an overall view of the relative magnitudes of the genotype (G), location (L), and Genotype×Location interaction (GL) variance terms. Location was the most important source of yield variation in either year accounting for 58.67 and 58.33% of the total variance in both first and second years, respectively. The large yield variation due to L, which is irrelevant to cultivar evaluation and mega environmental investigation, justifies selection of SREG procedures for analyzing the MET data (Segherloo *et al.*, 2010). In combined analysis of variance, location had the greatest effect accounting for 53.53% of the environment sum of squares (Table 3). The GEI sum of squares was about 8 times that of genotypes, indicating the importance of this source of variation (Table 3). Other researchers found this high percentage G×E and noted the importance of stability analysis and splitting of GEI to its parts (Flores *et al.*, 1998; Ssemakula *et al.*, 2008; Najafian *et al.*, 2010). Crossover interaction is present if there is at least one 2×2 (G×E) quadruple in which the difference between genotypes has opposite signs in the two environments (Moghaddam and Pourdad, 2009). Analysis of data shows the crossover type of GEI because the ranking of genotypes was not the same across environments. Check cultivar (Nosrat) showed the highest yield at the highest yielding environment, Karaj in the second year (Data not shown). To more investigate, the GEI partitioning was done based on AMMI model. AMMI analysis is a valuable tool for identifying genotypes with either specific or wide adaptation and this could be an important advantage of this method as compared with such other methods as joint regression based methods (Kvitschal *et al.*, 2009; Mortazavian *et al.*, 2009; Najafian *et al.*, 2010). The potential of AMMI analysis for describing G×L and G×E interactions in different crops has been proved (Nachit *et al.*, 1992; Yau *et al.*, 1995) on wheat, (Fox *et al.*, 1990) on triticale, (Adugna, 2008) on sorghum, (Argillier *et al.*, 1994) maize, (Annicchiarico

Table 4. ANOVA results of barley grain yield during the two years of evaluation.

Year	Source	DF	Sum of squares	Explained (%)
First	Location (L)	6	391.02	58.67
	Genotypes (G)	19	42.96	6.44
	GL	114	232.44	34.87
Second	Location (L)	6	377.86	58.33
	Genotypes (G)	19	31.70	4.89
	GL	114	238.15	36.76

et al., 2010) on Lupin and (Voltas *et al.*, 1999; Rodriguez *et al.*, 2008) on barley. This method revealed the first four terms of AMMI as significant, using an approximate *F*-statistics (Gollob, 1968). Computing the noise and signal of the model revealed that the AMMI model with a first multiplicative term was adequate for cross-validation of the yield variation as explained through GEI. Regarding the data, Root Mean Square Prediction Differences (RMSPD) of different AMMI models, Ockham's Hill was extremely flat. For instance, RMSPD for AMMI0 was 1,162 but for AMMI2, it amounted to 1,179, which differs by only one in the third decimal place–about a 1% difference. Several researchers proposed using first two IPC axes and believed these two to be enough for AMMI model (Gauch and Zobel, 1996; Ilker *et al.*, 2009). On the other hand, simpler AMMI1 model also merits because AMMI1 often generates as many mega-environments as practical agricultural considerations. Thus, the approximation of actual interaction pattern of the 20 barley genotypes with 14 environments was best cross-validated with the first multiplicative terms of genotypes and environments that were easily visualized with the aid of a biplot (Figure 1). AMMI1 model is a rank 2 model, that is, it has two numbers for each genotype and each environment (namely a mean and an IPC score) (Gauch ,1992). GGE biplot defines an ideal genotype, based on both mean performance and stability across environments (Aina *et al.*, 2009). The GGE biplot is superior to the AMMI1 graph in mega-environment analysis and genotype evaluation because it explains more G+GE than AMMI (Yan *et al.*, 2007). The GE biplot for AMMI1 explained about 75% of the yield variation. In this biplot, the abscissa showed the main effects and the ordinate the first multiplicative axis term (PC1). The solid line connecting environment markers indicated the year-to-year variation within an individual location. The genotypes close to ordinate expressed general adaptation, whereas the further genotypes depicted more specific adaptation to environments (Ebdon and Gauch, 2002). Therefore, genotypes like G19 and G13 with large absolute PC1 scores were better

