

AMMI ANALYSIS OF ADAPTABILITY AND YIELD STABILITY OF PROMISING LINES OF BREAD WHEAT (*Triticum aestivum* L.)

F. A. Kadhem

Prof.

F. Y. Baktash

Prof.

fadelbaktashi@yahoo.com

Dept. of Field Crops - Coll. of Agric. – Univ. of Baghdad

ABSTRACT

Additive main effects and multiplicative interactions (AMMI) model analysis was performed to assess and to quantify the magnitude of genotype by environment interaction and yield stability of bread wheat genotypes. Fifteen promising lines generated from a crossing program among six bread wheat (*Triticum aestivum* L.) pure lines were used in a randomized complete block design with four replications for five consecutive years (2009-2014). AMMI analysis of variance showed that the environment effect was a predominant source of variation (67.6% of the treatment SS) followed by GE interaction (21.1 %) and genotype effect (8.6%). First two interaction principal component axes (IPCA) cumulatively explained 92.75% of total interaction effects. A graphical interpretation of the AMMI analysis and GSI index incorporating the AMMI stability value (ASV) and the yield capacity of the different genotypes in a single non-parametric index were useful for discriminating genotypes with superior and stable grain yield. Based on AMMI biplot, G10 had general adaptability, and Based on ASV and Genotype stability index (GSI) genotypes G10, G15, and G2 revealed the highest stability. It seems that various measures of stability from AMMI model indicate similar aspects of yield stability and GEI nature.

Key words: AMMI, stability, G x E interaction, ASV, GSI.

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كاظم و بكتاش

تحليل الفعل الاضافي الرئيس والتداخل المضاعف للتكيف واستقرارية حاصل الحبوب لخطوط واعدة من حنطة الخبز

(*Triticum aestivum* L.)

فاضل يونس بكتاش

استاذ

fadelbaktashi@yahoo.com

فوزي عبد الحسين كاظم

استاذ

قسم المحاصيل الحقلية – كلية الزراعة – جامعة بغداد

المستخلص

اجري تحليل التباين حسب نموذج تحليل الفعل الاضافي الرئيس والتداخل المضاعف لتقييم وتحديد قيمة التداخل الوراثي البيئي وثباتية حاصل الحبوب لتراكيب وراثية من حنطة الخبز (*Triticum aestivum* L.). خمسة عشر خطوط واعدة مستنبطة من برنامج تهجين متبادل لستة خطوط نقية من حنطة الخبز، اختبرت وفق تصميم القطاعات الكاملة المعشاة واربعة مكررات لخمسة سنوات متتالية (2009 – 2014). بينت نتائج تحليل التباين لتحليل الفعل الاضافي الرئيس والتداخل المضاعف سيادة تأثير البيئات (67.6% من مجموع مربعات المعاملات)، يتبعها تأثير التداخل (21.1 %) ومن ثم تأثير التراكيب الوراثية (8.6%). ان مجموع ما فسر من المكونين الرئيسين الاول والثاني (PCA1 و PCA2) هو 92.75 % من مجموع مربعات التداخل. ان مقياس الثباتية (ASV) مفيد لتمييز ثباتية حاصل التراكيب الوراثية. كذلك اظهرت الرسوم البيانية المستخلصة من تحليل الفعل الاضافي والتداخل المضاعف للتراكيب الوراثية على ان التركيب الوراثي G10 اظهر تكيف وثباتية عامة، وعلى اساس قيمة ASV و مقياس ثباتية التراكيب الوراثية GSI اظهرت بان التراكيب الوراثية G10 ، G15 ، و G2 لها صفة الثباتية العالية. اظهرت الدراسة بان المقاييس المختلفة للثباتية المستنبطة من تحليل الفعل الاضافي تعطي مؤشرات متقاربة من ناحية ثباتية التراكيب الوراثية.

كلمات مفتاحية: AMMI، الثبات، التداخل الوراثي × البيئي، ASV، GSI.

