Electronic Journal of Plant Breeding

Research Article

Yield stability analysis in multi-environment trials of hybrid rice (Oryza sativa L.) in Northern India using GGE Biplot Analysis

Somanagoudra Chandrashekhar[1], Raman Babu[2], P. Jeyaprakash[3], R. Umarani[4], K. Bhuvaneshwari[5] and S. Manonmani[6]

[1]Ph.D Scholar, Centre for Plant Breeding and Genetics,
[2]Pioneer Hi-Bred Pvt. Ltd., Multi Crop Research Center, Wargal, Hyderabad, Telangana, India.
[3]AC&RI, Trichy
[4]FC&RI, Mettupalayam
[5]Department of Entomology,
[6*]Department of PGR, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India.
E-Mail: chandrashekharss@gmail.com

Abstract

This study was carried out to evaluate the performance of rice cultivars for grain yield stability performance analysis and wide adaptation by GGE biplot method. An experiment was conducted to evaluate 8 rice (Oryza sativa L.) hybrids, 2 check varieties for their stability at 6 different locations, viz Patna, Purnia, Lucknow, Gosaiganj, Barabanki and Prayagraj during rainy 2018 season representing different agroclimatic zones of Uttar Pradesh and Bihar. GGE biplot methodology was utilised to find out the grain yield performance and stability of rice cultivars examined over six environments. GGE biplot analysis considers both genotype (G) and GE interaction effects and graphically displays Genotype Environment interaction in a two-way table. GGE biplot is an effective method based on principal component analysis (PCA) to fully explore multi environment data. The significant Genotype by Environment interaction effects for yield infers that genotypes reaction was different over different environments, indicating that the genotype selection must be specific to the growing conditions. Based on the analyses, genotypes H2, H3 and H5 were high yielding and highly stable genotypes. Hybrid H6 at Environment 4 and hybrid H4 at Environment 3 performed well. Environments E1, E2, E5 and E6 were suitable evaluating environments for this set of rice cultivars.

Keywords
Rice, Stability, GGE biplot, Multi environment testing.

INTRODUCTION

Rice (Oryza sativa L.,) is the most important cereal crop and it is being grown round the year in various agro-climatic zones across geographies and seasons in India. The rice genotypes including breeding material interact differently with different environmental conditions. Apart from the decrease in production due to biotic & abiotic stresses, non-availability of genotypes tailored to specific growing environments account for the steady decline in the area, production and yield in rice. Therefore, designing breeding programs to evaluate and assess the adaptation and stability of rice cultivars is of prime concern. Therefore, it is of prime importance to evaluate and select genotype(s) showing a high degree of stability of performance over a wide growing environment (Das *et al.* 2010). Precise knowledge on the nature and magnitude of genotype × environmental interaction is important in understanding the stability in yield of a variety or a hybrid before it is being recommended for a given growing situation. Panwar et al. (2008) and Young and Virmani (1990) observed multiple levels of magnitude of heterosis over different locations and urged the need to evaluate hybrids in different locations/environments to identify wide

adaptable genotypes with high yield. Therefore, the study was designed to evaluate the stability parameters of the popular rice hybrids. The genotypes were evaluated at various agroclimatic zones in Uttar Pradesh and Bihar in the present investigation. A relatively novel concept of GGE biplot methodology was utilised to assess the stability of grain yield performance of the hybrids which were evaluated across six growing environments in Central Eastern part of India comprising of two major rice growing states., Uttar Pradesh and Bihar.

To assess the magnitude of Genotype x Environment interactions and to assess stability , there are many methods available such as, pooled ANOVA, stability analysis and multivariate methods. Pooled or Combined analysis of variance (ANOVA) is the commonly used method to assess and identify the presence of Genotype x Environment interactions in experiments involving variable environmental conditions, but the main concern in stability evaluation method is the assumption of homogeneity of variance among the tested environments. Zobel et al., 1988 reported that though combined ANOVA stability analysis method helps to determine variance components generated by different factors (Genotype x Environment, genotype and environment), this method doesn't allow response of the genotypes measurement in the nonadditive term (Zobel *et al*. 1988). AMMI (additive main effect and multiplicative interaction) model proposed

