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Evaluation of Yield Stability and Adaptability of Boro Rice (*Oryza sativa* L.) Genotypes in Bangladesh Using AMMI and GGE Biplot Analyses

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ABSTRACT

Genotype × environment (G × E) interaction is a critical consideration in rice breeding, as it determines the adaptability and stability of genotypes across diverse agroecological zones. This study aimed to explore the most suitable and stable Boro rice genotypes for Bangladesh. In this study, seven rice genotypes were evaluated in Boro season across twelve locations in Bangladesh during the 2024 Boro season to investigate genotype-environment interaction (GEI) and yield stability performance. The experiment utilized three replications of a completely randomized block design. The analyses were performed through the Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype plus Genotype × Environment (GGE) biplot models. The AMMI analysis revealed that environment accounted for the largest proportion of total variation (51.9%), followed by G × E interaction (16.7%) and genotype (3.7%) The AMMI identified genotypes G2 and G6 as stable, high-yielding genotypes. The GGE biplot analysis accounted for 78.4% of the total G × E interaction, with identifying G2 and G6 as elite genotypes for broad adaptation with high yield potential. Both the AMMI and GGE analyses consistently identified genotypes G2 and G6 as stable and emerge as elite genotypes for broad adaptation with high yield potential, while G1 and G5 show strong performance in specific environmental sets. The combined use of AMMI and GGE analyses effectively captured both yield stability and adaptability patterns, supporting that G2 was broadly adapted, high-yielding entries suitable for rice development program in Bangladesh.

Keywords: Rice, Boro, GxE, GGE biplot, AMMI, Stability, Adaptability

INTRODUCTION

Rice (*Oryza sativa* L.) serves as the primary staple food for a large portion of the global population, contributing nearly 20% of the world's dietary energy supply. Over the past three decades, Bangladesh has achieved remarkable progress in rice production and is widely recognized as a nation of rice growers and consumers (Fukagawa & Ziska, 2019; Hashim *et al.*, 2021; Mainuddin *et al.*, 2021)

To meet the increasing food demand of its growing population, Bangladesh must enhance genotypic adaptability, adopt improved

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agricultural technologies, and strengthen water management practices (Rahman *et al.*, 2023). The adaptability of rice genotypes to diverse and changing environments plays a pivotal role in ensuring yield stability across different locations and years. Moreover, the development and deployment of high-yielding genotypes are fundamental to sustaining the country's food security through enhanced productivity and yield consistency (Penna *et al.*, 2023).

Rice is cultivated in Bangladesh throughout the year under three distinct seasons Aus, Aman, and Boro. Among them, Boro rice is one of the major contributors to national rice production. Despite having a favorable subtropical climate for Boro cultivation, the average yield in Bangladesh remains relatively low compared to other Asian countries such as Indonesia and Malaysia. Variations in Boro rice yield are influenced by multiple factors, including genotypic differences, regional and seasonal conditions, inefficient nutrient management, pest and disease incidence, and various abiotic stresses such as drought, flooding, salinity, temperature extremes, and poor soil fertility. These factors collectively contribute to yield reduction and instability across environments in Bangladesh (Akter *et al.*, 2023).

When a genotype is evaluated under different growing conditions, its performance often varies significantly, a phenomenon referred to as genotype × environment (G×E) interaction (Allard & Bradshaw, 1964; Kang, 2004). Genotype × environment (G×E) interaction analysis provides a framework to assess how genotypes respond to variations in environmental conditions. Among various statistical tools, the Additive Main Effects and Multiplicative Interaction (AMMI) model and the Genotype plus Genotype × Environment (GGE) biplot are widely applied to study G×E interactions. These two statistical analyses (AMMI and GGE) were adopted in multi-environment (MET) two-way data matrices (Zhang *et al.*, 2016). In recent years, GE interaction has been only taken into account in AMMI analyze, but genotype effects were ignored while evaluating genotypes comprehensively. On the other hand, GGE biplot model has been considered as highly effective method to identify genotype difference and evaluation test environment (Ding *et al.*, 2007). Increasingly, crop breeders have used GGE biplot widely for evaluating mean performance, stability of cultivars (Kang *et al.*, 2006) and discrimination of test sites (Dimitrios *et al.*, 2008). By using both models, rice breeders can get robust and interpretable results for making decisions to select stable genotypes for rice breeding program or identifying a location-specific variety/genotype for rice production. The AMMI model combines analysis of variance for main effects with principal component analysis for interaction effects, while GGE biplot uses environment-centered principal components to graphically display genotype performance across environments. Despite methodological differences, both approaches provide comparable insights, allowing breeders to identify stable genotypes and environment groupings with minimal crossover interactions (Gouch & Zobel, 1996; Mohan *et al.*, 2023). However, limited studies have jointly applied both AMMI and GGE models to Boro rice genotypes across Bangladesh's major agrological zones, leaving uncertainty about adaptability under different stress conditions. Therefore, G×E analysis has become a standard component of plant breeding programs (Gupta *et al.*, 2022). Many studies in rice have explored various concepts and applications of G×E interaction analysis. (Poli *et al.*, 2018; Hashim *et al.*, 2021; Panda *et al.*, 2023; Anshori *et al.*, 2024; Ghazy *et al.*, 2024).

