AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments

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ABSTRACT: The genotype × environment interaction has a direct effect on genotypes stability and adaptability in different environmental conditions. In this sense, plant breeders look for genotypes that have general adaptability, or they look for genotypes that have specific adaptability for specific environments. In this regard, 20 chickpea genotypes were used in a randomized complete block design with three replications under two rainfed and irrigated conditions for 4 consecutive growing seasons (2008-2011). AMMI analysis showed that chickpea grain yield was significantly (p<0.01) affected by environments (E), genotypes (G) and genotype × environment interaction (GEI) indicating the presence of genetic variation and possible selection of stable entries. 81.62% of the total sum of squares was justified by environmental fluctuations exhibiting that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. GEI was further partitioned by principal component analysis. The first three multiplicative axis terms (PCA1, PCA2 and PCA3) explained 48.37, 25.54 and 16.17% (90.08%) of GEI sum of squares, respectively. According to AMMI1 biplot G2, G8, G11, G14 and G19 (adaptive group 1) exhibited specific adaptability for rainfed environments: E3, E5 and E7 with grain yield less than mean and positive interaction. Genotypes G4, G5, G6, G12, G16 and G17 (adaptive group 2) revealed specific adaptation for irrigated environments E4, E6 and E8 with high grain yield more than mean yield and positive interaction. The accessions G3, G7, G13, G18 and G18 (adaptive group 3) on the IPCA= 0 showed stability and general adaptability with grain yield close to mean yield and negligible interaction. The entries G1, G9 and G10 (adaptive group 4) were identified with specific adaptability for irrigated environment E2 with positive interaction and G20 (adaptive group 5) was screened with general adaptability for stress and non-stress environments (close to IPCA = 0) with high grain yield more than mean yield and negligible interaction.

Key words: Chickpea, genotype × environment interaction, AMMI model, biplot.

INTRODUCTION

Chickpea is the third most important pulse crop in the world, representing 14% of total world pulse production (Kelley et al., 1994). Chickpea is grown on 700,000 ha in Iran and ranks fourth in the world after India, Pakistan and Turkey. It occupies about 64% of the areas grown to food legumes in the country, which is 5.1% chickpea growing area in the world and produces 2.75% of global production. Chickpea productivity in Iran is less than half of the world average yield. Chickpea with 17-24% protein and 41-50.8% carbohydrates is one of the most important food crops (Witcombe and Erskine, 1984; Zali et al., 2011).

Iran is currently one of the world's largest net importers of agricultural products, importing about 30% of its requirements. Rapid population growth is expected to increase the demand for food. Iran is working towards increasing its agricultural efficiency. To increase its efficiency, the agricultural sector of Iran is attempting to improve chickpea production with identification and introduction of stable and adaptive cultivars (Ebadie Segherloo et al., 2008).

However, high yield is often associated with decreased yield stability (Calderini and Sailer, 1999; Padi, 2007). The terms 'stability' or 'adaptability' refer to consistent high performance of genotypes across diverse sets of environments (Romagosa and Fox, 1993). Yield is a complex quantitative trait, and such traits are often controlled by many genes, influenced by prevailing environmental conditions, with each gene having a small effect. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials (Luquez et al., 2002).
Genotypes tested in different locations or years often have significant fluctuations in yield due to the response of genotypes to environmental factors such as soil fertility or the presence of biotic and abiotic environmental stresses (Kang, 1993). These fluctuations are often referred as genotype × environment interaction (GEI).

GEI affects breeding progress because it complicates the demonstration of superiority of any genotype across environments and the selection of superior genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Another undesirable effect of GEI includes low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll, 1963; Alghamdi, 2004). Therefore, the magnitude and nature of GEI determine the features of a selection and testing program.

Various methods have been proposed to measure the stability of genotypes over environments. However, no single method can adequately explain cultivar performance across environments (Dehghani et al., 2006). These methods can be classified into two groups: graphical (GGE biplot an performance plots) and non-graphical [parametric (univariate and multivariate) and non-parametric]. Multivariate models include a wide range of methods such as principal component analysis (PCA) (Gower, 1967), cluster analysis (Mungomery et al., 1974) and additive main effects and multiplicative interaction models (AMMI) (Gauch and Zobel, 1988).

