Evaluation of phenotypic stability in bread wheat genotypes using GGE-biplot

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ABSTRACT: The objective of this study was to explore the effect of genotype (G) and genotype × environment interaction (GEI) on grain yield of 16 bread wheat genotypes (Triticum aestivum L.) in five different environments. Yield data were analyzed using the GGE biplot method. Environment (E) explained 59.39% of the total variation, whereas G and GEI captured 9.39% and 14.34%, respectively. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 44.3% and 24.5% of GGE sum of squares (SS), respectively. Collective analysis of the biplots suggested three bread wheat mega-environments in Ilam Province. The first mega-environment contained environments: E2 with genotypes B2 and B7. Genotype B9 gave the highest performance in environment E1 and E3 and genotypes B8, B9, B3 and B2 revealed the highest performance in environments E4 and E5. Genotypes B9, B8, B3 and B2 exhibited the highest mean yield and genotypes B6 and B16 displayed the poorest mean yield. The highest stability was attributed to genotypes B8, B10, B16, B1 and B11. On the other hand, E3 and E5 were the best representative of the overall environments and the most powerful to discriminate genotypes performance.

Key words: bread wheat, genotype × environment interaction, GGE biplot, stability

INTRODUCTION

Understanding the relationship between crop performance and environment has long been a key issue for plant breeders and geneticists. Crop performance, the observed phenotype, is a function of genotype — variety or cultivar, environment, and GEI. GEI is said to occur when different cultivars or genotypes respond differently to diverse environments. Researchers agree that GEI is important only when it is significant and causes significant change in genotype ranks in different environments, i.e., different genotypes are superior in different environments (Yan and Kang, 2003).

Agricultural researchers have long been cognizant of the various implications of GEI in breeding programs (Mooers, 1921; Yates and Cochran, 1938). GEI has a negative impact on heritability. The lower the heritability of a trait, the greater the difficulty in improving that trait via selection. Understanding the structure and nature of GEI is important in plant breeding programs because a significant GEI can seriously impair efforts in selecting superior genotypes relative to new crop introductions and cultivar development programs (Shafii and Price, 1998).

The detection of GEI in trials has led to the development of procedures that are generically called stability analyses. The numerous stability statistics available to the plant breeder and to the production agronomist provide different strategies and approaches of dealing with GEI.

Stability is an important concept for plant breeders interested in analyzing GEI data (Denis et al., 1996). Some researchers prefer to use the term sensitivity analysis instead of stability analysis (Dyke et al., 1995). Stability has many concepts. The static concept of stability implies that a genotype has a stable performance across environments, with no among-environment variance, i.e., a genotype is nonresponsive to increased levels of inputs. This type of stability, also referred to as biological concept of stability (Becker, 1981), is not desirable in production agriculture. The dynamic concept implies that a genotype’s performance is stable, but for each environment, its performance corresponds to the estimated or predicted level. The estimated or predicted level and the level of actual performance should agree (Becker and Leon, 1988). This concept has been referred to as the agronomic concept (Becker, 1981). Lin et al. (1986) classified stability statistics into four groups: (i) Group A — based on deviation from average genotype effect (DG); represents sums of squares (ii) Group B — based on GEI; represents sums of squares
GGE biplot software (Yan, 2001). The basic model for a GGE Biplot is:

\[ Y_{ij} = \mu + \alpha_i + \beta_j + \Phi_{ij} \]

The probability of outperforming a check (Eskridge, 1996), and Kang's rank-sum method (Kang, 1988, 1993) are effective, account for the underlying interaction (Shafii and Price, 1998). Integrating results obtained from biplot graphics with those of the genotypic stability analyses allows clustering of genotypes based on similarity of response and the degree of stability of performance across environments (Shafii and Price, 1998). The AMMI model or variations thereof (e.g., factor regression or FANOVA) have been used for interpreting GEI in various situations (Baril, 1992; Gutierrez et al., 1994; Yan and Hunt, 1998). Biadditive factorial regression models, which encompass both factorial regression and biadditive AMMI models, also have been evaluated (Brancourt-Hulmel et al., 2000). The shifted multiplicative model (SHMM) (Crossa et al., 1996; Cornelius et al., 1996), the nonparametric methods of Hühn (1996) that are based on cultivar ranks, analyses based upon the probability of outperforming a check (Eskridge, 1996), and Kang's rank-sum method (Kang, 1988, 1993) are some of the other methods that have been considered by plant breeders. The methods of Hühn (1996) and Kang (1988, 1993) integrate yield and stability into one statistic that can be used as a selection criterion.