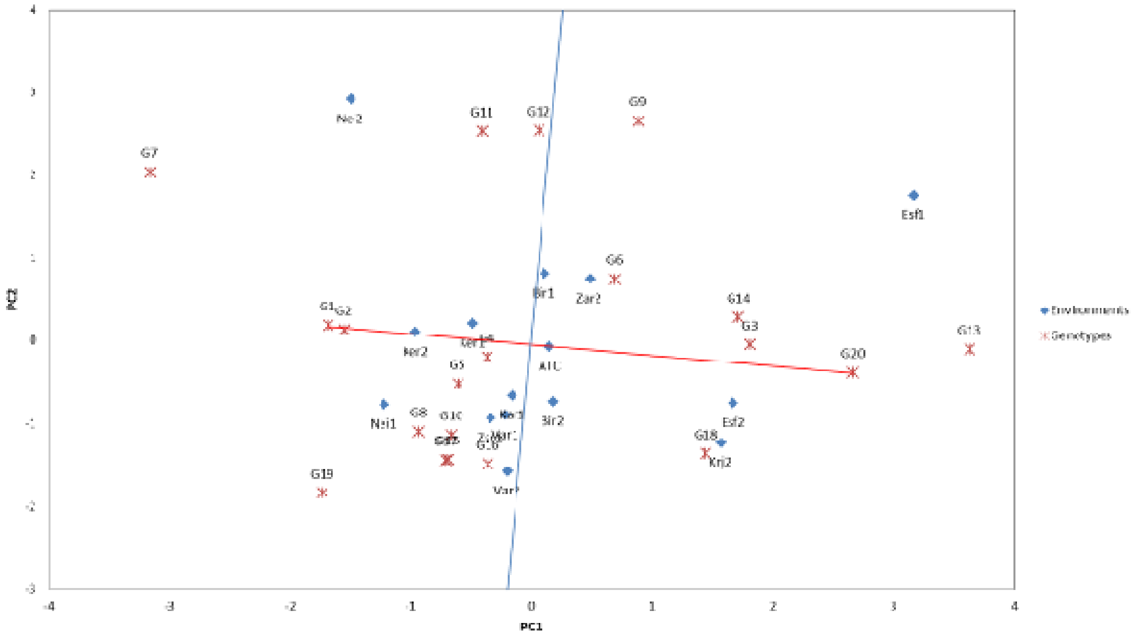

Figure 1. Comparison of two check (G1 and G20) cultivars in different environments. GGE biplot obtained from Site REGression (SREG) analysis.

adapted to Neishabour and Esfehan in the first year, respectively (Figure 2). Specific adaptation can be characterized as positive coincidence of plant phenology with such environmental reducing events as frost damage in winter and/or terminal drought. So, in a particular area with a well characterized environment, specific adaptation is the key point for yield improvement (Najafian *et al.*, 2010). The best genotype should combine high yield and stable performance across a range of production environments. Among the three high yielding genotypes G1, G4 and G14, G4 can be best judged based on stability and grain yield with combined low absolute PC1 score and high yield. Birjand exhibited the relatively smaller variation in the interaction (PC1 score) from year to year, while Esfehan had the largest (Figure 2). This indicated that the relative ranking of genotypes were more stable in Birjand than in Esfehan. Esfehan was described as a location that combined larger main effects with larger interaction effects making it a less predictable location for barley variety evaluation. Pattern analysis, employs both ordination and classification techniques. Using pattern analysis in AMMI model, genotype and environment of the same response will be grouped (Farshadfar, 2008; Pourdad and Mohammadi, 2008). Pattern analysis can be employed to recognize genotypes with the same response pattern in different environments because of co-exploiting of clustering and ordering merits. By use of this method, genotypes can be selected not only with regard to the stability but also concerning to the high yield. This beneficence has been used successfully in different studies (Chapman *et al.*, 1997; Bertero *et al.*, 2004; Mortazavia *et al.,* 2009). Pattern analysis of genotypes and environments based on first IPC and grain yield showed three distinct clusters. For example, results showed G13 and Esfehan in first year in the same cluster and G4, G5 and G16 with BI2, NE2, KR1 and VA1 in a distinct group. Biplot of IPC1 and IPC2 covers 53.2% of GE interaction (Figure 3).

