Advances in Research

16(2): 1-9, 2018; Article no.AIR.43488
ISSN: 2348-0394, NLM ID: 101666096

GGE Biplot Analysis of Multi-environment Yield Trials for Wheat in Northern India

Bhushan Kumar[1], Ekta Hooda[1] and B. K. Hooda[1*]

[1]*Department of Mathematics and Statistics, CCS HAU-Hisar, Haryana, India.*

Authors' contributions

This work was carried out by the first author BK as part of his M. Sc. thesis, who also performed the statistical analysis. The second author EH managed the analyses of the study, updated literature and wrote the first draft of the present manuscript. The overall supervision and monitoring work was done by the third author BKH.

Article Information

DOI: 10.9734/AIR/2018/43488
Editor(s):
(1) Dr. Martin Kröger, Professor, Computational Polymer Physics, Swiss Federal Institute of Technology (ETH Zürich), Switzerland.
Reviewers:
(1) Enver Kendal Kiziltepe, Mardin Artuklu University, Turkey.
(2) Watcharin Soonsuwon, Prince of Songkla University, Thailand.
(3) Marcin Studnicki, Warsaw University of Life Science, Poland.
Complete Peer review History: http://www.sciencedomain.org/review-history/26094

Original Research Article

Received 16th June 2018
Accepted 22nd August 2018
Published 4th September 2018

ABSTRACT

A GGE Biplot provides an efficient graphical procedure for identification of favourable genotypes and mega-environment analysis. It displays the Genotype main effect (G) and genotype-by-environment (GE) interaction in two dimensions. It also possesses an extra property in the evaluation of the test environment by discriminating power versus representativeness view. Wheat breeders aim to develop superior genotypes characterised by high grain yield and other desirable quality traits. Presence of G × E interaction makes it difficult to identify the high yielding and most stable genotypes. Mega-environment analysis and genotype evaluation were conducted for 23 genotypes of wheat in six environments/states of Northern India during 2013-14. Delhi environment was observed as the most discriminating while Uttar Pradesh was reported as the least discriminating. The genotype WH1105 was observed to be the most favourable followed by PBW698 for Northern Zone of India.

**Corresponding author: E-mail: bkhooda@gmail.com;*

Keywords: Singular value decomposition; G×E interaction; GGE Biplots; Mega-environment analysis; genotype evaluation.

1. INTRODUCTION

The indigenous cropping pattern is not sustainable as farmers in developing and undeveloped countries want maximum benefit from agriculture through the increased crop productivity. They are always searching for the high yielding varieties. But a high yielding variety in one region may not be high yielding in one or more other regions. The reason for the non-uniform performance of a variety is not only due to change in the environment but also because of the genotype and environmental interaction. The G × E interaction is a complex factor and makes the breeding program comprehensive and expensive. In particular, the creation of different genotypes from parents and testing their adaptability in a region makes it a multi-year research program.

Breeders conduct multi-location trials (METs) to develop superior genotypes and to meet the challenges posed by climatic and environmental factors. They evaluate genotypes on the basis of yield and recommend cultivar for the production in a region. The ANOVA technique is not of much use in varietal selection because it does not consider the positivity and negativity of factors. In general, the performance and stability of a particular genotype are not uniform in all environments. It may also occur that most of the variations are due to the performance of genotypes in some specific environments. If the three factors of yield (G, E, and GE) simultaneously come in the analysis for every pair of genotype and environment, then selection of cultivars becomes simple for the targeted region. It is G × E which makes the selection of cultivar complex. If G × E is non-significant then a genotype having the best performance in one environment will have similar performance in all other environments. However, such a situation does not occur in practice. Though variation in yield due to the environment is greater than the variation due to genotype and G x E interaction, G + GE are relevant to cultivar evaluation as indicated by Yan and Tinker [1].