The multivariate model, AMMI appeared to be able to extract a large part of the genotype - environment interaction and was efficient in analyzing interaction patterns (Zobel et al., 1988). Gauch (1992) reported that multivariate models captured a large portion of the genotype × environment interaction sum of squares clearly separating main and interaction effects, and the model often provided an agronomically meaningful interpretation of the data. Differences in genotype stability and adaptability to environment can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita et al., 2010). AMMI model is known as other names like Fanova, bilinear model and bi-additive model. In AMMI method firstly, the main additive effects of genotype and environment are considered by variance analysis, and then are analyzed by principal characteristics of remain value from variance analysis model (Gauch and Zobel, 1997). Totally, AMMI follows three basic purposes: firstly, is an appropriate method for primary analysis of performance tests. Secondy, explain the effect of genotype × environment. Thirdly, performance estimate is done by more accuracy. The amount of estimate accuracy by AMMI method is like increasing repetition number (Gauch, 1992).

The objective of this study was to evaluation of adaptation and stability of some advanced and promising chickpea genotypes in one of the most important production areas of Iran, Kermanshah.

### MATERIALS AND METHODS

#### Plant materials

In order to identify stable and high performance genotypes of chickpea (Table 1) a randomized complete block design (RCBD) with three replications was carried out in two different environments (rainfed and irrigated) for four growing seasons (2008-2011) (8 environments E1 to E8) in the Campus of Agriculture and Natural Resources of Razi University of Kermanshah, Iran (47° 20’ N, 34° 20’ E and 1351 m above sea level). The maximum and minimum temperatures were 44°C and –27°C and the average rainfall was 478 mm. The soil of experimental field was clay loam with a pH of 7.1.

Each plot consisted of five rows of 1.5 meter length. Row to row and hill-to-hill distances were kept at 30 and 10 cm, respectively. Data on seed yield were taken from the middle three rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

<table>
<thead>
<tr>
<th>Genotype Codes</th>
<th>Genotype names</th>
<th>Genotype Codes</th>
<th>Genotype names</th>
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</thead>
<tbody>
<tr>
<td>G1</td>
<td>X96TH54</td>
<td>G11</td>
<td>X95TH12</td>
</tr>
<tr>
<td>G2</td>
<td>FLIP-82-150C</td>
<td>G12</td>
<td>X96TH46</td>
</tr>
<tr>
<td>G3</td>
<td>FLIP-00-40C</td>
<td>G13</td>
<td>FLIP-82-245</td>
</tr>
<tr>
<td>G4</td>
<td>S96085</td>
<td>G14</td>
<td>X95TH154</td>
</tr>
<tr>
<td>G5</td>
<td>Bivanidi</td>
<td>G15</td>
<td>ILC482</td>
</tr>
<tr>
<td>G6</td>
<td>S925274</td>
<td>G16</td>
<td>FLIP-99-26C</td>
</tr>
<tr>
<td>G7</td>
<td>S91181</td>
<td>G17</td>
<td>X96TH41K4</td>
</tr>
<tr>
<td>G8</td>
<td>S95349</td>
<td>G18</td>
<td>X95TH469</td>
</tr>
<tr>
<td>G9</td>
<td>Hashem</td>
<td>G19</td>
<td>FLIP-82-115</td>
</tr>
<tr>
<td>G10</td>
<td>ARman</td>
<td>G20</td>
<td>FLIP-00-6C</td>
</tr>
</tbody>
</table>

The objective of this study was to evaluation of adaptation and stability of some advanced and promising chickpea genotypes in one of the most important production areas of Iran, Kermanshah.
Biometrical genetic analysis
AMMI model

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

$$y_{ger} = \mu + \delta_g + \beta_e + \sum \lambda_n \gamma_{gn} \delta_{en} + P_{ge} + \varepsilon_{ger}$$

Where \( y_{ger} \) is the yield of genotype (G) in environment (E) for replicate (r), \( \mu \) is the total yield mean, \( \delta_g \) is the main effect of genotype or the genotype (G) mean deviation (genotype mean minus total yield mean), \( \beta_e \) is the main effect of environment or the environment (E) mean deviation, \( \lambda_n \) is the singular value for IPCA axis N (N is the number of remain PCA axis in AMMI model: \( N \)). \( \gamma_{gn} \) is the genotype (G) eigenvector value for IPCA axis N, \( \delta_{en} \) is the environment (E) eigenvector value for IPCA axis N, \( P_{ge} \) is the residual or noise and \( \varepsilon_{ger} \) is the error (if the test has repetition). It should be mentioned that Eigen Values \( \lambda_n \) and \( \beta_e \) are without unit. But the single value of \( \delta_{en} \) has a performance unit (Gauch, 1992).

