GGE Biplot and AMMI Analysis of Yield Performance of Barley Genotypes across Different Environments in Iran

S. M. M. Mortazavian¹, H. R. Nikkhah², F. A. Hassani³, M. Sharif-al-Hosseini⁴, M. Taheri⁵, and M. Mahlooji⁶

ABSTRACT

Twenty promising barley lines were evaluated at seven research stations in Iran, during two cropping seasons. The analysis of variance on grain yield data showed mean squares of environments, genotypes and Genotype×Environment Interaction (GEI) as significant, respectively accounting 60.38, 4.52 and 35.09% of treatment combination sum of squares. To find out the effects of GEI on grain yield, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) and Sites Regression (SREG) GGE biplot analysis. Mega-environmental investigation is the most suitable way to utilize GEI. "Which-won-where" pattern was followed with three distinct mega-environments found in the barley assessment. Entries G5 and G6 showed general adaptability while G7 and G13 exhibited specific adaptation to Neishabour and Esfehan, respectively. Considering both techniques, genotype G1 revealed high grain yield along with yield stability. With regard to barley assessment, Esfehan was identified as a location with larger main effects interaction, making it a less predictable location for barley variety evaluation. The results finally indicated that AMMI and GGE biplot are informative methods to explore stability and adaptation pattern of genotypes in practical plant breeding and in subsequent variety recommendations. In addition, finding mega-environments help to identify the must suitable barley cultivars that can be recommended for areas within the mega-environment in either one or more test locations.

Keywords: Adaptation, Bi-linear method, SREG, Stability analysis.

INTRODUCTION

The considerable variation in crop circumstances, because of climatic conditions and different soil constituents, cause large annual variations in yield performance of crops. This is mainly because of low heritability of yield as a typical quantitative trait. Thus, grain yield could be affected by not only genotype, but also by environment as well by and genotypexenvironment interactions. In this context, Multi Environment Trials (METs) are important for studying yield stability, adaptation and as well for a prediction of yield performance of genotypes across environments. Typically, environment expresses most of the total yield variations, while genotype and GenotypexEnvironment Interaction (GEI) are usually less effective (Yan and Kang, 2003; Dehghani et al., 2009). A large GEI variation usually hinders

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the accuracy of yield estimation and reduces
the correlation between genotypic and
phenotypic values. GEI is a universal
phenomenon when different genotypes are
tested in a number of environments, and is
an important issue for plant breeders and
agronomists to predict cultivar behavior in
different locations across different years
prior to any cultivar recommendation.
Cultivars can be selected as based upon rank
differences or difference in amount.
Depending upon a researcher’s aim, specific
or general adaptability may be considered as
a main selection factor. Various methods
have been introduced in trying to deduce
cultivar reaction in different situations.
Additive Main Effects and Multiplicative
Interaction (AMMI) analysis is one of the
popular parametric but multivariate methods
to predict adaptation and stability of
cultivars. The usefulness of the method to be
applied to some different crops has been
noted by many researchers (Abay and
Bjørnstad, 2009; Alwala et al., 2010;
Annicchiarico et al., 2010). Zobel et al.
(1988) proposed the name AMMI first, but
the actual statistical method itself goes back
to work by Pike and Silverberg (1952) and
Williams (1952). AMMI analysis uses
Analysis of Variance (ANOVA), followed
by Principal Component Analysis (PCA)
applied to the sums of squares allocated
through ANOVA to GxE interaction. This
method leads to identification of stable and
adapted genotypes whether specific or
general. AMMI is useful in delineating
mega-environments by determining the
which-wins-where pattern, that is, which
genotype wins in which environments
(Gauch, 1992; Gauch and Zobel, 1997).
AMMI is successfully employed to estimate
stability, adaptation and GxE explanation of
different crops. Because of multivariate
nature of environment and effect on GEI,
many scientists believe this method to be
useful in exploiting and judging about variations (Sarial et al., 2008; Adugna,
2010; Annicchiarico et al., 2010;
Hassanpanah, 2011). Some researchers have
employed pattern analysis to identify