The genotype by environment data is represented in matrix form in which rows represent genotypes and columns represent environments. Introduced by Gabriel [2], biplot is a pictorial representation of a matrix in a plane by vectors for each row and each column such that scalar product of a row vector and a column vector is the corresponding row-column element of the matrix. In fact, biplot is a fusion of two plots, one plot of row factors (genotypes) and another plot of column factors (environments). Bradu and Gabriel [3] applied biplot to agricultural data from a cotton performance trial to illustrate their diagnostic role in model selection. Yan and Kang [4] used GGE biplot to cultivar evaluation and mega-environment investigation with the primary goal to identify superior cultivar for the target region.

According to Yan and Tinker [5] the GGE biplot allows for a comprehensive understanding of the target and test environments in addition to the effective evaluation of genotypes. They also suggested that a GGE biplot helps in understanding the target environment as a whole, whether it consists of single or multiple mega environments. Yan et al. [6] concluded that (G + GE) biplot analysis has wider adaptability in breeding programs and is superior to AMMI in mega-environment analysis and genotype evaluation. It possesses extra property in the evaluation of the test environment by discriminating power versus representativeness view which is not possible in AMMI biplot. Grange et al. [7] showed that the ‘R' package BiplotGUI provides a graphical user interface for construction, interaction, and manipulation of biplots. Bishnoi and Hooda [8] studied yield stability and association among parametric and non-parametric stability measures for wheat in Northern India.

Kumar [9] Applied GGE biplot methodology suggested by Yan et al. [10] for interpretation of G x E interaction based multi-environment trials data on wheat. Kendal [11,12] used ANOVA and GGE Biplot analysis of multi-environment yield trials to examine stability and genotypic superiority of barley cultivars. Kendal and Sener [13] applied GGE biplot analysis to examine the effects of G × E interaction on grain yield, its components, and quality characteristics in spring durum wheat and observed significant differences among cultivars in grain yield, yield components, and other quality traits.

Therefore, the present study was intended towards the construction and application of GGE biplots for interpretation of genotype versus environment interactions data for wheat yield in Northern India. Mega-environment analysis and genotype evaluation was conducted for 23 genotypes of wheat and was evaluated in 6 environments/states of Northern India (Delhi, Uttar Pradesh, Haryana, Uttrakhand, Punjab and Rajasthan) during 2013-14 under All India Coordinated Wheat and Barley Improvement Project.

2. MATERIALS AND METHODS

2.1 Data

The secondary data (Table 1) on 23 genotypes of wheat were evaluated in six states of Northern India (Delhi, Uttar Pradesh, Haryana, Uttrakhand, Punjab and Rajasthan) in randomised complete block design during 2013-14 under All India Coordinated Wheat and Barley Improvement Project have been used for the present study.

2.2 Model for GGE Biplot Analysis [5]

Let **Y** = $(y_{ij})_{n\times p}$ be the GE data matrix representing the mean grain yield of n = 23 wheat genotypes evaluated at p = 6 environments or states (Delhi, Uttar Pradesh, Haryana, Uttrakhand, Punjab and Rajasthan) in Northern Zone of India. In terms of the effects, the basic model for constructing a GGE biplot from GE data is given by

$$y_{ij} = \mu + g_i + e_j + \varphi_{ij} + \varepsilon_{ij}, \qquad (2.1)$$

i = 1, 2 , …n; j = 1, 2 ….p

Where y_{ij} is the average yield of i^{th} genotype in environment j^{th}; μ is overall or grand mean; g_i is the genotypic main effect; e_j is the environmental main effect; ϕ_{ij} is an interaction between g_i and e_j and ε_{ij} is the residual of the model associated with the genotype *i* in environment j. A GGE biplot is constructed by subjecting the environment-centred GGE Data to Singular Value Decomposition (SVD). The GGE data matrix is decomposed into three component matrices as:

$$\mathbf{Y = ULV^T} \qquad (2.2)$$

Where U (n × p) and V(p × p) are column orthonormal matrices, i.e. $\mathbf{U}^T\mathbf{U}$ = I = $\mathbf{V}^T\mathbf{V}$ and **L** is the diagonal matrix of non-zero eigen values of $\mathbf{YY}^T$ or $\mathbf{Y}^T$ **Y**. The columns of **U** (genotype eigenvector matrix) are eigenvectors of $\mathbf{YY}^T$ and columns of V (environment eigenvector matrix) are eigenvectors of $\mathbf{Y}^T$ **Y**.