INTRODUCTION

As a result of the fast increase of the world population, cereal crops becoming more important in human nutrition. Wheat (*Triticum sp.*) is commonly considered as strategically important crop. The grain of wheat is represents elementary source of nutrition for large part of human population. It is necessary to increase wheat production to meet nutrition needs of increasing world populations. Wheat is the most important cereal crop in the world and is produced on highest acreage, its production areas between 215-220 million ha and production of more than 671 million metric ton (1). Wheat genetic improvement objectives include obtaining cultivars capable of expressing their maximum potential yield and quality in diverse environments (2). This make necessary to know and define the environment in which a variety can express its maximum potential yield and quality. The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. However, attaining this goal is made more complicated by (GEI) genotype-environment interactions (3). Genotype-by-environment interaction (GEI) is frequent in multi-environment trials, and represents differential responses of genotypes across environments The existence of genotype-environment interaction (GEI) complicates the identification of superior genotypes for a range of environments and calls for the evaluation of genotypes in many environments to determine their true genetic potential (2, 4, 5). The big challenges facing the specialists in biometrical genetics is to find the perfect stability analysis of genotypes across wide rage range of environment. Lin *et al.* (6); Becker and León (7), Crossa (8) and Hohls (9) discussed a wide range of methods available for the analysis of GEI and stability and it can be divided into four groups: 1) the analysis of components of variance, 2) stability analysis, 3) qualitative methods and 4) multivariate methods. Albert (10) clearly stated that the multivariate models such as AMMI can summarize patterns and relationships of genotypes and environments successfully, as well as provide a valuable prediction assessment, although Becker and León (7) stated that multivariate methods are too sophisticated to provide a simple measure

of yield stability which allows a ranking of genotypes. It is clearly showing the adaptation of genotypes to environments and can be used to identify the superior genotypes in relation with the environments and years. The aim of the AMMI analysis is to model the interaction effects through a principal component model (11). The AMMI model was developed by Gabriel (12) and Gollob (13), and has been applied and extended by many other authors in many fields and disciplines (14, 15, 16). An important characteristic of this method is the possibility of obtaining plots of the principal components kept in the analysis of the AMMI model, and plots of the scores of PC s axes against the mean yield (12). Genotype and environment scores can be plotted on the same graph and used to visually identify stability and the similarity between genotypes and environments. The current study was conducted to interpret Genotype x Environment (GE) interaction obtained by AMMI analysis of yield performance of 15 bread wheat genotypes over 5 environments, to visually assess how yield performances vary across environments on a biplot and to group the cultivars having similar response patterns across varying environments together.

MATERIAL AND METHODS

Yield performance of Fifteen promising lines generated from a crossing program among six bread wheat (*Triticum aestavum* L.) pure lines (Alfateh, A3031, M.2, IPA99,A4.10, and Abu-Ghraib 3) started 2001 and 2002, using half diallel method. A single plant selection was used for six years. Some of promising lines from that program (Table 1) were evaluated during five years (2009-2014). The experiments were laid out in Randomized Complete Block Design with 4 replications in each year. The experimental unit was 3 x 2 m, which consist of 15 row 0.20 m apart. Fertilizers applications was 100 kg ha⁻¹ of triple super phosphate (45% P₂O₅) applied during soil preparations. Nitrogen fertilizer as urea (46% N) was used at rate of 200 kg ha⁻¹, splitting in three applications, during third leave initiation, stem node initiation, and booting stage. Experiments were planted in the second half of November each year. Hand weeding and irrigations were applied when needed. Harvesting was done for the two

middle rows of each plot, and grain yield was adjusted by converting plot yield (at 14% moisture content) to seed yield per hectare.

STATISTICAL ANALYSIS

Before data analysis, homogeneity of residual variance was determined by Bartlett's test (17) and the data collected was homogenous ($\chi^2_{19\text{ df}} = 28.72$ $P > 0.05$). Then, data for grain yield were pooled to perform the analysis of variance across years. Since the pooled analysis of variance considers only the main effects, the additive main effect and multiplicative interaction model (AMMI) was computed. The main idea of the AMMI models is: (i) first apply the additive of the variance model (ANOVA) to a two-way table (in the present case with genotypes and

environments); and (ii) secondly apply the multiplicative principal component analysis (PCA) model to the residual from the additive model, in this case to the interaction, (18). The AMMI model with multiplicative terms can be written as:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$$

Where: Y_{ij} is the yield of genotype i in environment j ;

μ grand mean;

G_i the genotype mean deviations (the genotype means minus the grand mean);

E_j the environment mean deviations; λ_k the singular value for the PCA axis k ; γ_{ik} and α_{jk} are the genotype and environment PCA scores for PCA axis k ; K is the number of PCA axes.