genotype and environments with the same
reaction. In this method, ordering and
clustering methods are simultaneously
applied (Chapman et al., 1997; Kaya, et al.
2006; Mortazavian et al., 2009; DeLacy et
al., 2010). Chapman et al. (1997) used this
method and applied cluster analysis through
Ward method based on squared Euclidean
distance. Similar results have been reported
between AMMI and GGE biplot analysis
(Ilker et al., 2009). GGE biplot methodology
was initially developed for Multi-
Environment variety Trials (MET) data
analysis (Yan and Kang, 2003). Ilker et al.
(2009) offered these two as reliable methods
to evaluate maize experimental hybrids and
as well identify proper test environments.
AMMI analysis technique uses double
centered data while in GGE biplot
environment, centered data is made used of.
The present research was carried out to
interpret Genotype-Environment (GxE)
interaction effects on barley grain yield via
AMMI analysis, find out stability and
adaptation pattern of genotypes using visual
assessment technique of GGE biplot, and
determine the most suitable genotypes while
combining a high level of grain yield with
yield stability.

MATERIALS AND METHODS

Twenty diploid barley genotypes (Coded
G1 to G20) were grown in national
advanced regional yield trials. Pedigrees of
investigated genotypes are presented in
Table 1. The experiments were conducted
across 14 environments, throughout two
crop seasons, 2009-2010, over seven
research stations namely:: Karaj,
Neishabour, Esfehan, Zarghan, Varamin,
Birjand, and Kerman. The characteristics of
these sites are listed in Table 2. The
experimental design employed, was a
Randomized Complete Block Design
(RCBD) of three replications. The
experimental plots were 6 m in length with
1.2 m of width. All the cultural practices
were carried out as recommended. The
### Table 1. Pedigree of the investigated genotypes.

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Entry Code Pedigree</th>
<th>Overall mean in all environments</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>Check-1 (Nosrat)</td>
<td>6.098</td>
</tr>
<tr>
<td>G2</td>
<td>LB.Moghan/Gloria’S'/Copla’s’/3/Arar/L.527</td>
<td>5.409</td>
</tr>
<tr>
<td>G3</td>
<td>L.527/NK1272//Alanda/3/Alanda-01*2</td>
<td>5.838</td>
</tr>
<tr>
<td>G4</td>
<td>24569/3/L.640/Bgs//Cel</td>
<td>6.018</td>
</tr>
<tr>
<td>G5</td>
<td>Np106/Minn14133/Gva/Doluis/3/Numar</td>
<td>5.523</td>
</tr>
<tr>
<td>G6</td>
<td>Comp-74-K</td>
<td>5.630</td>
</tr>
<tr>
<td>G7</td>
<td>ZARJOU/80-5151//K-332/1</td>
<td>5.157</td>
</tr>
<tr>
<td>G8</td>
<td>Gloria’s’/Copal’S’/Alger</td>
<td>5.731</td>
</tr>
<tr>
<td>G9</td>
<td>TOCTE</td>
<td>5.594</td>
</tr>
<tr>
<td>G10</td>
<td>Hma-02//11012-2/CM67/3/Alanda</td>
<td>5.162</td>
</tr>
<tr>
<td>G11</td>
<td>Eldorado//Alanda/Zafraa</td>
<td>5.369</td>
</tr>
<tr>
<td>G12</td>
<td>Kitchin/SLB60-35</td>
<td>5.895</td>
</tr>
<tr>
<td>G13</td>
<td>TOCTE/ESPERANZA//QUINA</td>
<td>5.385</td>
</tr>
<tr>
<td>G14</td>
<td>Lignee 527/NK1272//ILB 70-63</td>
<td>6.103</td>
</tr>
<tr>
<td>G15</td>
<td>Mammmut/Gloria’S’/Come’S’</td>
<td>5.491</td>
</tr>
<tr>
<td>G16</td>
<td>Kavir *2/Zdm 938</td>
<td>5.797</td>
</tr>
<tr>
<td>G17</td>
<td>Kavir /3/Roho//Alger/4/Kavir/Zdm 938</td>
<td>5.637</td>
</tr>
<tr>
<td>G18</td>
<td>Avi/Emir/Espe//SV.Mari/3/Rihane</td>
<td>5.520</td>
</tr>
<tr>
<td>G19</td>
<td>Reaserch/Kavir</td>
<td>5.487</td>
</tr>
<tr>
<td>G20</td>
<td>Check-2 (3rd EBYTM81-8(Deir Alla106//Hem/Bc/3/Rihane’S’))</td>
<td>5.683</td>
</tr>
<tr>
<td><strong>Mean</strong></td>
<td></td>
<td><strong>5.616</strong></td>
</tr>
</tbody>
</table>