Table 1. Mean wheat grain yield (q/ha) of 23 wheat genotypes evaluated at six locations in Northern India during 2013-14

Genotype	Delhi	Haryana	Punjab	Rajasthan	Uttar Pradesh	Uttarakhand
PBW 697	44.8	53.9	63.2	50.7	48.1	69.8
TL 2995	46.8	45.8	50.8	41.4	44.6	51.6
WH 1156	40.9	52.0	52.2	53.7	48.5	59.7
PBW 681	45.9	54.0	60.0	54.4	49.8	55.8
DBW 95	56.4	59.0	56.0	45.2	49.7	62.9
HD 3128	56.4	54.9	48.2	51.5	54.3	63.6
WH 1157	31.3	52.2	51.1	56.6	46.1	55.7
WH 1138	45.8	56.6	57.3	54.8	48.0	57.8
PBW 677	43.7	52.8	61.4	49.8	49.0	59.5
HD 3132	53.8	54.3	55.7	57.0	49.6	63.4
WH 1154	49.6	57.0	60.1	51.5	51.0	56.6
PBW 692	51.1	56.8	54.7	58.3	49.4	53.6
PBW 698	50.7	53.5	59.2	60.2	47.6	63.5
HD 3133	39.4	48.3	42.2	50.7	46.5	54.4
HUW 675	53.3	53.2	53.6	53.1	51.1	58.7
K 1204	48.2	54.8	53.1	53.4	47.8	54.1
PBW 695	39.7	51.6	54.9	55.0	50.1	57.1
HUW 666	46.1	55.6	56.7	51.3	47.9	55.9
HD 2967	52.2	51.5	50.7	50.7	50.4	60.7
DPW 621-50	50.2	55.2	55.2	57.1	49.8	61.3
WH 1105	52.9	59.4	59.9	49.2	50.0	66.2
DBW 88 (I)	36.5	53.9	59.9	52.1	50.3	63.8
HD 3086 (I)	44.5	57.3	59.5	59.2	47.5	60.4

The model for a GGE biplot based on SVD for the first two principal components is given by

$$y_{ij} - \mu - \bar{y}_j = \xi_{i1}\lambda_1\eta_{1j} + \xi_{i2}\lambda_2\eta_{2j} + \varepsilon_{ij} \qquad (2.3)$$

Where, y_{ij} is the average yield of genotype i in environment j; $\bar{y}_j$ is the average yield over all genotypes in environment j; λ_1 and λ_2 are the singular values for PC_1 and PC_2 respectively; ξ_{i1} and ξ_{i2} are the respective PC_1 and PC_2 scores for genotype i; η_{1j} and η_{2j} are the respective PC1 and PC2 scores for environment *j.*

To display PC_1 and PC_2 in a biplot, the equation (2.3) may be rewritten as:

$$y_{ij} - \mu - \bar{y}_j = \xi^*_{i1}\eta^*_{1j} + \xi^*_{i2}\eta^*_{2j} + \varepsilon_{ij} \qquad (2.4)$$

Where, $\xi^*_{ir} = \lambda_r^k \xi_{ir}$ and $\eta^*_{rj} = \lambda_r^{1-k}\eta_{rj}$, with r = 1, 2 and $0 \le k \le 1$. GE biplot is constructed by using scores derived from the first two PCs and plotting ξ^*_{i1} and η^*_{1j} against ξ^*_{i2} and η^*_{2j} in the same scatter plot. The R package based algorithm has been used for the construction of various biplots in this study [9].

3. RESULTS AND DISCUSSION

Table 2 shows the analysis of variance of G × E data for North India. The sum of squares and the percentage of variability along with respective degrees of freedom has been presented.

Table 2. Analysis of variance of G × E data for North India

Source	d.f.	S.S.	% variability
Genotypes	22	851.68	19.27
Environments	5	2012.27	45.52
G × E	110	1556.88	35.22

Analysis of variance had split the effects of genotypes, environments and G × E interaction. It is obvious from the analysis that variability in grain yield due to G × E interaction (35.22%) was more than the grain yield due to genotypes (19.27%). Also, environments accounted for 45.52% indicating that grain yield was likely to be more influenced by the environmental sites as compared to the G component. The contribution of GE to total variation was also higher as compared to the G component indicating a lesser scope for genetic improvement for this trait.

