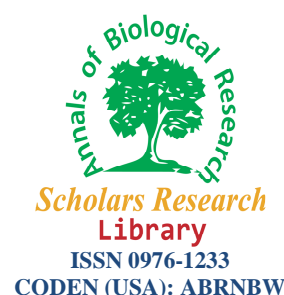




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## Evaluation of genotype $\times$ environment interaction in chickpea using measures of stability from AMMI model

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### ABSTRACT

This research was carried out to study stability analysis and comparison between some measures of stability from AMMI model in 17 chickpea genotypes, in RCBD with four replications in five different research stations of Iran across two years (2004-2005). Spearman's rank correlation was used to measure the relationship between measures of stability from AMMI model. To understand better relationships among these methods, principal component analysis, was performed. The first two PCs explained 87.65% of the variance of original variables. The relationships among the different stability statistics from AMMI model are graphically displayed in a biplot of PC<sub>1</sub> and PC<sub>2</sub>. The results also revealed that stability measures can be classified into three groups. The first group included, SIPC<sub>4</sub>, EV<sub>4</sub>, MASV, Dz<sub>4</sub>, AV<sub>(AMGE)}</sub>, W<sub>i(AMMI)}</sub> and FA<sub>i</sub> which were correlated with mean yield. The second group consists of ASV, Da<sub>4</sub>, B<sub>i</sub> and Za<sub>4</sub> which were correlated with mean yield too. Group 3 consist of FP<sub>i</sub> that was not associated with the more stability methods and mean yield. This measure may not be as good as the other methods. The results of the correlation matrix and the PC analysis between different measures of stability from AMMI model showed that all measures (except for FP<sub>i</sub>) can be used for evaluating the responses of chickpea genotypes to changing environments. Eventually, according to all measures of stability from AMMI model (except for FP<sub>i</sub>) and regarding the high mean yield, genotype G<sub>13</sub> (FLIP 97-114) was recommended for national release in Iran, as it adequately demonstrated wide adaptation across environments.

**Key words:** AMMI model, principal component analysis (PCA) and Spearman's rank correlation

**Abbreviation:** AMGE: Sum across environments of the GEI modeled by AMMI; AMMI: Additive main effects and multiplicative interaction; ASV: AMMI stability value; AV<sub>(AMGE)}</sub>: Absolute value of the sum across environments; B<sub>i</sub>: Stability statistic based on the first IPC axes of the first two IPC axes; Da<sub>i</sub>: Parameter of Annicchiarico (1997); Dz<sub>i</sub>: Distance of IPC point with origin in space; EV: Averages of the square eigenvector values; FA<sub>i</sub>: Stability statistic based on the first IPC axes based on fitted AMMI model; GEI: Genotype  $\times$  environment interaction; FP<sub>i</sub>: Stability statistic based on the first IPC axes of the first IPC axes; MET: Multi environmental trial; MASV: Modified AMMI stability value; SIPC: Sums of the absolute value of the IPC scores; SVD: Singular value decomposition; W<sub>i(AMMI)}</sub>: Wruck's ecovalance in term of AMMI; Za<sub>i</sub>: Absolute value the relative contribution IPCs to the interaction

## INTRODUCTION

Legumes are important source of good quality protein in the diets of people and are valuable as animal feed. Chickpea (*Cicer arietinum* L.) is Iran's most important food legume crop, comprising nearly 64% of the area grown to food legumes in the country. Iran's chickpea area represents 5.1% of the world's total chickpea area and produces 2.75% of global chickpea production [14].

The most important GE effects for targeting cultivars or for selection of material are the crossover type affecting top-yielding genotypes [2]. The importance of GEI in national cultivar evaluation and breeding programs have been demonstrated in almost all major crops, including chickpea genotypes [4, 13, 18]. Various statistical models have been developed to quantify GEI and identify relatively stable genotypes across different locations and years.

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach [6]. According to Gauch and Zobel (1988) [7], AMMI model can be used to analyze multi-location trials. Some methods are based on the additive main effects and multiplicative interaction model, e.g., AMMI stability value (ASV), parameter of Annicchiarico (1997) [1] ( $Da_i$ ), distance of IPC point with origin in space ( $Dz_i$ ), stability statistic based on the first IPC axes ( $FP_i$ ), stability statistic based on the first two IPC axes ( $B_i$ ), stability statistic based on fitted AMMI model ( $FA_i$ ), Wruck's ecovalance in term of AMMI ( $W_{i(AMMI)}$ ), modified AMMI stability value (MASV), sums of the absolute value of the IPC scores (SIPC), sum across environments of the GEI modeled by AMMI (AMGE), averages of the square eigenvector values (EV), absolute value of the sum across environments ( $AV_{(AMGE)}$ ), and absolute value the relative contribution IPCs to the interaction ( $Za_i$ ).

