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Stability analysis of bread wheat landraces and genotypes using GGE-BIPLOT

Fatemeh Bavandpori[*], Jafar Ahmadi, Sayyed Mohssen Hossaini

Department of Crop production and Breeding, Imam Khomeini International University, Iran

Abstract
The objective of this study was to explore the effect of genotype (G) and genotype ×environment interaction (GEI) on grain yield of 20 bread wheat genotypes (*Triticumaestivum* L.) insix different environments.The experiment was conducted in randomized complete block design(RCBD) with three replications under two conditions(irrigated and rainfed). Yield data were analyzed using the GGE biplot method. Environment (E)explained 81.05% of the total variation, whereas G and GEI captured 3.83% and 11.54%,respectively. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensionalGGE biplot and explained 34.3% and 23.2% of GGE sum of squares (SS), respectively. Collective analysis of the biplotsuggested four bread wheat mega-environments in Kermanshah Province.The firstmega-environment contained environments:E1, E5 and E6 with genotype G12followed by genotypes G16, G9, G5 and G17. Genotype G20followed by genotypes G19, G2 and G18 gave thehighest performance in environment E2. GenotypeG6 followed by genotypes G11, G3, G4 and G8thehighest performance in environments E3.GenotypesG1and G15 followed by genotype G7gave thehighest performance in environment E4.Genotypes12(WC-47403), 9(PISHGAM 2) exhibited the highest meanyield and Stability. Furthermore, the best genotypes were 12(WC-47403), 9(PISHGAM 2), 19(WC-4968), 18(WC-47472) and 20(WC-47528) idealgermplasm in order to introduce in the breeding programs.

***Corresponding Author:** Fatemeh Bavandpori ✉ f.bavandpori@yahoo.com

Introduction

Understanding the relationship between crop performance and environment has long been a key issuefor plant breeders and geneticists. Crop performance, the observed phenotype, is a function of genotypevariety or cultivar, environment, and GEI. GEI is said to occur when different cultivars or genotypes responddifferently to diverse environments. Researchers agree that GEI is important only when it is significant andcauses significant change in genotype ranks in different environments, i.e., different genotypes are superior indifferent environments (Yan and Kang, 2003).Agricultural researchers have long been cognizant of the various implications of GEI in breedingprograms (Mooers, 1921; Yates and Cochran, 1938). GEI has a negative impact on heritability. The lower theheritability of a trait, the greater the difficulty in improving ofthe trait. Understanding the structureand nature of GEI is important in plant breeding programs because a significant GEI can seriously impair effortsin selecting superior genotypes relative to new crop introductions and cultivar development programs (Shafiiand Price, 1998).The detection of GEI in trials has led to the development of procedures that are generically calledstability analyses. The numerous stability statistics available to the plant breeder and to the productionagronomist 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 stableperformance across environments, with no among-environment variance, i.e., a genotype is non-responsive toincreased levels of inputs. This type ofstability, 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 orpredicted level and the level of actual performance should agree (Becker and Leon, 1988). This concept hasbeen referred to as the agronomic concept (Becker, 1981). Lin *et al.* (1986) classified stability statistics into fourgroups: (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, (iii) Groups C and D: based on either DG or GEI; represent regression coefficient or deviations from regression. Lin *et al.* (1986) further assigned the four groups to three classes of stability: (1) Group A: Type 1 stability, (2) Groups B and C: Type 2 stability (3) and Group D: Type 3 stability.In Type 1 stability, which is equivalent to biological stability, a genotype isregarded as stable if its variance among environments is small. In Type 2 stability, which is equivalent to agronomic stability, a genotypeis regarded as stable if its response to environments is parallel to the mean response of all genotypes in a test.In Type 3 stability, a genotype is regarded as stable if the residual mean square following regression ofgenotype performance or yield on environmental index is small (Lin *et al.,* 1986). Lin and Binns (1988a)proposed a Type 4 stability concept on the basis of predictable and unpredictable non-genetic variation; thepredictable component related to locationsand the unpredictablecomponent related to years. They suggestedthe use of a regression approach for the predictableportion. The mean square for years-within-locations foreach genotype as a measure of the unpredictable variation was referred to as Type 4 stability.

GGE biplot analysis was recently developed to use some of timefunction of these methods jointly. Thebiplot method originated withGabriel (1971), and its use was subsequently expanded by Kempton (1984) andZobel*et al.*(1988). The extensive usefulness of GGEbiplot, where G = genotype effect and GE = genotypeby environment effect, has only recently been elucidated (Yan, 2001).The GGE biplotis a

multi-faceted tool in quantitative genetic analyses and plant breeding. In addition todissectingGEI, GGE biplot helps analyze genotypebytrait data, genotypebymarker data, and diallelcrossdata (Yan *et al.,*2000, 2001; Yan, 2001; Yan and Hunt, 2002; Yan and Rajcan, 2002). These aspects makeGGE biplot a mostcomprehensive tool inquantitative 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, Yanand Tinker, 2005), 2) genotype evaluation(the mean performance and stability) and 3) environmentalevaluation (the power to discriminate among genotypes in target environment).