The GGE Biplot analysis can be used to combine the additive genotypic effect with the multiplicative effect of G× E and then decompose them into principal components using the singular value decomposition technique [2,12]. Results obtained by the SVD of the GGE matrix effects showed that out of the six principal components (PCs), first two PCs accounted for 53.46% of variation caused by G + GE, where PC1 and PC2 accounted for 29.68% and 23.79% of the total variation, respectively.

A biplot of G × E data quantified the factors i.e., genotypes and environments and presented these factors as vectors on a plot. The dot product of a pair of genotypes and environment factors provided a yield of that factor. The analysis considered GGE biplots to discuss the following six aspects in reference to the wheat grain yield data from the six environments of Northern India.

3.1 Similarity and Dissimilarity among Genotypes

The GGE biplot (Fig.1) of wheat grain yield data consisted of 23 genotypes and six environments of Northern India and had been shown by the environment vectors as Delhi, Uttar Pradesh, Haryana, Uttrakhand, Punjab and Rajasthan (Table 1). The plot was row metric and preserved the properties of genotypes (rows) of the data shown in Table 1. The distance between the two genotypes in the biplot approximated the difference between them. So, this GGE biplot can be considered appropriate for visualisation of similarity and dissimilarity among genotypes. It was found that groups like (TL2995, PBW697), (HD3128, WH1157) and (WH1157, DBW95) were dissimilar while WH1138, PBW681 and PBW677 were similar type of genotypes.

3.2 Relationships among Test Environments

Fig. 2 is a column metric preserving the environment-vector view of GGE biplot for the data presented in Table 1. The biplot explained 53.46% of the total variation of the environment-centered G × E data. The dotted lines connecting environments to the biplot origin are called environment vectors. The cosine of the angle between any pair of the environment vectors measures the correlation between them. Fig. 2 indicates that the environments of Haryana and Uttrakhand had a high positive correlation (acute angle) in Northern India for wheat cultivation. Presence of strong negative correlation (obtuse angle) between Delhi and Rajasthan was an indication of strong crossover GE, implying that GE is moderately large. The lengths of the environment vectors were the standard deviations of environments and indicated their capacity of genotype differentiation. So, Delhi environment came out to be the most powerful environment for genotype differentiation based on the present study for wheat cultivation in Northern India.