A biplot was constructed in the dimension of first two principal components, using a singular-value decomposition (SVD) procedure [5, 10]. For a better description of the interaction, both first and second PCA scores of genotypes and environments are may be considered for plotting. Here second PCA scores of genotypes and environments are plotted against their respective first PCA scores. Biplot formulation of interaction will be successful only when significant proportion of GEI is concentrated in the first or first two PCA axes. When F tests mandates to retain more than 2 axes in the AMMI model, the biplot formulation of interaction will fail. Subsequently, the stability conclusions made based on biplots will be imprecise [12]. In this cases, one may be interested to consider the procedures that accumulate considerable proportion of interaction SS (all the  $N'$  significant PCA axes or all possible  $N$  axes) to make the stability conclusions more reliable. Another remark that can be made on biplots is that, when the stability differences among the genotypes are very close it will be difficult to distinguish the genotypes with respect to the stability. Because of the limitations of biplot concerning stability conclusion, we attempt to derive a more comprehensive stability measures retaining all possible  $N'$  PCA axes (fitted AMMI model).

The objectives of this study were to (i) evaluate the adaptation and stability of some advanced and promising chickpea genotypes selected from the Iran/ICARDA collaborative project in the environments of Iran, (ii) the reliability of stability conclusions improves with increase in the number of PCA axes and (iii) study the relationships, similarities and dissimilarities among some measures of stability from AMMI model.

## MATERIALS AND METHODS

This study was carried during 2004 and 2005 in five different research stations in Iran. The locations consist of Ghachsaran, Gorgan, Ilam, Kermanshah and Lorestan. These genotypes were developed at different research institutes/ stations of Iran and that of the International Center for Agricultural Research in the Dry Areas (ICARDA), Syria. The names, origin and genotypic codes of these genotypes are given in Table 5. Experimental layout was a randomized complete block design with four replications in each environment. Each plot consisted of four rows of 4 meter length. Row to row and hill-to-hill distances was kept at 30 and 10 cm, respectively. Data on seed yield were taken from the middle two rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

### Measures of Stability from AMMI Model

The model AMMI analysis was used to investigate GEI. The model AMMI equation is [7]:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \sum_{k=1}^N \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij} + \varepsilon_{ijk}$$

Where  $Y_{ijk}$  is the yield of genotype G in environment E for replicate r,  $\mu$  is the total yield mean,  $\alpha_i$  is the genotype G mean deviation (genotype mean minus total yield mean),  $\beta_j$  is the environment E mean deviation,  $\lambda_k$  is the singular value for IPCA axis N,  $\gamma_{ik}$  is the genotype G eigenvector value for IPCA axis N,  $\delta_{jk}$  is the environment E eigenvector value for IPCA axis N,  $\rho_{ij}$  is the residual, and  $\varepsilon_{ijk}$  is the error.

Thirteen stability parameters were derived from AMMI analyses. Parameters of AMMI (SIPC, EV and AMGE) according to the below equations was proposed by Sneller et al (1997) [15]. The first AMMI statistics, sums of the absolute value of the IPC scores (SIPC) for the  $i$ th genotype and  $N'$  was the number of IPC that were retained in the AMMI model via  $F$  tests [8].

$$SIPC_i = \sum_{k=1}^{N'} |\lambda_k^{0.5} \gamma_{ik}|$$

The closer the SIPC scores are to zero, the more stable the genotypes are across test environments [11]. The absolute value of first IPCA scores represented the simplest measure of yield stability. The next AMMI stability statistic (EV) was suggested by Sneller et al (1994) [15], and is averages of the squared eigenvector values, for the  $j$ th cultivar and  $N'$  were the number of IPC which were significant.

$$EV_i = \sum_{k=1}^{N'} \frac{\gamma_{ik}^2}{N'}$$

The next AMMI statistics (AMGE) is the sums across environments of the GEI modeled by AMMI, where E is the number of environments.

$$AMGE_i = \sum_{j=1}^E \sum_{k=1}^{N'} \lambda_k \gamma_{ik} \delta_{jk}$$

$N'$  was the number of IPC which were significant. Also the lower these parameters, the more stable a genotype is to environments.

Another stability parameter of AMMI according to the below equation was proposed by Annicchiarico (1997) [1].

$$Da_i = \sqrt{\sum_{k=1}^{N'} (\lambda_k \gamma_{ik})^2}$$

The statistic coefficient ( $Da_i$ ) for test of treatments or test years is calculated as follows:

$$Dz_i = \sqrt{\sum_{k=1}^{N'} \gamma_{ik}^2}$$

Where  $Dz_i$  is the distance of interaction principal component (IPC) point with origin in space,  $N'$  is the number of significant IPCs, and  $\gamma_i$  is the score of  $i$ th treatment in IPCs. The  $Dz_i$  gives the interaction estimate, and the treatment with the lowest value of the statistic  $Dz_i$  would be more stable [19].

Purchase (1997) [11] developed the AMMI stability value (ASV) based on the AMMI model's  $IPCA_1$  and  $IPCA_2$  scores for each genotype. ASV was calculated using as suggested by Purchase (1997) [11]:

$$ASV_i = \sqrt{\frac{SSIPC_1}{SSIPC_2} (PC_1)^2 + (PC_2)^2}$$

Where, ASV is the AMMI stability value, SS, sum of squares,  $IPCA_1$ , interaction of principal component analysis one,  $IPCA_2$ , interaction of principal component analysis two.

A parameter as modified AMMI's stability value (MASV) is introduced as below formula:

$$MASV_i = \sqrt{\sum_{k=1}^{N'-1} \left( \frac{SSIPC_n}{SSIPC_{n+1}} \right) (PC_n)^2 + (PC_{N'})^2}$$

In this modified AMMI stability parameter, all significant IPCs were used.

