Stability of Chickpea (*Cicer arietinum* L.) Landraces in National Plant Gene Bank of Iran for Drylands

M. Pouresmael1, H. Kanouni2, M. Hajihasani3, H. Astraki4, A. Mirakhorli5, M. Nasrollahi6, and J. Mozaffari1

ABSTRACT

Identification of high performance stable genotypes is an important objective for chickpea production in drylands of Iran. Hence, the stability of 12 chickpea local landraces and three check cultivars were evaluated during three consecutive cropping seasons (2010-2013). The experiments were laid out as a randomized complete block design with four replications in four locations. Combined analysis of variance was performed to verify the existence of differences among genotypes. AMMI analysis was performed to analyze the residual multiplicative interaction. The stability was estimated through ranking of genotypes based on different quantitative stability parameters including IPCA score, AMMI Stability Value (ASV), Sustainability Index (SUI), and Genotype Selection Index (GSI). Main effects of year, location, and genotype as well as their two- and three-way interaction effects were significant (P≤ 0.01) for grain yield. Significant effect of genotype, location, and year interaction implied presence of genetic variability which provides an opportunity to identify new superior genotypes for each location. AMMI analysis showed that the three main components accounted for 62% of the total genotype by environment interaction. Based on the results, the landraces G1, G2, G3, G8, and G12 had the highest average performance and stability compared to check cultivars and could be used in breeding programs for the development of new chickpea varieties.

Keywords: AMMI analysis, *Cicer arietinum* L., High yielding, Local genotypes, Rainfed.

INTRODUCTION

Chickpea harvested area in Iran is about 463,000 ha, of which the vast majority is in dryland areas (98.43%) (Agricultural Statistics, 2016). Spring cultivation of chickpea in Iran is common; hence, the plant has to use the moisture stored in the soil profile to complete its life cycle and the grain filling stage usually faces dehydration due to increase in evaporation from the soil and transpiration from the plant. Thus, the national average chickpea yield falls down from 1,392 kg ha\(^{-1}\) in irrigated land to 402 kg ha\(^{-1}\) in dryland (Agricultural Statistics, 2016).

Chickpea reproductive growth phase is sensitive to water shortage and erratic and inadequate amount of rainfall during this phase is one of the main reasons of yield reduction. Therefore, identification and introduction of appropriate genotypes for dryland farming is one of the major attempts...
towards the efficient use of water and soil resources of the country (Ebadi Segherloo et al., 2008).

Yield is a complex quantitative trait that is often controlled by several genes and influenced by environmental conditions. The importance of Genotypes by Environment Interaction (GEI) in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops (Najafian et al., 2010; Zali et al., 2011; Kendal et al., 2016; Sayar et al., 2013; Kendal and Doğan, 2016).

Among the multivariate methods, the Additive Bain effects and Multiplicative Interaction (AMMI) analysis is widely used for GEI investigation. The AMMI model combines ANOVA for the genotype and environment main effects with principal components analysis to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of GEI, with a minimum number of degrees of freedom (Gauch and Zobel, 1996). This method captures a large portion of the GEI sum of squares; it clearly separates main and interaction effects and often provides meaningful interpretation of data (Gauch and Zobel, 1996; Crossa et al., 1990). The degree of complexity of AMMI estimation model is dependent on crop species, germplasm diversity and the range of environmental conditions (Malhotra and Singh, 1991; Atta et al., 2009; Acikgoz et al., 2009; Kilic, 2014; Mortazavian et al., 2014; Kendal and Tekdal, 2016; Sayar et al., 2013).

The GEI have been studied by different researchers in chickpea and in other important agricultural crops (Arshad et al., 2003; Sabaghpour et al., 2006; Yaghotipoor and Farshadfar, 2007; Yadav et al., 2010; Bakhsh et al., 2011; Hamayoon et al., 2011; Imtiaz et al., 2013; Kendal and Sayar, 2016). Researchers almost describe stable genotypes using different parametric and non-parametric or univariate and multivariate statistical methods. Shafi et al. (2012) used stability parameters according to Eberhart and Russel methods to identify genotypes with stable performance across various environments. Mahtabi et al. (2014) studied phenotypic stability of chickpea genotypes using univariate parametric statistical methods. Kanouni et al. (2015) used AMMI model to analyze for seed yield stability of chickpea genotypes in the western cold zone of Iran. Farshadfar et al. (2011) explored the effect of genotype and genotype-environment interaction on grain yield of 17 chickpea genotypes using the GGE Bi-plot method. Wricke’s ecovalence analysis and AMMI analysis were used by Tilahun et al. (2015) to examine the magnitude of environmental effect on yield of chickpea genotypes in Ethiopia. Rashidi et al. (2013) studied phenotypic stability in chickpea genotypes over stress and non-stress environments using AMMI analysis. Johnson et al. (2015) used mean performance and regression coefficient and deviation from regression for stability analysis of seed yield and its components in chickpea.