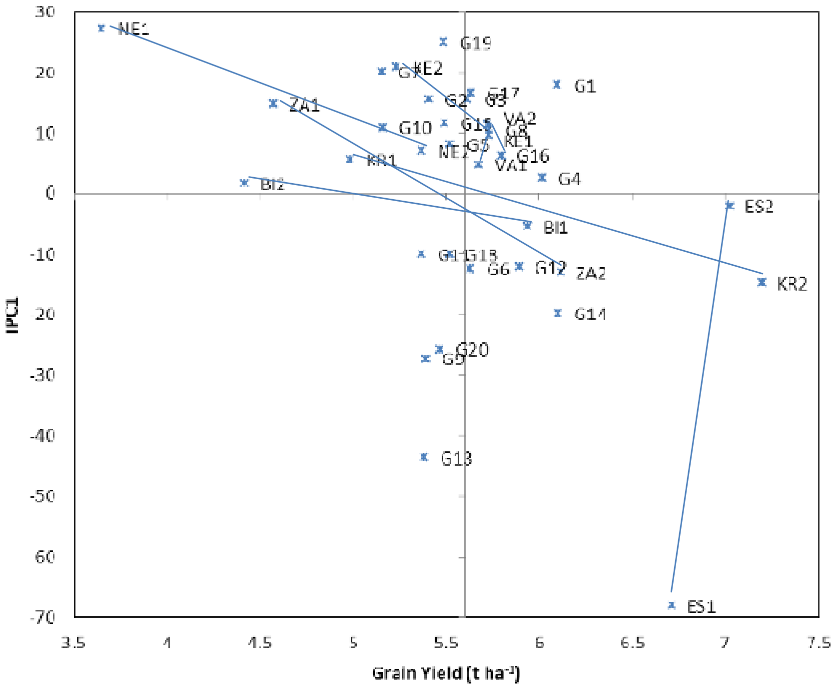

Figure 2. Biplot of mean grain yield (t ha^{-1}) and first IPCA axis (AMMI1) of barley genotypes and environments.

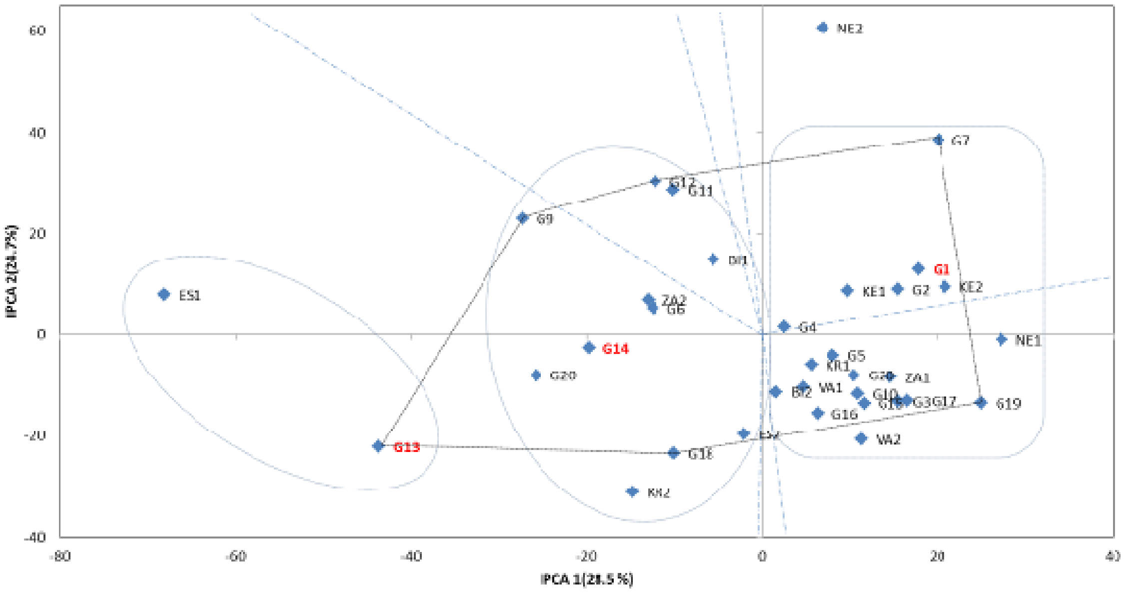

Figure 3. Pattern analysis biplot of first two IPC components of AMMI model shows "which-won-where" results. The winner genotypes in each mega environment are G13, G14 and G1.

Genotypes located near the plot origin were less responsive than the genotypes farther from the center of biplot. Genotypes G13, G9, G11, G12, G7, G19 and G18 benefit from specific adaptations. The genotypes G7 and G13 have the specific adaptation to NE2 and ES1, respectively because of their angle being acute, i.e. less than 90° and their GE interaction positive. Figure 3, shows pattern analysis and also "which-won-where" pattern of genotypes and locations. The locations fell into three sector or mega-environments: G1 was the best genotype for the first sector. Genotype G14 wins in the second sector and while genotype G13 in the third sector (Table 5). A criterion that is required to suggest different mega-environments is higher variation among-groups rather than within-groups. It is a common criterion for clustering (Yan and Kang, 2003). Second, there are different winning cultivars in different test environments. As shown in Figure 2, all the genotypes and environments are clustered in three groups, based upon pattern analysis. Rectangular segment contains two vertex cultivars, G7 and G19, but among genotypes in this part G1 yielded the highest. Then, Genotype G1 is the check cultivar and representative of the best genotype in sectors G7 and G19. The majority of locations including NE1, ZA1, KE1, KR1, VA1, KE2, VA2, NE2, and BI2 were located in mega-environment 1 in which genotype 1 is the winner. The performance of genotypes in relation to check cultivars (G1 and G20) is reflected in Figure 1. A connector line was drawn to connect the checks, with

Table 5. Winning genotypes based on SREG analysis of variance for grain yield in 3 mega-environments.

