

STABILITY ANALYSIS OF BREAD WHEAT LANDRACES AND LINES USING BIOMETRICAL GENETIC MODELS

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In order to evaluate yield stability of twenty genotypes of bread wheat, an experiment was conducted in randomized complete block design (RCBD) with three replications under irrigated and rainfed conditions in Razi University of Kermanshah for three years (2011-2013). Combined analysis of variance showed highly significant differences for the GEI. Stability determined by AMMI analysis indicated that the first two AMMI model (AMMI1–AMMI2) were highly significant ($P<0.01$). The GEI was three times higher than that of the genotype effect. The results of Biplot AMMI₂ showed that, genotypes WC-47359, WC-47472, WC-4611, WC-47388 and WC-47403 had general adaptability. Based on the ASV and GSI, the genotypes number WC-47403 and WC-47472 revealed the highest stability. GGE biplot analysis of yield displaying main effect G and GEI justified 57.5 percent of the total variation. The first two principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 34.3, 23.2 of GGE sum of squares (SS), respectively. Genotypes WC-47403, PISHGAM2 exhibited the highest mean yield and stability. Based on the results obtained the best genotypes were WC-47403, PISHGAM2, WC-4968, WC-47472 and WC-47528 for breeding programs.

Key words: Adaptability, AMMI and GGE biplot analyses, Genotype × Environment Interaction, Yield Stability

Abbreviations:

RCBD (randomized complete block design); AMMI (additive main effect and multiplicative interaction); ANOVA (analysis of variance); ASV (AMMI stability value); GE (genotype environment); GEI (genotype environment interaction); IPCA (interaction principal component axes); PCA (principal component analysis); TSS (total sum of squares); GSI (Genotype Selection Index).

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INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a major food grain in Iran, thus improving yield and yield stability is the principal objective of wheat breeding programs (RAM *et al.*, 2007). To study wheat genotypes with wide or specific adaptation to different environments, multi-location yield trails are grown each year. These have resulted to empirical identification of superior cultivars, some of which have been released in several countries (BASFORD *et al.*, 2004). The environments involve a wide range of photoperiods and temperatures which could cause large genotype (G) \times environment (E) interactions (GEI), specifically in the semi-arid areas. Large crossover-type GEI, especially among high yielding lines gives incorrect suggestions to farmers across all test environments. Quantification of GEI and comprehension its physiological bases are needed to breed effectively for superior environments (THOMASON and PHILLIPS, 2006). Most yield trails are used only to determine which cultivars give the highest average seed yield, and therefore valuable recommendation for planting by farmers.

Understanding the structure and nature of GEI is important in plant breeding programs because a significant GEI can seriously impair efforts in selecting superior genotypes relative to new crop introductions and cultivar improvement programs (SHAFII and PRICE, 1998). The detect of GEI in trials has led to the development of procedures that are generically called stability analyses. The available numerous stability statistics to breeders and to the production agronomist provide different strategies and approaches of dealing with GEI. Stability is an important concept for plant breeders interested in analysing GEI data (DENIS *et al.*, 1996; AYED *et al.*, 2016).

Stability analysis could be introduced by graphical and non-graphical methods. Graphical methods including biplot extracted from AMMI, GGE biplot and performance plot. Non graphical methods consist of parametric and non-parametric approaches. Two types of biplots, the AMMI biplot (GAUCH, 1988; GAUCH and ZOBEL, 1997) and the GGE biplot (YAN *et al.*, 2000; MA *et al.*, 2004) have been made widely to visualize genotype \times environment interaction. Compared to the methods of joint regression and type B genetic correlation, AMMI as well as GGE biplot analysis integrates some features from all of them. The differences of the two methods, GGE biplot analysis is based on environment-centred principal component analysis (PCA), whereas AMMI analysis is referred to double centred PCA (YAN *et al.*, 2007). A new approach known as genotype selection index (GSI) was recommended by FARSHADFAR (2008). Using AMMI stability value (ASV) and mean yield, GSI incorporates both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with stability and high mean yield.

The additive main effects and multiplicative interactions (AMMI) and genotype plus GE interaction (GGE) biplot models are introduced as a powerful tools for effective analysis, identify high yielding and adapted cultivars and interpretation of MET data in plant breeding programs (SABAGHNIA *et al.*, 2013; MOHAMED *et al.*, 2013; NAROU RAD *et al.*, 2013; HOMMA, 2015; BORNHOFEN *et al.*, 2017; ASHRAFUL ALAM *et al.*, 2017).

The objectives of this study were (i) to apply AMMI models and GGE biplot to identify bread wheat genotypes that have both high mean yield and stable yield performance across different environments for semi-arid areas of Iran, and (ii) to study the similarities, relationships and dissimilarities among yield - stability statistics carried out to quantify GE interaction effects on yield and to determine stable entries within the genotypic pool used in this study.

MATERIALS AND METHODS

Experimental Layout and Genetic Materials

In order to determine stability of 20 bread wheat cultivar or lines (Table 1) field experiments were conducted for three consecutive years (2011- 2013) under two different conditions (irrigated and rainfed) at Kermanshah (34° 21' N latitude, 47° 9' E longitude and 1319 m altitude), Iran. The experimental layout at each environment was randomized complete block design with three replications. Climate of the region is classified as semi-arid with mean annual rainfall of 379.3 mm. Minimum and maximum temperatures at the research station were 5.9 and 22.6°C, respectively. Each plot consisted of five rows with 5 meter length. Row distance was 20 cm with seed density 400 per m². Data on seed yield were taken from the middle two rows of each plot. The environments were considered as random factors while genotypes as fixed factors.