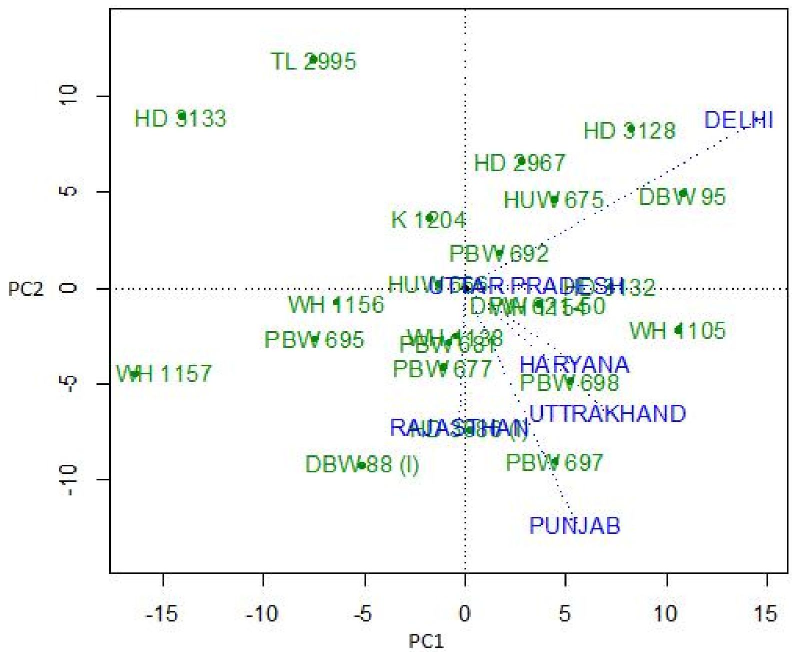

Fig. 1. Differentiation of genotypes in GGE biplot for Northern India wheat data

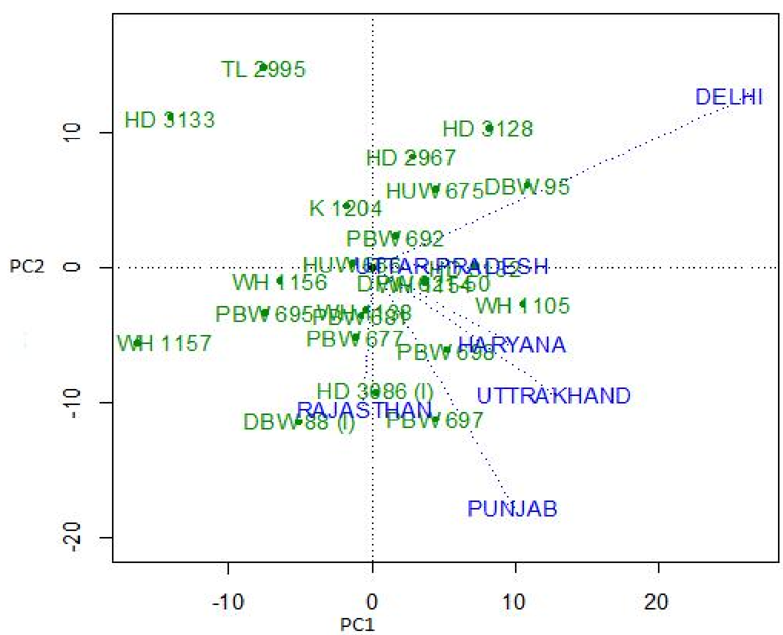

Fig. 2. Differentiation of environments in GGE biplot for Northern India wheat data

3.3 Mega-environments Analysis ('Which One Where' GGE Biplot)

Figs. 1 and 2 are congruent with respect to genotype and environment positions. The environments in this plot have also been shown as points where the only difference is that of the lines added to the plot. It is column-metric preserving biplot, so properties of the environments are retained exactly. Lines are added to extract extra information from column metric preserving GGE biplot. The additional information is about both the genotypes and environments by the division of the total trial areas into homogeneous groups with respect to genotype performances. An irregular convex polygon has been formed such that all genotypes come inside the polygon. Perpendicular lines are added on all sides of the polygon. The biplot in Fig. 3 provide superior or winner genotype in certain mega-environment. This biplot consists of four mega-environments identified as Delhi and Uttar Pradesh as one while Uttrakhand and Punjab form by two test locations. Haryana and Rajasthan form separate mega-environments consisting of only one test location each. The winner's genotypes at the vertex of the polygon were DBW95, PBW697, WH1105 and DBW88(I) for respective mega-environments.

3.4 Evaluation of Test Environment in Northern India on the Basis of GGE Biplot

Evaluation of environments helps in identification of test environments that effectively identify superior genotypes for a mega-environment. An ideal test environment is one which possesses the properties of discriminativeness of genotypes and representativeness of the mega environments. Correlation between a pair of environments is evaluated by the cosine of the angle between them. For evaluation of representativeness (Fig. 4), the target environment has been shown by an arrow on the Average-Environment Axis (AEA) by taking an average of all environments. Here, the angle between the target and the test environment is the representative of one another. The average environment has the average coordinates of all test environments and is often represented by a small circle at the end of the arrow.

The discriminating property was observed by the standard deviation of the environment (column) in G $\times$ E data. More standard deviation of the environment indicates more discriminating power of environment for genotypes [10]. Haryana environment with the smallest angle with the AEA (Fig. 4) had the highest representativeness of the experiment while Rajasthan with the largest angle with AEA had the lowest representation. The concentric circles on the biplot help in visualising the lengths of the environment vectors. It is proportional to the standard deviation within the respective environments and measures the discriminativeness power of the environments. It was observed that the Delhi environment was the most discriminating while Uttar Pradesh was the least discriminating environment.