for the interpretation of Genotype x environment using biplots stands out owing to presence of various technical interpretations available (Duarte and Vencovsky, 1999). An alternate method proposed by Yan *et al.,* (2000) in which AMMI was modified and named as GGE biplot method, has been used for Genotype x environment analysis. In this Biplot method, GGE analysis pools effect of genotype with GE (multiplicative effect) and submits them to principal component analysis, the resultant biplot is named as GGE biplot. Yan, 2001 reported that GGE biplot method of stability analysis considers genotype (G) and Genotype by Environment interaction effects both and displays GE interaction graphically in a two-way table. GGE biplot method is an alternate effective method for full exploration of multi-environment data which is based on PCA (Principal Component Analysis). GGE biplot method of stability analysis is a useful and efficient tool for finding out ideal locations that optimized hybrid genotypes performance with the aim of using the limited resources in an effective way was reported by Fan *et al*. (2007).

MATERIALS AND METHODS
Present investigation was carried out during *Kharif* 2018 in which 8 popular rice hybrids and 2 varietal checks (Table 1) were evaluated along with the newly synthesised hybrids at six locations *viz.,* Patna (E1), Purnea (E2) in Bihar, Lucknow(E3), Gosaiganj (E4), Barabanki (E5) and

Table 1. Details of the rice genotypes evaluated in the study

SI No	Code	Genotype	Remarks
1	H1	25P35	Early maturity hybrid by Pioneer
2	H2	27P22	CVRC released hybrid in IME
3	H3	27P31	CVRC released hybrid in IME
4	H4	27P37	CVRC released hybrid in IME
5	H5	28P67	CVRC released hybrid in IM
6	H6	BSBArize6444 Gold	National Hybrid check in AICRP IM
7	H7	PHB71	CVRC released hybrid in IME
8	H8	USWUS312	National Hybrid check in AICRP IME
9	V1	MTU1010	Regional Check in AICRP
10	V2	NDR359	Regional Check in AICRP

Prayagraj (E6) in Uttar Pradesh (Fig 1). In this study only released hybrids along with varieties were studied for their adaptability. The weather factors during crop growth period are presented in Table1. The experimental design used in the study was Randomized Block Design (RBD) having two replications, having a plot size of 3.5-meter-long with 0.5 meter allay, with 20 x 15 cm spacing, accommodating 40 plants per entry per replication. Standard crop management practices as applicable were followed in all the six environments. Yield data was recorded at harvest and plot data harvested was converted to T/ha at 14% MST by extrapolating plot yield to hectare.

The data generated was analyzed using R studio software. Biplot graph yield means were plotted against the scores of first principal component of interaction (IPCA1) and

GEI were analyzed. Similarly, data was analysed for discriminativeness vs representativeness ranking of environments and ranking of genotypes relative to ideal environment and ranking of environment based on ideal genotype was also performed. Mega-environments and winning genotypes in a given set of environments was identified by using option "which-won-where".

In Biplot graphs genotypes and environments scores are represented as vectors in a two-dimensional space. The genotypes and environments vectors drawn from the origin (0, 0) to the end points are determined by their scores. Angle of less than 90^0 or larger than 270^0 between a cultivar vector and a site vector indicates that the genotype having a positive response at a growing environment and a negative response when the angle is somewhere

Fig. 1. Map view of test environments

between 90° and 270°. The cosine of the angle between two environments or between two genotypes denotes the correlation of the two environments or between two genotypes. Zero angle between environment or genotypes denotes positive correlation of 1, and an angle of 90° (or -90°) denotes a correlation of 0 and an angle of 180° a negative correlation of 1.

The data was analysed for each locations and combined analysis was carried out for grain yield to test the significance of G x E interaction. In the combined ANOVA, genotypes were considered as fixed effects, while environments, replications, genotype by environment interaction and all other sources of variation were considered as random effects with test of significance at LSD of 0.05. Grain yield data was subjected to GGE biplot analysis to assess the stability and the pattern of response of hybrids tested in six different environments. Biplots were generated using the 2 principal components viz., Principal Component1 (PC1) and Principal Componet2 (PC2). Principal components were derived from environment cantered trait means for each environment. The data were not transformed (Transform = 0), standardized (Scale = 1), and were environment-cantered (Centring = 2).

The analyses and generation of Biplots was done using the R programming language in R studio. The GGE biplot equation used is as follows:

$$Yij - Yj = \lambda 1 \xi i1 \eta j1 + \lambda 2 \xi i2 \eta j2 + \varepsilon ij$$

Where:
Yj is the average yield across all genotypes in environment **j**;
λ1 and λ2 are the singular values for **PC1** and **PC2**;
ξi1 and ξi2 are the **PC1** and **PC2** scores for genotype i;
ηj1 and ηj2 are the **PC1** and **PC2** scores for environment j;
εij - residual associated with the genotype i in environment j.

