

GGE Biplot Based Stability Analysis of Durum Wheat Genotypes Using Statistical Package *GGEbiplotGUI*

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ABSTRACT

The investigation was aimed to identify stable genotypes of durum wheat which can perform consistently under multiple environments. The experiment was conducted in Research Area of CCS Haryana Agricultural University, Hisar during rabi 2015-16. In the present investigation seven released varieties of durum wheat were evaluated on four environments (timely *vs* late sown, irrigated *vs* drought) in randomized block design with three replications. Grain yield data was collected from randomly selected five plants of each genotype and used to carry out GGE biplot analysis using the R software and *GGEbiplotGUI* package. Analysis of variance revealed significant genetic variability among the genotypes. Significant variability was also observed due to both environment and GEI. The four environments were grouped into three major groups. Both irrigated environments were grouped together and were more alike for genotypic comparisons. Genotype WHD 948 was the most stable genotype in all the environments.

Highlights

- ① Significant variability for genotype, environment and their interaction was recorded.
- ① Four environments were grouped into two groups.
- ① Genotype WHD 948 was found most stable under different environments.

Keywords: GGE biplot, wheat, R software, *GGEbiplotGUI*, stability

Durum wheat (*Triticum durum* Desf.) is an important cereal and used for preparations of various food items such as bulgur, macaroni, and cakes. Although this species has less area than bread wheat (*T. aestivum*) but due to its importance in food industries it is grown all around the world with an annual production of 40 to 50 million tons (Kendal 2019). Demand of wheat is expected to increase in near future due to the increasing population. Plant breeders have always tried to improve the genotypic potential of crops to feed the huge population. But at present various abiotic stresses are causing severe challenges for breeders (Verma *et al.* 2020). In case of wheat, heat and drought are the major abiotic stresses. Under such situations it becomes necessary to breed genotypes which can tolerate these harsh conditions (Dehghanian 2006). In the process of crop improvement, assessment of genotypes under

multiple environments is important task. Evaluation of genotypes under different environments become more important under the present situations of climate change where plants are subjected to different stresses during a single growing season. Due to presence of high interaction of genotypes with environments cause change in ranking of genotypes under different environments (Letta *et al.* 2008; Jalata 2011; Farshadfar *et al.* 2012). The main problem of this type of evaluation is that data generated from multi environment experiment has multiple dimensions and analysis of this data becomes difficult. Graphical analysis of this type of data makes analysis easier. GGE biplot analysis is one of such techniques which not only help in graphical representation of data but also preserve all the information of the data (Yan *et al.* 2000). This technique removes irrelevant environment



from the data and analyzes the genotype by combining the genotypic variability with genotype x environment interactions (GEI) (Samonte *et al.* 2005). The main advantage of using this method is that stable genotypes can be identified easily and environments can be divided into groups based on their correlations with each other (Yan and Kang 2003; Yan and Tinker 2006). In recent years the use of this method has increased due to the need to develop varieties for the changing climatic conditions. But still there is lack of information among researchers about how to use this method. During the initial stage of this method a software 'GGEbiplot' was developed which was very easy for researchers of biology sciences (Yan 2001). This software although generate good figures but all the features are not available with the trial version. Secondly today researchers are shifting to one easy software R (R Core Team 2016). This software is very easy and freely available to researchers. R contains various statistical packages to carry out different type of analysis. 'GGEbiplotGui' is one of such packages used to analyze the multi-environment data. This package can be used directly to represent data into graphical forms. The present experiment was designed to evaluate durum wheat genotypes under multiple environment conditions. Further only seven genotypes and four environments are evaluated here so that readers can get an idea about how to analyze GGE biplot using this package.

MATERIALS AND METHODS

Experimental material

The present investigation was carried out in Research Area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University. The experiment was conducted during *rabi* 2015-16. For this experiment randomly selected seven durum genotypes namely; WHD 896, WHD 912, WHD 943, WHD 948, PDW 291, PDW 233, PDW 314 were used.

Environments and experimental design

The genotypes were evaluated under four environmental conditions i.e. timely sown irrigated condition (E1), late sown irrigated condition (E2), timely sown rainfed condition (E3), and late sown rainfed condition (E4). After restricting these

conditions other recommended packages and practices were followed throughout the cropping season of wheat. The experiment was conducted in Randomized Block Design (RBD) with three replications.

Data collection and statistical analysis

In the present experiment data was collected from randomly selected five plants from each genotype. Plants were tagged and harvested separately at the time of maturity. Threshing of these plants was done and grain yield of each plant was weighted. The data was then analyzed for the stability of genotypes and grouping of environments based on GGE biplot analysis given by Yan *et al.* (2000). For the data analysis, R software was used. GGE biplot was generated using statistical package 'GGEbiplotGUI'. This package can be downloaded in R by using the command 'install.package(GGEbiplotGUI) and can be loaded for analysis by the command 'library(GGEbiplotGUI)'. Grain yield of seven genotypes from the above four environments was saved in a comma separated file (.csv) and imported into R studio. After this biplot was generated by a simple command 'GGEbiplot(data_file)'. Different types of biplots can be generated by using the option 'biplot analysis'.