Table1. Genotype code and the name of 20 bread wheat lines and cultivars

No.	Code	Name	Mean yield	
			irrigated	rainfed
1	G1	Geravandi-17	527.04	190.33
2	G2	WC-47536	486.03	254.14
3	G3	WC-4919	453.17	143.29
4	G4	WC-4868	422.54	175.95
5	G5	WC-5046	397.76	251.26
6	G6	WC-4995	332.96	137.91
7	G7	Pishgam-1	564.15	139.96
8	G8	WC-4536	394.21	144.82
9	G9	Pishgam-2	545.86	169.95
10	G10	WC-47582	523.98	152.39
11	G11	WC-47359	411.18	148.76
12	G12	WC-47403	556.98	290.17
13	G13	WC-47388	494.83	179.08
14	G14	WC-4611	446.27	186.68
15	G15	WC-4515	467.94	193.84
16	G16	Pishtaz	590.98	167.93
17	G17	Moghan-3	462.45	166.69
18	G18	WC-47472	511.59	204.03
19	G19	WC-4968	595.94	292.39
20	G20	WC-47528	481.77	283.14

Statistical Analysis

Combined analyses of variance, Bartlett's test and mean comparison were done using MSTAT-C and SPSS statistical software. The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by CROSSA *et al.* (1991). Biplot based on the singular value decomposition (SVD) of GE contains only the GE interaction and can be referred to as a GE biplot. In compare a biplot based on the SVD of G and GE contains only G plus GE, and will be characterized as a GGE biplot (WEIKAI *et al.*, 2000). The GE biplot

was projected for 20 genotypes tested at six environments (E1, E2, E3, E4, E5, and E6). Clustering was computed for the genotype score using an agglomerate hierarchical algorithm based on Ward's method (FARSHADFAR, 1998) and the result of cluster grouping for the genotype PCA score was projected in the biplot of PCA1 and PCA2, and the biplot of PCA1 and mean yield. The IRRISTAT software was used for combined analysis of variance and AMMI analysis. The AMMI stability value (ASV) was calculated as explained by PURCHASE *et al.* (2000). Based on the rank of mean grain yield of genotypes (RY_i) across environments and rank of AMMI stability value ($RASV_i$) a selection index called GSI was calculated for each genotype which incorporates both mean grain yield and stability index in single criteria (GSI_i) as: $GSI_i = RASV_i + RY_i$. Analysis of variance on grain yield was conducted by GGE biplot software to detect the effect of environment (E), genotype (G) and GE interaction. The environments were considered as random effects and the genotypes as fixed factors. Coefficients between pairs of environments were computed *via* SAS 9.2 software. The first two components resulted from principal components were used to draw a biplot by GGE biplot software (YAN, 2001).

RESULTS

Combined Analysis of Variance

The results of combined analysis of variance (Table 2) indicated high significant difference ($P < 0.01$) for genotypes \times environments (locations and years) interaction. Mean comparison using Duncan's multiple rang test (Table 1) revealed maximum grain yield for genotypes G19, G16, G7 and G12 (595.94, 590.98, 564.15 and 556.98 g/m², respectively) in irrigated conditions whereas minimum grain yield was attributed to genotype G6 (332.96 g/m²). In rainfed conditions, maximum grain yield belonged to genotypes G19 and G12 (292.39 and 290.17 g/m², respectively) while minimum grain yield was related to genotype G6, G7 and G3 (137.91, 139.96 and 143.59 g/m², respectively).

Table 2. Combined analysis of variance for grain yield over different rainfed and irrigated conditions

S.O.V	DF	MS
Year (Y)	2	4359238**
Location (L)	1	7555663**
I \times Y	2	929220**
Error 1	12	6920
Genotype (G)	19	45126**
G \times Y	38	34873**
G \times L	19	23885**
G \times L \times Y	38	21152**
Error 2	228	3146
C.V%		16.57

*: significant at 1% level of probability.

AMMI Analysis of GE Interaction

The yield sum square was partitioned into genotype, environment and GE interaction. GE interaction was further partitioned by principal component analysis (Table 3). The results of AMMI analysis indicated that 11.54% of total variability was justified by GE interaction, 81.05% by environment and 3.83% by genotype. The ordination technique detected high significant differences for IPC1, IPC2, IPC3 and IPC4. The first interaction principal component (IPC1) explained 42.54% of variability of GE, followed by IPC2 (34.68%), IPC3 (15.31%) and

IPC4 (5.80%). Therefore, 77.22% of the GE sum of squares was justified by AMMI1 and AMMI2. The contribution of IPC1 in the GE interaction was greater than that of IPC2, IPC3 and IPC4. The greatest interaction being found for genotypes 20 and 7 while the least interaction for genotypes 13, 14 and 18.

Table 3. AMMI analysis of grain yield in bread wheat over rainfed and irrigated conditions

S.O.V	DF	SS	SS%	MS
Genotype(G)	19	857403	3.83 ^a	45126 ^{**}
Environment(E)	5	18132570	81.05 ^a	3626516 ^{**}
G×E	95	2582796	11.54 ^a	27187 ^{**}
IPC ₁	23	1098639	42.54 ^b	47767 ^{**}
IPC ₂	21	895707	34.68 ^b	42653 ^{**}
IPC ₃	19	395475	15.31 ^b	20814 ^{**}
IPC ₄	17	150024	5.80 ^b	8825 [*]
noise	15	42920	1.66 ^b	2861
Error	240	800328	3.57 ^a	3335
Total	359	22373066		

a: total sum of squares percent, b: GE sum of squares percent.

