Stability analysis of groundnut (*Arachis hypogaea* L.) genotypes using AMMI and GGE biplot models and ideal genotype selection indicator

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**Abstract**

A study on stability analysis was carried out on groundnut (*Arachis hypogaea* L.) genotypes grown at multilocation over two crop seasons. Based on additive main effects and multiplicative interaction (AMMI) analysis, the first two IPCAs explained 91.93% of the GEI variation (74.84 and 17.09% for IPCA1 and IPCA2, respectively). Based on AMMI 2, the best genotype for environments RA1 and RA2 was 201. The genotypes, ICG192 and ICG130 were found suitable for environments TA1 and TA2, respectively. ICG178 was better adapted to environment MA2, whereas ICG140 and the control NC2 were the best genotypes for environment RA2. In the GGE biplot, PC1 and PC2 explained 81.22 and 13.33% of the total GGE variance. Based on the ideal genotype selection index (IGSI), the genotypes, ICG115, ICG201, and ICG178 were stable and can be used in the breeding programs to develop new varieties.

**Keywords:** Adaptability, AMMI analysis, *Arachis hypogaea*, GGE biplot, stability

**Introduction**

Groundnut (*Arachis hypogaea* L.) is an important annual oilseed and protein crop cultivated on approximately 31.57 million hectares with a production of about 53.64 million tons worldwide (FAOSTAT 2022). Peanut cultivation in Iran covers an area of around 3800 hectares, yielding about 9100 tons, with 90% of the country’s peanuts coming from the Guilan and Ardabil provinces (Anonymous 2022). The prevailing groundnut variety in the region is “Goli” or “NC2”, known for its low harvest index and extended growing period (Nobahar et al. 2019). Therefore, evaluating new germplasm is crucial for developing high-yielding cultivars in the region. Environmental conditions play a significant role in the variation of agricultural traits in peanuts (Bonchev et al. 2018), and the performance of peanuts is strongly influenced by environmental factors (Gulluoglu et al. 2016). Therefore, studying the stability of peanut genotypes to identify a suitable variety is essential for maximizing yield potential for the regions (Kasno and Trustinah 2015). Additionally, research on peanut stability can contribute to the development of resilient and adaptable peanut varieties that can ultimately lead to a more secure and sustainable peanut production system in the region.

Significant GxE interactions (GEI) reduce the association between genotype and phenotype, making it hard to identify superior genotypes, thus affecting breeding progress (Delacy et al. 1996). Understanding the GEI and stability analysis can help plant breeders select stable genotypes. Several stability procedures have been developed to explain the GE interaction. These stability methods can be divided...
into two broad groups: parametric and non-parametric (Lin et al. 1986). The most common approach is parametric analyses. Some of the researchers highlighted significant interactions between environments and genotypes for grain yield in annual crops such as groundnut (Minde et al. 2017; Lal et al. 2021), wheat (Kaya and Sahin 2015; Wardofa and Ararsa 2020), pearl millet (Reddy et al. 2022), soybean (Goksoy et al. 2019; Cubukcu et al. 2021), mustard (Nowosad et al. 2017), canola (Zali et al. 2015), and maize (Shojaei et al. 2021) and with limited occasion in perennial crops like sugarcane (Yarawad et al. 2023) and tea (Kottawa-Ararachi et al. 2022). Multivariate methods include additive main effects and multiplicative interaction models (AMMI) (Gauch and Zobel 1988). In addition, the GGE biplot methodology as a superior approach for the graphical analysis of multi-environmental data (Yan and Kang 2003), that provides the possible identification of high-yield and stable genotypes (Karimizadeh et al. 2013).

The ideal genotype selection index (IGSI) is based on the technique for order of preference by similarity to the ideal solution (TOPSIS) introduced by Hwang et al. (1993) as a multi-criteria decision-making technique. This method was used by Zali et al. (2015) to include different stability analysis methods in ranking genotypes and selecting the most stable genotypes. In the SIIG method, all the calculated stability indices of the genotypes are converted to a single index with a value in the range of 0-1, which makes it easier to determine the stable genotypes. It has been used to select the most stable genotypes by considering the different stability parameters (Zali et al. 2015; Najafi Mirak et al. 2018). Keeping in view the above, the objectives of the present study were to: (i) investigate the GE interactions on groundnut genotypes yield across different environments; (ii) compare parametric, AMMI stability, and GGE biplot analysis and, (iii) select groundnut genotypes with a high and stable yield based on ideal genotype selection index (IGSI).