Plant Genetic Resources for Food and Agriculture (PGRFA) are the biological cornerstone of global food security. The agricultural diversity and genetic resources for food crops need to be used efficiently both to maintain current levels of food production and to confront future challenges. Crop production in all countries relies on genetic resources originating from all over the world. Chickpea dryland farming in Iran almost rely on samples received from international research centers such as ICARDA (International Center Agricultural for Dryland Area) and ICRISAT (The International Crops Research Institute for the Semi-Arid Tropics) and there is negligible attention to native landraces. Landraces locally adapted to the environmental conditions of the places where they have traditionally been grown are key component of PGRFA. This wealth of genetic diversity has been preserved during the natural process of domestication and cultivation (Yesmin et al., 2014). Today, due to climate change and need for higher genetic diversity to cope with this
phenomenon, dependency on national landraces is felt necessary. Comprehensive assessments of materials housed in gene banks can compensate risks resulting from climate change (Jarvis et al., 2008).

Different studies have demonstrated that the seed yield of chickpea in the Central and West Asia and North Africa region can be substantially increased by changing the planting season from the traditional spring to winter (Imtiaz et al., 2013). However, farmers prefer chickpea planting in the spring. Therefore, developing suitable high yielding cultivars is needed for spring sowing or dual season sowing (Imtiaz et al., 2013). This way, farmers have a chance to select suitable cultivars for spring or winter sowing depending on their local environmental or agro-climatic conditions (Imtiaz et al., 2013).

Iran is one of the countries of origin of chickpea. Chickpea collection of National Plant Gene Bank of Iran (NPGBI) contain 3365 accessions of Desi and 2012 accessions of Kabuli type chickpea, ranked as sixth collection among major chickpea collections in the world (FAO, 2010). The accessions of this collection are very diverse and all imaginable variations in the international descriptor are present in this collection. Hence, evaluation of these valuable resources to find out their undiscovered potential is urgent and will help breeders to work towards the proper utilization of these landraces for parental selection and linkage map construction for discovery of useful alleles (Yesmin et al., 2014).

For this purpose, 12 accessions of Kabuli chickpea landraces, which were identified as terminal drought stress tolerant in previous NPGBI projects (Pouresmael et al., 2012; Pouresmael et al., 2009), were compared with three commercial cultivars for spring sowing in four provinces of Iran. This study aimed to estimate the adaptability and yield stability of chickpea landraces using AMMI analysis to compare national landraces, introduce genotype with high performance and stability for breeding cycle, and to achieve the full potential under variable and unstable conditions of the dryland areas.

**MATERIALS AND METHODS**

In order to compare and identify the most stable and high yielding genotypes, multi-environment trials were conducted at the Agricultural and Natural Resources Research Station of Borujerd, Sararod, Sanandaj and Urmia located in four provinces of Iran, respectively, Lorestan, Kermanshah, Kurdistan and West Azerbaijan, during three cropping seasons (2010–2013). In total, 15 genotypes, including 12 Iranian Kabuli chickpea landraces provided by NPGBI (Table 1) and three common commercial cultivars (Hashem, Azad, and Arman) were evaluated and compared to each other for agronomical traits and performance point of view for spring sowing under dryland conditions. Experiments were carried out in a randomized block design with four replications. Each plot was 0.9 m wide and 3 m long, consisting of three rows of a single genotype. The inter-row and interplant spacing were 30 cm and 7 cm, respectively. Planting was done in the second half of March. Total rainfall, seasonal maximum and minimum temperature, and humidity percentage during cropping seasons (March–July) are shown in Table 2. Standard agricultural practices including fertilizer, weeds and diseases control was done in each location, based on need. Plants were harvested manually, grain yields were determined according to IBPGR (1993) and combined analysis of variance was performed for each environment (year by location integration) to verify the existence of differences among genotypes. AMMI analysis was used to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the GEI. The sum of squares of the GEI was divided into Interaction Principal Component Axis (IPCA), which
### Table 1. The accession number of used chickpea materials in the study.