The objective of this studywas to use GGEbiplot to evaluate thegrainyieldstability and to identify bread wheat genotypes that have both high mean yield andstable yield performance across different environments forsemiarid areas of Iran.

Materials and methods

Plant materials

This study was carried in 2011-2013 in six different environments in Kermanshah province in Iran. A set of 20 bread wheat genotypes selected from advanced experiments ofresearch stations were used asexperimental material (Table 1). Experimental layout was a randomized complete block design with three replications in each location(34° 21´ N latitude,47° 9´ E longitude and 1319 m altitude). Climateof the region is classified as semi-arid with meanannual rainfall of 379.3 mm. Minimum and maximumtemperatures at the research station were 5.9 and22.6˚C, respectively. Each plot consisted of five rows with5 meter length. Row distance was 20cm and 400 per m²seed density, respectively. Data on seed yieldwere taken from the middle two rows of each plot. At harvest time,the seed yield was determined for eachgenotype at each test environments.

Statistical analysis

Analysis of variance on grain yield was conducted by GGE biplot software to determine the effect ofenvironment (E), genotype (G) and GE interaction.The environments were considered as random effects and the genotypes as fixed factors. Coefficients between pairs of environments 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 GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and GGE concept (Yan *et al.,* 2000) was also used to visually analyze and identify the genotypic stability of genotypes. The graphs generated based on "which-won-where"pattern, ranking of genotypes on the basis of yield and stability, comparison of genotypes to an idealgenotype and ranking of genotypes relative to the test environment with the highest yielding performance(Farshadfar *et al.,* 2012).

Results and discussion

The ANOVA for grain yield in six different environments was presentedinTable 2. There were significant differences among the environments (E), genotypes (G) and G×E interaction (P<0.01). Significant E, G and G×E interaction explained 81.05%, 3.83% and 11.54% of the total sum of squares, respectively(%TSS).The first and second interaction principal component analysis (IPCA1 andIPCA2) explained 42.54 and 34.68% of the G×E variation, respectively. GGE stands for genotype main effect (G) plus genotype by environment interaction (GE) and the GGEconcept 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 consideredsimultaneously, not alone or separately, for appropriate genotype evaluation (Yan, 2002).

Which-Won-Where Pattern of genotypes

According to GGE analysis, ideal genotypes are those

that should have large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability). Also, ideal test environments should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments) (Yan and Rajcan, 2002). The polygon view of a GGE-biplot explicitly displays the which-won-where pattern, and hence is a succinct summary of the GEI pattern of a MEYT data set (kaya *et al.,* 2006). A polygon view for GGE analysis of grain yield of studied genotypes in six environments were given in Fig.1, which formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed inside the polygon. The vertex genotypes were G12, G20, G6, G15 and G1. These genotypes were the best or the poorest genotypes in

some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang, 2003). 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.

Table 1. Genotypes code and the name of 20 bread wheat genotypes.

No.	Code	Name
1	G1	GERAVANDI-17
2	G2	WC-47536
3	G3	WC-4919
4	G4	WC-4868
5	G5	WC-5046
6	G6	WC-4995
7	G7	PISHGAM-1
8	G8	WC-4536
9	G9	PISHGAM-2
10	G10	WC-47582
11	G11	WC-47359
12	G12	WC-47403
13	G13	WC-47388
14	G14	WC-4611
15	G15	WC-4515
16	G16	PISHTAZ
17	G17	MOGHAN-3
18	G18	WC-47472
19	G19	WC-4968
20	G20	WC-47528

In this study, the genotypes fell in five sectors and the test environments fell in two sectors. The first sector consists of E1, E5 and E6 environments (irrigated environment year 2011, irrigated environment year 2013 and rainfed environment year 2013, respectively), which had the genotype G12 followed by genotypes G16, G9, G5 and G17 as the specific

adaptable genotypes. The second sector consists of G20 followed by genotypes G19, G2 and G18 that this group had specific adaptation with E2 (rainfed environment year 2011). In this interpretation, the third sector consists of G6 followed by genotypes G11, G3, G4 and G8 that this group had specific adaptation with E3 (irrigated environment year 2012).