*; ** significant at the 5% and 1% probability levels, respectively.

Table 4. Values of interaction principal components (IPC) for bread wheat genotypes and environments

Genotype	IPC1	IPC2	IPC3	IPC4
G1	-6.480	0.795	0.858	-1.417
G2	8.261	-4.894	-1.597	0.563
G3	-2.313	4.481	5.824	2.778
G4	3.466	3.361	-0.333	2.592
G5	6.499	2.724	3.324	-6.110
G6	1.461	11.879	-5.090	-1.897
G7	-9.322	-2.189	-3.196	3.124
G8	0.699	7.482	-0.285	2.266
G9	-6.304	-9.371	-3.236	-3.569
G10	-3.941	-1.380	-3.123	4.127
G11	1.383	2.226	-8.684	-0.576
G12	-1.249	-3.618	6.831	-7.718
G13	-1.164	2.985	3.374	3.008
G14	0.124	-3.348	-8.350	-3.376
G15	-3.400	4.830	0.562	-2.305
G16	-6.220	-7.211	3.853	2.606
G17	-2.255	4.090	6.000	0.262
G18	-0.037	-2.445	0.954	-0.452
G19	7.731	-5.976	1.574	5.282
G20	13.061	-4.420	0.741	0.811

Environment					
E1	-7.055	-18.250	-7.123	0.541	
E2	21.791	-4.092	2.442	-0.250	
E3	-0.546	10.026	-6.740	7.905	
E4	-2.551	8.682	-5.804	-1.694	
E5	-7.547	-0.837	14.894	5.019	
E6	-4.092	4.471	2.330	-11.520	

AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

AMMI stability value (ASV) discriminated genotypes G12 (3.93), G18 (2.45), G13 (3.31), G14 (3.35) and G11 (2.80) as the stable genotypes, respectively (Table 5).

Genotype Selection Index (GSI) discriminated G12 (7.00) and G18 (9.00) with general adaptability and high grain yield for rainfed and irrigated conditions which were in agreement with the results of biplot analysis (Table 5).

Table 5. First and second IPC scores, ASV_i and GSI_i of genotypes investigated

Genotype	Mean yield	IPC1	IPC2	ASV _i	GSI _i
G1	358.69	-6.480	0.795	7.99	18.00
G2	370.09	8.261	-4.894	11.25	21.00
G3	298.23	-2.313	4.481	5.30	25.00
G4	299.25	3.466	3.361	5.42	25.00
G5	324.51	6.499	2.724	8.42	26.00
G6	235.44	1.461	11.879	12.01	38.00
G7	352.06	-9.322	-2.189	11.64	26.00
G8	269.51	0.699	7.482	7.53	30.00
G9	357.90	-6.304	-9.371	12.15	26.00
G10	338.18	-3.941	-1.380	5.03	17.00
G11	279.97	1.383	2.226	2.80	20.00
G12	423.58	-1.249	-3.618	3.93	7.00
G13	336.95	-1.164	2.985	3.31	14.00
G14	316.47	0.124	-3.348	3.35	18.00
G15	330.89	-3.400	4.830	6.38	22.00
G16	379.45	-6.220	-7.211	10.50	18.00
G17	314.57	-2.255	4.090	4.94	21.00
G18	357.81	-0.037	-2.445	2.45	9.00
G19	444.16	7.731	-5.976	11.21	16.00
G20	382.46	13.061	-4.420	16.62	23.00

Pattern Analysis

The AMMI2 biplot (Fig. 1) explained 77.22% of the GE interaction. It was observed that most of the genotypes and environments scattered around the biplot. Rainfed condition (E2) had the greatest GE with positive interaction. The rainfed environments (E4 and E6), showed negative and almost average interaction. The irrigated environment (E3) exhibited the least

interaction (near to 0). The environments E3, E4, E6, E2 and E1 indicated longer vectors and were farther from the centre of the biplot. Based on IPCA1 genotypes G13, G14 and G18 had low interaction and consequently high stability, but genotypes G20 and G7 displayed high interaction and low stability. The genotypes G3, G15 and G17 revealed specific adaptation and positive GE interaction with environments E4 and E6 (because their angle is less than 90°). Genotypes G20, G2 and G19 showed specific adaptation with environment E2 (rainfed environment 2011), with acceptable grain yield, while genotypes G9, G16, G7 and G10 exhibited specific adaptability with environments E1 and E5 (irrigated environment 2011 and irrigated environment 2013 respectively). The genotypes G6, G8, G15, G3 and G17 indicated specific adaptation with environments E3, E4 and E6 (irrigated environment 2012, rainfed environment 2012 and rainfed environment 2013, respectively). Genotypes G5 and G4 had specific adaptation with environment E2 (rainfed environment 2011) with lower grain yield. Genotype G1 had specific adaptation with environment E5 (irrigated environment 2013). Finally G18 could be introduced as a stable genotype with high performance and yield. Based on the AMMI2 model, genotypes G12 and G18 could be recommended as the most stable genotypes for rainfed and irrigated conditions.