Mega-environment	Environment		Mega-environment	Env.	Mega-environment	Env.
G1	Nei1	Nei2	G14	Bir1	G13	Esf1
	Ker1	Ker2		Esf2		
	Var1	Var2		Zar2		
	Zar1	Bir2		Kar2		
	Kar1					

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perpendicular lines made. As shown in Figure 3, G1 yielded more than G20 in Kerman, Neishabour and Varamin in both years while G20 yielded more than G1 in Esfehan in both years and in Zarghan and Karaj during the second year. Genotype G1 yields higher in most environments than G20. The GGE biplot of SREG analysis was employed to show the relative adaptation of genotype with the highest grain yield, G14, across environments (Figure 4). The length of environment projections onto G14 axis assessed the performance of G14 at different environments, relative to other genotypes. The broken perpendicular line to the G14 axis and passing through the origin, divided the environments where G14 would yield above and below averages. Hence, G14 would yield the highest in Esfehan in both years followed by Karaj in the second year, Zarghan in the second year and Birjand in both years. Figure 5 shows the "Average Environment Coordination" (AEC) of the GGE biplot for 20 barley genotype evaluations regarding the mean *vs.* stability. This AEC is based on genotype-focused Singular Value Partitioning (SVP) (Yan and Kang, 2003). Because of the inner-product property of the biplot, the projections of the genotype markers on the “average environment axis” are proportional to the rank-two approximation of the genotype means representing the main effects of the genotypes (Yan *et al.*, 2007). Genotype G4 has the shortest AEC ordinate so it is the most stable genotypes while G9 is the least stable genotype placed above average mean performance. With regard to both stability and high mean performance G13, G20, G3, G18, G14, G6 and G9 are preferred. Considering AMMI1 and GGE SREG results, G14 and G1 are recommended as the ideal ones among the genotypes.

CONCLUSIONS

Having yield stability and economic profitability is an important and complicated issue for breeders and farmers. Successful cultivars should be adapted to a broad range of environmental conditions to produce consistent yields everywhere. Hence, the information on GE interaction and stability is of paramount importance for barley breeders and farmers. The genotypes used in

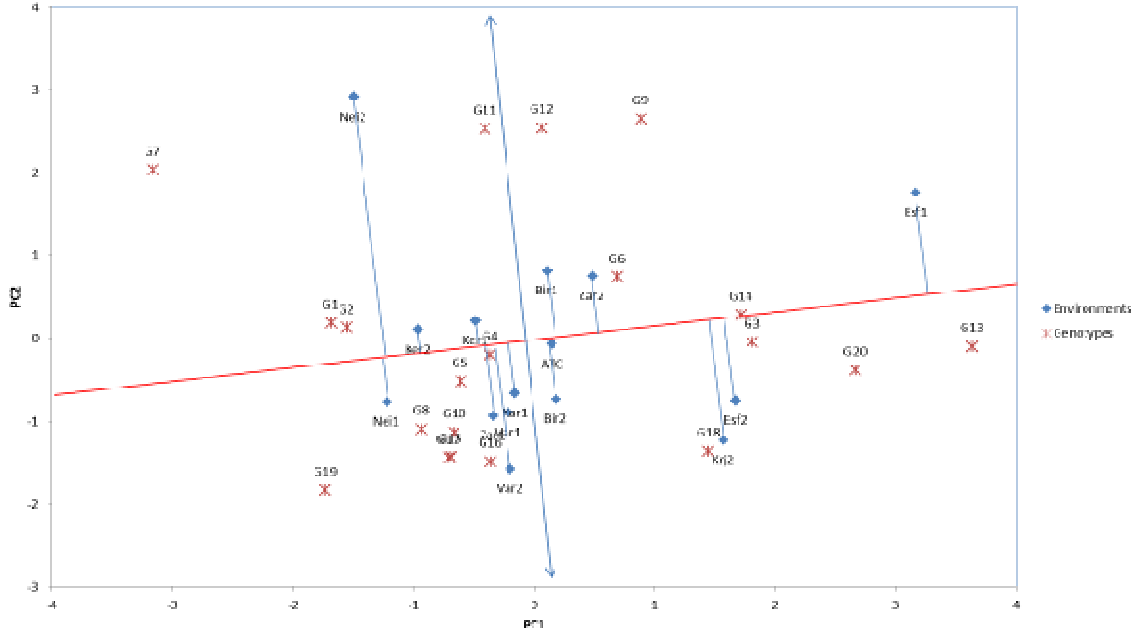

Figure 4. GGE biplot of SREG analysis showing the performance of the genotype with the highest grain yield, G14, at different locations.

