

GENOTYPE-ENVIRONMENT (G×E) INTERACTION, STABILITY AND ADAPTABILITY STUDY ON GRAIN YIELD IN ADVANCED RICE LINES

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Abstract

Stability and adaptability of a rice genotype is crucial to release it as a variety for commercial cultivation in a wide range of growing conditions. The present study was conducted during 2020-21 to assess the Genotype×Environment (G×E) interaction and to identify the stable rice lines for varietal development. Nine rice genotypes consisting advanced lines and released variety were investigated for stability in grain yield across three environments by Additive Main effects and Multiplicative Interaction (AMMI) and the Genotype Main Effect and Genotype by Environment interaction effects (GGE) analyses. AMMI and GGE analyses revealed significant G×E interactions indicating the variability among the genotypes and environments. As per AMMI1 and AMMI2 biplot models the genotypes BN-P-317 and BN-P-318 were identified as the best performer and suited for the environment Jamalpur. GGE biplot analysis showed that the genotypes BN-P-114, BN-P-115 and BN-P-317 were adapted to the environment Jamalpur, whereas BN-P-318 was more suitable for Nalitabari. According to GGE biplot-genotype view graph, the genotype BN-P-317 was identified as the ideal genotype for grain yield followed by BN-P-318. The GGE biplot- polygon view graph showed that the genotype BN-P-317 performed better in both the environments Jamalpur and Nalitabari. The genotypes BN-P-317 and BN-P-318 could be selected for further evaluation to release as variety.

Key words: AMMI, GGE, G×E interaction, Rice

Introduction

Rice is a staple food crop for half of the world's population, and its cultivation is widely adapted in different agroecological zones. Although the wide adaptation, rice cultivation is becoming challenging due to the adverse effect of climate change. Climate change increases the variability in weather conditions and negatively impacts the genotype × environment (G×E) interactions which adversely affects the yield potential of rice varieties (Khumairoh *et al.*, 2018).

There is a need to develop stable and widely adapted varieties that can ensure superior yield and quality performance across a wide range of environmental conditions for sustainable rice production. Thus, success in a breeding program lies in developing a variety that is widely adapted to diverse environments (Malosetti *et al.*, 2013, Andiku *et al.*, 2020).

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The stability of a quantitative trait like yield potential is a cumulative result of different interactions between the genetic make-up of the variety and the conditions where the variety is cultivated (Malosetti *et al.*, 2013). Moreover, the grain yield of rice is a complex polygenic trait (Renukadevi and Subbalakshmi 2006) and is largely affected by environmental conditions like precipitation, temperature, humidity and other biotic and abiotic factors.

Before releasing a crop variety for commercial cultivation, it is very important to understand the genotype by environment interaction (Sabaghpour *et al.*, 2012). The performance of the newly developed lines is compared across different environmental conditions for assessing the interaction. Multi-environment trial (MET) is decisive in identifying a stable genotype across the environments or detecting the most suitable environment for a specific genotype (Yan *et al.*, 2000). Cultivars grown in different environments react differently, and this reaction is the G×E interaction. The study of G×E interaction is important for the plant breeders to select the suitable varieties releasing for commercial cultivation. A number of studies have been conducted to evaluate the yield stability of rice in diverse environmental conditions (Cooper and Somrith, 1997; Flores *et al.*, 1998; Ouk *et al.*, 2007; Anandan *et al.*, 2009; Katsura *et al.*, 2016).

Combined analysis of variance can quantify the G×E interactions but cannot explain it (Asnake *et al.*, 2013). Several statistical models have been developed to explain the G×E interaction. But more than one model should be applied for getting the best comparison (Lubadde *et al.*, 2017). Additive Main effects and Multiplicative Interaction (AMMI) and the Genotype Main Effect and Genotype by Environment interaction effects (GGE) models are widely applied to analyze the G×E interaction in a MET (Nyaligwa *et al.*, 2018). AMMI determine the G×E interaction by analyzing the main effects (additive effect) and the non-additive residual effect through the analysis of variance (ANOVA) and principal component analysis (PCA) (Crossa and Cornelius, 1997). However, GGE biplots exhibit both genotype and genotype by environment difference for a trait (Crossa *et al.*, 2002). Stability and adaptability of a specific variety can be detected by studying the G×E interaction analyzed with AMMI and GGE biplot models (Jadhav *et al.*, 2019). Thus, the present study was conducted to evaluate the grain yield performance of advanced rice lines for their stability and adaptability across three environments.