Grain yield is a complex quantitative trait influenced by both genetic and environmental factors. A desirable genotype should not only provide high yield but also perform consistently across diverse agroecological environments. Assessing genotype × environment (G×E) interaction is therefore critical in plant breeding to determine the adaptability and stability of improved lines before their commercial release (Dewi *et al.*, 2014).

The present study applied both AMMI and GGE biplot analyses to evaluate the adaptability and stability of seven rice genotypes for grain yield across twelve locations in Bangladesh. The objectives were to identify high-yielding and stable genotypes, and determine potential mega-environments, and identify ideal genotypes and environments suitable for rice production areas in Bangladesh.

MATERIALS AND METHODS

Test Genotypes and Locations

The trial was conducted during the 2024–25 Boro (dry) season across twelve locations in Bangladesh, representing distinct agroecological zones (Table 1). These included Barishal (tidal submergence area), Satkhira (salinity-affected area), Rangpur (cold-prone areas), and Habiganj (Haoar area) Gazipur, Kushtia, Rajshahi, Sonagazi, Cumilla, Gopalganj, Bhanga, and Sirajganj (favorable areas). In this study, five advanced rice genotypes from BRRI Regional Station, Barishal and two check varieties were evaluated (Table 1).

Experimental Design and Crop Management

The experiment was conducted across multiple environments following a randomized complete block design (RCBD) with three replications. Within each environment, seven genotypes were randomized independently. In addition to individual environment analyses, data from all environments were pooled across environments to perform a combined analysis of variance (ANOVA) for assessing genotype × environment interactions and stability performance.

Forty-day-old seedlings were transplanted into 10.8 m^2 plots, each consisting of 10 rows with 27 hills per row, at a spacing of 20 × 20 cm with one seedling per hill. Fertilizers were applied at 260:100:120:110:11 kg ha^{-1} of urea, TSP, MP, gypsum, and $ZnSO_4$, respectively. Nitrogen was top-dressed in three splits: 15 days after transplanting (DAT), 30 DAT, and five days before panicle initiation, while the remaining fertilizers were applied during final land preparation. Standard agronomic and crop protection practices were followed according to BRRI guidelines (BRRI, 2010). Grain yield was determined from the harvest of the entire plot, as no border rows were excluded, and the yield was adjusted to 14% moisture content.

In addition to grain yield, ancillary agronomic traits such as days to 50% flowering, plant height, growth duration, number of effective tillers per hill, and panicle number per hill (pAcp) were also recorded during the trial. However, only grain yield data were used for the present genotype × environment (G×E) analysis.

Data Collection and Statistical Analysis

Grain yield data were subjected to combined analysis of variance (ANOVA) across environments to partition the effects of genotype (G), environment (E), and their interaction (G×E). AMMI and GGE biplot analyses were performed using R software (version 4.4.2) and PBTools (version 1.3, IRRI). In the model genotypes were treated as both fixed and random and environments were treated as fixed, and replications nested within environment as random effects. Data normality was not checked before analysis.

The Grain mean yield was analyzed using STAR 2.0.1 version. In the AMMI approach, main effects were first analyzed using ANOVA, followed by principal component analysis (PCA) of the residuals to interpret G×E interaction patterns. In parallel, the GGE biplot method was employed to visualize both genotype main effects (G) and G×E interactions (GE) in a single framework, facilitating the identification of high-yielding and stable genotypes as well as the delineation of mega-environments (Hashim *et al.*, 2021).