RESULTS AND DISCUSSION
The combined ANOVA displayed significant variation among cultivars (G) and growing locations (Environments) signifying the performance variation among test environments. Genotype X Environment interaction was highly significant enumerating the presence of strong genotype (G) x location (E) interaction. Genotype has the highest portion of variance in the total variance for grain yield (26.822) while locations and G x Location contributed 5.222 and 0.721, respectively (Table 3). G x E mean square significance allude that expression of trait will not

Table 2. Locations details of the six test environments

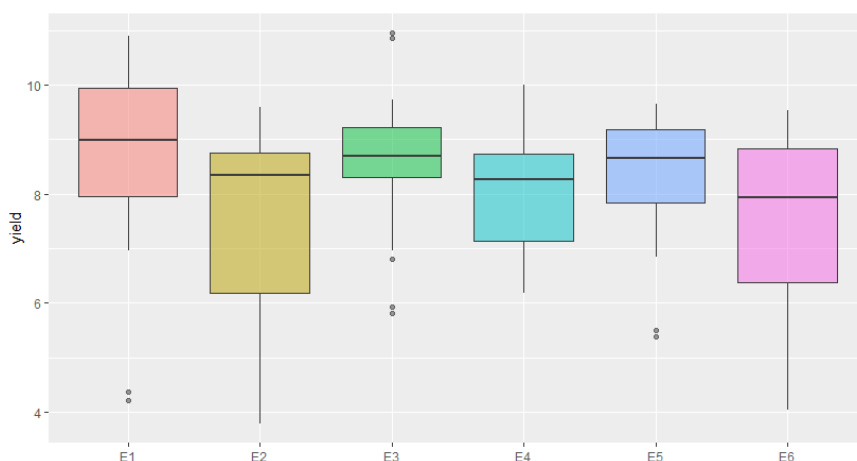| Factor/Location	E1	E2	E3	E4	E5	E6
Longitude	85.38025	87.26771	80.78606	81.07975	81.10857	81.83063
Latitude	25.71797	25.84294	26.74992	26.6353	26.92813	25.56773
Average Max Temperature	34.6	34.0	35.4	35.4	35.4	35.6
Average Min Temperature	25.7	25.5	24.8	24.8	24.8	25.4
Total Rainfall during crop	613.1	829.5	1282.3	1084.5	983.5	646.3

Fig 2. Box view of tested environments with yield

Table 3. Mean sum of squares (ANOVA) for grain yield across 6 locations

Source of Variation	DF	Mean squares for Grain Yield
Genotype	170	26.822***
Rep	1	0.006
Location	5	5.222***
GE*Location	850	0.721***
Residuals	1025	0.011
Mean		8.09
CV		19.6

Signif.codes:0'***'0.001'**'0.01'*'0.05'.'0.1' ' 1

be same across the growing locations/environments and yield ranks among location vary. Mean grain yield of 8.09 t/ha was recorded across six locations (Table 3). The average grain yield in each of the location, distribution is depicted in the fig. 2. Location E1 was highest yielding location (Patna) followed by E3 (Lucknow) whereas location E6 was lowest yielding (Prayagraj).

GGE bi plot analysis were conducted for 10 genotypes including two varieties in six environments. The 92.27% of total variation was expressed by PC1 axis 1 and 3.35% by PC2. PC1 and PC2 together accounted for 95.62% of Genotype **+** Genotype x Environment variation for grain yield. The results are presented in different sections

Hudzenko *et al.,* (2019) reported that analysis of data generated in multi environment trials using GGE biplot method have been theoretically substantiated and practically implemented by various studies and they signified the usage of this method for selecting the "best" spring barley breeding lines in the final stage of breeding process. Fig 3. is a basic bi plot that explains how environments and genotypes were scattered. Based on Figure 3, 6 locations can be grouped to three mega-environments for practical evaluation purposes. Locations E1, E2, E5 and E6 into one group, E4 and E3 are other two mega environments. There is no relationship between

environments E4 and E3. Genotypes H3, H2 and H5 have stable performance in E1, E2, E5 and E6 environments. Genotype H6 has high interaction with environment E4 and genotype H4 has high interaction towards environment E3, which means these genotypes are well adapted to those environments. The other genotypes H1, H7, H8, V1 and V2 are unstable and no interaction with environments.