Materials and Methods

Experimental design and plant materials

The experiment was conducted at three environments *viz.* Mymensingh, Jamalpur and Nalitabari of Bangladesh during dry season in 2020-21. Nine genotypes consisting of eight blast resistant advanced rice lines and one released variety were used in the study (Table 1). The experiment was carried out following the randomized complete block design (RCBD) with three replications. Thirty-five-day-old seedlings were transplanted to the field in a 3.0 m × 2.0 m size plot with 20 cm spacing between rows and 15 cm between plants within row. All the recommended management practices were adopted to raise a healthy crop under all

the tested environments. Each line was harvested separately and grain yield was assessed plot basis. Grain yield was recorded at 14% moisture level and finally converted to t ha⁻¹.

Table 1. List of genotypes used in the study

Code	Genotype	Origin	Variety status	Special attributes
G1	BN-P-102	IRRI	Pure line	Blast resistant & HYV
G2	BN-P-110	IRRI	Pure line	Blast resistant & HYV
G3	BN-P-114	IRRI	Pure line	Blast resistant & HYV
G4	BN-P-115	IRRI	Pure line	Blast resistant & HYV
G5	BN-P-120	IRRI	Pure line	Blast resistant & HYV
G6	BN-P-310	IRRI	Pure line	Blast resistant & HYV
G7	BN-P-317	IRRI	Pure line	Blast resistant & HYV
G8	BN-P-318	IRRI	Pure line	Blast resistant & HYV
G9	BRR1 dhan58	Bangladesh	Released variety	HYV

Statistical analysis

Combined ANOVA was constructed based on the grain yield data using RStudio (RStudio Team, 2020). The homogeneity test of the variance was conducted by the Barlette methods (Bartlett, 1932). The combined ANOVA was proceeded further to assess the G×E interaction and stability of the genotypes across the three locations. AMMI and GGE biplot multivariate models were used to determine the genotype and environment interaction and its relationship with stability parameters. AMMI and GGE biplot were constructed using PB Tools ver. 5 statistical software (<http://bbi.irri.org/products>) and RStudio (RStudio Team, 2020). The AMMI and GGE model are a combination of ANOVA and PCA. The analytical models are given as:

$$Y_{ij} = \mu + \delta_i + \beta_j + \sum_{k=1}^K \lambda_k \delta_{ik} \beta_{jk} + \epsilon_{ij} \text{ (AMMI model)}$$

$$Y_{ij} = \mu + \beta_j + \sum_{k=1}^K \lambda_k \delta_{ik} \beta_{jk} + \epsilon_{ij} \text{ (GGE model)}$$

Where, Y_{ij} is the mean yield of i^{th} genotype in j^{th} environment, μ is the overall mean, δ_i is the genotypic effect, β_j is the environment effect, λ_k is the singular value for PC axis k: δ_{ik} is the genotype eigenvector value for PC axis n, β_{jk} is the environment eigenvector value for PC axis k and ϵ_{ij} is the residual error assumed to be normally and independently distributed (0, σ^2/r), σ^2 is the pooled error variance, and r is the number of replicates (Cossa *et al.*, 2002; Gauch *et al.*, 2008).

Results and discussions

Combined analysis of variance

A wide variation was observed among the tested genotypes for grain yield across the environments (Table 2). In the environment Mymensingh, grain yield ranged from 4.34 to 5.75 t ha⁻¹ with 5.42 t ha⁻¹ as median, whereas it ranged from 5.00 to 6.20 t ha⁻¹ and 4.90 to 6.20 t ha⁻¹ in Jamalpur and Nalitabari, respectively (Fig. 1). After confirming the homogeneity of the variance across the environments through the Bartlett test, a combined analysis of variance was performed. It revealed highly significant differences among the

genotypes for grain yield (Table 3). Homogeneity of variance indicates that the genetic variances among the genotypes are inherent. According to the combined ANOVA, the grain yield was significantly affected by genotype (36.45%), environment (16.08%) and G×E interaction (38.88%) (Table 3). The significant mean sum of squares for genotypes indicates the divergence of the tested lines/varieties for the mean yield potential (Xu *et al.*, 2014). The significant G×E interaction effect confirms the diverse response of the genotypes to the differences in the environmental conditions (Jadhav *et al.*, 2019).