GGE biplot analysis was recently developed to use some of time function of these methods jointly. The GGE biplot method originated with Gabriel (1971), and its use was subsequently expanded by Kempton (1984) and Zobel et al. (1986). The extensive usefulness of GGE biplot, where G = genotype effect and GE = genotype-by-environment effect, has only recently been elucidated (Yan, 2001).

The GGE biplot is a multi-faceted tool in quantitative genetic analyses and plant breeding. In addition to dissecting GEI, GGE Biplot helps analyze genotype-by-trait data, genotype-by-marker data, and diallel cross data (Yan et al., 2001; Yan, 2001; Yan and Hunt, 2000, 2002; Yan and Rajcan, 2002). These aspects make GGE biplot a most comprehensive tool in quantitative genetics and plant breeding.

GGE Biplot is an effective tool for: 1) mega environment analysis (e.g. "which-won-where" pattern), where by specific genotypes can be recommended to specific mega environment (Yan and Kang, 2003, Yan and Tinker, 2005), 2) genotype evaluation (the mean performance and stability) and 3) environmental evaluation (the power to discriminate among genotypes in target environment).

The objectives of this study were to (1) interpret G main effect and GE interaction obtained by SREG analysis of yield performances of 16 bread wheat genotypes over five environment; (2) application of the GGE biplot technique to examine the possible existence of different mega environments in wheat growing; (3) visual assessment of yield variation across environments based on the GGE biplot and (4) application of this method to determine discriminating ability and representativeness of the environments.

**MATERIALS AND METHODS**

**Plant materials**

This study was carried in 2005-2006 in five different locations in Ilam province in Iran. A set of 16 bread wheat genotypes selected from advanced experiments of research stations were used as experimental material (Table 1). Experimental layout was a randomized complete block design with four replications in each location. Each plot consisted of six rows of 6 meter length. Row distance was 20cm and seed distance was 2cm, respectively. Data on seed yield were taken from the middle two rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

**Statistical analysis**

Analysis of variance on grain yield was conducted by Genstat software to determine the effect of environment (E), genotype (G) and GE interaction. Coefficients between pairs of locations were computed via SAS 9.2 software. The first two components resulted from principal components were used to obtain a biplot by GGE biplot software (Yan, 2001). The basic model for a GGE Biplot is:

\[ Y_{ij} = \mu + \alpha_i + \beta_j + \Phi_{ij} \]
Or
\[ \bar{Y}_{ij} - \mu - \beta_i = \alpha_i + \Phi_{ij} \]

Where \( Y_{ij} \) is the expected yield of genotype \( i \) in environment \( j \), \( \mu \) is the grand mean of all observations, \( \alpha_i \) is the main effect of genotype \( i \), \( \beta_j \) is the main effect of environment \( j \), and \( \Phi_{ij} \) is the interaction between genotype \( i \) and environment \( j \).

Instead of trying to separate G and GE, a GGE biplot model keeps G and GE together and partitions this mixture GGE into two multiplicative terms:
\[ \bar{Y}_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \epsilon_{ij} \]

where \( g_{i1} \) and \( e_{1j} \) are called the primary scores for genotype \( i \) and environment \( j \), respectively; \( g_{i2} \) and \( e_{2j} \), the secondary scores for genotype \( i \) and environment \( j \), respectively; and \( \epsilon_{ij} \) is the residue not explained by the primary and secondary effects. A GGE biplot is constructed by plotting \( g_{i1} \) against \( g_{i2} \), and \( e_{1j} \) against \( e_{2j} \) in a single scatter plot. The primary scores can be obtained through singular value decomposition (SVD) of the GGE or through regression of GGE against genotype main effects.

**RESULTS AND DISCUSSION**

The ANOVA for grain yield in five different environments using the SREG analysis is presented in Table 2. There were significant differences among the environments (E), genotypes (G) and G×E interaction. Significant E, G and G×E interaction explained 59.39%, 9.39% and 14.34% of the total sum of squares respectively. In the SREG analysis this is the first and second interaction principal component analysis (IPCA1 and IPCA2) explained 8.86% and 4.59% of the G×E variation, respectively.