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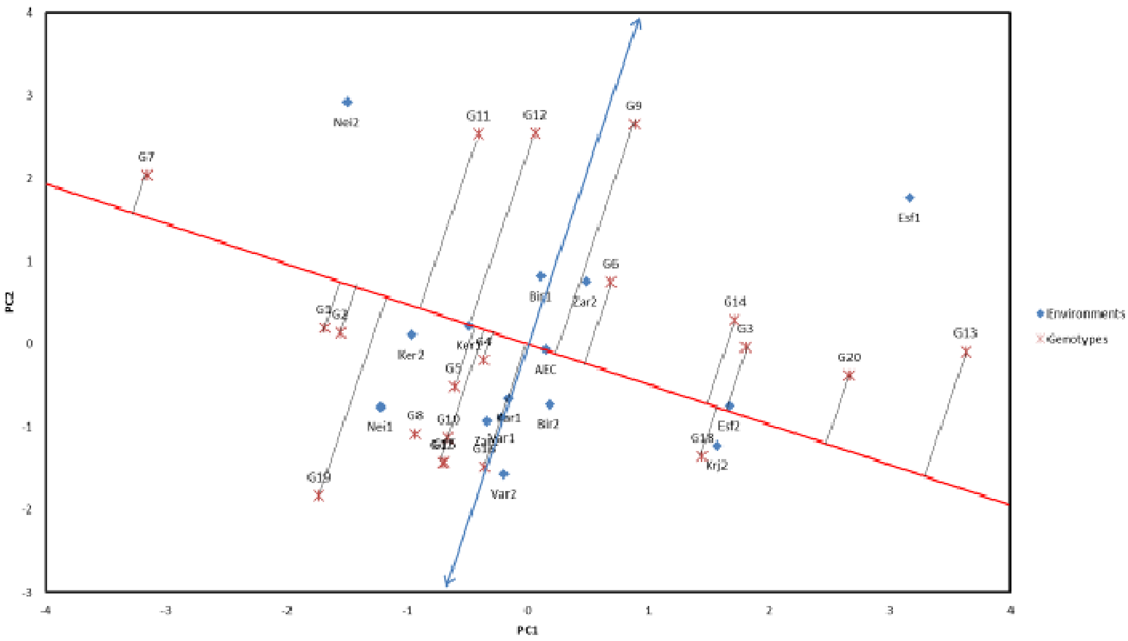

Figure 5. The mean *vs.* stability view of GGE biplot for the evaluated barley genotypes.

this study did not exhibit a uniform stability and response pattern to different environments. It was shown throughout the study that the GGE biplot graphic analysis complements the AMMI biplot stratification, defining mega-environments and the cultivars that optimize performance in such mega-environments. Analysis through GGE biplot approach in the present research revealed 3 barley mega-environments in Iran. Finding mega environments encompasses several advantages. Parsimony of evaluation cost is equivalent to an important profit. Genotype assessment can be done only in one location in each mega environment instead of in all the locations. For instance, G1 has specific adaptation to Kerman, Varamin and Neishabour while G14 is adapted to Zarghan and Karaj. Drawing "Which-Won-Where" pattern as based on environment values is more informative than locations because it involves both locations and years while retaining key information regarding years. The more climatic variations in a specific location, the less precise the mega environment identifications. Criterion to recommend a location as a profit mega environment is as large as enough to the presence of a winning genotype during different years in the same location. In this way, small mega environment 3 could be ignored because G13 wins only in one environment, Esf 1, and in the other year, Esf 2, genotype G14 is the winner. The most interesting genotype is G1 that wins in nine environments, including Neishabour, Kerman, and Varamin in both years. For the other four locations, G14 wins in only one of the two years, mostly with G1 winning in the other year, except for Esfehan 1st year. It should be noticed that GE interactions associated with locations are relatively repeatable and increase mega-environments, whereas GE associated with years are relatively unrepeatable and decrease mega-environments. Then, the best recommendation would be G1 throughout the test region. In a comparison of two control genotypes, G1 (Nosrat) benefits from similar responses with more genotypes rather than G20 and can be proved by more crowded of genotypes in the G1 part rather than G20. This conclusion is true for adaptation to different environments, too. Different researches on evaluation of barley genotypes under drought stressed conditions have identified Nosrat genotype as tolerant (Zare, 2012; Eivazi, *et al.*, 2013). In case of stress damages, such as drought or freezing damage, tolerant genotypes change their phonological development to escape or bear the stringency conditions and in this case they will show specific adaptation to locations of the stress conditions. Although barley is frequently considered by farmers as the safest and easiest annual cool-season crop to grow for grain yet, it can be reduced in grain yield. The lowest mean grain yield is related to Neishabour 2nd year that has the lowest minimum and maximum temperatures during the cropping season. Neishabour is a temperate to cold location with the risk of frost damage, especially to spring genotypes. Then genotypes adapted to this location are of the specific adaptation to low temperatures. Stations of Esfehan 1st year and Birjand 2nd year with the lowest rainfall and high temperatures are among the drought-prone regions, with water deficit being one of their characteristics especially in terminal stages of barley growth. Then genotypes with specific adaptation to these stations would be the drought tolerant genotypes.