Stability parameters of AMMI according to the below equation was proposed by Raju (2002) [12], that develop four measures of stability by retaining varying number of axes in the AMMI model. When the first PCA axis only is retained in the AMMI model, to develop a measure  $FP_1$  as

$$FP_i = \lambda_1^2 \gamma_{i1}^2$$

However the absolute value of  $\gamma_{i1}^2$  alone is sufficient for comparison. Since  $\lambda_1^2$  is same for all the genotypes. The comparison of genotypes for stability based on this measure will be equivalent to the comparison based on Biplot with first PCA axis.

If retain the first two PCA axes in the AMMI model, to develop a measure  $B_i$  as

$$B_i = \sum_{k=1}^2 \lambda_k^2 \gamma_{ik}^2$$

Stability comparisons based on this measure will be equivalent to the comparisons based on biplot with first two PCA axes.

Also consider the measure based on fitted AMMI model by retaining  $N'$  axes. Where  $N'$  is determine by the F test.

$$FA_i = \sum_{k=1}^{N'} \lambda_k^2 \gamma_{ik}^2$$

The proposed stability measure  $W_{i(AMMI)}$  which accommodates all possible PCA axes is shown equivalent to Wricke's ecovalence.

$$W_{i(AMMI)} = \sum_{k=1}^N \lambda_k^2 \gamma_{ik}^2$$

Where  $\lambda_k$  is the singular value for IPCA axis N,  $\gamma_{ik}$  is the genotype g eigenvector value for IPCA axis N.

Also for effective interpretation of GEI via AMMI model two parameters as  $AV_{(AMGE)}$  and  $Za_i$  is introduced as below formulas:

$$AV_{(AMGE)} = \sum_{j=1}^E \sum_{k=1}^{N'} |\lambda_k \gamma_{ik} \delta_{jk}|$$

$AV_{(AMGE)}$  method is actually absolute value of the sums across environments of the GEI modeled by AMMI (AMGE) [15].

$$Za_i = \sum_{k=1}^{N'} |\delta_k \gamma_{ik}|$$

Where  $Za_i$  is absolute value the relative contribution IPCs to the interaction,  $\delta_k$  is percent IPCSS to the interaction SS and  $N'$  was the number of IPC that were retained in the AMMI model via  $F$  tests.

Spearman's coefficient of rank correlation ( $r_s$ ) was employed [16] to statistically compare the stability indices used in this study. Spearman's rank correlation coefficient ( $r_s$ ) can be described as:

$$r_s = 1 - \frac{6 \sum d_i^2}{(n-1)n(n+1)}$$

Ranking numbers are whole numbers and when two or more equal ranking numbers occur, the average of the ranking numbers that they otherwise would have received, are ascribed to each genotype. The measures of stability from AMMI analysis were compared using their ranks for each genotype via calculating Spearman's rank correlation [16]. Calculations were performed by GENSTAT and Excel software using the full data (including all replicates data) for AMMI model. The correlation of the parameters and its significance level was determined by using the software package STATISTICA. To understand better relationships among stability methods, principal component analysis (PCA), was performed.

## RESULTS AND DISCUSSION

The AMMI analysis of variance of mean yield ( $\text{kg ha}^{-1}$ ) of 17 chickpea genotypes tested in 10 environments is presented in Table 2. The analysis showed that chickpea grain yield was significantly ( $p < 0.01$ ) affected by environments (E), genotypes (G) and genotype  $\times$  environment interaction (GEI). Environment significantly explained about 81.62% of the total sum of squares due to treatments. A large yield variation explained by environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. In multi environmental trial (MET), environment explains 80% or higher of the total yield variation [17]. Only the small portion that is, 1.67% of the total sum of squares due to treatments was attributed to genotypic effects. GEI significantly explained 16.71% of the treatments variation in grain yield. The magnitude of the GEI sum of squares was about 10 times larger than that for genotypes, indicating that there were sizeable differences in genotypic response across environments. Analysis of GEI is vital for breeders in order to design the dissemination strategies for new varieties. It is important to identify cultivars with specific and general adaptation.

The application of AMMI model for partitioning of GEI (Table 2) revealed the first four terms of AMMI were significant using an approximate F-statistic [9]. The Gollob's test most often retains the multiplicative axis terms of little practical relevance that is, axis with a low proportion of explained GE variation. In this study, the first four multiplicative axis terms explained 48.62, 28.23, 9.68 and 7.73% of GEI sum of squares, respectively. The four IPCAs retained by Gollob's F-test accounted for 84.9% of GE interaction. The AMMI model revealed that there was a more complex interaction of GE and which it could not facilitate graphical visualization of the genotypes in low

dimensions and so it is essential to use an alternative procedure to interpretation of GEI using AMMI parameters. The four IPCAs accounted for 84.9% of the total interaction, the remaining 15.1% being the residual or noise, which is not interpretable and thus discarded [11]. The AMMI model used in this research exhibited a more complex interaction which required a maximum of two PC axes to account for considerable amount of variation in the GEI. Also eigenvectors and four first IPCs for each genotype over all environments is given in table 5.