The fourth sector consists of G13, G10 and G14. The genotypes of group four did not show specific adaptation by environments. The fifth sector consists of G1 and G15 followed by genotype G7 showed specific adaptation with E4 (rainfed environment year 2012) (Fig.1).

Table 2. Analysis of variance for grain yield of 20 bread wheat genotypes in six environments.

S.O.V	DF	SS	%SS	MS
Genotype(G)	19	857403	3.83	45126[**]
Environment(E)	5	18132570	81.05	3626516[**]
G×E	95	2582796	11.54	27187[**]
IPC$_1$	23	1098639	42.54	47767[**]
IPC$_2$	21	895707	34.68	42653[**]
Error	240	800328	3.57	3335
Total	359	22373066	-	-

[**]: Significant at 1% statistical level.

Mean performance and stability of the genotypes
Yield performance and stability of genotypes were evaluated by 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. Fig.2 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, G12, G16, G9, G1, G18, G7, G15, G5, G17 and G19 had the highest mean yield. The double-arrowed line is the AEC ordinate; it points to greater variability (poorer stability) in either direction. Thus, genotypes G1, G7, G15, G19 and G16 were relatively unstable (Fig.2).

Discriminating ability and representativeness of the test environment
GGE biplot discriminating ability and representativeness is an important measure of the testing environments.

The concentric circles on the biplot as shown in Fig.3 help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminatory ability of the

environments.
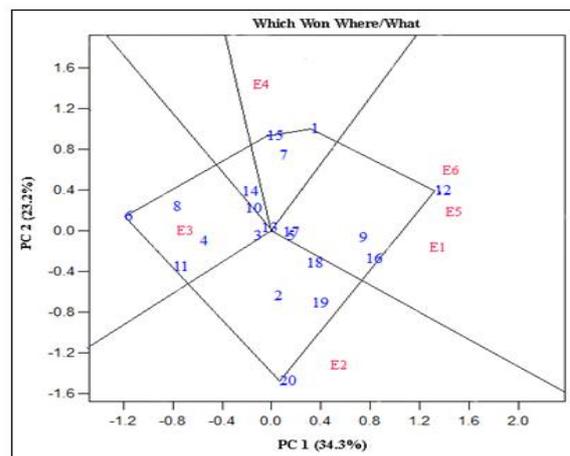
Fig. 1. Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments.

Therefore, among the six environments, E5 and E6 (irrigated and rainfed environments year 2013) were the most discriminating (informative). Environments E2 and E4 (rainfed environments years 2011 and 2012) were lower discriminating. Environment E3 (irrigated environment year 2012) was the least discriminating. Test environments that are consistently non-discriminating (non-informative), provide little information on the genotypes and, therefore, should not be used as test environments. The average environment (represented by the small circle at the end of the arrow) has the average coordinates of all test environments, and Average-

Environment Axis (AEA) or Average-Tester-Axis (ATA) (Yan, 2002) is the line that passes through the average environment and the biplot origin.
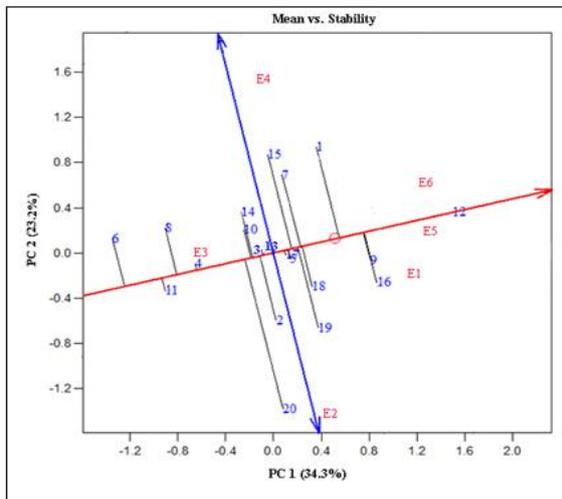
Fig. 2. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for themeans performance and stability of genotypes.

A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, E5 and E6 is the most representative whereas E3 is the least representative in their respective year. Test environments (locations) that are both discriminating and representative (e.g., E5) are good test environments for selecting generally adaptable genotypes. Discriminating but non-representative test environments like E3 are useful for selecting specifically adapt-able genotypes if the target environments can be divided into mega-environments or they are useful for culling unstable genotypes if the target environment is a single mega-environment (Fig.3).