<table>
<thead>
<tr>
<th>Genotype No</th>
<th>Accession number</th>
<th>Genotype No</th>
<th>Accession number</th>
<th>Genotype No</th>
<th>Accession number</th>
<th>Genotype No</th>
<th>Accession number</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>KC215171</td>
<td>G5</td>
<td>KC215671</td>
<td>G9</td>
<td>KC215995</td>
<td>G13</td>
<td>Arman</td>
</tr>
<tr>
<td>G2</td>
<td>KC215296</td>
<td>G6</td>
<td>KC215686</td>
<td>G10</td>
<td>KC216066</td>
<td>G14</td>
<td>Azad</td>
</tr>
<tr>
<td>G3</td>
<td>KC215654</td>
<td>G7</td>
<td>KC215767</td>
<td>G11</td>
<td>KC216084</td>
<td>G15</td>
<td>Hashem</td>
</tr>
<tr>
<td>G4</td>
<td>KC215664</td>
<td>G8</td>
<td>KC215843</td>
<td>G12</td>
<td>KC216325</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Table 2. Environmental code, soil characteristics and agro climatic information of different locations used in the study.

<table>
<thead>
<tr>
<th>Location</th>
<th>Geographic information</th>
<th>Soil characteristics</th>
<th>Experiment</th>
<th>Climatic information</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Longitude and latitude</td>
<td>Altitude (m)</td>
<td>Texture</td>
<td>pH</td>
</tr>
<tr>
<td>Borujerd</td>
<td>48° 55 E</td>
<td>Loam</td>
<td></td>
<td>7.8</td>
</tr>
<tr>
<td></td>
<td>33° 40 N</td>
<td>1476</td>
<td>(Sand 20%, Silt 46%, Clay 25%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sararod</td>
<td>47° 19 E</td>
<td>Silty Clay Loam</td>
<td></td>
<td>7.4</td>
</tr>
<tr>
<td></td>
<td>34° 20 N</td>
<td>1351</td>
<td>(Sand 9%, Silt 47%, Clay 44%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sanandaj</td>
<td>48° 08E</td>
<td>Loam</td>
<td></td>
<td>7.4</td>
</tr>
<tr>
<td></td>
<td>35° 43 N</td>
<td>2120</td>
<td>(Sand 21%, Silt 30%, Clay 49%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urmia</td>
<td>45° 09 E</td>
<td>Sandy/Loamy Silty</td>
<td></td>
<td>7.4</td>
</tr>
<tr>
<td></td>
<td>37° 21 N</td>
<td>1520</td>
<td>(Sand 17%, Silt 44%, Clay39%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
reflects the standard portion in which each axis corresponded to a particular AMMI model. Combined analysis of variance and mean comparison were performed using SPSS 16.1 and the AMMI analysis was done using GenStat 12. The genotype adaptability was estimated through ranking of genotypes based on different quantitative stability parameters including:

**IPCA SCORE**

The larger the *IPCA* (Interaction Principal Component Analysis) scores, either negative or positive, indicate the more specific adaptation of a genotype to a certain environments. Smaller *IPCA* scores indicate the lower contribution of the GEI and more genotype stability (Purchase *et al*., 2000).

**AMMI Stability Value (ASV)**

The AMMI stability value was calculated as described by Purchase *et al*., (2000); the lower ASV values indicate greater stability of a genotype.

**Sustainability Index (SUI)**

The sustainability index for each genotype was calculated as previously described by Babar Manzoor *et al*. (2009):

\[ SUI = \left( \frac{Y - \sigma_m}{YM} \right) \times 100 \]  
(1)

Where, *Y*, *σm* and *YM* stand for the average performance, the standard deviation and the best performance of a genotype, respectively. The sustainability index values were arbitrarily divided into three stability groups as follows: low (up to 35%), medium (36 to 70%) and high (71 to 100%).

**Genotype Selection Index (GSI)**

Genotype Selection Index (GSI), was calculated using the following formula:

\[ GSI = RASV + RY \]  
(2)

Where, *RASV* and *RY* are the rank of AMMI stability value and mean grain yield rank of a genotype, respectively (Farshadfar, 2008).

Additionally, Biplot graph interpretation based on the additive main effects (genotype and environment) and the effect of the G×E interaction were used for determination of ideal (more stable and high yielding) genotypes. An ideal genotype is a genotype with high yield average and high *IPCA* values close to zero. An undesirable genotype is a genotype with low yield average and high *IPCA* values (Kendal *et al*., 2016; Sayar, 2017). Besides, GGE Biplot was employed to analyze the multi environmental trial data.