Calculations were performed by GENSTAT and Excel software using the full data (including all replicates data) for AMMI model.

RESULTS AND DISCUSSION

Combined analysis of variance

AMMI analysis of 20 chickpea genotypes tested in 8 environments showed that chickpea grain yield was significantly (P<0.01) affected by environments (E), genotypes (G) and genotype × environment interaction (GEI) (Table 2) indicating the presence of genetic variation and possible selection of stable entries. 81.62% of the total sum of squares was justified by environmental fluctuations exhibiting 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 (Yan, 2002). Only a small portion (6.31%) of the total sum of squares was attributed to genotypic effects. GEI significantly explained 12.57% of the treatments variation in grain yield. The magnitude of the GEI sum of squares was about 2 times larger than that of genotypes, indicating sizeable differences in genotypic response across environments. As GEI was significant therefore we can further proceed and calculate phenotypic stability (Farshadfar, 2008).

AMMI model and pattern analysis

In AMMI model, principal component analysis is based on the matrix of deviation from additivity or residual, while pattern analysis employs both classification and ordination techniques. In this respect both the results of AMMI analysis, the genotype and environment will be grouped based on their similar responses (Gauch, 1992; Pourdad and Mohammadi, 2008).

GEI was further partitioned by principal component analysis (Table 1). Ordination technique using an approximate F-statistic (Gollob, 1968) revealed high significant differences for IPC1, IPC2 and IPC3. 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 three multiplicative axis terms explained 48.37, 25.54 and 16.17% of GEI sum of squares, respectively.

The first three interaction principal components (IPC1, IPC2 and IPC3) retained by Gollob’s F-test accounted for 90.08% of GE interaction. Corrected grain yield can be obtained by AMMI1, AMMI2 and AMMI3 for each environment and used as a selection criteria in breeding programs. In general the importance of AMMI model is in reduction of the noise even if principal components do not cover much of the GESS (Gauch and Zobel, 1988; Gauch, 1992).

The AMMI model revealed that there was a more complex GEI which could not facilitate graphical visualization of the genotypes in low dimensions, so it is essential to use an alternative procedure to interpret GEI using AMMI parameters. The three IPCAs accounted for 90.08% of the total interaction, the remaining 9.92% being the residual or noise, which is not interpretable and thus discarded (Purchase, 1997). 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 three first IPCs for each genotype over all environments are given in Table 2. The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments (Gauch and Zobel, 1996; Purchase, 1997; Martin and Alberts, 2004). The greater the IPCA scores, the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

Biplot analysis
To have a better discussion on the biplots resulted from the AMMI analysis we must consider the following points (Kempton, 1984; Kroonenberg, 1995):

(i) The center of biplot shows the mean of a genotype or an environment.
(ii) A long distance of a genotype (or an environment) from the center of biplot indicates a large interaction with that genotype (or environment).
(iii) The long length of a genotype on the environmental vector reveals more deviation from the mean and vice versa.
(iv) The angle between the vectors of a genotype and an environments shows that the interaction is positive or negative.

Identifying high yielding stable genotypes

To investigate the main effects and interactions, AMMI1 biplot was constructed for yield. In Figure 1, AMMI1 biplot of additive main effects or mean yield are shown along the abscissa and the ordinate represents the first IPCA or multiplicative interaction. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. Biplot space of Figure 1 is divided into 4 sections from low yielding environments in sections 1 (up left) and 4 (low left) to high yielding environments in sections 2 (up right) and 3 (low right). It is clear from the Biplot of Figure 1 that the points for environment are more scattered than the point for genotypes indicating that variability due to environments is higher than that due to genotypes difference which is in complete agreement of ANOVA (Table 2). On the bioplot, the points for the generally adapted genotypes would be at right hand side of grand mean levels (this suggests high mean performance) and close to the line showing IPCA = 0 and (this suggests negligible or no G x E Interaction).

According to the AMMI model, the genotypes which are characterized by means greater than grand mean and the IPCA score nearly zero are considered as generally adaptable to all environment.

However, the genotype with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments.

According to Figure 1: G2, G8, G11, G14 and G19 (adaptive group 1) exhibited specific adaptability for rainfed environments: E3, E5 and E7 with grain yield less than mean. As the genotypes and environments of first adaptive group have the same sign on the IPCA axis, their interaction is positive. Genotypes G4, G5, G6, G12, G16 and G17 (adaptive group 2) revealed specific adaptation for irrigated environments E4, E6 and E8 with high grain yield more than mean yield and positive interaction. The accessions G3, G7, G13, G18 and G18 (adaptive group 3) on the IPCA= 0 showed stability and general adaptability with grain yield close to mean yield and negligible interaction. The entries G1, G9 and G10 (adaptive group 4) were identified with specific adaptability for irrigated environment E2 with positive interaction and G20 (adaptive group 5) was screened with general adaptability for stress and non-stress environments (close to IPCA = 0) with high grain yield more than mean yield and negligible interaction.