3.5 Evaluation of Wheat Genotype in Northern India on the Basis of GGE Biplot

For the general release of a breed, genotypes were evaluated with respect to the average performance and stability of the genotypes. The test environment evaluation axis is helpful in search of such properties (Fig. 4). As discussed earlier, the axis passing through this virtual environment is called AEA while a perpendicular axis overlaid on the biplot is called average coordination axis (ACA). Projections of a genotype on AEA and ACA axes are the mean yield and stability of the respective genotypes. Taking both factors into consideration it was observed that the genotypes WH1105 and PBW698 were more suitable for cultivation in the experimental region (Northern Zone of India) (Fig. 5).

3.6 Ranking of Genotypes on the Basis of GGE Biplot

As discussed earlier (Fig. 4), inspite of considering two factors, genotypes may be ordered by a single factor. This is accomplished by defining ideal genotypes. The distances from ideal genotype decrease either mean yield or stability or both. Distances are considered as indicators of ranks in the evaluation of genotypes. Similarly, WH1105 was the most favourable genotype followed by PBW698 and DPW621-50 (Fig. 6). Onward all genotypes may be ranked in decreasing order by inspection of distances from the centre of the circle.

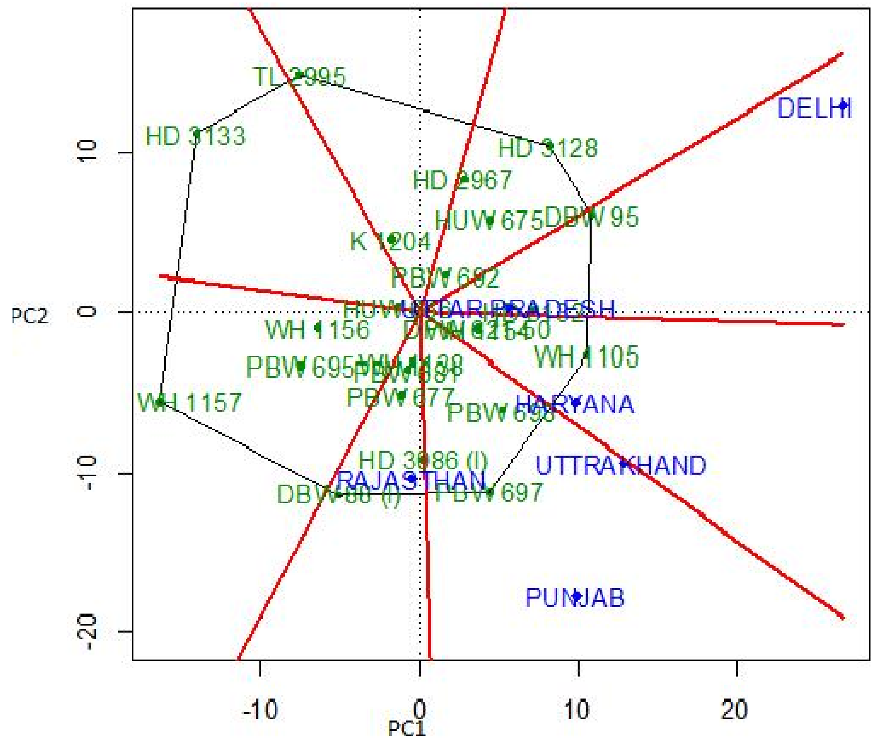

Fig. 3. Which won where GGE Biplot for Northern India wheat data

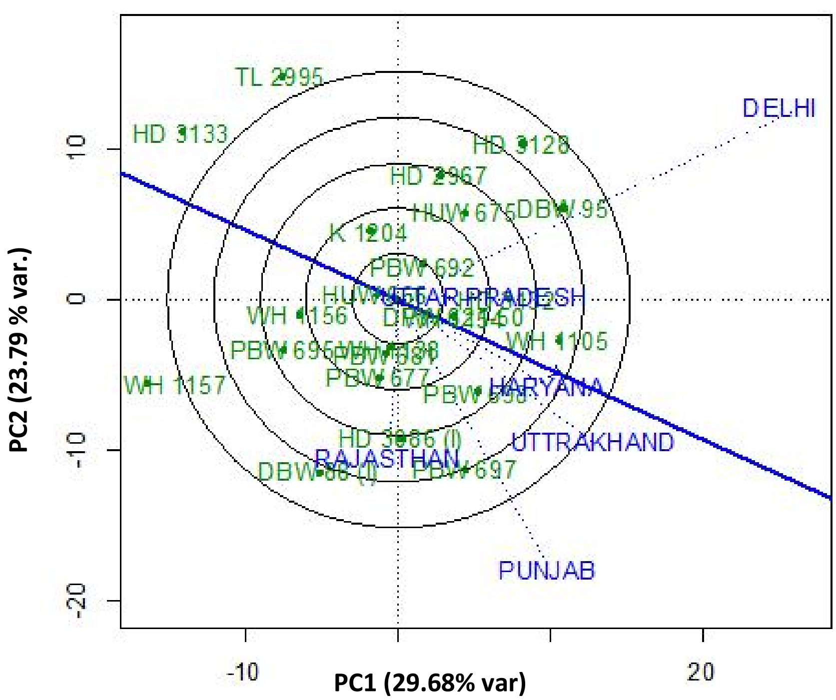