### Table 2. Stations, geographical locations and overall mean of grain yield in each location.

<table>
<thead>
<tr>
<th>Locations</th>
<th>Year</th>
<th>Location code</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Altitude (m)</th>
<th>Annual rainfall (mm)</th>
<th>Min temp (°C)</th>
<th>Max temp (°C)</th>
<th>Mean grain yield (t ha⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Karaj</td>
<td>1st</td>
<td>Krj1</td>
<td>35 49 N</td>
<td>50 58 E</td>
<td>1300</td>
<td>309.9</td>
<td>8.8</td>
<td>21.4</td>
<td>4.98</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Krj2</td>
<td></td>
<td></td>
<td></td>
<td>221.6</td>
<td>9.8</td>
<td>22.9</td>
<td>7.19</td>
</tr>
<tr>
<td></td>
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<td></td>
</tr>
<tr>
<td>Neishabour</td>
<td>1st</td>
<td>Nei1</td>
<td>36 22 N</td>
<td>58 82 E</td>
<td>1250</td>
<td>261.1</td>
<td>7.2</td>
<td>21.5</td>
<td>3.65</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Nei2</td>
<td></td>
<td></td>
<td></td>
<td>181.8</td>
<td>7.5</td>
<td>23</td>
<td>5.37</td>
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<tr>
<td>Esfahan</td>
<td>1st</td>
<td>Esf1</td>
<td>32 39 N</td>
<td>51 40 E</td>
<td>1590</td>
<td>104.6</td>
<td>9.5</td>
<td>24</td>
<td>6.86</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Esf2</td>
<td></td>
<td></td>
<td></td>
<td>199.4</td>
<td>9.8</td>
<td>24.5</td>
<td>7.17</td>
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<td></td>
</tr>
<tr>
<td>Zarghan</td>
<td>1st</td>
<td>Zar1</td>
<td>29 46 N</td>
<td>52 44 E</td>
<td>1590</td>
<td>398.3</td>
<td>8.2</td>
<td>24.8</td>
<td>4.57</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Zar2</td>
<td></td>
<td></td>
<td></td>
<td>317.7</td>
<td>8.4</td>
<td>25.6</td>
<td>6.12</td>
</tr>
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<td></td>
</tr>
<tr>
<td>Varamin</td>
<td>1st</td>
<td>Var1</td>
<td>35 32 N</td>
<td>51 65 E</td>
<td>918</td>
<td>161.7</td>
<td>11.1</td>
<td>24.6</td>
<td>5.68</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Var2</td>
<td></td>
<td></td>
<td></td>
<td>129.2</td>
<td>11.4</td>
<td>25.9</td>
<td>5.72</td>
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<td></td>
</tr>
<tr>
<td>Birjand</td>
<td>1st</td>
<td>Bir1</td>
<td>32 88 N</td>
<td>59 22 E</td>
<td>1491</td>
<td>219.3</td>
<td>8.6</td>
<td>23.8</td>
<td>5.94</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Bir2</td>
<td></td>
<td></td>
<td></td>
<td>75.7</td>
<td>9.3</td>
<td>25.7</td>
<td>4.42</td>
</tr>
<tr>
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<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Kerman</td>
<td>1st</td>
<td>Ker1</td>
<td>30 17 N</td>
<td>57 04 E</td>
<td>1755</td>
<td>122.6</td>
<td>8.1</td>
<td>25</td>
<td>5.73</td>
</tr>
<tr>
<td></td>
<td>2nd</td>
<td>Ker2</td>
<td></td>
<td></td>
<td></td>
<td>78.3</td>
<td>7.4</td>
<td>25.7</td>
<td>5.23</td>
</tr>
</tbody>
</table>