AMMI Analysis was also conducted and the stability of genotypes was predicted on the basis of mean performance and the magnitude of IPCA1 scores in soybean (Zobel et al. 1988), maize and wheat (Crossa et al. 1990), sorghum (Zavala-Garcia et al. 1992), barley (Romagossa et al. 1993) and chickpea (Zali et al., 2011)

Identifying favorable environments for chickpea genotypes

Environment that appears almost in a perpendicular line have similar means and those that fall almost in a horizontal line have similar interaction pattern. AMMI1 biplot (Figure 1) thus exhibited that environment differed in main and interactions. The environment E1 and E5 had similar main effect but differed in interaction with genotypes. The ranking in such environments is likely to be quite variable, thus making it complex to produce variety recommendations. Further the environment E2, E4, E6 and E8 were the highest yielding and highly interacting, hence are most suitable only for the specifically adapted genotypes.

<table>
<thead>
<tr>
<th>S.O.V</th>
<th>Df</th>
<th>Sum of square</th>
<th>SS% (ð)</th>
<th>Mean of square</th>
</tr>
</thead>
</table>

Table 2. Partitioning of the sum of squares (SS) and mean of squares (MS) from the AMMI analysis of 20 chickpea advanced genotypes yield performance evaluated across 8 environments
Table 3. Genotypes, mean, eigenvector and interaction principal component of mean yield for chickpea genotypes

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Mean</th>
<th>Eigenvectors for genotypes</th>
<th>Interaction principle component</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Y1</td>
<td>Y2</td>
<td>Y3</td>
</tr>
<tr>
<td><strong>G1</strong></td>
<td>169.3</td>
<td>-0.227</td>
<td>0.132</td>
</tr>
<tr>
<td><strong>G2</strong></td>
<td>153.1</td>
<td>-0.323</td>
<td>-0.351</td>
</tr>
<tr>
<td><strong>G3</strong></td>
<td>154.9</td>
<td>0.055</td>
<td>-0.197</td>
</tr>
<tr>
<td><strong>G4</strong></td>
<td>176.7</td>
<td>0.407</td>
<td>0.228</td>
</tr>
<tr>
<td><strong>G5</strong></td>
<td>153.4</td>
<td>0.038</td>
<td>0.090</td>
</tr>
<tr>
<td><strong>G6</strong></td>
<td>166.2</td>
<td>0.149</td>
<td>-0.117</td>
</tr>
<tr>
<td><strong>G7</strong></td>
<td>144.7</td>
<td>-0.005</td>
<td>0.181</td>
</tr>
<tr>
<td><strong>G8</strong></td>
<td>132.3</td>
<td>-0.251</td>
<td>0.525</td>
</tr>
<tr>
<td><strong>G9</strong></td>
<td>171.4</td>
<td>-0.229</td>
<td>-0.181</td>
</tr>
<tr>
<td><strong>G10</strong></td>
<td>163.1</td>
<td>-0.153</td>
<td>-0.066</td>
</tr>
<tr>
<td><strong>G11</strong></td>
<td>133.1</td>
<td>-0.118</td>
<td>0.079</td>
</tr>
<tr>
<td><strong>G12</strong></td>
<td>214.2</td>
<td>0.339</td>
<td>0.338</td>
</tr>
<tr>
<td><strong>G13</strong></td>
<td>156.3</td>
<td>0.050</td>
<td>-0.004</td>
</tr>
<tr>
<td><strong>G14</strong></td>
<td>140.3</td>
<td>-0.292</td>
<td>-0.190</td>
</tr>
<tr>
<td><strong>G15</strong></td>
<td>182.6</td>
<td>0.123</td>
<td>-0.184</td>
</tr>
<tr>
<td><strong>G16</strong></td>
<td>181.2</td>
<td>0.117</td>
<td>0.042</td>
</tr>
<tr>
<td><strong>G17</strong></td>
<td>199.8</td>
<td>0.444</td>
<td>-0.421</td>
</tr>
<tr>
<td><strong>G18</strong></td>
<td>154.5</td>
<td>0.050</td>
<td>-0.112</td>
</tr>
<tr>
<td><strong>G19</strong></td>
<td>125.1</td>
<td>-0.250</td>
<td>0.109</td>
</tr>
<tr>
<td><strong>G20</strong></td>
<td>168.7</td>
<td>0.070</td>
<td>0.087</td>
</tr>
<tr>
<td>Eigenvalue</td>
<td>270.52</td>
<td>196.56</td>
<td>156.40</td>
</tr>
</tbody>
</table>

ns, * and **: non-significant, significant at 5% and 1% probability level, respectively
Figure 1. Biplot of the first interaction principal component axis (IPCA1) versus mean yields.