Ranking of genotypes relative to the ideal genotype
An ideal genotype should have the highest mean performance and be absolutely stable (that is, performs the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it (Fig.4). Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype

evaluation (Yan and Tinker, 2006). A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Because the units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype-focused scaling (Fig.2), the units of the AEC abscissa (mean yield) and ordinate (stability) should also be in the original unit of yield.
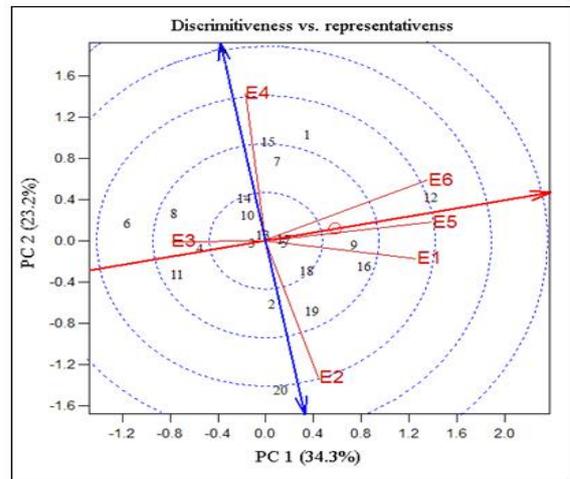
Fig. 3. Discriminating ability vs. representativeness of test environments.

The unit of the distance between genotypes and the ideal genotype, in turn, will be in the original unit of yield as well. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important (Farshadfar *et al.,* 2012; Yan, 2002). Fig.4 revealed that G12, which fell into the center of concentric circles, was the ideal genotype in terms of higher yielding ability and stability, compared with the rest of the genotypes. In addition, G9 and G16, located on the next consecutive concentric circle, may be regarded as desirable genotypes. G6 genotype was the weakest genotype according ranking (Fig.4).

Ranking of environments relative to the ideal environment
The ideal environment is represented by an arrow pointing to it (Fig.5). Although such an ideal environment may not exist in reality, it can be used as

a reference for genotype selection in the MEYTs. An environment is more desirable if it was closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan *et al.,* 2000).
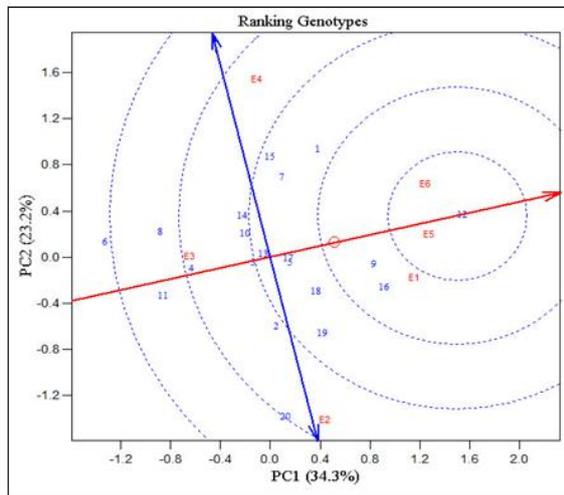
Fig. 4. GGE biplot based on genotype-focused scaling for comparison of the genotype with ideal genotype.
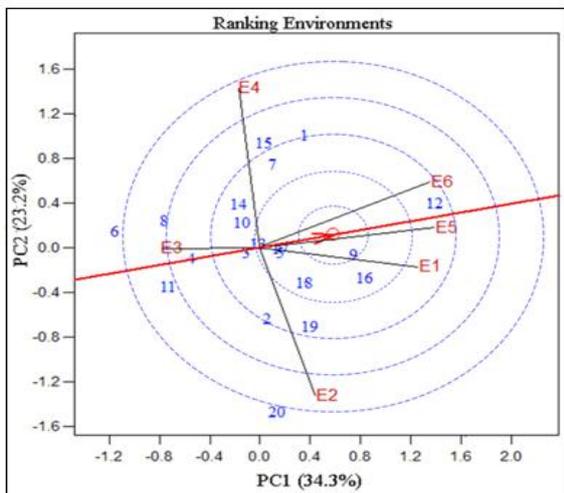
Fig. 5. GGE biplot based on environment-focused scaling for comparison of the environment with ideal environment.

The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments. Therefore, E1 and E5 (irrigated environment years 2011 and 2013) was the most ideal environments. E6

and E3 (rainfed environment year 2013 and irrigated environments year 2012) were the next ranking environments. E2 and E4 (rainfed environments years 2011 and 2012) were the weakest environments according ranking (Fig.5).

Conclusion

The 20 bread wheat genotypes showed very high variation for grain yield. The five test environments were classified into four mega-environments. Genotypes 12 (WC-47403), 9 (PISHGAM 2) exhibited the highest mean yield and Stability. Furthermore, the best genotypes were 12 (WC-47403), 9 (PISHGAM 2), 19 (WC-4968), 18 (WC-47472) and 20 (WC-47528) ideal germplasm in order to introduce in the breeding programs.

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