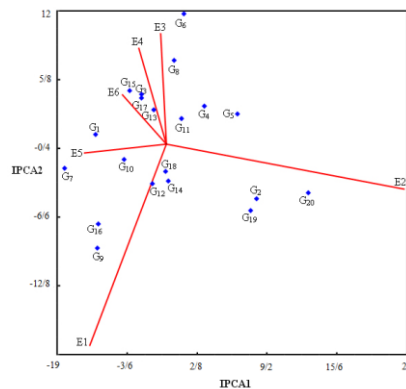


Fig.1. Biplot analysis of GE interaction based on AMMI2 model for first two interactions principal component scores

Which-Won-Where Pattern of genotypes

A polygon view of GGE biplot of grain yield for studied genotypes in six environments is given in Fig.2, which formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed inside the polygon. The vertex genotypes were G12, G20, G6, G15 and G1. In this study, the genotypes fell in five sectors and the test environments fell in two sectors. The first sector consists of E1, E5 and E6 environments (irrigated environment 2011, irrigated environment 2013 and rainfed environment 2013, respectively), which had the genotype G12 followed by genotypes G16, G9, G5 and G17 as the specific adaptable genotypes. The second sector consists of G20 followed by genotypes G19, G2 and G18. This group displayed specific adaptation with E2 (rainfed environment 2011). In this interpretation, the third sector consists of G6 followed by genotypes G11, G3, G4 and G8. This group showed specific adaptation with E3 (irrigated environment 2012). The fourth sector including G13, G10 and G14. The genotypes of group four did not show specific adaptation by environments. The fifth sector consists of G1 and

G15 followed by genotype G7 indicating specific adaptation with E4 (rainfed environment 2012) (Fig.2).

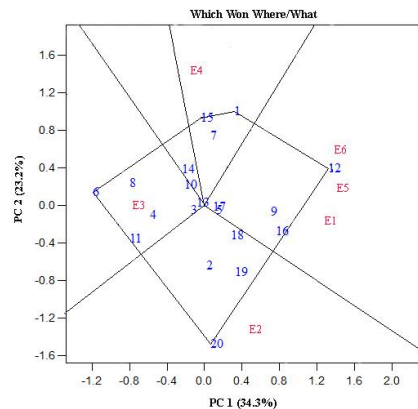


Fig.2. Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments

Mean performance and stability of genotypes

Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes with zero GEI, as represented by an arrow pointing to it (Fig.3). Within a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments. The single-headed line is the AEC ordinate, it points to higher mean yield across environments. Thus, G12, G16, G9, G1, G18, G7, G15, G5, G17 and G19 revealed the highest mean yield. The double-headed line is the AEC abscissa; it points to greater variability (poorer stability) in either direction. Thus, genotypes G1, G7, G15, G19 and G16 were relatively unstable (Fig.3).

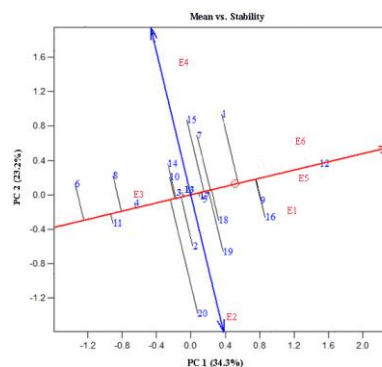


Fig.3. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes

Ranking of genotypes relative to the ideal genotype

A genotype is more desirable if it is located closer to the ideal genotype. Therefore, using the ideal genotype as the centre, concentric circles were drawn to help to visualize the distance

between each genotype and the ideal genotype. Because the units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype-focused scaling (Fig.4), the units of the AEC abscissa (mean yield) and ordinate (stability) should also be in the original unit of yield. Figure 4 revealed that G12, which fell into the centre of concentric circles, was the ideal genotype in terms of higher yielding ability and stability, compared with the rest of the genotypes. In addition, G9 and G16, located on the next consecutive concentric circle, may be considered as desirable genotypes. According to the ranking, G6 genotype was the weakest genotype.

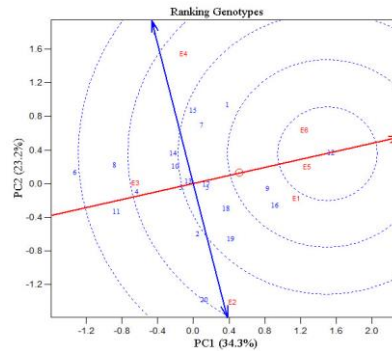


Fig.4. GGE biplot based on genotype-focused scaling for comparison of the genotype with ideal genotype
Ranking of environments relative to the ideal environment

Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the MEYTs. An environment is more desirable if it is closer to the ideal environment. The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments. Thus, E1 and E5 (irrigated environment 2011 and 2013) was the most ideal environments. E6 and E3 (rainfed environment 2013 and irrigated environments 2012) were the next ranking environments. E2 and E4 (rainfed environments 2011 and 2012) were the weakest environments according to ranking (Fig 5).