Plots' crops were harvested mechanically. Data on seed yield were converted to t ha⁻¹ and combined analysis of variance across the test environments of stations vs. years was undertaken. Adaptability and phenotypic stability analyses were performed through AMMI method as described in Zobel et al. (1988) using the following statistical model:

\[
Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{K} \lambda_k \alpha_k \gamma_{jk} + r_{ij} + e_{ij}
\]

The employed GGE biplot as based on the Sites Regression (SREG) linear-bilinear
(multiplicative) model (Cornelius et al., 1996) can be written as:

\[ Y_{ij} = \mu + \sum_{k=1}^{t} \lambda_k \alpha_i \gamma_j + \epsilon_{ij} \]

where \( Y_{ij} \) is the mean response of genotype \( i \) in the environment \( j \); \( \mu \) is the overall mean; \( \alpha_i \) the fixed effect of genotype \( i \) (\( i = 1, 2, \ldots, g \)); \( \epsilon_{ij} \) is the random effect of environment \( j \) (\( j = 1, 2, \ldots, e \)); \( \epsilon_{ij} \) is the average experimental error; the GxE interaction is represented by the factors; \( \lambda_k \), a unique value or singular value of the \( k^{th} \) Interaction Principal Component Analysis (IPCA), (\( k = 1, 2, \ldots, t \), where \( t \) stands for the maximum number of estimable main components), \( a_{ik} \) is a singular value for the \( i^{th} \) genotype in the \( k^{th} \) IPCA, \( y_{jk} \) is a unique value of the \( j^{th} \) environment in the \( k^{th} \) IPCA; \( r_{ij} \) the error for the GxE interaction or AMMI residue (noise present in the data); and \( k \) the characteristic non-zero roots, \( k = [1, 2, \ldots, \min(G - 1, E - 1)] \).

Analysis of variance was performed using SAS software (SAS Institute, 1996). AMMI analysis of GxE interaction and calculation of Root Mean Square Prediction Differences (RMSPD) were processed using MATMODEL 3.0 (Gauch, 1997). GGE biplot was employed to analyze the Multi-Environment Trial (MET) data and find "which-won-where" pattern of MET data. The model used for the GGE interaction biplot analysis was an environment-centered model with no-scaling.

RESULTS AND DISCUSSION

The combined analysis of variance for grain yield data is given in Table 3. All the sources except entry×year were significant. Significant interactions were resulted from the changes in the relative ranking of the genotypes or changes in the magnitudes of differences between genotypes from one environment to another. Significant difference between two years suggests the different reactions of genotypes from a year to another. The same interpretation can be expressed for locations. The significant GxL effect demonstrated different responses of genotypes to the variation in environmental conditions of location indicating the necessity of testing barley varieties at multiple locations. Analysis of variance

### Table 3. Combined and AMMI analysis of variance for barley grain yield (t ha\(^{-1}\)) genotypes across environments.