### AMMI stability measure

Thirteen measures of stability from AMMI model and the mean yield for each genotype over all environments are given in table 3. Genotypic rank differences over environments indicated the presence of crossover GEI [3]. This was confirmed by the significant effect of the GEI in the analysis of variance (Table 2) and indicated the need to assess the response of the genotypes to environmental variation. The 17 genotypes were ranked with respect to their stability with each of the thirteen measures of stability from AMMI model such that lesser the value of the rank more is the stability. The stability rank orders displayed by these thirteen measures of stability from AMMI model was presented in table 4.

According to results of tables 3 and 4 for  $B_i$  stability parameter genotypes  $G_{13}$ ,  $G_8$  and  $G_9$  were the most stable genotypes whereas for  $FA_i$  stability parameter genotypes  $G_8$ ,  $G_{13}$  and  $G_9$  were the most stable genotypes and for  $W_{i(AMMI)}$  stability parameter genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  were the most stable genotypes too. In these methods genotype  $G_{15}$  was the most unstable genotype but had relatively high mean yield performance.  $FP_i$  stability parameter which derived from these methods revealed that genotypes  $G_{15}$ ,  $G_{16}$  and  $G_{13}$  were the most stable genotypes while genotypes  $G_{10}$ ,  $G_{17}$  and  $G_1$  were the most unfavorable genotypes. Overall according to  $B_i$ ,  $FA_i$  and  $W_{i(AMMI)}$  parameters, genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  had the most stability and genotype  $G_{13}$  could be introduced as the most favorable genotype with both high mean yield and stability.  $FP_i$  measure is equivalent to biplot with first PCA axis and  $FA_i$  measure is equivalent to biplot with first two PCA axes for ranking of genotypes. The stability measure  $W_{i(AMMI)}$  which accommodates all possible PCA axes is equivalent to Wruck's ecovalence [12].

Results of Sneller et al (1997) [15] stability statistics are shown in Table 3, and the ranks of genotypes according to these measures are given in Table 4. According to the  $EV_4$ ,  $SIPC_4$ , and  $AMGE_4$  parameters, the genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  were considered stable in comparison with the other genotypes.  $AV_{(AMGE)}$  like these methods identified  $G_8$ ,  $G_9$  and  $G_{13}$  as the most stable genotypes, although genotypes  $G_8$  and  $G_9$  had the lowest mean yield. Also results of Zhang et al (1997) [19] ( $Dz_4$ ) and Annicchiarico's (1997) [1] ( $Da_4$ ) stability statistics were similar to these measures. These methods calculated based on fitted AMMI model by retaining  $N'$  is determined by the F tests.

The ASV as described by Purchase (1997) [11] and MASV are comparable with the other stability parameters of AMMI model in the study of GEI. Table 4 indicates the ranks of genotypes according to ASV values and MASV for each genotype. Results of ASV parameter showed that genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  were the most stable. The most unstable were genotypes  $G_{10}$ ,  $G_{15}$  and  $G_4$ . Although, ASV parameter was reported to produce a balanced measurement between the two first PC's ( $PC_1$  and  $PC_2$ ) scores, but it seems that this parameter is useful when the portion of explained total variation was relatively high [14]. The results of the modified AMMI's stability value (MASV) which benefits all four significant IPCs, indicated that genotypes  $G_{13}$ ,  $G_8$ ,  $G_9$  and  $G_3$  were most stable which genotype  $G_{13}$  had relatively high mean yield performance whereas genotypes  $G_{15}$ ,  $G_5$  and  $G_4$  were the most unstable genotypes which had relatively high mean yield performance (Table 4). ASV measure is equivalent to biplot with first two PCA axis and MASV measure is equivalent to plot with first four PCA axes for ranking of genotypes.

According to the ranks of genotypes (table 4) the lowest  $Za_4$  was observed genotype for  $G_8$  followed by  $G_{13}$  and  $G_9$  (Table 3). According to  $Za_4$ ,  $G_{13}$  was the most stable genotype with the mean yield ( $1718 \text{ kg ha}^{-1}$ ) higher than total yield mean (average of all genotypes yield  $1702 \text{ kg ha}^{-1}$ ). The highest  $Za_4$  was belonging to  $G_4$  followed by  $G_{10}$  and  $G_{12}$  that only  $G_4$  had high mean yield than total yield mean.

The significant GEI, its complexity, and the changes in ranks of genotypes across environments suggest a breeding strategy of specifically adapted genotypes in homogeneously grouped environments. The AMMI procedure used in this study indicated a more complex interaction which required four PC axes to account for considerable amount of variation in the GEI. Therefore, it is clear those parameters which use the number of IPC that were retained in the AMMI model via F tests ( $SIPC_4$ ,  $EV_4$ ,  $AV_{(AMAG)}$ ,  $AF_1$ ,  $Da_4$ ,  $Dz_4$ ,  $Za_4$  and MASV) are better than those parameters which use the first of IPC ( $FP_1$ ) or the first two of IPC ( $B_i$  and ASV). Also, the ASV and  $B_i$  uses two IPC scores to

produce a balanced measurement between them, and can be useful in situations which two first IPCs counted considerable amount of GEI and the portion of explained total variation was relatively high. However, it seems that there is not a way to consider all of these parameters simultaneously, and some of them should be used in each research regarding number of significant IPCs [12, 13]. Also using  $SIPC_4$ ,  $EV_4$ ,  $AV_{(AMAG)}$ ,  $AF_i$ ,  $Da_4$ ,  $Dz_4$ ,  $Za_4$  and  $MASV$  parameters is a way to consider all of significant IPC simultaneously.