In fig. 4, polygon view of the GGE biplot is depicted and it indicates the ideal genotype in each given location. The presence of two or more environments within a sector indicates that a single genotype has the highest yield in those environments. If environments fall into different sectors; it means that different genotypes perform well in different environments (Yan and Tinker., 2005 and Yan *et al*., 2010). In this study, genotypes H6, H4 and V1 were high response genotypes, genotype H6 had more response in environment E4, genotype H4 had more response towards environment and genotype V1 had no much response towards the environments considering it unstable genotype. Genotypes H2, H3, H5 and H7 which are present at origin of the vertex, denotes that these genotypes are unresponsive to the environments and stable genotypes across environments.

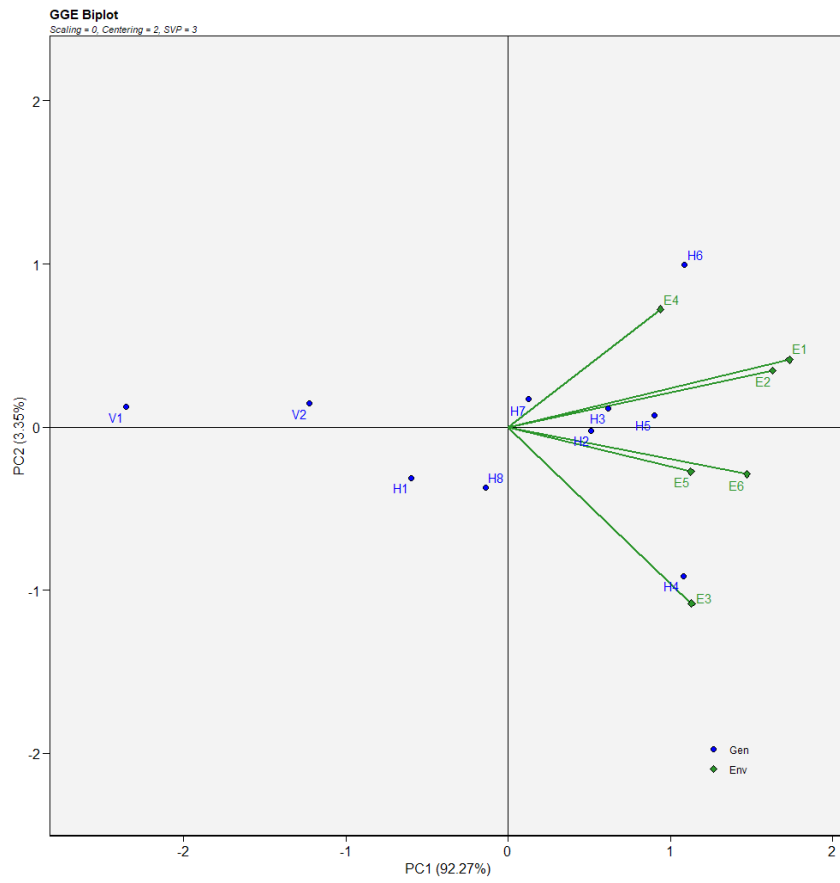Biplot view in fig. 5 depicts that the "ideal" environment

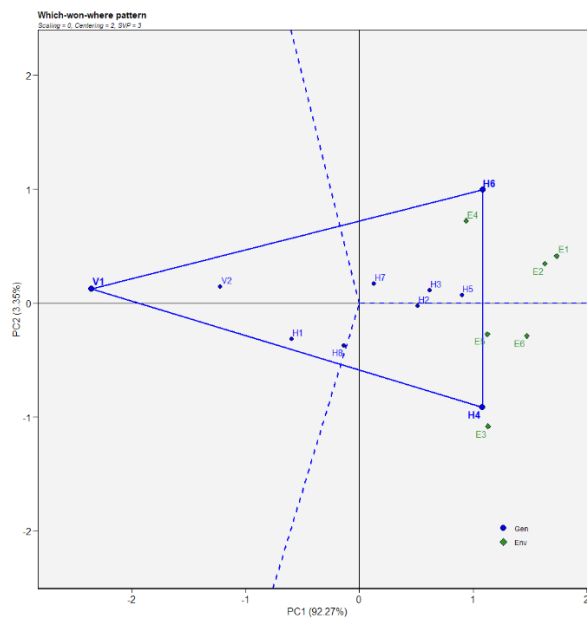**Fig. 3. basic bi plot view with genotypes and environments**