Fig. 4. Evaluation of environments for Northern India wheat data

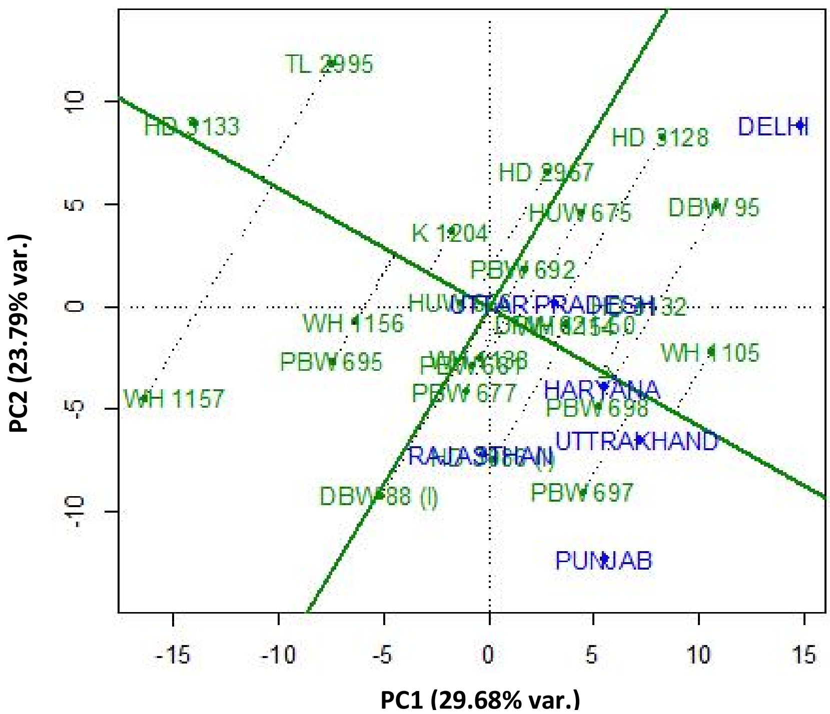

Fig. 5. Mean versus stability biplot for Northern India wheat data

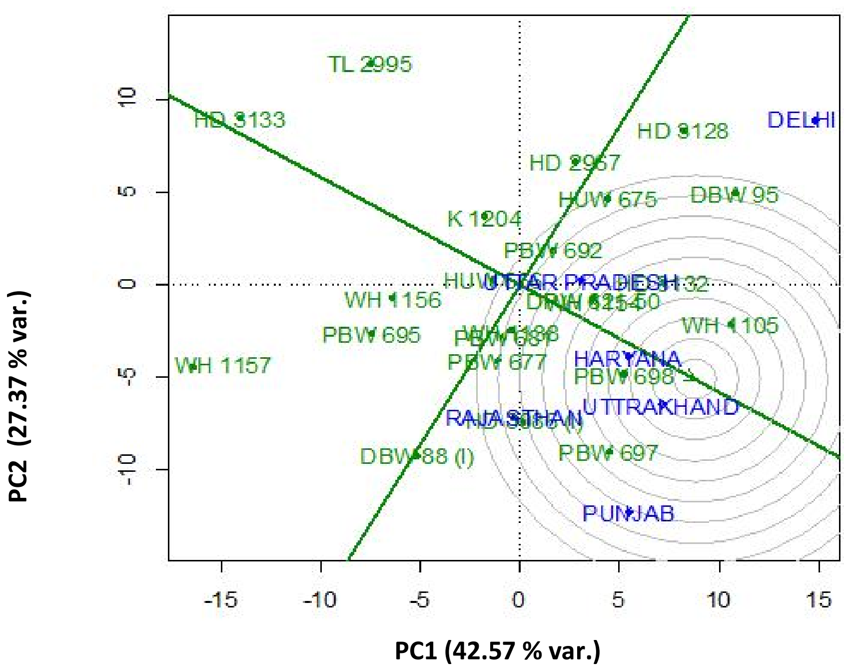

Fig. 6. Ranking of genotypes in biplot for North India wheat data

4. CONCLUSIONS

Evaluation of genotypes and interpretation of genotype versus environment interaction for wheat grain yield in Northern India was studied using GGE Biplots. Genotype pairs such as (TL2995, PBW697), (HD3128, WH1157) and (WH1157, DBW95) were found to be dissimilar while WH1138, PBW681 and PBW677 were observed to be the most similar genotypes.

Haryana environment having the smallest angle with the Average Environment Axis (AEA) had the highest representativeness of the experiment while Rajasthan with the largest angle with AEA had the lowest representation. Delhi environment was observed to be the most discriminating while Uttar Pradesh as the least discriminating. The genotype WH1105 was observed to be the most favourable followed by PBW698 for North Zone of India.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Yan W, Tinker NA. An integrated biplot system for displaying, interpreting and exploring genotype by environment interactions. Crop Sci. 2005;45:1004-1016.
2. Gabriel KR. The biplot graphic display of matrices with application to principal component analysis. Biomet. 1971;58(3): 453-465.
3. Bradu D, Gabriel KR. The biplot as a diagnostic tool for models of two-way tables. Technomet. 1978;20:47-68.