#### **Relationship between mean yield and measures of stability from AMMI model**

Spearman's rank correlation [16] was determined for each pair of mean yield and measures of stability from AMMI model (table 6). Mean yield showed highly significant ( $P < 0.01$ ) positive rank correlation with all measures (except for  $FP_i$  and  $AMGE_4$ ).

$B_i$  method and  $ASV$  revealed positive correlation ( $0.96^{**}$ ) compared to the other measurements. Stability comparisons based on these measures will be equivalent to the comparisons based on biplot with first two PCA axes. Also  $B_i$  exhibited high significant positive correlation with most of the stability measures (except for  $FP_i$  and  $MAGE_4$ ).  $FP_i$  measure indicated the greatest deviation from other procedures.  $FA_i$  and  $W_{i(AMMI)}$  were highly significantly positively correlated with the measures  $SIPC_4$ ,  $EV_4$ ,  $AMGE_4$ ,  $ASV$ ,  $MASV$ ,  $Dz_4$ ,  $AV_{(AMGE)}$ ,  $Za_4$ ,  $Da_4$  and mean yield (except for  $FP_i$  and  $MAGE_4$ ).

Sneller et al (1997) [15] stability statistics ( $SIPC_4$  and  $EV_4$ ) and Annicchiarico's (1997) [1] stability statistic ( $Da_4$ ) showed the highest significant positive correlation with more methods ( $ASV$ ,  $MASV$ ,  $Dz_4$ ,  $AV_{(AMGE)}$ ,  $Za_4$ ,  $B_i$ ,  $FA_i$  and  $W_{i(AMMI)}$ ) and non-significant correlation with  $AMGE_4$  and  $FP_i$ . Also the statistics  $AMGE_4$  showed the greatest deviation from all the other procedures.

Procedure  $Za_4$  exhibited high significant positive correlation with most of the stability measures (except for  $AMGE_4$ ) and mean yield.

To better understand the relationships among the measures of stability from AMMI model, principal component analysis (PCA), based on the rank correlation matrix (table 3) was used. The first four PCAs explained 87.71% (73.93 and 13.72 by  $PCA_1$  and  $PCA_2$ , respectively) of the variances in the original variables (fig. 1). The relationships among different stability parameters are graphically displayed in a biplot of  $PCA_1$  and  $PCA_2$  (Fig. 1). The  $PCA_1$  and  $PCA_2$  axes mainly distinguish the measures of stability from AMMI model in different groups. Mean yield groups with procedures  $SIPC_4$ ,  $EV_4$ ,  $Dz_4$ ,  $AV_{(AMGE)}$ ,  $W_{i(AMMI)}$ ,  $B_i$  and  $FA_i$  which we refer to group 1 stability measures. The PCs axes separated measures  $ASV$ ,  $Za_4$ ,  $B_i$  and  $Da_4$  (We refer to as group 2) and  $FP_i$  was separated from the other classes (we refer to as group 3) (fig. 1).

Group1 included the sums of the absolute value of the IPC scores ( $SIPC_4$ ), averages of the square eigenvector values ( $EV_4$ ), modified AMMI stability value ( $MASV$ ), distance of IPC point with origin in space ( $Dz_4$ ), absolute value of the sum across environments ( $AV_{(AMGE)}$ ), Wruck's ecovalance in term of AMMI ( $W_{i(AMMI)}$ ), stability statistic based on the fitted AMMI model ( $FA_i$ ) and mean yield. According to results of group 1, the genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  were considered stable in comparison with the other genotypes, although genotypes  $G_8$  and  $G_9$  had the lowest mean yield. Also genotype  $G_{13}$  could be introduced as the most favorable genotype with both high mean yield and stability.

Group 2 included the AMMI stability value ( $ASV$ ), parameter of Annicchiarico (1997) [1] ( $Da_4$ ), stability statistic based on the first IPC axes of the first two IPC axes ( $B_i$ ) and Absolute value the relative contribution IPCs to the interaction ( $Za_4$ ).

These stability methods were positively and linearly correlated with each other. All these parameters were significantly correlated with mean yield. Therefore, these parameters allow the identification of genotypes adapted to environments with favorable growing conditions. Also Group 2 stability measures, revealed that genotypes  $G_8$ ,  $G_9$  and  $G_{13}$  with the lowest values for this stability parameters were stable genotypes, but only genotype  $G_{13}$  had the highest mean yield and also genotypes  $G_{10}$  and  $G_{15}$  with highest values was unstable (tables 3 and 4).

Stability statistics employed in this study quantified stability of genotypes based on yield or stability or yield and yield stability. But both yield and stability of performance should be considered simultaneously to exploit the useful effect of GEI and to make selection of the genotypes more precise and refined.

Group 3 included stability statistic based on the first IPC axes of the first IPC axes (FP<sub>1</sub>). This parameter was not significantly correlated with mean yield. FP<sub>1</sub> stability parameter which derived from other methods revealed that genotypes G<sub>15</sub>, G<sub>16</sub> and G<sub>13</sub> were the most stable genotypes while genotypes G<sub>1</sub>, G<sub>17</sub> and G<sub>10</sub> were the most unfavorable genotypes.