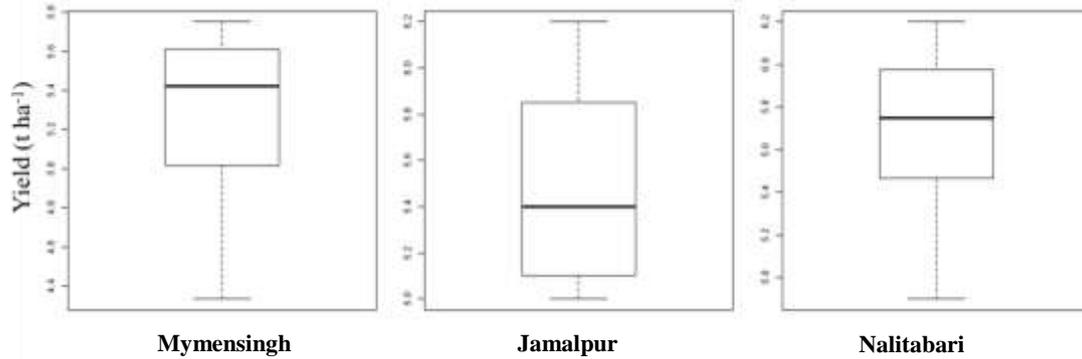


Fig. 1. Box plot of genotype performance for grain yield across the three environments

Table 2. Phenotypic variability and descriptive statistics of grain yield of nine genotypes for three environments

Code	Environment	Parameters								
		Min	Max	Mean	Var	SE	CV	Skewness	Kurtosis	IQR
E1	Mymensingh	4.34	5.75	5.28	0.15	0.07	7.37	-0.61	-0.36	0.59
E2	Jamalpur	5.00	6.20	5.49	0.17	0.08	7.57	0.41	-1.34	0.75
E3	Nalitabari	4.90	6.20	5.69	0.14	0.07	6.58	-0.73	-0.34	0.51

Min = Minimum, Max = Maximum, Var = variance, SE = Standard Error CV = Coefficient of Variation, IQR = Interquartile Range

Table 3. Combined analysis of variance of grain yield for rice genotypes evaluated at three environments

Source	df	SS	MS	Explained SS (%)
Genotype (G)	8	5.26	0.66***	36.45
Repeat (E)	6	0.06	0.01	0.42
Environment (E)	2	2.32	1.16***	16.08
G×E	16	5.61	0.35***	38.88
Residuals	48	1.19	0.02	8.25
Total	80	14.43	0.18	
Chi square Value (Bartlett's Test)	2		0.29	

NB: ***indicates significance at $p < 0.001$ probability level
df = degree of freedom; SS = Sum of squares; MS = Mean of squares

AMMI and GGE analysis of variance

The AMMI analysis of variance indicates that the genotypes and environments contributed 26.26% and 11.58% of the total sum of squares, respectively, whereas 28.00% of the total sum of squares was attributed by G×E interaction effects (Table 4). A larger genotype sum of square than the environment, indicates the substantial differences among the genotypes (Bose *et al.*, 2014). A considerable portion of variation explained by environments indicating that the environments were diverse. It might be due to the divergence in precipitation pattern, temperature regime and other biotic and abiotic factors (Zewdu *et al.*, 2020). The AMMI model demonstrates the presence of significant genotype by environment interaction. This interaction was portioned in the first two interaction principal component axis (IPCA) and these two components were significant at $p < 0.001$ in a postdictive assessment (Table 4). The first two principal components explain the contribution of genotype and their environment. The PC1 (71.1) and PC2 (26.9) values together explained 100% of the G×E interaction which means the interaction of the studied 9 genotypes can easily be predicted by using this two IPCAs (Gauch and Zobel, 1996). Previously it was reported that the first two IPCAs contribute more to explain the G×E interactions (Susanto *et al.*, 2015; Jadhav *et al.*, 2019; Senguttuvel *et al.*, 2021).

The principal components from the GGE analysis explain the contribution of genotype, environment and the interaction of G×E (Malosetti *et al.*, 2013). From the GGE analysis it was observed that the PC1 value (50.3) was higher than PC2 (37.3) and PC2 (12.4) (Table 5). Higher PC1 implies the higher contribution of genotype in the total sum of squares (Malosetti *et al.*, 2013; Jadhav *et al.*, 2019).