4. Yan W, Kang MS. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL; 2003.
5. Yan W, Tinker NA. Biplot analysis of multi-environment trial data. Canad. J. of Plant Sci. 2006;86:623-664.
6. Yan W, Kang MS, Woods MB. Cornelius PL. GGE Biplot vs. AMMI Analysis of Genotype-by-Environment data. Crop Sci. 2007;47:641-653.
7. Grange AL, Roux NL, Lubbe SG. Biplot GUI: Interactive biplots in R. J. of Stat. Soft. 2009;30(12):1-37.
8. Bishnoi S, Hooda BK. Yield stability and association among parametric and non-parametric stability measures for wheat (*Triticum aestivum L.*) genotypes in northern region of India. Inter Jour of Agri Environ and Biotech. 2018;11(1):103-109.
9. Kumar B. Biplots and their application in multi-environment trials data analysis. Unpublished M. Sc. submitted to CCS HAU-Hisar; 2017.
10. Yan W, Hunt LA, Sheng Q, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 2000;40:597- 605.
11. Kendal E. GGE Biplot analysis of multi-environment yield trials in barley (*Hordeum vulgare* L) cultivars. Ekin J. of Crop Breeding and Genetics. 2016;2-3:90-99.
12. Oral E, Kendal E, Dogan Y. Selection the best barley genotypes to multi and special environments by AMMI and GGE biplot models. Fresenius Environmental Bulletin. 2018;27(7):5179-5187.
13. Kendal1 E, Sener O. Examination of genotype × environment interactions by GGE biplot analysis in spring durum wheat. Indian J. Genet. 2015;75(3):341-348.

Peer-review history:
The peer review history for this paper can be accessed here:
http://www.sciencedomain.org/review-history/26094