**RESULTS AND DISCUSSION**

AMMI for seed yield of 15 chickpea genotypes at 12 environments are presented in Table 3. The analysis revealed that Kabuli chickpea yield were significantly (P≤ 0.01) affected by Environments (E), Genotypes (G), and GEI. The main effects of environments and genotypes accounted for 44.23 and 4.8%, respectively. Genotype by environment interaction effect attributed to 28.9% of the total sum of squares. Similarly, Sayar (2017) reported that the most effective factor on yield performance of genotypes was the environmental effect (42.23%). It was followed by GEI effect (36.13%) and genotype effect (21.64%).

Large amount of environment sum of squares imply that environment has created main portion of variations in seed yield in dryland cultivation of Kabuli chickpea in Iran. Similarly, Tilahun *et al*. (2015) reported that the main portion of Kabuli chickpea seed yield variations in Ethiopia was created by environment. The magnitude of the genotype by environment sum of squares was two times more than that for genotypes, indicating that there were considerable differential in genotype responses across environments. Formerly, the presence of significant genotype by environment interactions for chickpea and
different crops reported by many agricultural researchers (Singh and Bejiga, 1990; Duzdemir, 2011; Farshadfar et al., 2011, 2013; Sayar et al., 2013; Tilahun et al., 2015; Mortazavian et al., 2014; Kanouni et al., 2015; Sayar and Han, 2016; Kendal and Sayar, 2016). Significant effect of GEI implied the importance of stability analysis and splitting of GEI to its parts (Najafian et al., 2010; Mortazavian et al., 2014).

GEI sum of square was significantly (P≤ 0.01) affected by five principal components (IPCA 1 to IPCA 5). The IPCA1 and IPCA2 components accounted for 25.6 and 20.8% of the total GEI sum of squares, respectively (Table 3).

### Stability Analysis of Genotypes

The first two components coefficients of GEI are the simplest method to select stable genotypes (Annicchiarico, 1997; Grausgruber et al., 2000; Purchase et al., 2000; Mohammadi et al., 2008; Kilic, 2014, Sayar et al., 2016). Based on the results, the lowest amount of IPCA 1 belonged to G15, G7, G12 and G14, respectively. Also, low amount of IPCA 2 was specialized to genotypes G10, G7, G13, and G12, respectively (Table 4). Genotypes with low amount of IPCA1 and IPCA2 scores have negligible role in genotype by environment interaction effect and IPCA1 and IPCA2 coefficient closer to zero, indicating genotype stability (Farshadfar et al., 2013; Kilic, 2014; Kendal et al., 2016; Sayar et al., 2016; Sayar, 2017).

AMMI Stability Value (ASV) is also one of parameters that are used to estimate genotypes stability. ASV, in fact, is distance of a special genotype from the origin coordinates of IPCA 1 against IPCA 2 two-dimensional scatter plot. Lower amount of ASV value shows greater stability of genotypes (Purchase et al., 2000). Genotypes G7, G12, G4 and G14, respectively, were the more stable genotypes because of having the lowest amount of ASV. Genotypes G2, G5, and G8 with a maximum amount of ASV were the less stable genotypes (Table 4). Genotypes G1, G12 and G14, respectively, were the more stable genotype because of having the lowest amount of GSI (Table 4). Genotypes G5, G15, G6 and G10 with a maximum amount of GSI were the less stable genotypes (Table 4).

Ranking genotypes based on yield mean values and coefficients of the first two GEI components (IPCA 1 and IPCA 2) showed that G14 and G12 genotypes with high yield and low coefficients were the most stable genotypes. Following these two genotypes, genotype G4 with medium yield and high stability was the best genotype (Table 4).