<table>
<thead>
<tr>
<th>SOV</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F Value</th>
<th>Explained % of E SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication (R)</td>
<td>2</td>
<td>0.854</td>
<td>0.427</td>
<td>ns</td>
<td>0.46</td>
</tr>
<tr>
<td>Environment (E)</td>
<td>13</td>
<td>830.956</td>
<td>63.919</td>
<td>**</td>
<td>63.60</td>
</tr>
<tr>
<td>Year (Y)</td>
<td>1</td>
<td>62.07</td>
<td>62.07</td>
<td>71.59 **</td>
<td>7.46</td>
</tr>
<tr>
<td>Location (L)</td>
<td>6</td>
<td>444.83</td>
<td>74.14</td>
<td>85.51 **</td>
<td>53.53</td>
</tr>
<tr>
<td>Entry (G)</td>
<td>6</td>
<td>324.06</td>
<td>54.01</td>
<td>62.29 **</td>
<td>38.99</td>
</tr>
<tr>
<td>GxE</td>
<td>247</td>
<td>482.99</td>
<td>1.96</td>
<td>1.95 **</td>
<td></td>
</tr>
<tr>
<td>IPCA 1</td>
<td>31</td>
<td>138.222</td>
<td>4.45</td>
<td>4.42 **</td>
<td>28.61</td>
</tr>
<tr>
<td>IPCA 2</td>
<td>29</td>
<td>119.737</td>
<td>4.128</td>
<td>4.10 **</td>
<td>24.79</td>
</tr>
<tr>
<td>IPCA 3</td>
<td>27</td>
<td>66.891</td>
<td>2.47</td>
<td>2.45 **</td>
<td>13.84</td>
</tr>
<tr>
<td>IPCA 4</td>
<td>25</td>
<td>49.135</td>
<td>1.965</td>
<td>1.95 **</td>
<td>10.17</td>
</tr>
<tr>
<td>Noise</td>
<td>135</td>
<td>110.402</td>
<td>0.817</td>
<td>0.81ns</td>
<td>22.85</td>
</tr>
<tr>
<td>Error</td>
<td>560</td>
<td>563.212</td>
<td>1.005</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>839</td>
<td>1890.59</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
</tbody>
</table>

\( CV = 16.58\% \)

* and **: Significant difference at 0.05 and 0.01 probability level, respectively.
Table 4. ANOVA results of barley grain yield during the two years of evaluation.

<table>
<thead>
<tr>
<th>Year</th>
<th>Source</th>
<th>DF</th>
<th>Sum of squares</th>
<th>Explained (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>First</td>
<td>Location (L)</td>
<td>6</td>
<td>391.02</td>
<td>58.67</td>
</tr>
<tr>
<td></td>
<td>Genotypes (G)</td>
<td>19</td>
<td>42.96</td>
<td>6.44</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>114</td>
<td>232.44</td>
<td>34.87</td>
</tr>
<tr>
<td>Second</td>
<td>Location (L)</td>
<td>6</td>
<td>377.86</td>
<td>58.33</td>
</tr>
<tr>
<td></td>
<td>Genotypes (G)</td>
<td>19</td>
<td>31.70</td>
<td>4.89</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>114</td>
<td>238.15</td>
<td>36.76</td>
</tr>
</tbody>
</table>
This method revealed the first four terms of AMMI as significant, using an approximate $F$-statistics (Gollob, 1968). Computing the noise and signal of the model revealed that the AMMI model with a first multiplicative term was adequate for cross-validation of the yield variation as explained through GEI. Regarding the data, Root Mean Square Prediction Differences (RMSPD) of different AMMI models, Ockham’s Hill was extremely flat. For instance, RMSPD for AMMI0 was 1,162 but for AMMI2, it amounted to 1,179, which differs by only one in the third decimal place—about a 1% difference. Several researchers proposed using first two IPC axes and believed these two to be enough for AMMI model (Gauch and Zobel, 1996; Ilker et al., 2009). On the other hand, simpler AMMI1 model also merits because AMMI1 often generates as many mega-environments as practical agricultural considerations. Thus, the approximation of actual interaction pattern of the 20 barley genotypes with 14 environments was best cross-validated with the first multiplicative terms of genotypes and environments that were easily visualized with the aid of a biplot (Figure 1). AMMI1 model is a rank 2 model, that is, it has two numbers for each genotype and each environment (namely a mean and an IPC score) (Gauch, 1992). GGE biplot defines an ideal genotype, based on both mean performance and stability across environments (Aina et al., 2009). The GGE biplot is superior to the AMMI1 graph in mega-environment analysis and genotype evaluation because it explains more G x GE than AMMI (Yan et al., 2007). The GE biplot for AMMI1 explained about 75% of the yield variation. In this biplot, the abcissa showed the main effects and the ordinate the first multiplicative axis term (PC1). The solid line connecting environment markers indicated the year-to-year variation within an individual location. The genotypes close to ordinate expressed general adaptation, whereas the further genotypes depicted more specific adaptation to environments (Ebdon and Gauch, 2002). Therefore, genotypes like G19 and G13 with large absolute PC1 scores were better