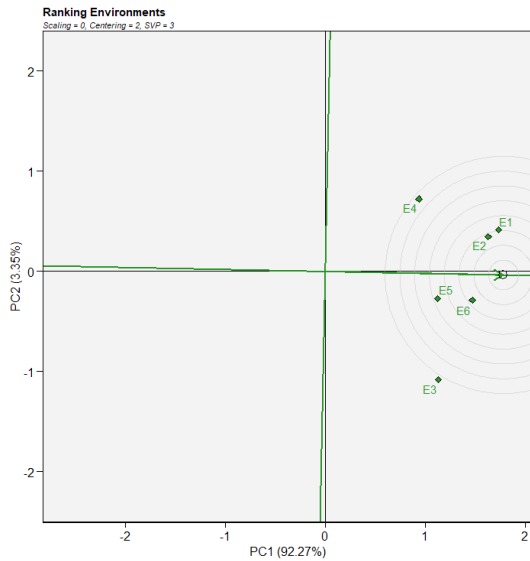

Fig. 4. Ranking of environments Biplot.

Fig. 5. Bi plot view with ranking the enviornments

is used as the center of a set of lines which serve as an indicator to assess the distance between an environment and the ideal environment. In this study, E2 and E1 are the ones which are nearest ideal environment, and therefore, is most desirable amongst six growing locations/environments. E3 and E4 were the lowest informative or suitable test locations/environments. The ranking of environments is as follows: E2 > E1 > E6 > E5 > E4 > E3.

GGE biplot provides excellent opportunity for identification of genotypes most adapted to a given environment with the help of visualization of the performance of different genotypes in each environment. In this study we are examining all tested six environments, in terms of genotype interaction with environment (Fig. 6). In Environment 1, genotypes H6 and H5 are high yielding genotypes and V1 and V2 are low yielding genotypes. In Environment 2, genotypes H6 and H5 are high yielding genotypes and V1 and V2 are low yielding genotypes. In Environment 3, genotypes H4 and H5 are high yielding genotypes and V1 and V2 are low yielding genotypes. In Environment 4, genotypes H6 and H5 are high yielding genotypes and
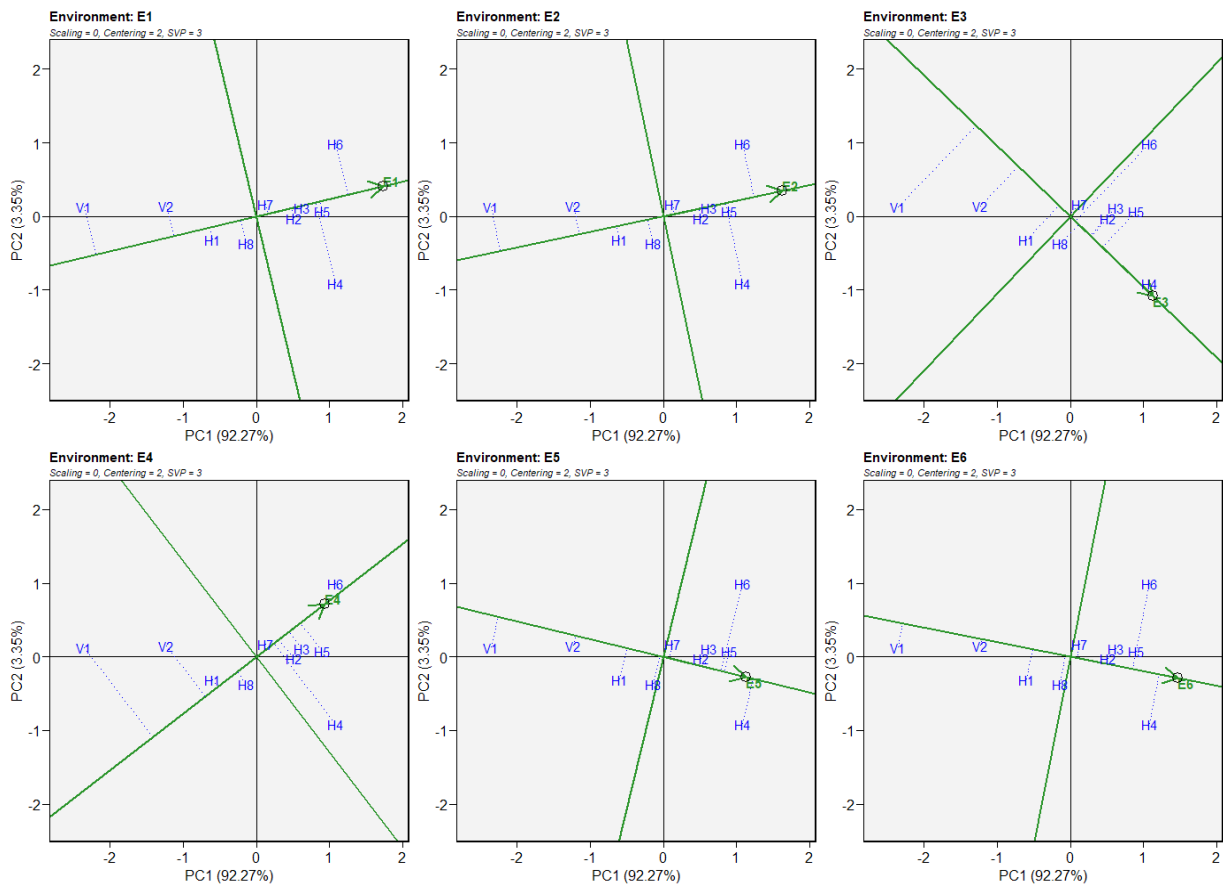