Table 1. Description of Rice Genotypes examined and corresponding location codes.

Genotype code	Genotype Name	Location code	Location Name
G1	BRBaNGR 324-1	E1	Barishal
G2	BRBaNGR 1256-1	E2	Bhanga
G3	BRBaNGR350-2	E3	Cumilla
G4	BRBaNGR736-1	E4	Gazipur
G5	BRBaNGR994-1	E5	Gopalganj
G6	BRRI dhan74(Ck)	E6	Habiganj
G7	BRRI dhan102(Ck)	E7	Kustia
		E8	Rajshahi
		E9	Rangpur
		E10	Satkhira
		E11	Sirajgonj
		E12	Sonagazi

RESULTS AND DISCUSSION

Mean Grain Yield Performance

The Table 2 presents the grain yield performance (t/ha) of seven rice genotypes (five advanced breeding lines and two checks) evaluated across twelve environments (E1–E12) in Bangladesh. Considerable variation in yield performance was observed among genotypes and across locations, indicating strong genotype × environment (G×E) interaction.

Table 2. Mean Performance of Grain Yield Across Environments.

Genotype	Yield ($t ha^{-1}$)												Ave.mean
Location	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	
G1	6.45 a	8.32 a	7.93a	5.37a	8.84 a	6.56 a	6.92a	7.97a	7.34c	8.17a	5.21ab	9.49a	7.38
G2	5.66 ab	7.81 a	7.14 ab	5.16a	8.17 ab	5.55 a	6.28ab	7.34a	7.09c	7.45a	5.08ab	6.82b	6.63
G3	5.95ab	8.01 a	7.20 a	4.72 a	6.90 b	6.18 a	5.11b	8.18a	7.02c	7.02a	6.38a	6.17b	6.57
G4	6.26ab	8.34 a	5.04 c	5.34a	8.63 a	5.83 a	6.25ab	7.31a	9.09ab	7.74a	4.67b	5.92b	6.71
G5	6.00 ab	8.60 a	5.80 bc	5.68 a	9.02 a	6.23 a	7.00a	7.64a	9.63a	7.90a	5.23ab	7.13b	7.16
G6	5.97 ab	8.05 a	6.95 ab	5.79 a	8.27 a	5.87 a	6.17ab	7.06a	6.93c	7.87a	5.17ab	7.07b	6.77
G7	5.07 b	8.14 a	7.11 ab	5.21 a	8.44a	5.213a	7.26a	8.04a	7.76bc	8.33a	6.14a	6.54b	6.94
Location Mean	5.91	8.19	6.74	5.32	8.33	5.92	6.43	7.65	7.84	7.79	5.41	7.03	
LSD at 0.05													0.6
CV (%)													8.45
Heritability(H2)													0.72

Means with the same letter are not significantly different

Across environments, the mean yield ranged from 6.63 t/ha to 7.38t/ha. G1 showed the highest yield among all genotypes across environments. On the other hand, G2 performed moderate to high yields in several environments (7.81 t/ha in E2; 8.17 t/ha in E5). G5 exhibited good performance across most locations, with the highest yields recorded in E5 (9.02 t/ha) and E9 (9.63 t/ha). Among the tested lines, G1 and G5 demonstrated better performance compared to checks. There is no significant difference among the G2 with checks and it showed almost similar performance to checks. Therefore, it is important to observe G×E interaction underscores the importance of multi-environment testing in selecting widely adapted and stable rice genotypes for Bangladesh's diverse agro-ecologies.

ANOVA and AMMI Analysis of Variance

The combined use of AMMI and GGE biplot analyses in this study offered a robust evaluation of genotype × environment (G×E) interaction among seven rice genotypes (G1–G7) across twelve environments (E1–E12). This dual-method approach, commonly applied in crop studies reaffirmed its value in dissecting patterns of stability and adaptability (Mohan *et al.*, 2023).

The AMMI analysis of variance (Table 3) showed that environment (E) was the largest source of variation, accounting for 51.9% of the total sum of squares (TSS) and was highly significant ($p < 0.001$). This indicates that yield performance of rice genotypes was strongly influenced by environmental differences, which is typical in multi-location trials.

Table 3. ANOVA and AMMI analysis of variance for grain yield across 12 environments.