G1 was included in the four superior genotypes in ten environments (Table 5). This genotype had the highest yield average, the medium amount of ASV and high interaction coefficients of the first two AMMI components (Table 4). G2 and G8,

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**Table 3.** Additive Main effects and Multiplicative Interaction (AMMI) analysis of variance for grain yield (g m⁻²) of the 15 Kabuli-type genotypes tested across 12 environments.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>Prob level</th>
<th>Explained (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes (G)</td>
<td>14</td>
<td>27499</td>
<td>1964</td>
<td>9.00</td>
<td>0.000</td>
<td>4.83</td>
</tr>
<tr>
<td>Environments (E)</td>
<td>11</td>
<td>251989</td>
<td>22908</td>
<td>32.88</td>
<td>0.000</td>
<td>44.24</td>
</tr>
<tr>
<td>G*E</td>
<td>154</td>
<td>164771</td>
<td>1070</td>
<td>4.90</td>
<td>0.000</td>
<td>28.93</td>
</tr>
<tr>
<td>IPCA1</td>
<td>24</td>
<td>42232</td>
<td>1760</td>
<td>8.06</td>
<td>0.000</td>
<td>25.6</td>
</tr>
<tr>
<td>IPCA2</td>
<td>22</td>
<td>34265</td>
<td>1558</td>
<td>7.13</td>
<td>0.000</td>
<td>20.8</td>
</tr>
<tr>
<td>IPCA3</td>
<td>20</td>
<td>26033</td>
<td>1302</td>
<td>5.96</td>
<td>0.000</td>
<td>15.8</td>
</tr>
<tr>
<td>IPCA4</td>
<td>18</td>
<td>21978</td>
<td>1221</td>
<td>5.59</td>
<td>0.000</td>
<td>13.3</td>
</tr>
<tr>
<td>IPCA5</td>
<td>16</td>
<td>17003</td>
<td>1063</td>
<td>4.87</td>
<td>0.000</td>
<td>10.3</td>
</tr>
<tr>
<td>Residual GxE</td>
<td>54</td>
<td>23259</td>
<td>431</td>
<td>1.97</td>
<td>0.0001</td>
<td>14.1</td>
</tr>
<tr>
<td>Total</td>
<td>719</td>
<td>569611</td>
<td>792</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Table 4: Grain yield mean (g m\(^{-2}\)), first and second Interaction Principal Components Analysis (IPCA), AMMI Stability Value (ASV) and Genotype Stability Index (GSI) of 15 chickpea genotypes over 12 environments.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Grain yield mean</th>
<th>Rank grain yield</th>
<th>IPCA 1</th>
<th>Rank IPCA 1</th>
<th>IPCA 2</th>
<th>ASV</th>
<th>Rank ASV</th>
<th>GSI</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>71.63</td>
<td>1</td>
<td>-2.66448</td>
<td>10</td>
<td>-2.04563</td>
<td>12</td>
<td>3.594013</td>
<td>7</td>
</tr>
<tr>
<td>G2</td>
<td>69.68</td>
<td>2</td>
<td>-4.60291</td>
<td>14</td>
<td>-0.727</td>
<td>5</td>
<td>5.156381</td>
<td>13</td>
</tr>
<tr>
<td>G3</td>
<td>63.81</td>
<td>4</td>
<td>-1.074</td>
<td>6</td>
<td>3.77919</td>
<td>13</td>
<td>3.962455</td>
<td>9</td>
</tr>
<tr>
<td>G4</td>
<td>58.25</td>
<td>9</td>
<td>0.51973</td>
<td>5</td>
<td>-1.40511</td>
<td>7</td>
<td>1.518743</td>
<td>3</td>
</tr>
<tr>
<td>G5</td>
<td>49.53</td>
<td>15</td>
<td>4.82565</td>
<td>15</td>
<td>-1.58415</td>
<td>8</td>
<td>5.581435</td>
<td>14</td>
</tr>
<tr>
<td>G6</td>
<td>55.96</td>
<td>11</td>
<td>4.55317</td>
<td>13</td>
<td>-0.83637</td>
<td>6</td>
<td>5.118504</td>
<td>12</td>
</tr>
<tr>
<td>G7</td>
<td>52.86</td>
<td>14</td>
<td>0.20587</td>
<td>2</td>
<td>0.56694</td>
<td>2</td>
<td>0.611189</td>
<td>1</td>
</tr>
<tr>
<td>G8</td>
<td>66.44</td>
<td>3</td>
<td>-1.35833</td>
<td>9</td>
<td>-0.05899</td>
<td>15</td>
<td>6.243459</td>
<td>15</td>
</tr>
<tr>
<td>G9</td>
<td>56.08</td>
<td>10</td>
<td>-1.29478</td>
<td>7</td>
<td>1.78842</td>
<td>10</td>
<td>2.293575</td>
<td>5</td>
</tr>
<tr>
<td>G10</td>
<td>54.25</td>
<td>12</td>
<td>-3.55412</td>
<td>12</td>
<td>0.43979</td>
<td>1</td>
<td>3.966168</td>
<td>10</td>
</tr>
<tr>
<td>G11</td>
<td>58.55</td>
<td>8</td>
<td>1.32486</td>
<td>8</td>
<td>1.93439</td>
<td>11</td>
<td>2.429162</td>
<td>6</td>
</tr>
<tr>
<td>G12</td>
<td>58.68</td>
<td>7</td>
<td>-0.27542</td>
<td>3</td>
<td>0.60718</td>
<td>4</td>
<td>0.679684</td>
<td>2</td>
</tr>
<tr>
<td>G13</td>
<td>62.88</td>
<td>5</td>
<td>3.29323</td>
<td>11</td>
<td>0.57413</td>
<td>3</td>
<td>3.697218</td>
<td>8</td>
</tr>
<tr>
<td>G14</td>
<td>62.36</td>
<td>6</td>
<td>0.28715</td>
<td>4</td>
<td>-1.60492</td>
<td>9</td>
<td>1.636211</td>
<td>4</td>
</tr>
<tr>
<td>G15</td>
<td>53.01</td>
<td>13</td>
<td>-0.18562</td>
<td>1</td>
<td>4.57211</td>
<td>14</td>
<td>4.576742</td>
<td>11</td>
</tr>
</tbody>
</table>