Table 4. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (t ha⁻¹) of rice genotypes across three environments

Source	Df	SS	MS	Explained SS (%)	Proportion	Accumulated
Genotype (G)	8	5.26	0.66***	26.26		
Repeat (E)	6	0.06	0.01	0.30		
Environment (E)	2	2.32	1.16***	11.58		
G×E	16	5.61	0.35***	28.00		
IPCA1	9	4.10	0.46***	20.47	73.1	73.1
IPCA2	7	1.51	0.22***	7.54	26.9	100
Residuals	48	1.19	0.02			
Total	96	20.03	0.21			

NB: ***indicates significance at P<0.001 probability level; IPCA=Interaction Principal Component Axis

Table 5. ANOVA and Sum of Squares percentage on G, E and G x E derived from analysis of variance for GGE stability model

Source of variation	df	Sum of Squares percentage
PC1	9	50.3
PC2	7	37.3
PC3	5	12.4

Stability analysis of genotypes for grain yield across the environments

In AMMI1 biplot, PC1 is plotted on vertical axis and mean yield on the horizontal axis. The genotypes that are perpendicular to each other have same mean yield performance and the genotypes which are on a horizontal line have the same interaction pattern (Ebdon and Gauch, 2002). As per AMMI1 biplot model the genotypes BN-P-110, BN-P-115, BN-P-120, BN-P-317 and BN-P-318 exhibited the high yield with high main (additive) effects as they are situated at the right side of the mean yield performance (Fig. 2). Among these 5 genotypes BN-P-115 and BN-P-317 had the positive IPCA1 score and the genotype BN-P-317 being the highest yield producing genotype. The genotype BN-P-317 was specially adapted to the environment Jamalpur. The genotypes or environments that have high PC1 score has large interaction effect irrespective of their positive or negative sign, whereas the genotypes having the low or near to zero PC1 value have less interaction and is considered as a stable genotype (Crossa *et al.*, 1990). The genotype BN-P-114 positioned the farthest from the origin indicates that it contributed the largest towards the interaction. The genotypes BN-P-102 and BN-P-310 produced grain yield lower than the average and with negative IPCA1 value. The genotype BRRi dhan58 also produced grain yield lower than the average but had IPCA1 value near to zero indicating its stability across the environments. The genotypes BN-P-115 and BN-P-318 also had IPCA1 value near to zero means these were also stable across the environments.

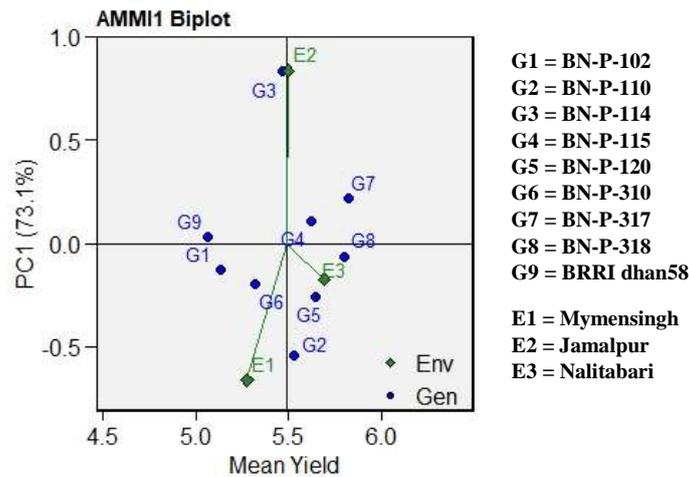


Fig. 2. AMMI1 biplot for grain yield ($t\ ha^{-1}$) of nine rice genotypes and three environments using genotypic and environmental IPCA scores

According to the AMMI2 biplot, the environments fall into three sections (Fig. 3). The genotypes BN-P-110, BN-P-114, BN-P-115 and BRRi dhan58 were more responsive as they are more distant from the origin. BN-P-114 and BRRi dhan58 were the best genotypes with respect to the best enhancing environment Jamalpur. The other genotypes BN-P-102, BN-P-120, BN-P-310, BN-P-317 and BN-P-318 were less sensitive to the environmental interactive forces as these are close to zero.

G×E interaction is a complex phenomenon and it can be simplified by GGE biplot analysis by dissecting this complex phenomenon into various PC (Yan and Tinker, 2006). GGE biplot-environment view can assess the relationship among the test environments. The relationship is visualized by the line connecting to the biplot origin and calculated by the cosine of the angle of two environments (Yan and Tinker, 2006). According to GGE biplot-environment view, environments Mymensingh & Nalitabari and Jamalpur & Nalitabari had positive relationship as they have acute angle (Fig. 4). But Mymensingh and Jamalpur had no relationship as they have a right angle. According to the GGE biplot, genotype BN-P-120 was more suitable for the environment Mymensingh. In Jamalpur, the genotypes BN-P-114, BN-P-115 and BN-P-317 were more adaptable and BN-P-318 was more suitable in Nalitabari.