Table 1. Pedigree, Origin, and Codes of Promising line

Genotype	Code	Pedigree	Origin
Alfateh	P1	C1-82-24/C168-3/3 CN02 / 711C/Tob-Swm6828-6AP-3-AP-OAP) x (Mexipak	Iraq
3103A	P2	Kanz/'S'/Kanz/S/ x ICW-91-0493-OTS-SAP-OTS-IAP-OP	Australian
M.2	P3	Ns732Hcr/Shix4414/Ccrolj'S'	Germany
IPA99	P4	Ures/Bows/3/Jup/B/2S1//Ure	CIMMYT
A4.10	P5	Kanz/3/S/ x ICW-91-0157-OBR-12AP-OTS-OAP	Australian
Abu-Ghraib3	P6	Ajeepa x Inia66R x Mexico24	Iraq
S12	G1	P5 x P4	
S52	G2	P4 x P1	
S76	G3	P6 x P3	
S83	G4	P4 x P2	
S94	G5	P4 x P3	
S97	G6	P5 x P3	
S102	G7	P2 x P1	
S118	G8	P6 x P1	
S123	G9	P6 x P5	
S130	G10	P5 x P4	
S148	G11	P5 x P2	
S152	G12	P6 x P2	
S155	G13	P4 x P3	
S175	G14	P5 x P1	
S177	G15	P6 x P1	

retained by the model; ρ_{ij} is the additional residue and ε_{ij} is the ij^{th} error associated with the model. replicated, an error term ε_{ijr} , which is the difference between the Y_{ij} mean and the single observation for replicate r , should be added. AMMI model, along with prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates. The interaction is explained in the form of a biplot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI components. The main purposes of the AMMI models were pointed out by Crossa (8): (i) model diagnosis (19); (ii) to clarify GEI (20, 21); and (iii) to improve the accuracy of yield

estimates (20, 21). The main effects in the additive part of the model (grand mean, genotype effect g_i and environment effect e_j) were analyzed using ANOVA. The least-squares fit to the additive part of the model were obtained in two steps. The first partition was between the treatment and the error. The block effect was removed from the error term during this fundamental partition. The treatments were then partitioned into additive effects of genotype and environment, and non-additive residual (i.e. genotype by environment interaction). Analysis of variance showed that the non-additive residual was significant (Table 2). Therefore, it was analyzed with help of principal component

analysis according to the multiplicative part of the model Principal component analysis. All the analyses were carried out using IRRISTAT (22) and MINITAB (23) software's, and GenStat Release 12.1 (24). To construct a biplot for the model with one principle component (AMMI1), means of genotypes (over all environments) and environments (over all genotypes) were plotted along the abscissa (x-axis). The interaction PCA (IPCA 1) scores for both genotypes and environments were plotted along the ordinate (y-axis). Consequently, displacement along the abscissa reflects differences in main effects, whereas displacement along the ordinate exhibited differences in interaction effects. When a model with two PCA axes was used, an additional biplot was constructed by plotting IPCA 2 scores against IPCA 1 scores. In this case, there are no additive effects exhibited on the biplot. The ordinate with IPCA2 scores is interpreted exactly the same way as the abscissa with IPCA 1 scores. In a biplot where, PCA 1 score is on the vertical axis and the mean yield on the horizontal, genotypes that appear almost on a perpendicular line had similar means and those that fall almost on a horizontal line had similar interaction patterns. Similarly, environment that occurred almost on a perpendicular line had similar means and those on horizontal lines had similar interaction patterns. Genotypes or environments with large PCA 1 scores, either positive or negative had large interactions, whereas genotypes with PCA 1 score of zero or nearly zero had smaller interaction (10).

AMMI STABILITY VALUE (ASV):

The AMMI stability value (ASV) as described by Purchase et al. (25) was calculated as follows:

$$ASV = \sqrt{\frac{IPCA1sumofsquare}{IPCA2sumofsquare} (IPCA1score)^2 + (IPCA2score)^2}$$