GGE stands for genotype main effect (G) plus genotype by environment interaction (GE) and the GGE concept is based on the understanding that genotype main effect (G) and genotype by environment interaction (GE) are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously, not alone or separately, for appropriate genotype evaluation (Yan, 2002). The graphical method was employed to investigate environmental variation and interpret of G×E interaction (Figure 1).

**Table 1. Genotype code and name of 16 bread wheat genotypes.**

<table>
<thead>
<tr>
<th>No.</th>
<th>Code</th>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>B1</td>
<td>Gen Bank-3</td>
</tr>
<tr>
<td>2</td>
<td>B2</td>
<td>Momchil/Kataya1</td>
</tr>
<tr>
<td>3</td>
<td>B3</td>
<td>Ok822822//Bow//Nkt/3/F41105w2.1</td>
</tr>
<tr>
<td>4</td>
<td>B4</td>
<td>Rsk/Nac//Sardari/5/Lr64//lz1813//093-44//3/NO57//4/Sut66</td>
</tr>
<tr>
<td>5</td>
<td>B5</td>
<td>Turkey PYT (1999-2000)-13</td>
</tr>
<tr>
<td>6</td>
<td>B6</td>
<td>Unknown-4</td>
</tr>
<tr>
<td>7</td>
<td>B7</td>
<td>Turkey KOVD – A (1999-2000) -16</td>
</tr>
<tr>
<td>8</td>
<td>B8</td>
<td>Ww33G/Vee&quot;s&quot;//Mrm//HD2172//Bloudan//Azd/3/San/Ald&quot;s&quot;//Avd</td>
</tr>
<tr>
<td>9</td>
<td>B9</td>
<td>T189</td>
</tr>
<tr>
<td>10</td>
<td>B10</td>
<td>Almaty Polukovilik</td>
</tr>
<tr>
<td>11</td>
<td>B11</td>
<td>Tam 200/Fundulea</td>
</tr>
<tr>
<td>12</td>
<td>B12</td>
<td>1D13.1/Mlt//Tui</td>
</tr>
<tr>
<td>13</td>
<td>B13</td>
<td>Fenkang 15/Sefid</td>
</tr>
<tr>
<td>14</td>
<td>B14</td>
<td>87 Zhong 291</td>
</tr>
<tr>
<td>15</td>
<td>B15</td>
<td>Azar - 2</td>
</tr>
<tr>
<td>16</td>
<td>B16</td>
<td>Sardari</td>
</tr>
</tbody>
</table>

**Table 2. Analysis of variance for grain yield of 16 bread wheat genotypes in five environments.**

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>%TSS</th>
</tr>
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<tbody>
<tr>
<td>Model</td>
<td>94</td>
<td>444043501.8</td>
<td>4723867.0**</td>
<td>86.82</td>
</tr>
<tr>
<td>Environment(E)</td>
<td>4</td>
<td>303734653.3</td>
<td>75933663.3**</td>
<td>59.39</td>
</tr>
<tr>
<td>Rep(E)</td>
<td>15</td>
<td>18907214.6</td>
<td>1260481.0**</td>
<td>3.7</td>
</tr>
<tr>
<td>Genotype(G)</td>
<td>15</td>
<td>48037561.1</td>
<td>3202504.1**</td>
<td>9.39</td>
</tr>
<tr>
<td>G×E</td>
<td>80</td>
<td>73364072.8</td>
<td>1222734.5**</td>
<td>14.34</td>
</tr>
<tr>
<td>IPCA1</td>
<td>18</td>
<td>32500284.25</td>
<td>1805571.35**</td>
<td>8.86</td>
</tr>
<tr>
<td>IPCA2</td>
<td>16</td>
<td>17974197.84</td>
<td>1123387.365**</td>
<td>4.59</td>
</tr>
<tr>
<td>Residuals</td>
<td>26</td>
<td>22889590.164</td>
<td>880368.85n.s</td>
<td>0.89</td>
</tr>
<tr>
<td>Error</td>
<td>255</td>
<td>67403189.20</td>
<td>299569.7</td>
<td>13.18</td>
</tr>
</tbody>
</table>