Materials and methods

Ten advanced lines of groundnut selected from the preliminary yield experiments along with a local cultivar, NC2 were evaluated at three different locations, namely, Talesh, Masal, and Rasht in Iran during the years, 2019–2020 and 2020–2021. Details about the environmental conditions during the crop season at experimental sites are given in Table 1. The materials were evaluated in a randomized complete block design with three replicates. Each plot included three rows of five meters long with a row space of 50 and 20 cm apart. Weed control was carried out through manual weeding at the 3-4-leaf stage. Triple superphosphate (150 kg ha⁻¹), potassium sulfate (100 kg ha⁻¹), and urea (60 kg ha⁻¹) were used as starter nitrogen at the planting time. The genotype × environment interaction was analyzed using the AMMI model as given in equation (1) (Gauch and Zobel 1988):

\[ Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n y_{in} \delta_{jn} + p_{ij} + \varepsilon_{ij} \]  

where: \( Y_{ij} \) is the mean yield of the \( i \)th genotype (\( i = 1, 2, \ldots, g \)) in the \( j \)th environment (\( j = 1, 2, \ldots, e \)), \( \mu \) is the grand mean, \( g_i \) and \( e_j \) are the genotype and environment deviations from the grand mean, respectively. \( \lambda_n \) is the singular value for IPCA axis \( n \), and \( y_{in} \) and \( \delta_{jn} \) are the genotype and environment eigenvectors for axis \( n \), respectively. \( N \) is the number of principal components retained in the model, \( p_{ij} \) is the AMMI residue, and \( \varepsilon_{ij} \) is pooled error. In addition, various AMMI-based stability statistics, including sums of the absolute value of the IPC Scores (SIPC, and SIPC,) (Sneller et al. 1997), AMMI statistic coefficient (D) (Zhang et al. 1998), averages of the squared eigenvector values (EV, and EV,) (Zobel et al. 1988), AMMI stability value (ASV) (Purchase 1997), genotype selection index (GSI) (Farshadfar 2008), Raju’s parameters of stability (FP, and B) (Raju 2002), Annichiarico’s stability measure (Da) (Annichiarico 1997), Zali’s parameter of stability (Za) (Zali et al. 2012) were calculated. Also, the biplot of IPCA1 against the genotypes and environments means (AMMI1) and the biplot of IPCA1 against IPCA2 (AMMI2) was plotted.

Using the Excel software, different parametric statistics, including Roemer’s environmental variance (SE) (Roemer 1917), Francis and Kannenberg’s coefficient of variation (CV) (Francis and Kannenberg 1978), Finlay and Wilkinson’s regression coefficient (b.) (Finlay and Wilkinson 1963), Eberhart and Russel’s model (SE) (Eberhart and Russel 1966), Pinthus’s coefficient of determination (R²) (Pinthus 1973), Wricke’s ecovalence (W²) (Wricke 1962), Shukla’s stability variance (σ²) (Shukla 1972), Plaisted and Peterson’s mean-variance component (\( \Theta \)) (Plaisted and Peterson 1959), Plaisted’s GEl variance component (\( \Theta_{gel} \)) (Plaisted 1960), Lin and Binns’s (1988a) intra-locational variance (\( \text{MS}_{\text{bar}} \)) (Lin and Binns 1988b), Lin and Binns’s (1988b) superiority index (P) (Lin and Binns 1988b) were also used to estimate stability.

In addition, the IGI (Hwang and Yoon 1981) indicator based on all the AMMI-based and parametric stability statistics was used to select the most stable genotypes. In this method, the best genotype is the one that is closest to the ideal genotype and has the highest distance from the most negative genotype. The IGI value is in the range of 0-1. If it is close to 1, the genotype is close to the ideal; else, the genotype is close to the non-ideal one if it is close to 0 (Zali et al. 2015).

Also, heatmaps based on Spearman rank correlation coefficients were plotted to evaluate relationships among parametric and AMMI stability statistics and grain yield (Average plot yield in kilograms was converted into per hectare). The analyses were carried out using SAS (V9.1.3) (SAS Institute, Inc.), R (V.4.2.2) (“metan”, “gplots” and
“ggcorrplot” packages) (Olivoto and Lucio 2020), Minitab (V.16.2.1) (MINITAB Inc 2010) and Excel software. Also, the GGE biplot analysis (Yan et al. 2000) was used to investigate genotype × environment interaction. Using the GenStat (V.12) software (GenStat 2009), the graphs based on the “which-won-where” pattern, ranking of genotypes based on the yield, and stability and comparison of genotypes with ideal genotype were generated.