### Table 5: Yield total average, four high performances AMMI recommended genotypes and yield improvement amount through planting of these genotypes in each environment.

<table>
<thead>
<tr>
<th>Environment</th>
<th>Yield total average (g m(^{-2}))</th>
<th>Four AMMI recommended genotypes</th>
<th>Yield improvement (g m(^{-2}))</th>
<th>Environment</th>
<th>Yield total average (g m(^{-2}))</th>
<th>Four AMMI recommended genotypes</th>
<th>Yield improvement (g m(^{-2}))</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>72.86</td>
<td>G2</td>
<td>44.86</td>
<td>E7</td>
<td>56.9</td>
<td>G8</td>
<td>2.53</td>
</tr>
<tr>
<td>E2</td>
<td>61.74</td>
<td>G8</td>
<td>15.92</td>
<td>E8</td>
<td>45.42</td>
<td>G3</td>
<td>19.24</td>
</tr>
<tr>
<td>E3</td>
<td>37.95</td>
<td>G1</td>
<td>31.63</td>
<td>E9</td>
<td>50.47</td>
<td>G2</td>
<td>22.44</td>
</tr>
<tr>
<td>E4</td>
<td>67.25</td>
<td>G8</td>
<td>15.22</td>
<td>E10</td>
<td>38.1</td>
<td>G1</td>
<td>17.8</td>
</tr>
<tr>
<td>E5</td>
<td>43.07</td>
<td>G8</td>
<td>17.83</td>
<td>E11</td>
<td>54.93</td>
<td>G1</td>
<td>6.89</td>
</tr>
<tr>
<td>E6</td>
<td>102.91</td>
<td>G3</td>
<td>20.89</td>
<td>E12</td>
<td>83.42</td>
<td>G2</td>
<td>4.65</td>
</tr>
</tbody>
</table>

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which showed high average for performance after G1, were superior in seven environments (Table 5). G3, G13, and G14 were superior in five environments and were categorized as the best genotypes, too (Table 5).

Sustainability index values, the average performance, the standard deviation, and the best performance of different genotypes are shown in Table 6. Genotypes divided into two categories based on $SUI$. Genotypes G1, G4, G6, G8, G13, and G14 with $SUI$ more than 35% were categorized in medium stability group. All other genotypes had $SUI$ less than 35% and were categorized in low stability group (Table 5). None of the genotypes were in the high stability group.

Differences in genotype stability and adaptability to environment can be considered through depicting a two-dimensional Biplot (Figure 1), of which the $x$-coordinate indicates the main effects (environment and genotype means) and the $y$-coordinate indicates the effects of the interaction, IPCA 1 or IPCA 2, (Vita et al., 2010, Kendal and Tekdal, 2016).

It is clear from Figure 1 that the points for environment are more scattered than the points for genotypes, indicating that variability due to environments is higher than that due to genotypes. This result is in complete agreement of ANOVA (Table 3). Values closer to the origin of $y$-coordinate provide a smaller contribution to the interaction and either direction away from the Biplot origin indicates greater genotype by environment interaction and reduced adaptability (Gauch, 1992).