![Figure 1](image-url). Comparison of two check (G1 and G20) cultivars in different environments. GGE biplot obtained from Site REGression (SREG) analysis.
adapted to Neishabour and Esfehan in the first year, respectively (Figure 2). Specific adaptation can be characterized as positive coincidence of plant phenology with such environmental reducing events as frost damage in winter and/or terminal drought. So, in a particular area with a well characterized environment, specific adaptation is the key point for yield improvement (Najafian et al., 2010). The best genotype should combine high yield and stable performance across a range of production environments. Among the three high yielding genotypes G1, G4 and G14, G4 can be best judged based on stability and grain yield with combined low absolute PC1 score and high yield. Birjand exhibited the relatively smaller variation in the interaction (PC1 score) from year to year, while Esfehan had the largest (Figure 2). This indicated that the relative ranking of genotypes were more stable in Birjand than in Esfehan. Esfehan was described as a location that combined larger main effects with larger interaction effects making it a less predictable location for barley variety evaluation. Pattern analysis, employs both ordination and classification techniques. Using pattern analysis in AMMI model, genotype and environment of the same response will be grouped (Farshadfar, 2008; Pourdad and Mohammadi, 2008). Pattern analysis can be employed to recognize genotypes with the same response pattern in different environments because of co-exploiting of clustering and ordering merits. By use of this method, genotypes can be selected not only with regard to the stability but also concerning to the high yield. This beneficence has been used successfully in different studies (Chapman et al., 1997; Bertero et al., 2004; Mortazavia et al., 2009). Pattern analysis of genotypes and environments based on first IPC and grain yield showed three distinct clusters. For example, results showed G13 and Esfehan in first year in the same cluster and G4, G5 and G16 with BI2, NE2, KR1 and VA1 in a distinct group. Biplot of IPC1 and IPC2 covers 53.2% of GE interaction (Figure 3).

![Figure 2](image)

**Figure 2.** Biplot of mean grain yield (t ha⁻¹) and first IPCA axis (AMMI1) of barley genotypes and environments.
Genotypes located near the plot origin were less responsive than the genotypes farther from the center of biplot. Genotypes G13, G9, G11, G12, G7, G19 and G18 benefit from specific adaptations. The genotypes G7 and G13 have the specific adaptation to NE2 and ES1, respectively because of their angle being acute, i.e. less than 90° and their GE interaction positive. Figure 3, shows pattern analysis and also “which-won-where” pattern of genotypes and locations. The locations fell into three sector or mega-environments: G1 was the best genotype for the first sector. Genotype G14 wins in the second sector and while genotype G13 in the third sector (Table 5). A criterion that is required to suggest different mega-environments is higher variation among groups rather than within-groups. It is a common criterion for clustering (Yan and Kang, 2003). Second, there are different winning cultivars in different test environments. As shown in Figure 2, all the genotypes and environments are clustered in three groups, based upon pattern analysis. Rectangular segment contains two vertex cultivars, G7 and G19, but among genotypes in this part G1 yielded the highest. Then, Genotype G1 is the check cultivar and representative of the best genotype in sectors G7 and G19. The majority of locations including NE1, ZA1, KE1, KR1, VA1, KE2, VA2, NE2, and BI2 were located in mega-environment 1 in which genotype 1 is the winner. The performance of genotypes in relation to check cultivars (G1 and G20) is reflected in Figure 1. A connector line was drawn to connect the checks, with