Where $\frac{IPCA1sumofsquare}{IPCA2sumofsquare}$

is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

GENOTYPE SELECTION INDEX (GSI): 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 (26), which incorporates both mean grain yield and stability index in single criteria

$$(GSI_i) \text{ as: } GSI_i = RASV_i + RY_i$$

RESULTS AND DISCUSSION

AMMI ANOVA

The analysis of variance of the AMMI model for 15 wheat promising lines (genotypes) over 5 environments (Table 2) revealed that the genotypes accounted for 8.6% of the total treatment SS, the environmental effect explained 67.6% , and the G x E interaction (GEI) effect captured 21.1%, were all significant (P < 0.001). The environments were diverse and caused for a great variation in grain yield, nevertheless wheat is grown in the open field and the yield is quantitative trait so the environmental factors are crucial determinant of yield expression. The five years, where the promising lines were tested, seem to be informative because of their contrasting weather conditions. This indicates the reason in causing most of the variation in grain yield, and that were clearly noticed in Fig.1 were E3, E4, and E5 were clustered together and characterized by more productive environments . Where as E1, and E2 were poor productive environments. Gauch and Zobel (3) reported that E accounts for about 80% of the total variation, while G and GEI each account for about 10% in normal Multi-environment trials (METs). The large E and GEI in this study suggest the possible existence of different mega-environments with different top-yielding genotypes (27). The GEI contribute more than twice of that of genotypes implying the need for investigating the nature of differential response of the genotypes to environments (Table 2). The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values (8,14). Similar findings were also obtained by Tarakanovas and Ruzgas (16), and Bavandpori et al (26) on the additive main

effect and multiplicative interaction analysis studies of wheat varieties.

Table 2. AMMI analysis of variance for grain yield (kg ha⁻¹) of 15 wheat promising lines grown at 5 environments

Source	df	SS	MS	F-cal	F_Prob.
Treatments	74	223.86	3.025	118.79	0.000
Genotypes	14	19.81	1.415	55.57	0.000
Environments	4	155.54	38.885	576.35	0.000
Block	15	1.01	0.067	2.65	0.001
Interactions	56	48.51	0.866	34.02	0.000
IPCA- 1	17	34.4	2.023	79.45	0.000
IPCA- 2	15	10.51	0.701	27.52	0.000
IPCA- 3	13	2.21	0.170	6.68	0.000
IPCA- 4	11	1.39	0.126	4.97	0.000
Error	210	5.35	0.025	*	*
Total	299	230.22	0.77		

The multiplicative variance of the sum of squares due to GEI was partitioned into IPCA-1, IPCA-2, IPCA-3 and IPCA-4 .). The first principal component axis (PCA-1) of the interaction captured 70.9% of the interaction sum of square in 30.35% of the interaction degrees of freedom. Similarly, the second principal component axis explained further 21.85% of the GEI sum of square. while IPCA3 and IPCA4 explained 4.5 and 2.8 % respectively. According to Crossa et al. (20) and Zobel et al. (21) in AMMI the first two interaction principal component axis best predictive model explains the interaction sum of squares. Conversely, Sivapalan et al. (28) recommended a predictive AMMI model with the first four PCAs. Further, interaction

principal component axes 3 and 4 captured mostly noise and did not help in prediction. 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 (20). Thus interaction of the 15 promising lines with 5 environments was best predicted by the first two principal components of GEI. Mean grain yield (kg ha⁻¹) of the 15 promising lines at 5 environments, their ranking orders and IPCA 1 and 2 are presented in Table 3. mean yield ranged from 5.089 for G15 to 5.981 of G9. With regard to IPCA 1 score, G15 and G3 gave the lowest scores respectively while G4 attained highest IPCA 1 score.

Table 3. Mean yield First and second IPCA and various yield-stability statistics investigated in wheat of 15 promising lines in 5 environments