RESULTS AND DISCUSSION

Analysis of variance

Grain yield in wheat is a complex trait as it has both genotypic and environmental origin (Farshadfar *et al.* 2013). In the present study it was found that yield of seven durum wheat genotypes varied across environments which proved that environment influenced this trait (Table 1).

Table 1: Mean grain yield of durum wheat varieties in the multi environment trial

Variety	Grain yield (g/plant)				Mean
	E1	E2	E3	E4	
WHD 896	22.00	12.63	12.37	14.20	15.30
WHD 912	24.83	13.03	10.30	10.00	14.54
WHD 943	22.93	16.17	9.60	11.37	15.02
WHD 948	28.90	18.57	18.30	7.90	18.42
PDW 291	22.23	12.63	13.43	9.73	14.51
PDW 233	22.90	13.87	15.30	10.80	15.72

PDW 314	24.13	15.13	14.60	9.80	15.92
Mean	23.99	14.58	13.41	10.54	15.63

E1: Timely sown irrigated environment; E2: Late sown irrigated environment; E3: Timely sown rainfed environment; E4: Late sown rainfed environment.

Pooled analysis of yield data for seven durum wheat genotypes from four environments was carried out to partition the total variability into its component parts. Analysis of variance (ANOVA) showed that the studied genotypes were significantly different from each other for grain yield (Table 2). Further highly significant variations were also noticed for environment and genotype \times environment interaction (GE). Only 28.10% of variability is caused by genotype itself. It is clear from the table that about 50.48% of variability was caused only by environment itself whereas its interaction with genotype contributed for about 7.38% of variability. It is clear from earlier studies that durum wheat has enough genetic variability for grain yield (Rathwa *et al.* 2018). Grain yield in wheat is affected by significant influence of environment (Kaya and Akcura 2014). Earlier researchers have also noticed significant interaction of genotypes with environment Solonechnyi *et al.* (2015). The significant interaction of genotype and environment is the major cause of change in ranking of genotypes under different environments (Matus-Cadiz 2003). This interaction also creates problems while selecting a genotype on the basis of grain yield (Crespo *et al.* 2017).

Table 2: Pooled analysis of variance for genotype, environment and GE on yield of durum wheat genotypes

Source of Variation	DF	Mean Sum of Squares	% SS
Genotype	18	6.301**	28.105
Environment	3	67.918**	50.489
Rep within environment	8	1.072	2.124
Genotype \times Environment	6	4.970**	7.388
Pooled Error	48	1.000	11.894
Total	83		

**Significant at $p > 0.01$, DF: Degree of freedom; SS: Sum of squares.

Variability explained by GGE biplot

Environmental effect can make the evaluation more confusing. In the present case about 50% of

variability was caused due to environment. Under such situation the data was further analyzed for genotype and genotype plus environment interaction (GGE) using the standard procedure of GGE biplot analysis suggested by Yan *et al.* (2000). In GGE biplot analysis the irrelevant environmental variance is separated from total variance and evaluation of genotypes are carried out only using two parameters viz. genotype and GEI (Yan and Kang 2003). Using this method two major principle components; PC1 and PC2 were calculated which accounted for 71.30% and 17.34% of variability respectively shown on x and y axis of GGE biplot (Fig. 1). The first two principle components accounted for a total of 88.64% of genetic variability for grain yield among these genotypes caused by G+GE interaction. In a similar study first two PCs were used to represent 88.50% of variability caused by GEI (Solonechnyi *et al.* 2015). When first two PCs can measure maximum variability exploration of other PCs become wasteful (Verma *et al.* 2020).

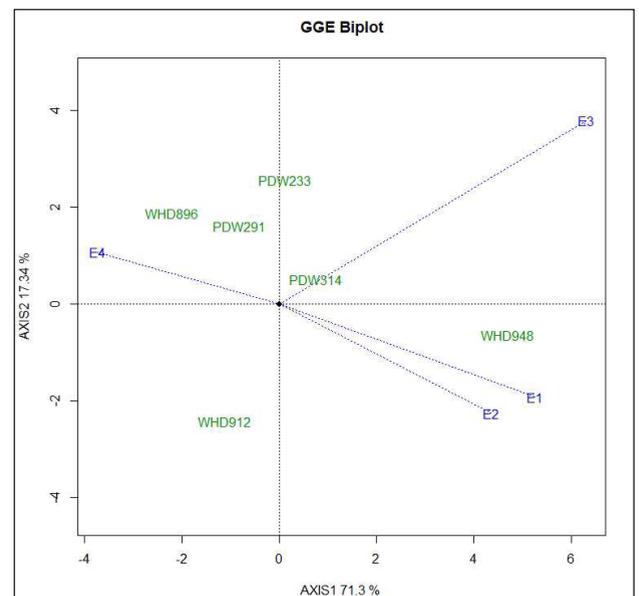


Fig. 1: Basic features of the GGE biplot. Note that about 88% of variability was explained by first two principal components

Grouping of environments

In our present GGE biplot, green color was used to indicate positions of genotypes on biplot whereas environments were represented by blue color. To get the maximum information from the biplot, black dotted lines were used to represent origin of biplot and blue dotted lines as environment vectors i.e. line joining the environments to the origin of biplot. The

environment vectors were formed by calculating standard deviations of genotypes in a particular environment. Thus, the length of environmental vectors can be utilized in identification of a suitable environment. In the present study, environment E3 had maximum length of environment vector (Fig. 2). Grouping of environments based on GGE biplot is more easy and valuable (Yan 2000).