**Relationships among test environments**

GGE biplot, which was based on environment focused scaling, was portrayed to estimate the model of environments (Figure 1). The vector view of the GGE biplot (Figure 1) provides a summary of the interrelationships among the locations. The lines that connect the test environments to the biplot origin are called environment vectors. The cosine of the angle between the vectors of two environments approximates the
correlation between them (Kroonenberg, 1995; Yan, 2002). The distance between two environments measures their dissimilarity in discriminating the genotypes. Thus, the five environments fell into three apparent groups: E2 formed group1, E1 and E3 formed group2 and E4 and E5 formed group3. The smallest angle between E4 and E5 implies that there was the highest correlation between them. The large angle between E2 and E3 indicates the poor correlation between these locations (Figure 1).

Figure 1. GGE biplot based on relationships among test environments.

Figure 2. Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments.

Figure 3. GGE biplot based on genotype-focused scaling for comparison the genotypes.
Which-Won-Where Pattern of genotypes

One of the most smart facial appearance of a GGE biplot is its facility to show the which-won-where model of a genotype by environment dataset (Figure 2). Many researchers find this use of a biplot intriguing, as it graphically addresses important concepts such as crossover GE, mega environment differentiation, particular adaptation, etc (Yan and Tinker, 2005). The polygon is created by involving the markers of the genotypes that are further away from the biplot source such that all other genotypes are restricted in the polygon. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments since they had the long distance from the origin of biplot. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. For example, lines 1 and 2 are perpendicular to side B3 – B8; line 3 is perpendicular to the side B9 – B6; line 4 is perpendicular to side B6 – B16; similarly, line 5 is perpendicular to side B16 – B12 and line 6 to side B12 – B3. These 6 lines divide the biplot into 6 sectors, and the environments fall into 2 of them (Figure 2). An interesting feature of this view of a GGE biplot is that the vertex genotype(s) for each sector has higher (sometimes the highest) yield than the others in all environments that fall in the sector (Yan, 2002). Thus, E4, E5, E1 and E3 fell into sector 2 delineated by lines 2 and 3, and the vertex genotypes for this sector were B8 and B9. Similarly, E2, fell into sector 6 delineated by lines 6 and 1, and the vertex genotype for this sector was B3 and B2.
**Ranking of genotypes based on yield and stability**

The ranking of 16 genotypes based on their mean grain yield and yield stability for 5 environments is shown in Figure 3. It has been reported that when PC1 in a GGE biplot approximates the G (mean performance), PC2 must approximate the G × E associated with each genotype, which is a measure of instability (Yan et al., 2000; Yan, 2002). The line passing through the biplot origin and the environmental average is indicated by circles and is known as the average environment coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores for all environments. Projection of genotype markers onto this axis should, therefore, approximate the mean yield of the genotypes. Thus, genotypes 9, 8, 3, 2, 15 and 13 had higher grain yield, followed by genotypes 10, 11, 7, 5, 4, 14, 12, 1, 6 and 16 for all dataset. The line which passes through the origin but is perpendicular to the AEC with double arrows represents the status of the genotypes stability. A position in either direction away from the biplot origin, on this axis, indicates greater G × E interaction and reduced stability (Yan, 2002). Therefore, genotypes 5, 7, 14 and 3 showed a more variable and less stable performance than the other genotypes. Genotypes 8, 10 and 16 were more stable than the others (Figure 4).

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method (Yan, 2001, 2002 and Yan and Hunt, 2002). Within a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments. Figure 5 is the average-environment coordination (AEC) view of the GGE biplot. The single-arrowed line is the AEC abscissa, it points to higher mean yield across environments. Thus, B9, B8, B3, B2 and B15 had the highest mean yield. The double-arrowed line is the AEC ordinate; it points to greater variability (poorer stability) in either direction. Thus, B5 and B7 were highly unstable whereas B8 and B10 were highly stable, followed by B16, B11 and B1.

**CONCLUSION**

The 16 bread wheat genotypes showed very high variation for grain yield. The five test environments were classified into three mega-environments. genotype B8 was the best performer in all environments, followed by B10, B16, B1 and B11. Genotypes B9 and B8 had the highest yield stability.

**REFERENCES**


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