G. code	E1*	E2	E3	E4	E5	Genotyp e mean	Yield rank	IPCA- 1 score	IPCA- 2 score	ASV	GSI
G1	4.927	4.488	5.513	5.794	5.955	5.335	9	-0.168	-0.205	0.548	11
G2	4.904	4.319	6.148	6.584	6.412	5.673	3	0.203	0.195	0.644	8
G3	4.773	3.873	5.96	6.12	5.924	5.33	10	0.123	0.192	0.417	11
G4	3.399	3.89	6.209	6.146	6.158	5.16	13	0.883	-0.041	2.68	28
G5	5.101	3.69	5.287	6.166	5.388	5.126	14	-0.287	0.326	0.93	23
G6	5.21	3.743	5.155	6.2	6.024	5.266	11	-0.293	0.508	1.027	21
G7	4.311	3.996	6.432	6.555	6.394	5.538	6	0.59	0.247	1.804	19
G8	5.059	4.872	5.765	5.823	6.072	5.518	7	-0.166	-0.418	0.653	13
G9	5.178	4.507	6.63	6.832	6.757	5.981	1	0.279	0.23	0.874	9
G10	5.674	4.518	6.198	6.208	6.388	5.797	2	-0.211	0.054	0.643	6
G11	4.114	4.18	6.201	6.299	6.166	5.392	8	0.538	-0.013	1.632	19
G12	6.128	4.425	5.063	6.238	6.136	5.598	4	-0.791	0.285	2.42	18
G13	4.641	4.766	5.531	5.586	5.282	5.161	12	-0.164	-0.675	0.838	19
G14	5.41	4.104	5.219	5.425	5.286	5.089	15	-0.589	-0.151	1.792	27
G15	4.843	4.906	6.209	6.108	5.712	5.555	5	0.053	-0.535	0.563	8
Mean	4.912	4.285	5.835	6.139	6.003	5.435					
IPCA	-1.34	-0.224	0.849	0.336	0.379						

AMMI Biplot

The most attractive feature of AMMI analysis is the construction of biplot graphs, through

combining the analysis of variance with multivariate analysis through principle component analysis. There are two basic

AMMI biplots, the AMMI 1 biplot, where the main effect (Genotype and Environments means) and IPCA-I scores are plotted against each other (Fig.1). AMMI 2 biplot where scores of IPCA-1 and IPCA-2 are plotted (Fig.2). In AMMI 1 biplot The differences among genotypes in terms of direction and magnitude along the X-axis (yield) and Y axis (IPCA 1 scores) are important. In the biplot display, genotypes or environments that appear almost on a perpendicular line of the graph had similar mean yields and those that fall almost on a horizontal line had similar interaction (10). Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. The score and sign of IPCA1 reflect the magnitude of the contribution of both genotypes and environments to GEI, where scores near zero are characteristic of stability, whereas higher score (absolute value) considered as unstable and specific adapted to certain environment (13). The characterization of each promising lines (genotypes) to mean grain yield and contribution to GEI by mean of IPCA1 (Fig.1) indicates that genotypes G7, G2, and G9 were specifically adapted to high yielding environments (E3, E4, and E5) with grain yield more than grand average yield (Fig 1), and with respect to their contribution to GEI (i.e. stability) the IPCA1 score, G7 was the most unstable genotype and also adapted to higher yielding environments, G2 was more stable in comparison to G7, G9, and G10. However, G3, G1, and G13 were low yield genotypes and relatively stable. On the other hand, G4, G5, G6, G14, and G11 were adapted to low yielding environment but not stable. G15, G3, G8, and G1 were near to zero IPCA 1 by which it was shown to have a higher stability for yield than other genotypes (Fig 1). The best genotype needs to combine good grain yield and stable performance across a range of production environments. For example, a genotype G15 can be judged based on its stability over the environments, which combined low absolute IPCA-I score with good grain yield, was the overall winner with less variable yield across the environments explaining its suitability as one of the leading promising line for such trials. The environments showed much variability in both

additive main effects and interactions (Table 1). The environment with most potential (E3, E4, and E5) having high positive IPCA-I score showed differential performance of genotypes for grain yield (table 2). The lowest yielding environment (E2) had recorded lowest but negative IPCA I score suggesting that all the genotypes poorly performed under this environment.

AMMI 2 Biplot

When IPCA1 was plotted against IPCA2 (Figure 2), genotypes; G10 was found closer or at a lesser distance from the center of the biplot when compared with other genotypes and that would be considered as most stable genotype with regard to its lesser contribution to GEI. On the contrary, G13, G4, G6, and G14 exhibit longer vector from origin indicating the high contribution of these genotypes to GEI (i.e. unstable genotypes). The AMMI2 biplot also revealed that the environments were divers and exhibits longer vectors from origin especially E1 and E2, and that imply their higher contribution to Environment Sum of Square. The longer vector of environments compared to genotypes explain the higher sum of square of environments as compared to Sum of squares of genotypes in the ANOVA table (Table 2). The best genotypes with respect to environments E1 were G12, G14 G10. Genotypes G13, G15, and G8 were best for environments E2. Whereas, G9, G7, G15, G4, and G11 were best for environments E3. Best genotypes for E4 and E5 were G9, G7, G2, G10 and G3.