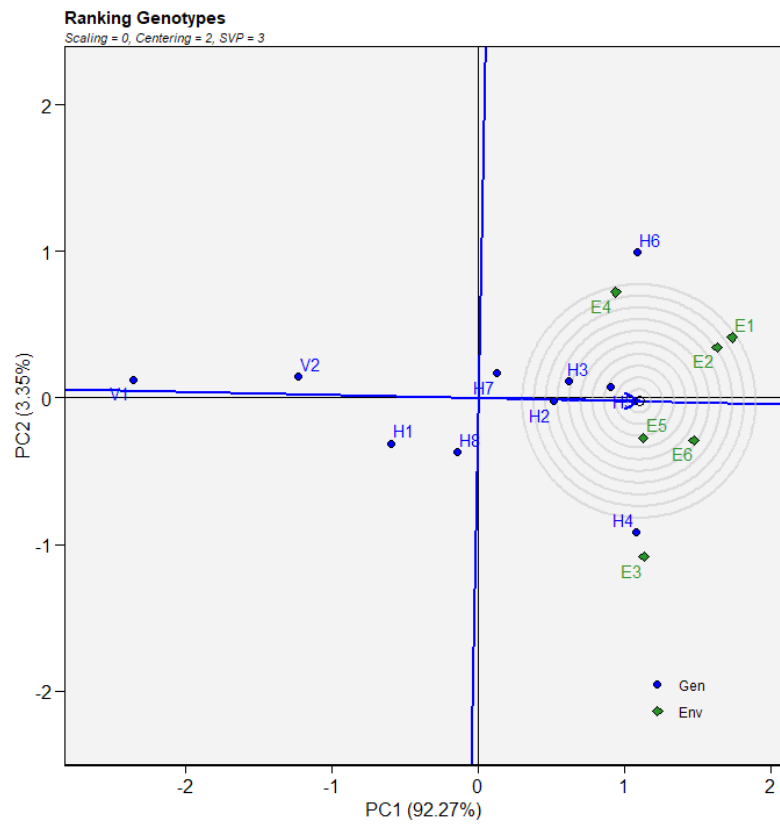
Fig. 6. Exaimining the test enviornment

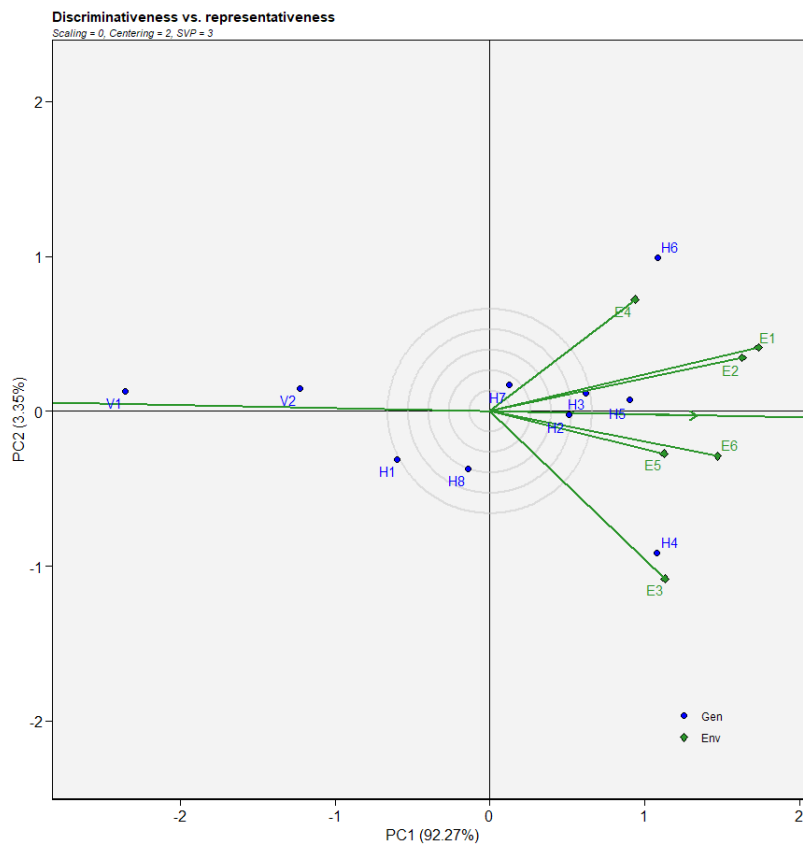Fig. 7. GGE Biplot view 'discriminating power and representativeness'

Fig. 8. Biplot view ranking of genotypes

V1 and V2 are low yielding genotypes. In Environment 5, genotypes H4 and H5 are high yielding genotypes and V1 and V2 are low yielding genotypes. In Environment 6, genotypes H4 and H5 are high yielding genotypes and V1 and V2 are low yielding genotypes. This particular biplot view clearly distinguishes the performance of genotypes in each environment.

The six locations E1, E2, E3, E4, E5, E6 are the ideal locations that can be considered as representative of the rice growing regions in Central Eastern part of India. Evaluation is done to identify growing locations/ environments that helps us to identify stable genotypes when evaluated under a group of environments. The representativeness and discriminating power view of GGE biplot analysis for this study are presented in Figure 7. E1 had longest vector followed by E3, while E5 had shortest vector. E2, E1, E6 and E5 were at the smallest angle to the average environment axis (AEA) followed by E4 and E3 were at largest angles to it. Yan and Rajcan., (2002) suggested that an ideal test environment is one which should effectively discriminate genotypes for their performance and represent all the growing environments. In this study among the six environments where study was conducted, the environments E1, E2, E5 and E6 represented the ideal testing environment, hence these locations are appropriate ones for selecting desired stable genotypes which represent the growing region.

Fig. 8 biplot attempts to juxtapose all cultivars with the "ideal" genotype which is represented by the dot with an arrow pointing to it, such genotype is stable and has the highest mean yield. In this BiPlot, the genotypes are ranked based on their distance from the ideal genotype. Genotypes H5, H3 and H2 are very close to dot representing the ideal genotype and have high grain yield compared to other genotypes in the study and can be considered as fairly stable genotypes among the tested environments (Fig. 8).