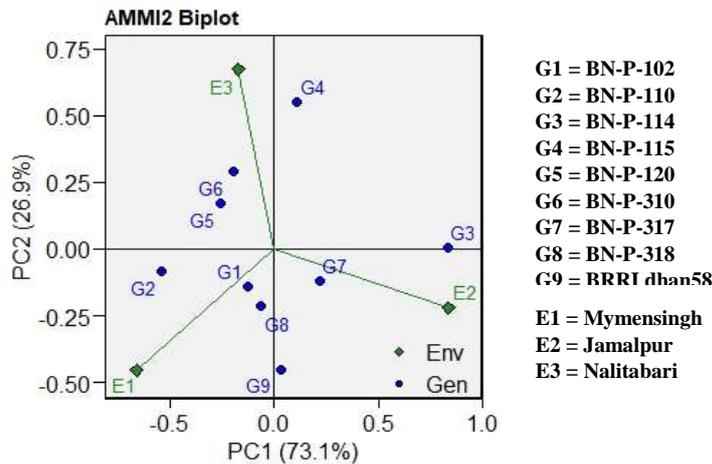


Fig. 3. AMMI2 biplot for grain yield (tha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of nine rice genotypes in three environments

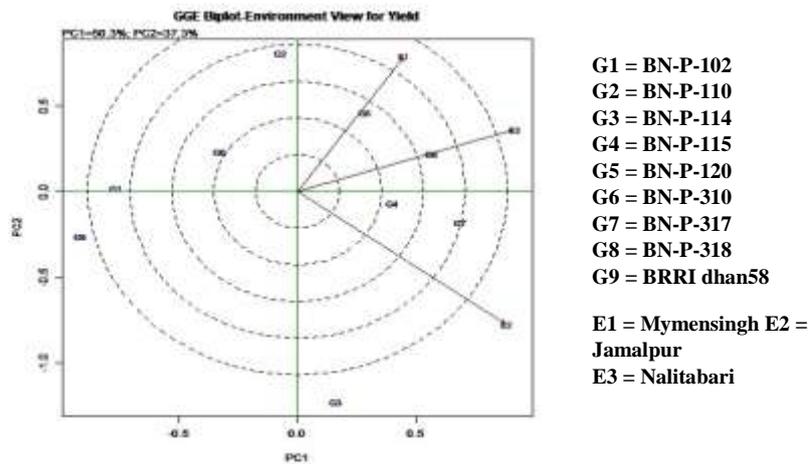


Fig. 4. GGE biplot for grain yield (t ha^{-1}) of nine genotypes tested in three environments

Adaptability of genotypes across the environments

Based on the GGE biplot-genotype and GGE biplot polygon view graph, adaptability of the genotypes was assessed across the environments. The ideal genotypes for grain yield were selected from the GGE biplot-genotype view graph and the best suited genotype for a specific environment was identified by the GGE biplot-polygon view graph. In GGE biplot-genotype graph, the genotype BN-P-317 was identified as the ideal for grain yield (Fig. 5). BN-P-318 which is next to the BN-P-317 in the ideal genotype graph was more stable than BN-P-317 as this genotype is closer to the average environment axis (AEA). Genotypes BN-P-115, BN-P-120, BN-P-317 and BN-P-318 were selected as more stable with high performance. The genotype BRRRI dhan58 was also more stable as closer to AEA but with below average performance. The genotypes BN-P-110 and BN-P-114 were highly environment specific as they located in distant position from the AEA.

In GGE biplot polygon view graph, different polygons comprise one or several environments and one or several genotypes are used to detect that which genotype is performing best in which environments (Jadhav *et al.*, 2019). According to the the GGE biplot-polygon view graph BN-P-110 and BN-P-120 were the most suitable genotypes in the environment Mymensingh. BN-P-317 and BN-P-318 were suitable genotypes for the environment Jamalpur and Nalitabari, respectively. Moreover, genotype BN-P-317 performed better in both the environments Jamalpur and Nalitabari (Fig. 6).