**Table 1 Geographical parameters for the location**

Location	Latitude	Longitude	Altitude (m)	Soil condition	
				Texture	Type†
Ghachsaran	30°10'N	50°50'E	669.5	Silt-Loam	Regosols
Gorgan	36°51'N	54°16'E	13.3	Sandy-Loam	Cambisols
Lorestan	23°26'N	48°17'E	1147.7	Silt-Loam	Regosols
Ilam	33°38'N	46°25'E	1363.4	Silt-Loam	Cambisols
Kermanshah	34°19'N	47°07'E	1322	Silt-Loam	Cambisols

†: Type, according to FAO system of soil classification

**Table 2 Partitioning of the sum of squares (SS) and mean of squares (MS) from the AMMI analysis of 17 chickpea advanced genotypes yield performance evaluated across 10 environments**

S.O.V	Df	Sum of square	SS% (δ)	Mean of square
Total	679	406191141		
Treatments	169	341964710		2023460**
Genotypes	16	5714705	1.67	357169 <sup>ns</sup>
Environments	9	2799105517	81.62	31011724**
Interactions	144	57144488	16.71	396837**
IPCA <sub>1</sub>	24	27566258	48.24	1148594**
IPCA <sub>2</sub>	22	16129482	28.23	733158**
IPCA <sub>3</sub>	20	5534116	9.68	276706**
IPCA <sub>4</sub>	18	4417457	7.73	245414**
Residuals	60	3497176	6.12	58286
Pooled error	510	64226431		125934

<sup>ns</sup> and \*\*: non-significant and significant at 1% probability level, respectively.

**Table 3 Mean yield and measures of stability from AMMI model for 17 chickpea genotypes**

No. genotypes	EV <sub>4</sub>	SIPC <sub>4</sub>	Da <sub>4</sub>	Dz <sub>4</sub>	AMGE <sub>4</sub>	AV (AMGE)	ASV	MASV	FP <sub>1</sub>	B <sub>i</sub>	FA <sub>i</sub>	W <sub>i(AMMI)</sub>	Za <sub>4</sub>	Mean yield
1	0.055	36.18	948.8	0.936	16.68	76.35	22.37	26.95	280.7	302.0	413.6	589.3	22.49	1774
2	0.049	29.16	894.2	0.831	-9.28	62.63	21.25	23.99	258.8	268.1	364.6	460.5	19.47	1610
3	0.042	26.77	652.3	0.821	24.41	60.76	13.47	19.47	92.8	115.8	244.8	417.1	15.08	1647
4	0.078	45.12	1089.6	1.039	21.65	97.33	24.65	37.68	253.9	427.5	576.3	591.6	27.61	1884
5	0.144	43.85	1051.4	1.063	-33.10	91.37	15.79	41.50	119.1	164.9	761.1	841.1	21.84	1734
6	0.037	31.02	750.7	0.861	-12.30	66.93	17.04	25.82	122.5	203.6	272.1	308.5	19.04	1631
7	0.098	41.10	957.0	1.020	-8.28	97.39	18.61	35.16	78.57	290.7	560.4	681.4	21.79	1838
8	0.013	17.78	462.6	0.643	-4.32	38.10	10.52	16.62	41.02	81.5	102.8	181.8	11.44	1579
9	0.021	20.65	540.8	0.705	-0.54	48.58	11.85	21.88	19.42	126.6	151.5	193.3	12.12	1579
10	0.053	33.36	1134.0	0.860	29.75	68.31	28.47	30.33	458.7	485.2	511.9	677.1	25.12	1688
11	0.051	30.18	827.6	0.860	10.35	57.47	18.11	25.99	190.0	193.2	346.6	382.0	18.12	1654
12	0.075	42.07	991.5	1.016	-32.50	94.24	22.05	31.92	216.2	332.9	503.2	542.2	24.78	1672
13	0.024	22.27	504.4	0.746	-2.21	49.23	9.69	20.61	19.0	80.5	149.9	228.3	11.80	1718
14	0.050	33.26	870.3	0.903	-5.92	77.31	19.91	29.58	152.5	288.2	368.5	501.8	21.47	1683
15	0.110	40.82	1242.4	1.006	-8.45	99.10	26.81	54.52	0.38	718.5	808.5	893.5	20.96	1835
16	0.056	29.76	761.9	0.869	17.09	65.71	15.21	31.20	10.5	223.8	342.3	472.2	15.13	1612
17	0.043	30.74	958.6	0.835	24.42	50.57	23.51	26.99	310.7	332.4	383.5	423.5	21.85	1796
Mean	<b>0.059</b>	<b>32.65</b>	<b>861.1</b>	<b>0.883</b>	<b>1.616</b>	<b>70.67</b>	<b>18.78</b>	<b>29.42</b>	<b>154.4</b>	<b>272.7</b>	<b>403.6</b>	<b>493.3</b>	<b>19.42</b>	<b>1702</b>