Source of variation	Df	Sum Square	Mean Square	F value	Pr(>F)	Proportion (%)	Accumulated (%)	%TSS
Environment(E)	11	268.938	24.4489	50.88	6.71E-14			51.9
Replication(R)	24	11.533	0.4806	1.53	6.54E-02			2.2
Genotype(G)	6	19.237	3.2062	10.23	2.02E-09			3.7
(G×E)	66	86.643	1.3128	4.19	3.77E-13			16.7
PC1	16	45.423	2.8389	9.06	0.00E+00	52.4	52.4	8.8
PC2	14	23.196	1.6569	5.29	0.00E+00	26.8	79.2	4.5
PC3	12	12.073	1.0061	3.21	4.00E-04	13.9	93.1	2.3
PC4	10	4.663	0.4663	1.49	1.49E-01	5.4	98.5	0.9
PC5	8	0.756	0.0945	0.30	9.65E-01	0.9	99.4	0.15
PC6	6	0.532	0.0887	0.28	9.46E-01	0.6	100.0	0.1
Residuals	144	45.111	0.3133					8.7
Total	317	518.105	1.6344					100

The %TSS indicates the proportion of total sum of squares explained by each source of variation. IPCA = Interaction Principal Component Axis. DF = degree of freedom, G x E = genotype by environment interaction, SS = sum of squares, %TSS = percent total sum of squares.

The genotypic effect (G) contributed only 3.7% of TSS, although it was highly significant, suggesting the presence of inherent but relatively small genetic variation for yield among the tested entries. In contrast, the genotype × environment interaction (GEI) explained 16.7% of TSS and was highly significant, demonstrating that genotypes responded inconsistently across environments, thus justifying the need for stability and adaptability analysis.

Partitioning of GEI into interaction principal component axes (IPCAs) showed that PC1, PC2, and PC3 together captured 93.1% of GEI variation, with PC1 alone contributing 52.4%. The significance of the first three IPCAs suggests that they are sufficient to describe the major crossover interactions among genotypes and environments. Higher-order IPCAs (PC4–PC6) explained only minor, non-significant portions of the interaction and were therefore less relevant. Residual variation accounted for 8.7% of TSS, which is acceptable for field trials.

These findings are consistent with previous studies in rice and other cereals, where the environment typically explains the largest proportion of yield variation, followed by GEI and a smaller contribution from genotypes. For example, Gauch & Zobel (1996) reported that environmental effects usually exceed 50% of TSS in AMMI models, while Purchase *et al.*

(2000) in maize and Yan & Tinker (2006) in wheat observed similar patterns. In rice, Huang et al. (2021) also reported that GEI accounted for 15–20% of yield variation, highlighting the importance of stability analysis in cultivar evaluation. Thus, these results confirm that environmental heterogeneity dominates rice yield performance, but genotype and GEI effects are critical for identifying stable, widely adapted varieties.

Genotype Performance and Stability

AMMI biplot for Yield Mean

The AMMI biplot (Fig. 1) explained a substantial proportion of the total variation, with PC1 and PC2 accounting for 52.4% and 26.8%, respectively. Together, these two components captured more than 79.2% of the genotype × environment (G×E) interaction, indicating a reliable representation of yield stability patterns which is a level of explanatory power consistent with effective G×E interpretation (Gauch, 2006; Akter *et al.*, 2014; Hasina *et al.*, 2015). In this biplot, genotypes and environments close to the origin are considered more stable, while those further away exhibit greater interaction with the environment. Genotypes G2 and G6 were located near the origin, suggesting their yield performance was stable across environments. Conversely, genotypes G1, G3, and G4 were positioned farther from the origin, displayed strong interaction and greater sensitivity to environmental changes. G5 show high yield potential, but their strong G×E interaction suggests they are suitable only for specific environments (not broadly adaptable). A similar type of findings has been reported in the literature on rice crops by Hasina *et al.*, (2015); Bose *et al.*, (2014), and Akter *et al.*, (2014).