Statistically significant Genotype x Environment at 0.05 or 0.01 LSD interaction for grain yield indicates the differential performance of genotypes across the test environments. Therefore, the selection of genotype should be specific to the environment and environments contribute significantly to performance variations of genotypes, which in turn also points to the fact that unpredictable environmental factors are the major constraints in breeding and selection for wide adaptable rice genotypes. Mary Ann *et al.,* (2019) in their study on high zinc rice varieties observed that genotype and environment interaction (G X E) is a major obstacle in breeding, thus an understanding of G X E interaction and identifying stable genotypes through multi-location evaluation will help in identifying potential lines for varietal release. Akter *et al.,* (2015) evaluated six varieties (4 hybrids & 2 varieties) over 5 environments and observed that G + GxE biplots are the good visual

multi -environmental trials data analysis tools and identified hybrids G2 & G3 were high yielding and stable and environment E3 was more stable. Srinivas Reddy *et al*., (2020) identified that the maize genotypes viz., G44, G105, G86, G97, G65 and G76 were higher yielding and most stable by using GGE biplot analyses and opined that these methods provide clear basis for determining stability and performance of the 106 single cross maize genotypes evaluated in their study across northern India in rainy 2018. In the current study based on the analyses, genotypes H2, H3 and H5 were high yielding and most stable genotypes. Genotype H6 at E4 and H4 genotype at E3 performed good, respectively. Environments E1, E2, E5 and E6 can be ideal test environments.