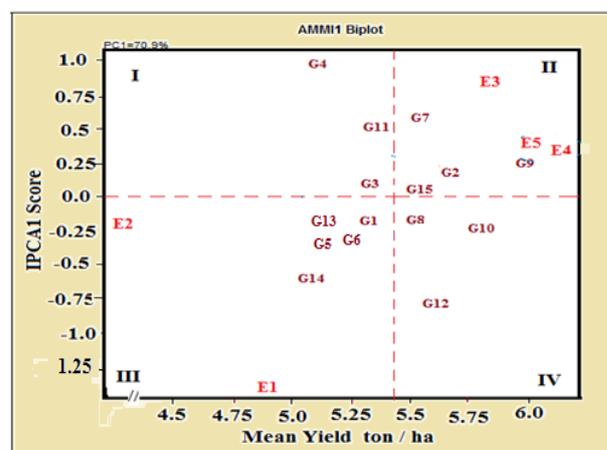


Figure 1 . AMMI 1 biplot for additive effects vs. IPCA1 in 15 promising lines of wheat from five environments

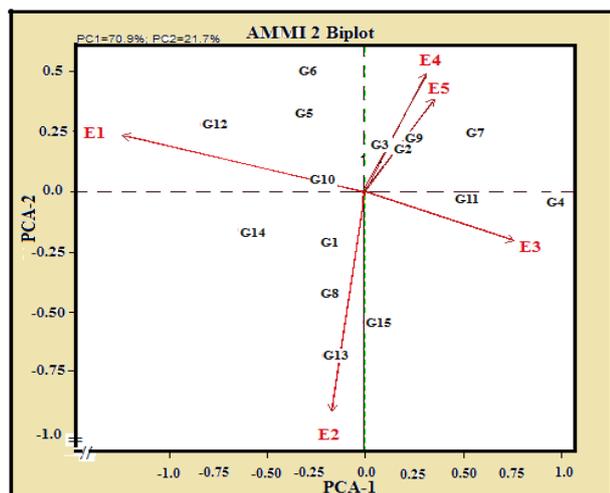


Figure 2 . AMMI2 biplot showing the two main axes of interaction (IPCA2 vs. IPCA1) in 15 promising lines from 5 five environments

AMMI stability value (ASV):

AMMI stability value was also computed to determine stability of the genotypes (Table 2). In fact ASV is the distance from zero in a two dimensional scatter gram of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores. Since the IPCA1 score contributes more to GE sum of scores, 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 distance from zero is then determined using the theorem of Pythagoras (25). In ASV method, a genotype with least ASV score considered as the most stable. Accordingly, genotypes G3, G1, G15, G10, and G2 had general adaptation, while genotypes G7, G12, and G4 were the most unstable. This was in agreement with Farshadfar (29) who has used ASV as one method of evaluating grain yield stability of bread wheat varieties. Similar reports were also observed by Fereny et al (31) who has studied adaptability and stability pattern of spring wheat using ASV and other stability parameters.

Genotype Selection Index (GSI)

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), hence there is a need for approaches that incorporate both mean and stability in a

single criteria. In this regard, as ASV takes into account both IPCA1 and IPCA2 that justify most of the variation of GE interaction, therefore the rank of ASV_i and rank of mean are incorporated in a single selection index namely Genotype Selection Index (GSI). The least GSI is considered as the most stable (Table 2) , in that regard the G10, G15, G2, and G9 were considered as most stable genotypes , whereas, G4, G14, and G5 are the least stable genotypes. These results were in agreement with the result of biplots.

Conclusion:

The results of this study confirm the importance of testing genotypes under representative environmental conditions to identify the best, stable and high yielding genotypes. Both yield and stability of performance should be considered simultaneously to reduce the effect of GE interaction and to make selection of genotypes more precise and refined. The analysis of variance for the AMMI model of grain yield showed that genotypes, environments, genotype x 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. A graphical interpretation of the AMMI analysis and GSI index incorporating the ASV and the yield capacity of the different genotypes in a single non-parametric index were useful for discriminating genotypes with superior and stable grain yield. Although the use of different methods to estimate the stability and adaptability of select genotypes has led to controversial results, Based on AMMI biplot, G10 had general adaptability, and Based on ASV and GSI indices genotypes G10,G15, and G2 revealed the highest stability. It seems that various measures of stability from AMMI model indicate similar aspects of yield stability and GEI nature.

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