EV<sub>4</sub>: Averages of the square eigenvector values, SIPC<sub>4</sub>: Sums of the absolute value of the IPC scores, Da<sub>4</sub>: parameter of Annicchiarico (1997), Dz<sub>4</sub>: Distance of IPC point with origin in space, AMGE<sub>4</sub>: Sum across environments of the GEI modeled by AMMI, AV (AMGE): Absolute value of the sum of the environments, ASV: AMMI stability value, MASV: Modified AMMI stability value, FP<sub>1</sub>: Stability statistic based on the first IPC axes of the first IPC axes, B<sub>i</sub>: Stability statistic based on the first IPC axes of the first two IPC axes, FA<sub>i</sub>: Stability statistic based on the first IPC axes based on fitted AMMI model, W<sub>i(AMMI)</sub>: Wruck's ecovalence in term of AMMI and Za<sub>4</sub>: Absolute value the relative contribution IPCs to the interaction.



Table 4 Ranks of 17 genotypes using mean yield and measures of stability from AMMI model

No. genotypes	EV <sub>4</sub>	SIPC <sub>4</sub>	Da <sub>4</sub>	Dz <sub>4</sub>	AMGE <sub>4</sub>	AV <sub>(AMGE)</sub>	ASV	MASV	FP <sub>i</sub>	B <sub>i</sub>	FA <sub>i</sub>	W <sub>i(AMMI)</sub>	Za <sub>4</sub>	Mean yield
1	11	12	9	12	10	11	13	8	15	12	11	12	14	5
2	7	5	10	5	7	7	11	5	14	9	8	8	8	15
3	5	4	4	4	13	6	4	2	7	5	4	6	4	10
4	14	17	15	16	12	16	15	15	13	15	15	13	17	1
5	17	16	14	17	17	13	6	16	8	4	16	16	13	6
6	4	9	5	9	9	9	7	6	9	7	5	4	7	13
7	15	14	11	15	5	15	9	14	6	11	14	15	12	2
8	1	1	1	1	3	1	2	1	5	2	1	1	1	16
9	2	2	3	2	1	2	3	4	4	3	3	2	3	16
10	10	10	16	7	15	10	17	11	17	16	13	14	16	8
11	9	7	7	7	8	5	8	7	11	6	7	5	6	11
12	13	15	13	14	16	14	12	13	12	14	12	11	15	9
13	3	3	2	3	2	3	1	3	3	1	2	3	2	7
14	8	11	8	11	4	12	10	10	10	10	9	10	10	12
15	16	13	17	13	6	17	16	17	1	17	17	17	9	3
16	12	6	6	10	11	8	5	12	2	8	6	9	5	14
17	6	8	12	6	14	4	14	9	16	13	10	7	11	4

Table 5 Genotypes names, origin, eigenvector and interaction principle component of mean yield for chickpea genotypes

Genotypes no.	Genotypes names	Origin	Eigenvectors for genotypes				interaction principle component							
			γ <sub>i1</sub>	γ <sub>i2</sub>	γ <sub>i3</sub>	γ <sub>i4</sub>	IPCA <sub>1</sub>	IPCA <sub>2</sub>	IPCA <sub>3</sub>	IPCA <sub>4</sub>				
1	FLIP 97-211	ICARDA	-0.327	-0.103	-0.187	-0.259	-16.754	-4.616	-6.413	-8.396				
2	FLIP 97-113	ICARDA	0.314	-0.068	0.006	0.303	16.088	-3.047	0.206	9.823				
3	FLIP 97-85	ICARDA	-0.188	-0.107	-0.030	0.349	-9.633	-4.795	-1.029	11.314				
4	FLIP 97-78	ICARDA	-0.311	0.294	0.327	0.148	-15.935	13.175	11.215	4.798				
5	FLIP 97-41	ICARDA	0.213	0.151	0.710	-0.056	10.913	6.767	24.350	-1.815				
6	FLIP 97-30	ICARDA	0.216	0.201	-0.220	-0.105	11.067	9.007	-7.545	-3.404				
7	FLIP 97-102	ICARDA	-0.173	0.325	0.038	-0.505	-8.864	14.564	1.303	-16.371				
8	FLIP 97-79	ICARDA	0.125	-0.142	-0.134	-0.013	6.405	-6.363	-4.596	-0.421				
9	X95TH1	ICARDA	0.086	0.231	-0.029	0.151	4.406	10.351	-0.995	4.895				
10	X95TH154	ICARDA	-0.418	-0.115	0.060	0.146	-21.417	-5.153	2.058	4.733				
11	FLIP 97-43	ICARDA	0.269	-0.040	-0.354	-0.076	13.783	-1.792	-12.140	-2.464				
12	FLIP 97-95	ICARDA	0.287	-0.241	0.123	-0.381	14.705	-10.800	4.218	-12.351				
13	FLIP 97-114	ICARDA	0.085	0.175	-0.236	-0.061	4.355	7.842	-8.094	-1.978				
14	X94TH45K10	ICARDA	0.241	0.260	-0.041	0.273	12.348	11.651	-1.406	8.850				
15	X95TH5K10	ICARDA	-0.012	-0.598	0.201	-0.201	-0.614	-26.797	6.894	-6.516				
16	X45TH150K1	ICARDA	-0.063	-0.326	-0.032	0.334	-3.228	14.609	-1.097	10.827				
17	Arman	Iran	-0.344	0.104	-0.204	-0.045	-17.625	4.660	-6.996	-1.458				
<b>Eigen value</b>			<b>2625.18</b>	<b>2008.08</b>	<b>1176.24</b>	<b>1050.89</b>								