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REFERENCES

1. Abay, F. and Bjørnstad A. 2009. Specific Adaptation of Barley Varieties in Different Locations in Ethiopia. *Euphytica*, **167(2)**: 181-195.
2. Adugna, A. 2008. Assessment of Yield Stability in Sorghum Using Univariate and Multivariate Statistical Approaches. *Hereditas*, **145(1)**: 28-37.
3. Adugna, A. 2010. Assessment of Yield Stability in Sorghum. *Afr. Crop Sci. J.,* **15(2)**: 83-92.
4. Aina, O., Dixon, A., Paul, I. and Akinrinde, E. 2009. G×E Interaction Effects on Yield and Yield Components of Cassava (Landraces and Improved) Genotypes in the Savanna Regions of Nigeria. *Afr. J. Biotechnol.,* **8(19)**: 4933-4945.
5. Alwala, S., Kwolek, T., McPherson, M., Pellow, J. and Meyer, D. 2010. A Comprehensive Comparison between Eberhart and Russell Joint Regression and GGE Biplot Analyses to Identify Stable and High Yielding Maize Hybrids. *Field Crops Res.,* **119**: 225-230.
6. Annicchiarico, P., Harzic, N. and Carroni, A. M. 2010. Adaptation, Diversity, and Exploitation of Global White Lupin (*Lupinus albus* L.) Landrace Genetic Resources. *Field Crops Res.,* **119 (1)**: 114-124
7. Argillier, O., Hébert, Y. and Barrière, Y. 1994. Statistical Analysis and Interpretation of Line ×Environment Interaction for Biomass Yield in Maize. *Agron. Sustain. Dev.,* **14(10)**: 661-672.
8. Bertero, H., De La Vega, A., Correa, G., Jacobsen, S. and Mujica, A. 2004. Genotype and Genotype-by-environment Interaction Effects for Grain Yield and Grain Size of Quinoa (*Chenopodium quinoa* Willd.) as Revealed by Pattern Analysis of International Multi-environment Trials. *Field Crops Res.*, **89(2-3)**: 299-318.
9. Chapman, S., Crossa, J. and Edmeades, G. 1997. Genotype by Environment Effects and Selection for Drought Tolerance in Tropical Maize. I. Two Mode Pattern Analysis of Yield. *Euphytica*, **95(1)**: 1-9.
10. Cornelius, P., Crossa, J., Seyedsadr, M., Kang, M. and Gauch, H. 1996. Statistical Tests and Estimators of Multiplicative Models for Genotype-by-environment Interaction. Genotype-by-environment Interaction. CRC Press, Boca Raton, FL, PP.199-234.
11. Dehghani, H., Sabaghnia, N. and Moghaddam, M. 2009. Interpretation of Genotype-by-environment Interaction for Late Maize Hybrids' Grain Yield Using a

Biplot Method. *Turk. J. Agric. For.,* **33(2)**: 139-148.