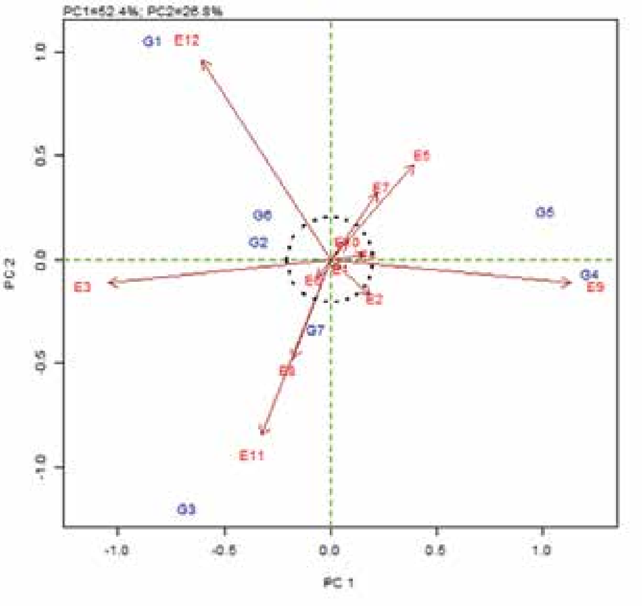

Fig. 1. AMMI biplot for Yield Mean.

Among environments, E12 and E3 were highly interactive, showing greater capacity to discriminate among genotypes, while E5 and E6 also contributed to G×E interaction. In contrast, environments clustered near the center, such as E2 and E7, were less interactive, reflecting more uniform genotypic responses. These results suggest that E12 and E3 are critical sites for identifying environment-specific adaptation, while E2 and E7 are more useful for testing general adaptability.

Ranking of Genotypes based on Yield and Stability performance

The GGE genotype view (Fig. 2) highlighted performance differences. Genotypes G2 and G6 were placed in the positive direction of the average environment axis (AEA), indicating good yield potential across environments. G7 was close to the AEA origin, suggesting stable though moderate performance. In contrast, G3 appeared at the upper extreme of the plot and G4 at the opposite lower side, indicating poor yield potential and strong interaction effects. Genotypes close to the ideal genotype center (represented by concentric circles) are considered more desirable. Here, G2 and G6 were closest, identifying them as high-yielding and broadly adapted entries.

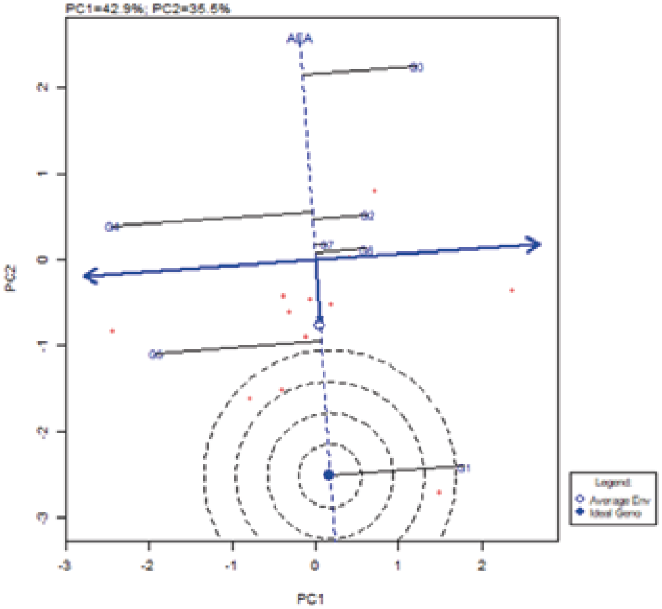

Fig. 2. GGE biplot genotype view showing the ranking of genotypes for both yield and stability performance over environment.

The estimation of genotype yield and stability (Fig. 2) was carried out using the average environment coordinates (AEC) method (Yan *et al.*, 2007). The average environment is defined by the average values of PC1 and PC2 for all environments and it is presented with a circle. The average ordinate environment (AOE) defined by the line which is perpendicular to the AEA (average environment axis) line and passes through the origin. This line divides the genotypes into those with higher yield than average and into those lower yield than average. The stability of genotypes is determined by their distance from the AE abscissa. Genotypes positioned closer to the abscissa are more stable than those farther away. In this study, the greatest stability in the high yielding group had genotypes G2 and G6, while the most unstable of all was G7. Although G1 showed the highest mean yield but it is unstable across the environment. Based on the ranking of the genotypes for both yield and stability performance were G2 and G6.

The results confirm that the AMMI and GGE models provide complementary insights AMMI quantifies stability, while GGE effectively visualizes adaptability and mega-environment. The identification of G2 and G6 as stable performers and G1 as a specifically adapted high-yielding genotypes for specific environment which is potential for rice breeding program advancement in Bangladesh.