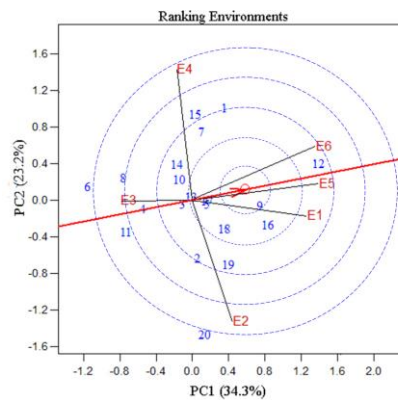


Fig.5. GGE biplot based on environment-focused scaling for comparison of the environment with ideal environment

DISCUSSION

Combined Analysis of Variance

The significant interactions of genotypes \times environments (locations and years) offer that grain yield of genotypes varied across irrigated and rainfed conditions. Significant differences for genotypes, environments and GE interaction showed the influence of environments in the GE interaction, genetic variability among the entries and possibility of selection for stable genotypes (Table 2). Genotypes of annual crops evaluated for grain yield on multi-locations, and years frequently show GE interaction that complicates the selection or recommendation of materials. CHANDRA *et al.* (1974) reported that GE interaction with location is more important than GE interaction with year. As GE interaction was significant, thus we can further proceed and evaluate phenotypic stability (FARSHADFAR and SUTKA, 2006; MOHAMMADI *et al.*, 2016). Coping with genotype-year or genotype-location-year interaction effects is possible only by selection for yield stability across environments defined as location year combinations (ANNICCHIARICO, 1997).

AMMI Analysis of GE Interaction

The partitioning of total sum of squares showed that the environment effect was a predominant source of variation followed by GE and genotype effect. The GE interaction was three times higher than that of the genotype effect, offering the possible existence of different environmental groups (Table 3). The benefits of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (FREEMAN, 1990). GAUCH and ZOBEL (1996) showed that AMMI1 with IPCA1 and AMMI2 with IPCA1 and IPCA2 are usually selected and the graphical representation of axes, either as IPCA1 or IPCA2 against main effects or IPCA1 against IPCA2 is generally informative. According to the opinion KILIÇ (2014); KADHEM and BAKTASH (2016), the analysis of variance for the AMMI model of grain yield showed that genotypes, environments, genotype \times environments interaction and AMMI components 1 and 2 were significant. Thus, both yield and PCA1 and PCA2 scores should be taken into account simultaneously to utilize the useful effect of GEI and to make recommendation of the genotypes more accurate. We obtained same results in this experiment as well. It showed that the GEI was an important source of yield variation and its biplots were powerful enough for visualizing the response patterns of genotypes and environments. The AMMI method is used for three main targets. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular datasets (GAUCH, 1988). Secondly, AMMI clarifies the $G \times E$ interaction and it summarizes patterns and relationships of genotypes and environments, the third use is to improve the accuracy of yield prediction. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (ZOBEL *et al.*, 1988; CROSSA, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes.

AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

As stability per se is not a desirable selection criterion, because the most stable genotypes would not necessarily give the best yield performance, therefore, simultaneous ranking of grain yield and ASV in a single non-parametric index entitled. Since the IPCA1 score contributes more

to GE sum of square (Table 5), it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total GE sum of squares. The AMMI model does not make provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according to their yield stability, the ASV measure was proposed by PURCHASE *et al.* (2000) to cope with this problem. In fact, ASV is distance from zero in a two dimensional scatter gram of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores. The distance from zero is then detected using the theorem of Pythagoras (PURCHASE *et al.*, 2000). In general the importance of AMMI model is in reduction of noise even if principal components do not cover much of the GESS (GAUCH, 1992; GAUCH and ZOBEL, 1996).

Stability per se should however not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (MOHAMMADI *et al.*, 2007); so there is a need for approaches that incorporate both mean grain yield and stability in single criteria. In this regard, as ASV takes into account both IPCA1 and IPCA2 that justify most of the variation of GE interaction, thus the rank of ASV and mean grain yield (RY_i) are incorporated in a single selection index namely Genotype Selection Index (GSI). The least GSI is considered as the most stable with high grain yield (Table 5). The ASV and GSI indicators have been used by many researches (KHAN *et al.*, 2014; HOMMA, 2015; ABATE *et al.*, 2015; KADHEM, and BAKTASH, 2016).

Pattern Analysis

Genotypes farther from the centre of biplot show specific adaptation. In order to evaluate specific adaptation and study of their stability, biplot diagram has used (Fig. 1). If two vector of genotype have small angle, two environments have high correlation. Genotype in centre of biplot axes means that genotype has general adaptation with environment. Vertical length of genotype vector on environment vector shows the amount of deviation of that genotype from means of that environment. According to what explained, in figure 1, biplot vector which comes from first and second principles, interaction for 20 studied genotypes in six environments have three configurations between environments. Genotypes toward the centre of biplot have zero interaction; thus have general adaptation with different mean grain yield. When length of genotype vector is longer, the amount of that genotype interaction with environment is more (NACHIT *et al.*, 1992). In pattern analysis genotypes are judged in grouping form and therefore save time and precision in interpretation and selection (WADE *et al.*, 1995; ALAGARSWAMY and CHANDRA, 1998; FARSHADFAR and SUTKA, 2003).

GGE stands for genotype main effect (G) plus genotype by environment interaction (GE) and the GGE concept is based on the comprehension that genotype main effect (G) and genotype by environment interaction (GE) are the two sources of variation that are relative to genotype evaluation and that they must be considered simultaneously, not alone or separately, for appropriate genotype evaluation (YAN, 2002).

Which-Won-Where Pattern of genotypes

The polygon view of a GGE-biplot explicitly displays the which-won-where pattern, and hence is a succinct summary of the GEI pattern of a MEYT data set (KAYA *et al.*, 2006; SABAGHNIA *et al.*, 2013; HOMMA, 2015; BORNHOFEN *et al.*, 2017). The genotypes that locating the farthest from the origin of biplot, are the best or the poorest genotypes in some or all of the

environments (YAN and KANG, 2003). Many researchers find this use of a biplot intriguing, as it graphically addresses important concepts such as crossover GE, mega environment differentiation, particular adaptation, etc. (YAN and TINKER, 2005). The polygon is created by involving the markers of the genotypes that are further away from the biplot source such that all other genotypes are restricted in the polygon. We obtained similar results based on Which-Won-Where Pattern of genotypes. The vertical lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them (Fig.2).