Table 6 Spearman's coefficient of rank correlation for mean yield and measures of stability from AMMI model of 17 chickpea genotypes

	EV <sub>4</sub>	SIPC <sub>4</sub>	Da <sub>4</sub>	AMGE <sub>4</sub>	Dz <sub>4</sub>	ASV	MASV	FP <sub>i</sub>	B <sub>i</sub>	FA <sub>i</sub>	W <sub>i(AMMI)</sub>	AV <sub>(AMGE)</sub>	Za <sub>4</sub>
SIPC <sub>4</sub>	0.868**												
Da <sub>4</sub>	0.819**	0.833**											
AMGE <sub>4</sub>	-0.218	-0.265	-0.034										
Dz <sub>4</sub>	0.918**	0.963**	0.737**	-0.329									
ASV	0.556*	0.654**	0.877**	0.169	0.511*								
MASV	0.936**	0.882**	0.862**	-0.203	0.903**	0.620**							
FP <sub>i</sub>	0.069	0.311	0.426	0.282	0.135	0.627**	0.056						
B <sub>i</sub>	0.627**	0.696**	0.873**	0.118	0.589*	0.961**	0.721**	0.466					
FA <sub>i</sub>	0.907**	0.909**	0.963**	-0.157	0.856**	0.779**	0.917**	0.304	0.794**				
W <sub>i(AMMI)</sub>	0.914**	0.855**	0.895**	-0.140	0.847**	0.689**	0.897**	0.181	0.730**	0.953**			
AV <sub>(AMGE)</sub>	0.880**	0.916**	0.782**	-0.333	-0.329	0.623**	0.870**	0.088	0.708**	0.875**	0.902**		
Za <sub>4</sub>	0.667**	0.848**	0.873**	0.078	0.921**	0.853**	0.706**	0.703**	0.833**	0.833**	0.750**	0.699**	
Mean	0.654**	0.745**	0.703**	0.108	0.671**	0.591*	0.676**	0.213	0.593*	0.765**	0.713**	0.662**	0.669**

\* and \*\*: significant at 5% and 1% probability level, respectively

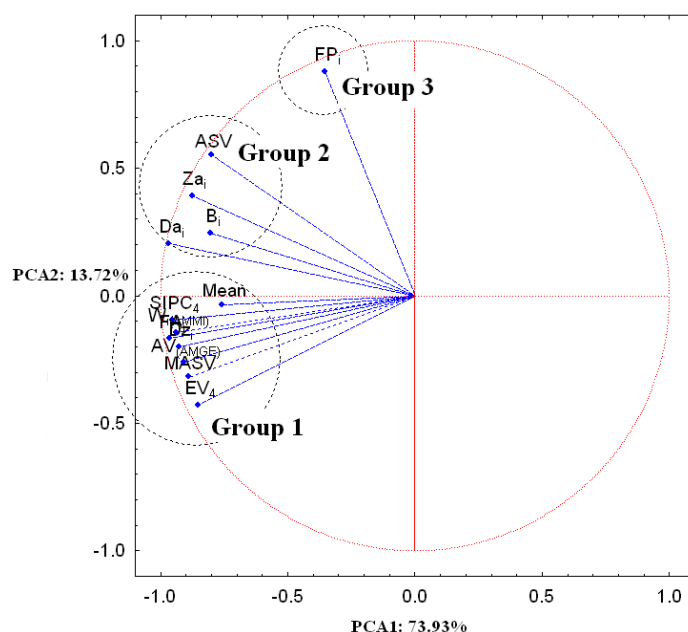


Fig 1 Principal component (PC<sub>1</sub> and PC<sub>2</sub>) analysis plot of ranks of yield stability, estimated by measures of stability from AMMI model using yield data from 17 genotypes grown in 10 environments and showing relationship among these statistics.

### CONCLUSION

In the present study some stability measures are proposed which are equivalent to biplot with first PCA axis and biplot with first two PCA axes for ranking purposes. The reliability of stability conclusions improves with increase in the number of PCA axes, which has been exploited while proposing the new measure of stability. Because of the limitations of biplots concerning stability conclusions, be attempted to derive a more comprehensive stability measure, retaining all possible  $N'$  PCA axes. The proposed stability measures are precise in the order in which amount of information increases.

It seems that various measures of stability from AMMI model indicate similar aspects of yield stability and GEI nature. More parameters use first four IPC (except for ASV, B<sub>i</sub>, FP<sub>i</sub>) and can explain 84.9 percent of variation for GE interaction, therefore according to all stability statistics and regarding the high mean yield, genotype G<sub>13</sub> (FLIP 97-114) was recommended for national release in Iran, as it adequately demonstrated wide adaptation across environments.

Za<sub>4</sub> Method exhibited high significant positive correlation with most of the stability measures (except for AMGE<sub>4</sub>) and mean yield. Therefore we propose that researcher use of Za<sub>4</sub> parameters for evaluating adaptability and stability of genotypes or cultivar because this parameters showed that they had high significant correlated with other parameters.

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