Figure 2. Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for chickpea genotypes.

**AMMI 2 biplot**

The IPCA 1 versus IPCA 2 biplot (i.e. AMMI 2 biplot) (Figure 2) explain the magnitude of interaction of each genotype and environment. The genotypes and environments that fall farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Osiru et al., 2009). A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment.
and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific environmental conditions. However, for the AMMI 2 model, IPCA2 scores was considered in interpreting GEI that captured 12.6% of the interaction sum of squares as suggested by Gauch and Zobel (1996). A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). Furthermore, when IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot (Figure 2), the more stable they are.

Figure 2 gives the AMMI2 biplot for yield. The IPCA 1 component accounted for 48.37 % of G×E interaction, while IPCA 2 accounted for only 25.54 % (Table 1). Distribution of genotype points in the AMMI II biplot revealed that the genotypes, G13, G16, G20 and G5 scattered close to the origin, indicating minimal interaction of these genotypes with environments. The remaining 14 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. On this basis, the genotypes G3, G18, G6, G15 and G17 had positive interaction with environments E4 and E6, hence exhibited specific adaptation with irrigated environments. G4 and G12 displayed positive interaction with irrigated environment E8. Genotypes G1, G11, G8 and G19 indicated specific adaptability and positive interaction with environments E5 and E7. The accessions G10, G9, G14 and G2 showed specific adaptability and positive interaction with environments E1, E3 and E2.

In Figure 2 genotypes and environments are depicted as points on a plane. The position of the point for genotype i is given by the estimates for the genotypic scores, similarly, the point coordinates for environment j originate from the estimates for the environmental scores. Distances from the origin (0,0) are indicative of the amount of interaction that was exhibited by either genotypes over environments or environments over genotypes (Thangavel et al., 2011). For example, the genotypes G17, G4, G12, G8, G2 and environments E2, E4, E6, E8, E5 and E7 displayed a highly interactive behavior, whereas the environments E1 and E3 exhibited low interaction. In a vector representation, the genotype and environment points determine lines starting at the origin (0,0). The interaction effect of genotype i in environment j is approximated by projecting the genotype point onto the line determined by the environmental vector, where distance from the origin provides information about the magnitude of the interaction. The angle between the vectors of genotype i and environment j tells us something about its nature: the interaction is positive for acute angles, negligible for right angles, and negative for obtuse angles. Genotypes G3, G18, G6, G15 and G17 showed acute angle with the vectors of E4 and E6 and obtuse angles with the vectors of environments E8, E5, E7, E2 and E1. Genotypes G4 and G12 exhibited acute angle with environments E6, E4 and E8, while obtuse angle with environments E5, E7, E2 and E1. The accessions G1, G11 and G19 revealed acute angle and positive interactions with vectors E1, E2, E3, E5, E7 and E1, where as obtuse angle and negative interaction with the vectors of environments E8, E4 and E6. The entries G10, G9, G14 and G2 displayed acute angle with the vectors of environments E1, E2 and E3, while showed negative interaction and obtuse angle with environments E4, E6 and E8. As the length of the vectors of genotypes G3, G18, G6, G15, G10 and G11 is shorter than the other ones hence they are more adapted to their specified environments, while G17, G4, G12 and G8 with longer vectors indicated more deviation from their specified environments.

REFERENCES

Martin J, Alberts A. 2004. A comparison of statistical methods to describe genotype × environment interaction and yield stability in multi-location maize trials. Faculty of Agriculture, Department of Plant Sciences (Plant Breeding) at the University of the Free State.
Vargas MV, Crossa J. 2000. The AMMI analysis and graphing the biplot. CIMMYT, INT., Mexico.
Witcombe JR, Erskine W. 1984. Genetic resources and their exploitation in chickpea (Cicer aritinum L.), faba beans and lentils. The Netherlands and ICARDA.