Mean performance and stability of the genotypes

Within a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments (Fig.3). Yield performance and stability of genotypes were evaluated by average environment coordination (AEC) method (YAN, 2002, YAN and HUNT, 2002; AL-UBAIDI *et al.*, 2013; MEHARI *et al.*, 2015; KARIMIZADEH *et al.*, 2016).

Ranking of genotypes relative to the ideal genotype

According to figure 4, an ideal genotype should have the highest mean performance and be absolutely stable (that is, performs the best in all environments). Although such an ideal genotype may not exist in fact, it can be used as a reference for genotype selection (YAN and TINKER, 2006). The unit of the distance between genotypes and the ideal genotype, in turn, will be in the original unit of yield as well (Fig.4). Thus, the ranking based on the genotype-focused scaling supposes that stability and mean yield are equally important (YAN, 2002; FARSHADFAR *et al.*, 2012).

Ranking of environments relative to the ideal environment

The ideal environment is represented by an arrow pointing to it (Fig.5). Therefore, using the ideal environment as the centre, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (YAN *et al.*, 2000; FARSHADFAR *et al.*, 2011).

CONCLUSION

According to similar results of AMMI and GGE biplot analyses obtained from our multi-environment trials data, both of these statistical methods can be used reliably by plant breeders. Both methods can be used successfully in determine suitable wheat genotypes and locations for Iranian climatic conditions. Results of this research revealed that stability analysis by AMMI model showed that environment and genotype \times environment interactions effects were significant. Analysis of genotype \times environment interactions indicated that four principal components were significant and 77.2 percent of interaction sum of square was related to the first two components. According to the biplot of AMMI₂, genotypes 11(WC-47359), 18 (WC-47472), 14 (WC-4611), 13 (WC-47388), 12 (WC-47403) had general adaptability. Based on ASV and GSI indices genotypes 12 (WC-47403) and 18 (WC-47472) revealed as the highest stability. The five test environments were classified into four mega-environments. Genotypes 12 (WC-47403), 9 (PISHGAM 2) exhibited the highest mean of yield and stability. Based on the results obtained, the best genotypes were 12 (WC-47403), 9 (PISHGAM 2), 19 (WC-4968), 18 (WC-47472) and 20 (WC-47528), ideal germplasm in order to introduce in breeding programs.

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REFERENCES

- ABATE, F., F. MEKBIB, Y. DESSALEGN (2015): Association of different parametric and non parametric stability models in durum wheat (*Triticum turgidum* Desf.) genotypes. *Int. J. Plant and Soil Sci.*, 7(4): 192-201.
- ALAGARSWAMY, G. and S. CHANDRA (1998): Pattern analysis of international sorghum multi-environment trials for grain-yield adaptation. *TAG*, 96: 397-405.
- ANNICCHIARICO, P. (1997): Additive main effects and multiplicative interaction (AMMI) analysis of genotype location interaction in variety trials repeated over years. *TAG*, 94: 1072-1077.
- ASHRAFUL ALAM, M.D., M.D. FARHAD, M.D. ABDUL HAKIM, N.CH. DEB BARMA, P. KUMAR MALAKER, M.D. MOSTOFA ALI REZA, M.D. AMIR HOSSAIN, M. LI (2017): AMMI and GGE biplot analysis for yield stability of promising bread wheat genotypes in Bangladesh. *Pak. J. Bot.*, 49(3): 1049-1056.
- AYED, S., A. OTHMANI, N. CHAIEB, S. BECHRIF, M. REZGUI, M.B. YOUNES (2016): Assessment of adaptability and stability of six Tunisian cereal genotypes under rainfed conditions and at two semi-arid environments. *Eur. Sci. J.*, 12(6): 1857 – 7881.
- BASFORD, K.E., WT. FEDERER, IH. DELACY (2004): Mixed model formulations for Multi-environment trails. *Agron. J.*, 96: 143-147.
- BORNHOFEN, E., G. BENIN, L. STORCK, L.G. WOYANN, T.H. DUARTE, M.G. STOCO, S.V. MARCHIORO (2017): Statistical methods to study adaptability and stability of wheat genotypes. *Bragantia, Campinas*, 76(1): 1-10.
- CHANDRA, S., M.S. SOHOO, K.P. SINGH (1974): Genotype environment interaction for yield in ram. *J. Res.*, 8: 165-168.
- CROSSA, J., H.G. GAUCH, R.W. ZOBEL (1990): Additive main effect and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci.*, 30: 493-500.
- CROSSA, J., P.N. FOX, W.H. PFEIFFER, S. RAJARAM, H.G. GAUCH (1991): AMMI adjustment for statistical analysis of an interactional wheat yield trail. *TAG*, 81: 27-37.
- DENIS, J.B., H.P. PIEPHO, F.A. VAN EEUWIJK (1996): Mixed models for genotype by environment tables with an emphasis on heteroscedasticity. *Technology de Biometrie, Laboratory de Biometrie, Institut Nationale de Research Agronomique, Versailles, France*.
- FARSHADFAR, E. (1998): Application of biometrical genetic in plant breeding. vol 2. Razi University press, Kermanshah, Iran.
- FARSHADFAR, E. and J. SUTKA (2003): Locating QTLs controlling adaptation in wheat using AMMI model. *Cereal Res. Comm.*, 31: 249-255.
- FARSHADFAR, E. and J. SUTKA (2006): Biplot analysis of genotype-environment interaction in durum wheat using the AMMI model. *Acta Agr. Hung.*, 54: 459-467.
- 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.
- FARSHADFAR, E., H. ZALI, R. MOHAMMADI (2011): Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot. *Ann. Biol. Res.*, 2(6): 282-292.
- FARSHADFAR, E., R. MOHAMMADI, M. AGHAEI, Z. VAISI (2012): GGE Biplot analysis of genotype \times environment interaction in wheat-barley disomic addition lines. *Aust. J. Crop Sci.*, 6(6): 1074-1079.