REFERENCES

Akter Anowara., M Jamil Hasan., Umma Kulsum., Rahman, M.H.,   Khatun, M and Islam, M.R. (2015). 'GGE Biplot Analysis for Yield Stability in Multi-environment Trials of Promising Hybrid Rice (Oryza sativa L.). *Bangladesh Rice J.* **19**(1):1 – 8. [Cross Ref]

Das, S., Mishra, R.C. and Das, S. R. (2010). 'G×E interaction, adaptability and yield stability of mid early rice genotypes'. *Indian Journal of Agricultural Research.* **44** (2): 104–11.

Duarte, J.B. and Vencovsky, R. (1999). 'Interaçãogenótipos x ambientes: umaintrodução à análise AMMI. RibeirãoPreto: SociedadeBrasileira de Genética', Série Monografias 9, 60.

Fan, X.M., Kang, M.S., Chen, H., Zhang, Y., Tan, J. and Xu, C. (2007). 'Yield stability of maize hybrids evaluated in multi–environment trials in Yunnan', China. *Agronomy Journal.* **99**(1), 220–228. [Cross Ref]

Hudzenko, V.M., Polishchuk, T.P., Sardak, M.O., Buniak, N.M. and V. A. Ishchenko (2019). 'Multi-environment trials of spring barley genotypes (Hordeum vulgare L.) in the final stage of breeding process'. *Electronic Journal of Plant Breeding,* **10** (4): 1435-1440. [Cross Ref]

Mary Ann Inabangan-Asilo., Mallikarjuna Swamy, B.P., . Amery F. Amparado., Gwen Iris L., Descalsota-Empleo., Emily C. Arocena & Russell Reinke (2019). 'Stability and G 3 E analysis of zinc-biofortified rice genotypes evaluated in diverse environments. *Euphytica* (2019) **215**:61. [Cross Ref]

Panwar, L. L., Joshi, V. N. and Ali, M. (2008). 'Genotype × environment in scented rice'. *Oryza*, **45** (1):103–9.

Srinivasa Reddy Boreddy., Ganesan, K.N., Ravikesavan, R., Senthil, N and Raman Babu. (2020). Genotype-by-environment interaction and yield stability of maize (Zea Mays L.) single cross hybrids. *Electronic Journal of Plant Breeding*, **11**(1) :184-191. [Cross Ref]

Yan, W., Hunt, L.A., Shengm, Q. and Szlavnics, Z. (2000). 'Cultivar evaluation and mega-environment investigation based on the GGE biplot'. *Crop Science* **40**(3), 597-605. [Cross Ref]

Yan, W. (2001). 'GGE biplot-A windows application for graphical analysis of multi-environment trial data and other types of two-way data'. *Agronomy Journal* **93**(5), 1111–1118. [Cross Ref]

Yan, W., and Rajcan, I. (2002). 'Biplot evaluation of test locations and trait relations for breeding superior soybean cultivars in Ontario'. *Crop Science.* **42**(1), 11–20. [Cross Ref]

Yan, W., and Tinker, N.A. (2005). 'An integrated biplot analysis system for display, interpreting, and exploring genotype x environment interaction'. *Crop Science.* **45**(3), 1004-1016. [Cross Ref]

Yan, W., Frégeau-Reid, J., Pageau, D., Martin, R., Mitchell-Fetch, J., Etienne, M., Rowsell, J., Scott, P., Price,M., de Haan, B., Cummiskey, A., Lajeunesse, J., Durand, J. and Sparry, E. (2010). 'Identifying essential test locations for oat breeding in Eastern Canada'. *Crop Science* **50**(2), 504– 515.

Young Y B and Virmani, S.S. (1990). 'Stability analysis of agronomic traits in rice hybrids and their parents'. *Oryza* **27**: 109–121.

Zobel, R.W., Wright, M.J. and Gauch, H.G. (1988), 'Statistical analysis of a yield trial', *Agronomy Journal* **80**(3), 388-393. [Cross Ref]