**Results and discussion**

**AMMI analysis**

The mean yields of 11 groundnut genotypes in six environments are presented in Table 2. The mean grain yield of genotypes over the environments ranged from 838.33 kg ha⁻¹ for 140 to 3776.67 kg ha⁻¹ for 192 (Table 2). Results of ANOVA based on the AMMI model of grain yield for 11 groundnut genotypes in 6 environments are shown in Table 3. Based on this table, the main effects of the environment (E), genotypes (G), and their interactions (G×E) were significant (p < 0.01), explained 57.47, 23.47, and 13.18% of the total variance, respectively. The first two interaction principal component analysis (IPCA1 and IPCA2) exhibited 91.93% (74.84 and 17.09%, respectively) of the G×E interaction variance (Table 3).

Also, the biplot of IPCA1 against the genotypes and environments means (AMMI1) and the biplot of IPCA1 against IPCA2 (AMMI2) are shown in Fig. 1a and 1b, respectively. Based on Fig. 1a, 192 and 128 were the high-yielding genotypes. The highest yield was also observed in TA2, TA1, and MA2 environments. Also, the ICG178, ICG115, and ICG176 genotypes had the lowest positive or negative IPCA1 scores. ICG130, ICG128, and ICG192 had the highest positive IPCA1 score, and NC2 and ICG208 had the highest negative IPCA1 score (Fig. 1a). TA2 had the highest positive IPCA1 score. The highest negative IPCA1 score was recorded in the RA1, RA2, and MA1 environments (Fig. 1a). Based on the AMMI2 biplot (Fig. 1b), the genotypes near the biplot origin communicated general adaptation, while the genotypes far from it delineated more specific adaptation to locations and showed higher GE interaction. Therefore, ICG192 and ICG130 were the best genotypes for environments TA1 and TA2, respectively. Also, ICG208 was the best for RA2; ICG140 and NC2 were better adapted to environments RA1 and MA1. In contrast, ICG178, ICG115, ICG201, and ICG176 were near to origin and therefore were identified as genotypes that have general adaptation in all studied environments.

The heatmap based on the different AMMI stability parameters and various parametric stability statistics of 11 groundnut genotypes is shown in Fig. 2a and 2b, respectively. Accordingly, based on most of these statistics, genotypes ICG178, ICG115, ICG176, and ICG201 had the lowest scores and were the most stable genotypes. However, NC2, ICG208, ICG130, and ICG192 having the highest values,
Table 2. Mean yield (kg ha⁻¹) of 11 groundnut genotypes in six environments

<table>
<thead>
<tr>
<th>Genotype</th>
<th>TA1</th>
<th>MA1</th>
<th>RA1</th>
<th>TA2</th>
<th>MA2</th>
<th>RA2</th>
<th>Mean yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>ICG130</td>
<td>2383.33</td>
<td>1716.67</td>
<td>1603.33</td>
<td>3160.00</td>
<td>2243.33</td>
<td>970.00</td>
<td>2012.78</td>
</tr>
<tr>
<td>ICG140</td>
<td>1971.67</td>
<td>1890.00</td>
<td>1828.33</td>
<td>2335.00</td>
<td>2230.00</td>
<td>838.33</td>
<td>1848.89</td>
</tr>
<tr>
<td>ICG113</td>
<td>2351.67</td>
<td>1946.67</td>
<td>1798.33</td>
<td>2945.00</td>
<td>2411.67</td>
<td>1053.33</td>
<td>2025.28</td>
</tr>
<tr>
<td>ICG115</td>
<td>2401.67</td>
<td>1783.33</td>
<td>1803.33</td>
<td>2720.00</td>
<td>2120.00</td>
<td>1293.33</td>
<td>2020.28</td>
</tr>
<tr>
<td>ICG128</td>
<td>3145.00</td>
<td>2156.67</td>
<td>1991.67</td>
<td>3411.67</td>
<td>2676.67</td>
<td>1533.33</td>
<td>2485.83</td>
</tr>
<tr>
<td>ICG176</td>
<td>2585.00</td>
<td>1823.33</td>
<td>1868.67</td>
<td>2730.00</td>
<td>2273.33</td>
<td>1053.33</td>
<td>2035.28</td>
</tr>
<tr>
<td>ICG178</td>
<td>2333.33</td>
<td>1803.33</td>
<td>1851.67</td>
<td>2540.00</td>
<td>2403.33</td>
<td>1003.33</td>
<td>1989.17</td>
</tr>
<tr>
<td>ICG192</td>
<td>3776.67</td>
<td>2390.00</td>
<td>2370.00</td>
<td>3531.67</td>
<td>3085.00</td>
<td>1810.00</td>
<td>2827.22</td>
</tr>
<tr>
<td>ICG201</td>
<td>2363.33</td>
<td>1996.67</td>
<td>1813.33</td>
<td>2468.33</td>
<td>2425.00</td>
<td>1405.00</td>
<td>2078.61</td>
</tr>
<tr>
<td>ICG208</td>
<td>2165.00</td>
<td>1770.00</td>
<td>1756.67</td>
<td>1488.33</td>
<td>2043.33</td>
<td>1020.00</td>
<td>1707.22</td>
</tr>
<tr>
<td>NC2 (control)</td>
<td>1620.00</td>
<td>1900.00</td>
<td>1866.67</td>
<td>1663.33</td>
<td>2093.33</td>
<td>1310.00</td>
<td>1742.22</td>
</tr>
<tr>
<td>Mean</td>
<td>2463.33</td>
<td>1925.15</td>
<td>1851.82</td>
<td>2635.76</td>
<td>2364.09</td>
<td>1198.64</td>
<td></td>
</tr>
</tbody>
</table>