- FREEMAN, G.H. (1990): Modern statistical methods for analyzing genotype–environment interactions. In: M.S. Kang (ed.), *Genotype × Environment Interaction and Plant Breeding*. Louisiana State University Agricultural Center, Baton Rouge, LA. 118-125 pp.
- GABRIEL, K.R. (1971): The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58: 453-467.
- GAUCH, H.G. (1988): Model selection and validation for yield trials with interaction. *Biometrics*, 44: 705-715.
- GAUCH, H.G. (1992): *Statistical analysis of regional yield trials. AMMI analysis of factorial designs*. Elsevier, New York.
- GAUCH, H.G. and R.W. ZOBEL (1996): AMMI analysis of yield trials. In: Kang MS, Gauch HG (eds) *Genotype by environment interaction*. CRC Press. Boca Raton, FL.
- GAUCH, H.G. and R.W. ZOBEL (1997): Identifying mega-environments and targeting genotypes. *Crop Sci.*, 37: 311–26.
- HOMMA, S.H. (2015): AMMI, stability and GGE biplot analysis of durum wheat grain yield for genotypes tested under some optimum and high moisture areas of Ethiopia. *Aca. J. Ento.*, 8(3): 132-139.
- KADHEM, F.A. and F.Y. BAKTASH (2016): AMMI analysis of adaptability and yield stability of promising lines of bread wheat (*Triticum aestivum* L.). *Iraq. J. Agri. Sci.*, 47: 35-43.
- KARIMZADEH, R., A. ASGHARI, R. CHINIPARDAZ, O. SOFALIAN, A. GHAFARI (2016): Application of GGE biplot analysis to evaluate grain yield stability of rainfed spring durum wheat genotypes and test locations by climatic factors in Iran. *Crop Breed. J.*, 4, 5 and 6 (2; 1 and 2): 41-49.
- KAYA, Y., M. AKCURA, S. TANER (2006): GGE-Biplot Analysis of Multi-Environment Yield Trials in Bread Wheat. *Turk. J. of Agric.*, 30: 325-337.
- KEMPTON, R.A. (1984): The use of biplots in interpreting variety by environment interactions. *J. Agric. Sci.*, 103: 123-135.
- KHAN, A.A., M.A. ALAM, M.R. KABIR (2014): AMMI analysis for stability and environmental effects on grain yield of eight spring wheat varieties (*Triticum aestivum* L.) in Bangladesh. *Bull. Inst. Trop. Agr., Kyushu. Univ.*, 37: 93-103.
- KILIÇ, H. (2014): Additive main effects and multiplicative interactions (AMMI) analysis of grain yield in barley genotypes across environments. *Tar. Bil. Der. J. Agric. Sci.*, 20: 337-344.
- MA, B.L., W. YAN., L.M. DWYER, J. FRÉGEAU-REID, H.D. VOLDENG, Y. DION, H. NASS (2004): Graphic analysis of genotype, environment, Nitrogen fertilizer, and their interaction on spring wheat yield. *Agron. J.*, 96: 169–80.
- MEHARI, M., M. TEFAY, H. YIRGA, A. MESELE, T. ABEBE, A. WORKINEH, B. AMARE (2015): GGE biplot analysis of genotype-by-environment interaction and grain yield stability of bread wheat genotypes in South Tigray, Ethiopia. *Comm. Bio. Crop Sci.*, 10(1): 17–26.
- MOHAMED, N.E.M., A.A. SAID, K.A. AMEIN (2013): Additive main effects and multiplicative interaction (AMMI) and GGE-biplot analysis of genotype × environment interactions for grain yield in bread wheat (*Triticum aestivum* L.). *Afr. J. Agric. Res.*, 8(42): 5197-5203.
- MOHAMMADI, R., A. ABDULAH, R. HAGHPARAST, M. ARMION (2007): Interpreting genotype- environment interactions for durum wheat grain yields using non-parametric methods. *Euphytica*, 157: 239–251.
- MOHAMMADI, R. and A. AMRI (2008): Analysis of Genotype × Environment interaction for grain yield in durum wheat. *Crop sci.*, 49: 1177-1186.
- MOHAMMADI, M., H. GHOJIGH, H. KHANZADEH, T. HOSSEINPOUR, M. ARMION (2016): Assessment of yield stability of spring bread wheat genotypes in multi-environment trials under rainfed conditions of Iran using AMMI model. *Crop Breed. J.*, 4, 5 and 6 (2; 1 and 2): 59-66.
- NACHIT, M.M., G. NACHIT, H. KETATA, H.G. GAUCH, R.W. ZOBEL (1992): Use of AMMI and linear regression models to analyze genotype-environments interaction in Durum wheat, *TAG*, 83: 597-601.
- NAROUY RAD, M.R., M. ABDUL KADIR, M.Y. RAFII, H.Z.E. JAAFAR, M.R. NAGHAVI, F. AHMADI (2013): Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum* L.) under normal and drought stress conditions. *Aust. J. Crop Sci.*, 7(7):956-961.