Based on Figure 1, some of the environments (E3, E4, E6, E8, and E10 and E12) and some of the genotypes (G2, G5, G6, G10 and G13) stood out with a high contribution to the interaction. Only in environments E1, E2, E4, E6, and E12, averages were recorded above the overall averages, indicating that these environments were favorable to obtain high mean performance for chickpea production.
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 (Rashidi et al., 2013). However, the genotypes with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments. Therefore, on the Biplot, the points for the generally adapted genotypes would be at right hand side of the grand mean levels (this suggests high mean performance) and close to the line showing IPCA equal to zero (this suggests negligible or no genotype by environment interaction).

It appears from Figure 1 that the majority of genotypes occupied an intermediate position, relatively similar to the check cultivars Azad (G14) and Hashem (G15). Genotypes G12 and G15 were the most stable genotypes, as indicated by values near the origin of the IPCA 1 axis, which is indicative of a smaller contribution to the

Table 6. Mean, Maximum, Minimum, standard deviation of yield (g m⁻²) and Sustainability Index (SUI %) of 15 chickpea genotypes over 12 environments.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Mean</th>
<th>Max</th>
<th>Min</th>
<th>SD</th>
<th>SUI (%)</th>
<th>Stability</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>71.43</td>
<td>113.3</td>
<td>38.46</td>
<td>23.47</td>
<td>39.07</td>
<td>Medium</td>
</tr>
<tr>
<td>G2</td>
<td>69.68</td>
<td>121</td>
<td>36.62</td>
<td>27.66</td>
<td>32.06</td>
<td>Low</td>
</tr>
<tr>
<td>G3</td>
<td>63.81</td>
<td>123.8</td>
<td>38.43</td>
<td>25.39</td>
<td>28.64</td>
<td>Low</td>
</tr>
<tr>
<td>G4</td>
<td>58.25</td>
<td>95.1</td>
<td>37.46</td>
<td>18.62</td>
<td>38.48</td>
<td>Medium</td>
</tr>
<tr>
<td>G5</td>
<td>49.53</td>
<td>77.9</td>
<td>24.82</td>
<td>19.42</td>
<td>35.68</td>
<td>Low</td>
</tr>
<tr>
<td>G6</td>
<td>55.96</td>
<td>85.5</td>
<td>30.78</td>
<td>19.15</td>
<td>39.74</td>
<td>Medium</td>
</tr>
<tr>
<td>G7</td>
<td>52.86</td>
<td>97.8</td>
<td>30.48</td>
<td>19.72</td>
<td>31.28</td>
<td>Low</td>
</tr>
<tr>
<td>G8</td>
<td>66.44</td>
<td>104.6</td>
<td>18.43</td>
<td>25.05</td>
<td>36.52</td>
<td>Medium</td>
</tr>
<tr>
<td>G9</td>
<td>56.08</td>
<td>109.1</td>
<td>32.36</td>
<td>22.81</td>
<td>28.14</td>
<td>Low</td>
</tr>
<tr>
<td>G10</td>
<td>54.25</td>
<td>107.5</td>
<td>25.28</td>
<td>25.76</td>
<td>24.46</td>
<td>Low</td>
</tr>
<tr>
<td>G11</td>
<td>58.55</td>
<td>106</td>
<td>33.75</td>
<td>20.41</td>
<td>33.21</td>
<td>Low</td>
</tr>
<tr>
<td>G12</td>
<td>58.68</td>
<td>104.9</td>
<td>36.72</td>
<td>20.27</td>
<td>33.79</td>
<td>Low</td>
</tr>
<tr>
<td>G13</td>
<td>62.88</td>
<td>100.7</td>
<td>35.72</td>
<td>18.92</td>
<td>40.30</td>
<td>Medium</td>
</tr>
<tr>
<td>G14</td>
<td>62.36</td>
<td>99</td>
<td>41</td>
<td>18.85</td>
<td>40.57</td>
<td>Medium</td>
</tr>
<tr>
<td>G15</td>
<td>53.01</td>
<td>113.9</td>
<td>26.35</td>
<td>25.88</td>
<td>21.98</td>
<td>Low</td>
</tr>
</tbody>
</table>

(Figure 1).

Figure 2. Polygon view of GGE Biplot (A) and the mega environments division (B) for the which-won-where pattern of 15 chickpea genotypes in 12 environments.
GEI. Following these two genotypes, genotypes G3, G4, G7, G8, G9, G11 and G14 showed greater stability and smaller contribution to the GEI. However, the yield mean of G7, G9, and G15 genotypes were less than the average, therefore, these genotypes could not be recommended. On the other hand, genotypes G3 and G8 were stable and their yield mean were more than overall average (Figure 1). Range of yield improvement through planting of G3 and G8 genotypes were estimated from 10 to 20.89 and from 6.22 to 42.86 g m\(^{-2}\) in different environment, respectively (Table 5).