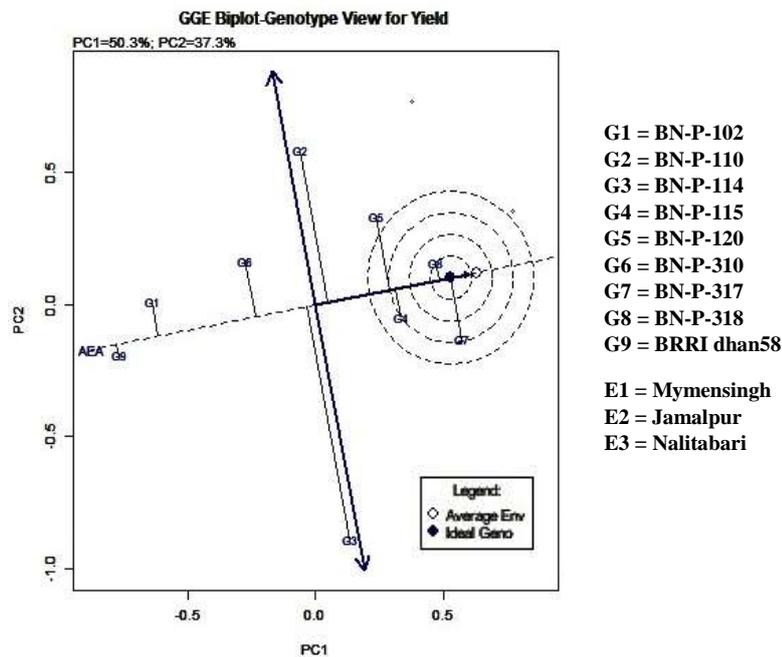


Fig. 5. GGE biplot-Genotype view, including performance of test genotypes in comparison to an estimated average environment and ideal genotype

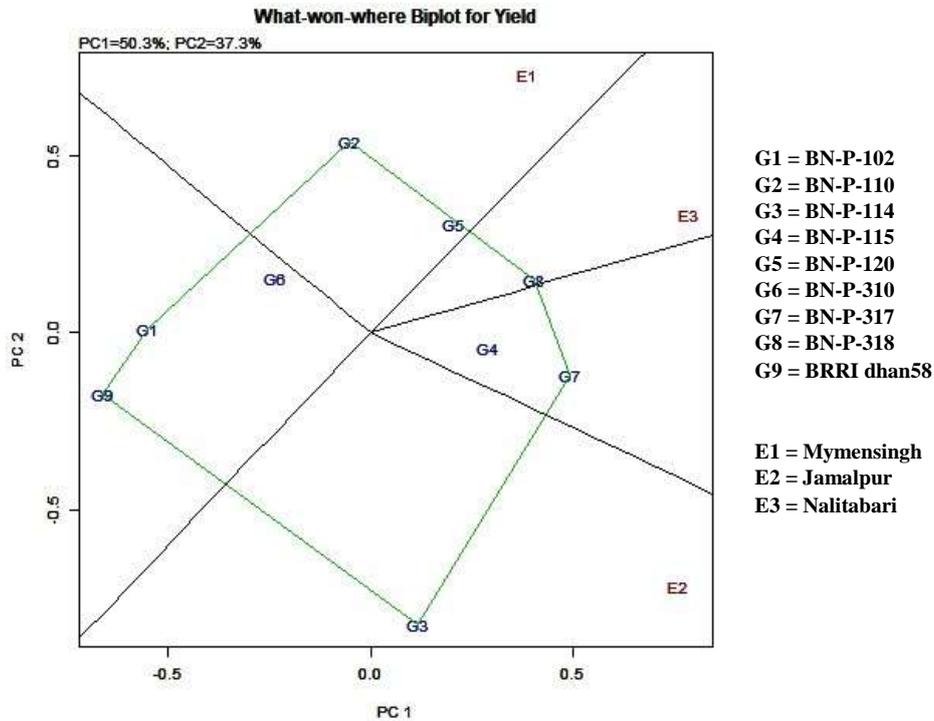


Fig. 6. Polygon views of the GGE biplot based on symmetrical scaling for ‘which-won-where’ pattern of rice genotypes in three environments showing genotype performed the best in particular environment.

Conclusion

The present research work reveals that the genotype BN-P-317 was the highest yield producer across the environments and the best suitable environment was Jamalpur. Moreover, BN-P-318 also can produce a high yield next to BN-P-317 and was more stable across the environments. These two advanced lines can be further evaluated and released as new varieties.

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