- PURCHASE, J.L., H. HATTING, C.S. VANDEVENTER (2000): Genotype \times environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *S. Afr. J. Plant Soil*, 17: 101-107.
- RAM, C., G. SHARMA, O. FERRARA, J. CROSSA, M.R. BHATTA, M.A. SUFIAN (2007): What grain yield and stability assessed through regional trials in the Eastern Gangetic Plains of Sought Asia. *Euphytica*, 157: 457-464.
- SABAGHNI, N., R. KARIMIZADEH, M. MOHAMMADI (2013): GGL biplot analysis of durum wheat (*Triticum turgidum* spp. *durum*) yield in multi-environment trials. *Bulg. J. Agric. Sci.*, 19: 756-765.
- SHAFII, B. and W.J. PRICE (1998): Analysis of genotype-by-environment interaction using the Additive Main Effects and Multiplicative Interaction model and stability estimates. *J. Agric. Biol. Environ. Stat.*, 3: 335-345.
- THAMSON, W.E. and S.B. PHILIPS (2006): Methods to evaluate wheat cultivar testing environment and improve cultivar selection protocols. *Field Crops Res.*, 99: 87-95.
- WADE, L.J., S. SARKARUNG, C.G. MELRAN, A. GUHEY, B. QUADER, C. BOONRITE, S.T. AMARANTE, A.K. SARAWGI, A. HAUGE, D. HARNPICHITRITAYA, A. PAMPLONA, M.C. BHAMRI (1995): Genotype by environment interaction and selection method for identifying improved rainfed lowland rice genotypes. International Rice Research Institute. P. O. box 933. Manila. Philippines, 883-900.
- YAN, W., L.A. HUNT, Q. SHENG, Z. SZLAVNICS (2000): Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.*, 40: 597-605.
- YAN, W., P.L. CORNELIUS, J. CROSSA, L.A. HUNT (2001): Two types of GGE biplots for analysis of multi-environment trial data. *Crop Sci.*, 41: 565-663.
- YAN, W. (2001): GGE biplot-A Windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron. J.*, 93: 1111-1118.
- YAN, W. and L.A. HUNT (2002): Biplot analysis of multi-environment trial data. In M. S. Kang (ed.). 289-303 pp.
- YAN, W. and I. RAJCAN (2002): Biplot analysis of sites and trait relations of soybean in Ontario. *Crop Sci.*, 42: 11-20.
- YAN, W. (2002): Singular-value partitioning in biplot analysis of multi-environment trial data. *Agron. J.*, 94: 990-996.
- YAN, W. and M.S. KANG (2003): GGE biplot analysis: a graphical tool for breeders, geneticists and agronomist. CRC Press, Boca Raton, Florida, 271 pp.
- YAN, W. and N.A. TINKER (2005): An integrated system of biplot analysis for displaying, interpreting, and exploring genotype \times environment interactions. *Crop Sci.*, 45: 1004-1016.
- YAN, W. and N.A. TINKER (2006): Biplot analysis of multi-environment trial data: principles and applications. *Can. J. Plant. Sci.*, 86: 623-645.
- YAN, W., M.S. KANG, B. M.A., S. WOODS, P.L. CORNELIUS (2007): GGE Biplot vs AMMI analysis of genotype-by-environment data. *Crop Sci.*, 47: 643-53.
- ZOBEL, R.W., M.J. WRIGHT, J.R. GAUCH (1988): Statistical analysis of a yield trial. *Agron. J.*, 76: 1-10.

ANALIZA STABILNOSTI DOMAĆIH POPULACIJA I LINIJA HLEBNE PŠENICE PRIMENOM BIOMETRIJSKOG GENETIČKOG MODELA

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Izvod

Da bi se procenila stabilnost prinosa dvadeset genotipova hlebne pšenice, eksperiment je sproveden u randomiziranom kompletnom blok dizajnu (RCBD) sa tri ponavljanja u sušnim uslovima navodnjavanja na Univerzitetu Razi u Kermanshahu tri godine (2011-2013). Kombinovana analiza varijanse pokazala je veoma značajne razlike za GEI. Stabilnost utvrđena AMMI analizom pokazala je da su prva dva AMMI modela (AMMI1-AMMI2) bila veoma značajna ($P < 0,01$). GEI je bila tri puta veća od genotipskog efekta. Rezultati Biplota AMMI2 pokazali su da su genotipovi WC-47359, WC-47472, WC-4611, WC-47388 i WC-47403 imali opštu adaptabilnost. Na osnovu ASV i GSI, genotipovi WC-47403 i WC-47472 pokazali su najveću stabilnost. GGE biplot analiza prinosa koji prikazuje glavne efekte G i GEI opravdava 57,5 % ukupne varijacije. Prve dve glavne komponente (PC1 i PC2) su korišćene da bi se napravio 2-dimenzionalni GGE biplot i objasnio 34.3, odnosno 23.2 GGE sume kvadrata (SS). Genotipovi WC-47403, PISHGAM2 su pokazali najveći prosečni prinos i stabilnost. Na osnovu dobijenih rezultata, najbolji genotipovi su WC-47403, PISHGAM2, WC-4968, WC-47472 i WC-47528 za programe oplemenjivanja.

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