Polygon view of GGE biplot analysis

The "which-won-where" view of the GGE biplot has been widely recognized as an effective visual tool for mega-environment analysis (Yan *et al.*, 2007). In this approach, a polygon is formed by connecting the vertex genotypes, with rays drawn from the origin of the biplot to each side of the polygon, thereby dividing the biplot into different sectors. Each sector represents a potential mega-environment, and the vertex genotypes located furthest from the origin are considered either the best or the poorest performers within those environments (Yan and Kang, 2003).

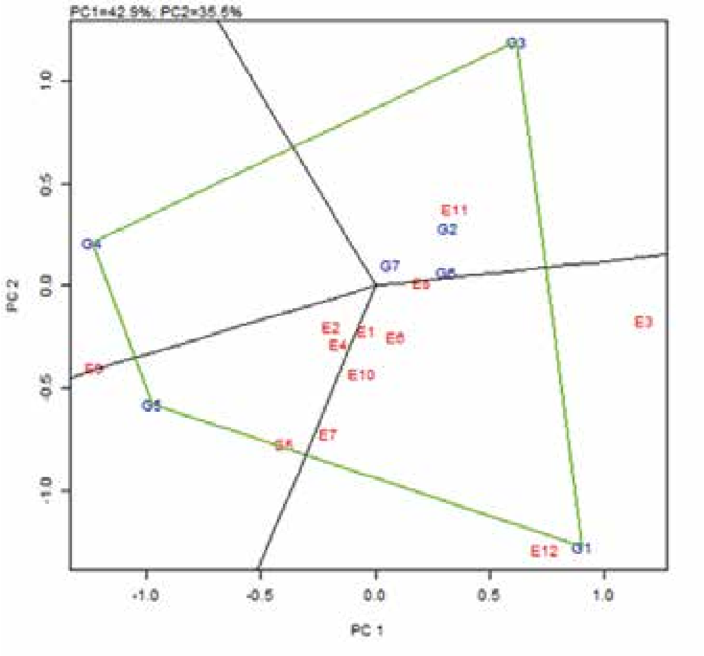

Fig. 3. The "which-won-where" view of the GGE biplot.

In this study, PC1 (42.9%) and PC2 (35.5%) together captured a large share of the total variation, indicating the GGE model effectively represents GEI (Fig. 3). Genotypes with positive PC1 scores were associated with higher yield performance, whereas those with negative scores were considered lower yielding, in agreement with the findings of Kaya et al. (2006). Similarly, the PC2 axis was indicative of genotype stability, where values closer to zero reflected stable performance across environments.

The polygon view identified G1, G3, G4, and G5 as vertex genotypes (Fig. 3), suggesting that these were either highly responsive or extremely poor performers across the test environments. For instance, G4 consistently showed poor performance, as they were positioned far from most environments, confirming their low adaptability and yield potential across sites. Conversely, environments such as E11, which clustered with genotypes G2, G6, and G7, were associated with relatively higher and stable yield performance, as reflected by their near-zero PC2 scores. Genotypes G1, G3, and G5 showed superiority in specific environments, indicating potential for targeted adaptation.

Overall, the analysis demonstrated the existence of distinct environmental groupings, with certain genotypes performing consistently well in specific environments while others exhibited poor adaptability. The clustering of environments and identification of vertex genotypes align with earlier findings that GGE genotypes align with earlier findings that GGE biplot analysis not only reveals mega-environment structures but also aids in selecting genotypes with wide or specific adaptability (Karimizadeh *et al.*, 2013). These results are highly relevant for targeted rice improvement, as they provide breeders with valuable insights into which genotypes are broadly stable, and which are best suited for specific ecological niches.

CONLUSION

This study demonstrated that environmental factors exert the strongest influence on rice grain yield, accounting for more than half of the observed variation. However, the significant genotype × environment interaction highlighted the importance of stability and adaptability testing in breeding programs. The AMMI analysis identified G2 and G6 as the most stable and high-yielding genotypes, while GGE biplot analysis further confirmed their wide adaptability across test environments. Conversely, G1, G3, and G5 were highly interactive and suggesting limited adaptability. Among environments, E12 and E3 were identified as key discriminative sites for evaluating genotype adaptability. The combined application of AMMI and GGE models thus proved effective in identifying genotypes with both wide and specific adaptation. These findings provide valuable insights for rice breeders aiming to select high-performing, stable genotypes suitable for multi-environment cultivation in Bangladesh.

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