The genotypes G4, G11, G12 and G14 were stable, and their performance was close to the overall average (Figure 1). Therefore, these genotypes could be recommended as stable genotypes. On the other hand, G1, G2, G5, G6, G10 and G13 were the most unstable genotypes because they were more distant from the Bi-plot origin.

In order to observe the pattern of interaction between genotype and environment and interpret the results, Bi-plot polygons were used (Yan and Kang, 2003). This polygonal view graphically addresses important concepts such as crossover GE, mega environment differentiation and specific adaptation and have been used in several research (Yan and Tinker, 2006; Farshadfar et al., 2011; Imtiaz et al., 2013; Mortazavian et al., 2014; Kanouni et al., 2015). Polygonal display of current study consisting of 15 genotypes in 12 environments is shown in Figure 2-A. In this figure, a polygon was made through connecting genotypes with highest distance to the origin of biplot. Genotypes located on the vertices of the polygon performed either the best or the poorest genotype in one or more locations. Genotypes G2, G3, G5, G8, and G15, which formed vertices of the polygon, had the longest distance from plot origin. G8, G2, and G3 were the best genotypes in their environment. G5 and G15 were the worst genotypes in their environment. Genotypes, G9, G12 and G4, which were close to the origin of coordinate, produced average yield in all experimental environments.

Five lines divided the Bi-plot to the five sections and environments fell in four sections, 3 of which were mega environment (Figure 2-B). Vertex genotype(s) for each sector has higher yield than the others in all environments that fall in the sector. The first mega environments consist of seven environments including E2, E5, E7, E3, E10, E11, and E12. G8 was the more stable and high yielding genotype of this sector. Similarly, E1, E6, and E9 were located in the second mega environment. G2 was the best genotype in the second sector. E8 alone was placed in an environmental group and G15 was the vertex genotype in this location. G5 was the vertex genotype in E4 and E10 environments (Figure 2).

Totally based on Figure 2, among 12 studied local landraces, yield of genotypes G1, G2, G3, G8, and G10 were more than the overall average. Genotypes G8, G5, and G6 were the more stable genotypes. Genotype G12 with lowest amount of both IPCA and yield near the overall average was also a remarkable genotype with general adaptation to all of the experimental environments. G12 was also a remarkable genotype from stability analysis indices like IPCA1 and IPCA2, and ASV point of view. Therefore, these genotypes could be recommended as new superior and more stable genotypes.

**CONCLUSIONS**

Results of the study showed that environmental effect is the most effective factor on grain yield of Kabuli type chickpea genotypes in Iran’s dryland conditions. And, with high grain yield averages, Kermanshah and Urmia locations were found as favorable environments for chickpea cultivation. The grain yield performance and stability status of G1, G2, G3, G8, and G12 landraces were found to be higher and better than that of the chickpea varieties used as check. Consequently, the superior chickpea landraces found in this study should be improved for grain production in Iran conditions.
REFERENCES

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44. Sayar, M. S., Anlarsal, A. E. and Başbag, M. 2016. Additive Main Effects and Multiplicative Interactions (AMMI)


تجزیه مدل اثرات اصلی افزایشی و ضریب پذیر (AMMI) به منظور تحلیل اثرات مقابل مورد استفاده قرار گرفت. پایداری زنوتیب ها از طریق رتبه بندی آنها بر اساس پارامترهای مختلف نظر ضرایب مولفه (GSI) و شاخص پایداری و شاخص انتخاب زنوتیب (ASV) امکانپذیر است. پایداری صحتی پارامتر رتبه تأثیر اثرات مختلف تجربه داشته و وجود افزایش این پارامتر در بیان واریانس ها و تغییرات اثر مقابل زنوتیب 

می‌کند. تجزیه و تحلیل AMMI محیط را توجیه می‌نماید. بر اساس نتایج به دست آمده، زنوتیب‌های G1، G2، G3، G4، G5، G6، G7، G8، G9، G10، G11 و G12 بالاترین میانگین عملکرد را داشته و از نظر پایداری عملکرد مشابه ارقام شاهد بودند. از این رو می‌توان در برنامه‌های اصلاحی برای توسعت ارقام جدید از این منابع ارزشمند استفاده نمود.