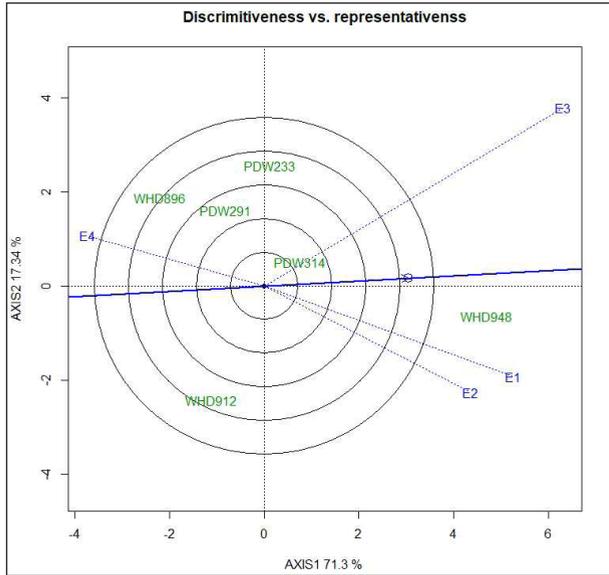


Fig. 2: Ranking of environments based on discriminating ability and representativeness

Thus, environment E3 had more discriminating power as genotypes perform differentially in this environment. All other environments had similar environment vectors and thus had same discriminating powers. The other information we get from environment vectors is the correlation between the environments. This correlation is a measure of cosine angular distance between two environment vectors. Larger the angle, lesser will be correlation between the environments and vice versa. In the present case, environment E1 and E2 were highly correlated while others with high angles were less correlated. Thus instead of E1 and E2 we can use either of these environment for future studies as both environments are alike and can give similar results. Another feature of GGE biplot is that environments can be grouped based on average or ideal environment. In Fig. 2, the bold and arrowed blue line was used to represent average environment. This line is called average environment coordinate (AEC) and the angle between this line and a test environment is used to

check the reliability power of that test environment (Braun *et al.* 1996). In present case, environment E4 and E1 had almost equal angle with AEC and had higher discriminating power than other environments. Thus out of these four environments only three environments i.e. E1, E2 and E3 are best and one can drop the fourth environment for genotypic assessment.

Stability of genotypes

The genotypes WHD 948 was best for three environments viz. E1, E2 and E3 whereas WHD 896 was most suitable for E4 (Fig. 3a). Variability in a genotype and its yield stability can be accessed by locating the genotype on AEC. From Fig. 3, it is clear that genotype WHD 948 is more stable and higher yielder than other genotypes. Genotypes WHD 943, WHD 912 and PDW 233 were situated away from ATC lines and thus varied from one environment to other. In other way we can say that performance of these three genotypes was changing across different environments (Fig. 3b). As GGE biplot can classify the genotypes according to their stability this technique is very useful for plant breeders (Hagos and Abay 2013; Sagar *et al.* 2014). GGE biplot has been utilized by Solonechnyi *et al.* (2015) to identify stable genotypes.

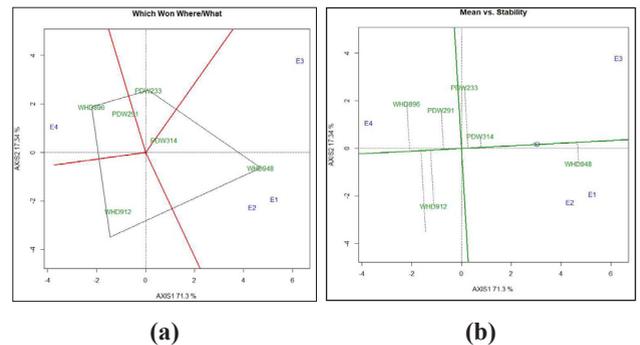


Fig. 3. (a) Polygon view of GGE biplot representing “which-won-where” pattern of genotypes and environments. **(b)** Average environment coordination (AEC) views of the GGE biplot based on environment-focused scaling for the means of performance and stability of genotypes

CONCLUSION

From this study it can be concluded that *GGEbiplotGUI* is one of user friendly package in R which can be used to study multiple environment data. Based on correlation matrices four environments can be classified into two groups. This suggests that when



there is no difference in irrigation, both normal and late sown environments can be used equally to evaluate the genotypes. Stability of genotype is a major concern for present day agriculture. In our study it is clear that the durum wheat genotype WHD 948 is most stable genotype.

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