TA1= Talesh 2019, MA1= Masal 2019, RA1= Rasht 2019
TA2= Talesh 2020, MA2= Masal 2020, RA2= Rasht 2020

Table 3. AMMI variance analysis for grain yield of 11 groundnut genotypes in six environments

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>%SS_E</th>
<th>%SS_G×E</th>
</tr>
</thead>
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<td>Environments</td>
<td>5</td>
<td>47924508</td>
<td>9584902</td>
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</tr>
<tr>
<td>Block/E</td>
<td>12</td>
<td>1643544</td>
<td>136962</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotypes</td>
<td>10</td>
<td>19568921</td>
<td>19568921</td>
<td>23.47</td>
<td></td>
</tr>
<tr>
<td>Interactions</td>
<td>50</td>
<td>10993520</td>
<td>219870</td>
<td>13.18</td>
<td></td>
</tr>
<tr>
<td>IPCA₁</td>
<td>14</td>
<td>8227809</td>
<td>587701</td>
<td>74.84</td>
<td></td>
</tr>
<tr>
<td>IPCA₂</td>
<td>12</td>
<td>1878765</td>
<td>156564</td>
<td>17.09</td>
<td></td>
</tr>
<tr>
<td>Residuals</td>
<td>24</td>
<td>886947</td>
<td>36956</td>
<td>8.07</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>132</td>
<td>4907633</td>
<td>37179</td>
<td>ns</td>
<td></td>
</tr>
</tbody>
</table>

ns, * and **: non-significant, significant at the 0.05 and 0.01 level of probability, respectively

were identified as the most unstable genotypes (Fig. 2a,b). So, we simultaneously used these parameters and the mean yield for selecting high-yield and stable genotypes based on the ideal genotype selection index (IGSI). Based on this method, genotypes with the closest IGSi values to 1 are recognized as stable genotypes. So, in comparison with other genotypes, ICG115, ICG201, ICG178, and ICG176 were identified as stable genotypes (Fig. 2c).

Spearman rank Correlation among various Stability Statistics

A heat map based on Spearman rank correlation coefficients was plotted to show the relationships of yield with parametric and AMMI-based stability statistics (Fig. 3). Mean yield (MY) positively correlated with $P_i$, GSI and negatively correlated with $\sigma_i^2$ and $GSI_i$ (Fig. 3). The findings reported earlier by Pourdad (2011), Kaya and Ozer (2014), and Goksoy et al. (2019) also support the present results on MY and Pi. In addition, a significant positive rank correlation was observed among all possible pairs of $W_i^2$, $\sigma_i^2$, $\theta_i$, $\sigma_{ij}^2$, $b_i$, $R_i^2$, $SIPC_i$, $SIPC_j$, $D_i$, $EV_i$, $EV_j$, ASV, $GSI_i$, $FP_i$, $B_i$, $Da_j$, $Da_i$, and $Z_{a_i}$.  

Fig. 1. AMMI 1 biplot (IPCA1 vs. mean) (a), and AMMI 2 biplot (IPCA 2 vs. IPCA 1) (b) for grain yield of 11 groundnut genotypes in six environments

Fig. 2. AMMI 1 biplot (IPCA1 vs. mean) (a), and AMMI 2 biplot (IPCA 2 vs. IPCA 1) (b) for grain yield of 11 groundnut genotypes in six environments...
Fig. 2. Heatmap and grouping of groundnut genotypes based on AMMI stability statistic (a), parametric stability statistics (b), and diagram of ideal genotype selection index (IGSI) of 11 groundnut genotypes (c). Green circles show selected genotypes having IGSI index higher than 0.75.