**Figure 3.** Pattern analysis biplot of first two IPC components of AMMI model shows "which-won-where" results. The winner genotypes in each mega environment are G13, G14 and G1.

**Table 5.** Winning genotypes based on SREG analysis of variance for grain yield in 3 mega-environments.

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perpendicular lines made. As shown in Figure 3, G1 yielded more than G20 in Kerman, Neishabour and Varamin in both years while G20 yielded more than G1 in Esfahan in both years and in Zarghan and Karaj during the second year. Genotype G1 yields higher in most environments than G20. The GGE biplot of SREG analysis was employed to show the relative adaptation of genotype with the highest grain yield, G14, across environments (Figure 4). The length of environment projections onto G14 axis assessed the performance of G14 at different environments, relative to other genotypes. The broken perpendicular line to the G14 axis and passing through the origin, divided the environments where G14 would yield above and below averages. Hence, G14 would yield the highest in Esfahan in both years followed by Karaj in the second year, Zarghan in the second year and Birjand in both years. Figure 5 shows the "Average Environment Coordination" (AEC) of the GGE biplot for 20 barley genotype evaluations regarding the mean vs. stability. This AEC is based on genotype-focused Singular Value Partitioning (SVP) (Yan and Kang, 2003). Because of the inner-product property of the biplot, the projections of the genotype markers on the “average environment axis” are proportional to the rank-two approximation of the genotype means representing the main effects of the genotypes (Yan et al., 2007). Genotype G4 has the shortest AEC ordinate so it is the most stable genotypes while G9 is the least stable genotype placed above average mean performance. With regard to both stability and high mean performance G13, G20, G3, G18, G14, G6 and G9 are preferred. Considering AMMIII and GGE SREG results, G14 and G1 are recommended as the ideal ones among the genotypes.

CONCLUSIONS

Having yield stability and economic profitability is an important and complicated issue for breeders and farmers. Successful cultivars should be adapted to a broad range of environmental conditions to produce consistent yields everywhere. Hence, the information on GE interaction and stability is of paramount importance for barley breeders and farmers. The genotypes used in

Figure 4. GGE biplot of SREG analysis showing the performance of the genotype with the highest grain yield, G14, at different locations.
Figure 5. The mean vs. stability view of GGE biplot for the evaluated barley genotypes.