12. DeLacy, I., Kaul, S., Rana, B. and Cooper, M. 2010. Genotypic Variation for Grain and Stover Yield of Dryland (Rabi) Sorghum in India 2. A Characterisation of Genotype×Environment Interactions. *Field Crops Res.,* **118(3)**: 236-242.
13. Ebdon, J. and Gauch, H. 2002. Additive Main Effect and Multiplicative Interaction Analysis of National Turfgrass Performance Trials. I. Interpretation of Genotype×Environment Interaction. *Crop Sci.*, **42(2)**: 489-496.
14. Eivazi, A. R., Mohammadi, S., Rezaei, M., Ashori, S. and Pour, F. 2013. Effective Selection Criteria for Assessing Drought Tolerance Indices in Barley (*Hordeum vulgare* L.) Accessions. *Intl. J. Agron. Plant. Prod.,* **4**:813-821.
15. Farshadfar, E. 2008. Incorporation of AMMI Stability Value and Grain Yield in a Single Non-parametric Index (GSI) in Bread Wheat. *Pak. J. Biol. Sci.*, **11(14)**: 1791-1796.
16. Flores, F., Moreno, M. and Cubero, J. 1998. A Comparison of Univariate and Multivariate Methods to Analyze G×E Interaction. *Field Crops Res.,* **56(3)**: 271-286.
17. Fox, P., Skovmand, B., Thompson, B., Braun, H. and Cormier, R. 1990. Yield and Adaptation of Hexaploid Spring Triticale. *Euphytica*, **47(1)**: 57-64.
18. Gauch, H. and Zobel, R. W. 1997. Identifying Mega-environments and Targeting Genotypes. *Crop Sci.*, **37(2)**: 311-326.
19. Gauch, H. G. 1992. Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs.Amsterdam.
20. Gauch, H. G. 1997. MATMODEL Version 3.0: Open Source Software for AMMI and Related analyses. Crop and Soil Sciences, Cornell University.
21. Gauch, H. G. and Zobel, R. W. 1996. AMMI Analysis of Yield Trials. In: "*Genotype-by-environment Interaction*", (Eds.):. Kang, M. S. and Gauch, H. G.. CRC Press, Boca Raton, FL, PP. 85-122.
22. Gollob, H. F. 1968. A Statistical Model which Combines Features of Factor Analytic and Analysis of Variance Techniques. *Psychometrika,* **33(1)**: 73-115.
23. Hassanpanah, D. 2011. Analysis of G×E Interaction Using the Additive Main Effects and Multiplicative Interaction (AMMI) in Potato Cultivars. *Afr. J. Biotechnol.,* **10(2)**: 154-158.
24. Ilker, E., Tonk, F. A., Caylak, O., Tosun, M. and Ozmen, I. 2009. Assessment of Genotype× Environment Interactions for Grain Yield in Maize Hybrids Using AMMI and GGE Biplot Analysis. *Turk. J. Field Crops*, **14(2)**: 123-135.
25. Kaya, Y., Akcura, M., Ayranci, R. and Taner, S. 2006. Pattern Analysis of Multi-environment Trials in Bread Wheat. *Commun. Biometry Crop Sci.*, **1(1)**: 63-71.
26. Kvitschal, M. V., Vidigal Filho, P. S., Scapim, C. A., Gonçalves-Vidigal, M. C., Sagrilo, E., Pequeno, M. G. and Rimoldi, F. 2009. Comparison of Methods for Phenotypic Stability Analysis of Cassava (*Manihot esculenta* Crantz) Genotypes for Yield and Storage Root Dry Matter Content. *Braz. Arch. Biol. Techn.*, **52**: 163-175.
27. Moghaddam, M. and Pourdad, S. 2009. Comparison of Parametric and Non-parametric Methods for Analysing Genotype×Environment Interactions in Safflower (*Carthamus tinctorius* L.). *J. Agr. Sci.*, **147(5)**:601.
28. Mortazavian, M., Bihamta, M., Zali, A., Taleii, A. and Chogan, R. 2009. Adaptability and Stability of Grain Yield Maize (*Zea mays*) Hybrids by Using Genotype Pattern Analysis Method (AMMI). *Iran. J. Field Crop Sci.,* **40(1)**: 147-159.
29. Nachit, M. M., Nachit, G., Ketata, H., Gauch, H. G. and Zobel, R. W. 1992. Use of AMMI and Linear Regression Models to Analyze Genotype-environment Interaction in Durum Wheat. *Theor. Appl. Genet.*, **83(5)**: 597-601.
30. Najafian, G., Kaffashi, A. and Jafar-Nezhad, A. 2010. Analysis of Grain Yield Stability in Hexaploid Wheat Genotypes Grown in Temperate Regions of Iran Using Additive Main Effects and Multiplicative Interaction. *J. Agr. Sci. Tech.,* **12**: 213-222.
31. Pike, E. W., Silverberg, T. R., Pike, E. and Silverberg, T. 1952. Designing Mechanical Computers. *Machine Design*, **24**:131-137.
32. Pourdad, S. S. and Mohammadi, R. 2008. Use of Stability Parameters for Comparing Safflower Genotypes in Multi-environment Trials. *Asian J. Plant Sci.,* **7**: 100-104.
33. Rodriguez, M., Rau, D., Papa, R. and Attene, G. 2008. Genotype by Environment Interactions in Barley (*Hordeum vulgare*

L.): Different Responses of Landraces, Recombinant Inbred Lines and Varieties to Mediterranean Environment. *Euphytica*, **163**:231-247.