Fig. 3. Heatmap showing the relationships among yield and parametric and AMMI stability statistics based on Spearman’s rank correlation coefficients. MY = Mean yield; SIPC = Sum of the absolute value of the IPC scores; $D_i$ = AMMI statistic coefficient; EV = Averages of the squared eigenvector values; $ASV_i$ = AMMI stability value; $GSI_i$ = Genotype selection index; $FP_i$ = Stability statistic based on the first IPC axes of the first IPC axes; $B_i$ = Stability statistic based on the first IPC axes of the first two IPC axes; $D_{a}$ = Parameter of Annicchiarico (1997); $Z_a$ = Absolute value the relative contribution IPCs to the interaction; $P_i$; superiority index; $S^2_{ev}$ = Environmental variance, $CV_i$ = Coefficient of variation; $MS_y/l$ = Intra-locational variance; $CV_y/l$ = Intra-locational coefficient of variation $W_{i}$ = Wricke’secovalence; $\sigma_i^2$ = stability variance of Shukla; $\theta_i$ = Plaisted and Peterson mean variance, $\theta^{(i)}$ = Plaisted interaction variance, $b_i$ = Regression coefficient; $S^2_{d_i}$ = Deviation from regression; $R^2_i$ = Coefficient of determination.

GGE biplot analysis

GGE biplot analysis was performed based on the mean yield of 11 groundnut genotypes in six environments. The first two PCs in the GGE biplot explained 94.56% of the total GGE variation (PC1 = 81.22% and PC2 = 13.33%). A polygon view of the GGE biplot showing the “which-won-where” pattern based on the mean yield and stability of 11 groundnut genotypes in six environments is shown in Fig. 4. The “which-won-where” view of the GGE biplot shows which genotypes performed better in which location.

The polygon is created by connecting the extreme genotypes, while all other genotypes are restricted in the polygon. Light rays perpendicular to the sides of the biplot divided the biplot into sectors. The apex genotype of each sector is the one with the highest yield in it. In this investigation, the vertex genotypes were ICG192, ICG128, ICG130, ICG140, NC2, and ICG208. The ray split the biplot into six sectors, but the environments fell into one of them (Fig. 4a). The apex genotypes in this sector were ICG192 and ICG128.

The ranking of 11 groundnut genotypes based on their mean yield and stability for six environments is shown in Fig. 4b. The line through the origin of the biplot is called the average environmental coordinate (AEC) axis. The AEC ordinate separates high-performing (right) and low-performing (left) genotypes. The line perpendicular to the AEC through the origin of the biplot indicates genotypic stability. Thus, the yield ranking of the genotypes was in the following order: ICG192 > ICG128 > ICG201 > ICG113 > ICG176 > ICG115 > ICG130 > ICG178 > ICG140 > NC2 > ICG208. Genotypes, ICG128, ICG178, and ICG140 were found highly stable owing to their closeness to the AEC axis, whereas ICG130, ICG208, and NC2 were highly unstable genotypes. Genotype ICG128 was a stable and high-yield genotype.
Evaluation of genotypes based on an ideal genotype by GGE biplot method

The evaluation of genotypes based on an ideal genotype is shown in Fig. 5. The ideal genotype has both a high mean yield and high stability. Although such an ideal genotype may not actually exist, it can be used as a reference for comparing genotypes (Yan and Kang 2003). The hypothetical ideal genotype is located at the center of the concentric circles in Fig. 5. A genotype close to the ideal genotype can be considered a desirable genotype. Based on the results of the present study, genotypes ICG192, ICG128, and ICG201 were close to ideal genotypes and could be considered desirable genotypes. Genotypes NC2, ICG208, and ICG140 were far from the ideal genotype and regarded as undesirable genotypes (Fig. 5). Several researchers have identified stable genotypes in different crops GGE biplot analysis, which has discriminatory ability. Recently, Zerehgar et al. (2023) applied multivariate analysis to identify the stable genotype of safflower under rainfed conditions also found an ideal genotype within the concentric circle or closest to the assumed ideal genotype with high and stable yield.

Authors’ Contribution
Conceptualization research (RAZ); Designing of the experiments (RAZ); Contribution of experimental materials (MMR); Execution of field/lab experiments and data collection (FFN, MMR); Analysis of data and interpretation (FFN, MMA); Preparation of the manuscript (FFN, RAZ, MMA).

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