This study did not exhibit a uniform stability and response pattern to different environments. It was shown throughout the study that the GGE biplot graphic analysis complements the AMMI biplot stratification, defining mega-environments and the cultivars that optimize performance in such mega-environments. Analysis through GGE biplot approach in the present research revealed 3 barley mega-environments in Iran. Finding mega environments encompasses several advantages. Parsimony of evaluation cost is equivalent to an important profit. Genotype assessment can be done only in one location in each mega environment instead of in all the locations. For instance, G1 has specific adaptation to Kerman, Varamin and Neishabour while G14 is adapted to Zarghan and Karaj. Drawing "Which-Won-Where" pattern as based on environment values is more informative than locations because it involves both locations and years while retaining key information regarding years. The more climatic variations in a specific location, the less precise the mega environment identifications. Criterion to recommend a location as a profit mega environment is as large as enough to the presence of a winning genotype during different years in the same location. In this way, small mega environment 3 could be ignored because G13 wins only in one environment, Esf 1, and in the other year, Esf 2, genotype G14 is the winner. The most interesting genotype is G1 that wins in nine environments, including Neishabour, Kerman, and Varamin in both years. For the other four locations, G14 wins in only one of the two years, mostly with G1 winning in the other year, except for Esfahan 1st year. It should be noticed that GE interactions associated with locations are relatively repeatable and increase mega-environments, whereas GE associated with years are relatively unrepeatable and decrease mega-environments. Then, the best recommendation would be G1 throughout the test region. In a comparison of two control genotypes, G1 (Nosrat) benefits from similar responses with more genotypes rather than G20 and can be proved by more crowded of genotypes in the G1 part rather than G20. This conclusion is true for
adaptation to different environments, too. Different researches on evaluation of barley genotypes under drought stressed conditions have identified Nosrat genotype as tolerant (Zare, 2012; Eivazi, et al., 2013). In case of stress damages, such as drought or freezing damage, tolerant genotypes change their phonological development to escape or bear the stringency conditions and in this case they will show specific adaptation to locations of the stress conditions. Although barley is frequently considered by farmers as the safest and easiest annual cool-season crop to grow for grain yet, it can be reduced in grain yield. The lowest mean grain yield is related to Neishabour 2nd year that has the lowest minimum and maximum temperatures during the cropping season. Neishabour is a temperate to cold location with the risk of frost damage, especially to spring genotypes. Then genotypes adapted to this location are of the specific adaptation to low temperatures. Stations of Esfehan 1st year and Birjand 2nd year with the lowest rainfall and high temperatures are among the drought-prone regions, with water deficit being one of their characteristics especially in terminal stages of barley growth. Then genotypes with specific adaptation to these stations would be the drought tolerant genotypes.

ACKNOWLEDGEMENTS

The authors would like to thank Prof. Hugh G. Gauch, from Cornell University for his kind help, suggestions and revision. The authors also acknowledge the Seed and Plant Improvement Institute (SPII) for providing the necessary facilities.

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تجزیه امی و GGE بای یالات عملکرد زنوتیب های جو در محیط های مختلف ایران

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چکیده

پیشینه و دو لای ایمیدیشی جو در هفت ایستگاه مختلف در ایران طی دو سال مورد بررسی قرار گرفتند. تجزیه واریانس عملکرد دانه نشان داد که میانگین مربعات محیط، زنوتیب و برهمکنش زنوتیب در محیط معنی دارد. و برنده 36، 38/3، 38/2 درصد از مجموع مربعات تیمار را تشکیل می‌دهد. به منظور پیدان تاریک مقابل زنوتیب در محیط تجزیه اثرات متقابل ضریب و اثرات اصلی جمع‌بندیر (AMMI) با یالات GGE SREG و BA گرفت. تجزیه الگو جهت اثرات آور استفاده یا باید استفاده قرار گرفت. با توجه به 1 RMSPD داده‌ها، مدل امی 621
انتخاب شد. الگوی "which-won-where" در بال شه و سه ابرمحمی مشخص گردید. زنوتیب های G6 و G5 سازگاری عمومی نشان داده و پایدارترین زنوتیب ها در آزمایش شناخته شدن. در حالیکه G13 بسیار زنوتیب ها سازگاری خصوصی نشان دادند نظیر G7 و G13 که ترتیب سازگاری خصوصی به نیشابور و اصفهان نشان دادند. با توجه به نتایج دو روش G4 بدلیل عملکرد بالا و پایداری عملکرد انتخاب شد. اصفهان بعنوان مکانی شناخته شد که بیشترین اثرات اصولی و اثرات مقابل را داشته و لذا جهت ارزیابی ارقام جو کمترین قابلیت پیش بینی را داراست. نتایج آزمایش نشان داد که روش امی و GGE روش های کارامدی در شناسایی الگوی سازگاری و پایداری زنوتیب ها در برنامه‌ها اصلاحی و توصیه رقیم هستند.