34. Sarial, A., Haile, J., Assefa, S. and Sareen, S. 2008. AMMI Analysis for Stability and Location Effect on Grain Yield and Its Components of Durum Wheat Genotypes. Sydney University Press, PP??
35. SAS Institute Inc. 1996. *SAS R User's Guide: Statistics.* Version 6, Cary.
36. Segherloo, A. E., Sabaghpour, S. H., Dehghani, H. and Kamrani, M. 2010. Screening of Superior Chickpea Genotypes for Various Environments of Iran Using Genotype Plus Genotype×Environment (GGE) Biplot Analysis. *J. Plant Breed.Crop Sci.,* **2(9)**: 286-292.
37. Ssemakula, G., Dixon, A. and Maziya-Dixon, B. 2008. Stability of Iron and Zinc Concentrations in Selected Genotypes of Cassava (*Manihot esculenta* Crantz) Tuberous Roots. *J. Food Agric. Environ.*, **6(3&4)**: 362-367.
38. Voltas, J., Van Eeuwijk, F., Sombrero, A., Lafarga, A., Igartua, E. and Romagosa, I. 1999. Integrating Statistical and Ecophysiological Analyses of Genotype by Environment Interaction for Grain Filling of Barley. I. Individual Grain Weight. *Field Crops Res.*, **62**:63-74.
39. Williams, E. J. 1952. The Interpretation of Interactions in Factorial Experiments. *Biometrika*, **39**:65-81.
40. Yan, W. 2002. Singular-value Partitioning in Biplot Analysis of Multienvironment Trial Data. *Agron. J.*, **94**: 990-996.
41. Yan, W. and Kang, M. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. CRC Press, Boca Raton, FL, 288 PP.
42. Yan, W., Kang, M. S., Ma, B., Woods, S. and Cornelius, P. L. 2007. GGE Biplot *vs.* AMMI Analysis of Genotype-by-environment Data. *Crop sci.,* **47**: 643-655.
43. Yau, S. K., Nachit, M. M., Ryan, J. and Hamblin, J. 1995. Phenotypic Variation in Boron-Toxicity Tolerance at Seedling Stage in Durum Wheat (*Triticum durum*). *Euphytica,* **83**: 185-191.
44. Zare, M. 2012. Evaluation of Drought Tolerance Indices for the Selection of Iranian Barley (*Hordeum vulgare*) Cultivars. *Afr. J. Biotechnol.*, **11**:15975-15981.
45. Zobel, R. W., Wright, M. J. and Gauch, H. G. 1988. Statistical Analysis of a Yield Trial. *Agron. J.*, **80**:388-393.

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تجزیه امی و GGE بای پلات عملکرد ژنوتیپ های جو در محیط های مختلف ایران

س. م. م. مرتضویان، ح. ر. نیکخواه، ف. ا. حسنی، م. شرف الحسینی، م طاهری، و م. مهلوجی

چکیده

بیست و دو لاین امیدبخش جو در هفت ایستگاه مختلف در ایران طی دو سال مورد ارزیابی قرار گرفتند. تجزیه واریانس عملکرد دانه نشان داد که میانگین مربعات محیط، ژنوتیپ و برهمکنش ژنوتیپ در محیط معنی دار بوده و بترتیب ۶۰/۳۸ درصد ، ۴/۵۲ درصد و ۳۵/۰۹ درصد از مجموع مربعات تیمار را تشکیل می دهد. به منظور پی بردن به اثرات متقابل ژنوتیپ در محیط ، تجزیه اثرات متقابل ضربی و اثرات اصلی جمع پذیر (AMMI) و بای پلات SREG GGE صورت گرفت. تجزیه الگو جهت بدست آوردن اطلاعات بیشتر مورد استفاده قرار گرفت. با توجه به RMSPD داده ها، مدل امی ۱

انتخاب شد. الگوی "which-won-where" دنبال شد و سه ابرمحیط مشخص شد. ژنوتیپ های G5 و G6 سازگاری عمومی نشان داده و پایدارترین ژنوتیپ ها در آزمایش شناخته شدند درحالیکه سایر ژنوتیپ ها سازگاری خصوصی نشان دادند نظیر G7 و G13 که به ترتیب سازگاری خصوصی به نیشابور و اصفهان نشان دادند. با توجه به نتایج دو روش G4 بدلیل عملکرد بالا و پایداری عملکرد انتخاب شد. اصفهان بعنوان مکانی شناخته شد که بیشترین اثرات اصلی و اثرات متقابل را داشته و لذا جهت ارزیابی ارقام جو کمترین قابلیت پیش بینی را داراست. نتایج ازمایش نشان داد که روش امی و بای پلات GGE روش های کارامدی در شناسایی الگوی سازگاری و پایداری ژنوتیپ ها در برنامه های اصلاحی و توصیه رقم هستند.

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