

Contents lists available at Banglajol

Bangladesh Rice Journal

journal homepage: www.banglajol.info/index.php/BRJ

Breeding for Resilience: Cross-Environment Stability of Rice Genotypes Combining High Yield and Major Disease Resistance

A Rahman¹, M R A Sarker¹, M R Hasan², M R Islam¹, M A Syed¹, M Adil¹, A K M Shalahuddin¹, M A Rahman³, R J Promee², N Tamanna¹, S Hossain⁴, M A I Khan⁵, M Khatun^{1*}

¹Plant Breeding Division, Bangladesh Rice Research Institute (BRRI), Gazipur-1701

²Bangladesh Rice Research Institute (BRRI), Regional station, Rangpur

³Bangladesh Rice Research Institute (BRRI), Regional station, Kushtia.

⁴Grain Quality and Nutrition Division, Bangladesh Rice Research Institute (BRRI), Gazipur-1701

⁵Bangladesh Rice Research Institute (BRRI), Regional station, Barishal

ARTICLE INFO

Keywords:

Rice
Disease resistance
Stability
MGIDI
Resilience

ABSTRACT

Rice production is severely affected by different stresses, especially biotic stresses. The current study was aimed to identify resilient genotypes with wider adaptation along with major disease resistance. Genotypes, BR11866-5R-277, BR11867-5R-118, BR11867-5R-331, BR12437-4R-164, BRRI dhan101, and BRRI dhan89 were identified as the most stable genotypes by utilizing GGE biplot and PCA analysis, whereas BR11869-5R-148, BR12125-6R-6, BR12125-6R-79, and BR13796-5R-102 exhibited site-specific adaptability for grain yield. MGIDI index demonstrated that BR11866-5R-277, BR11867-5R-331, and BRRI dhan89 were closest to the ideotype by combining multi-trait i.e., yield, growth duration, and plant height, with stability. Most of the genotypes met the national standard of grain quality. The genotypes BR11866-5R-277 and BR11867-5R-331 showed BB resistance and BR11867-5R-118, BR12125-6R-6, BR12125-6R-79, BR12450-4R-108, BR12450-4R-24 demonstrated blast resistance. The genotypes BR11866-5R-277 and BR11867-5R-119 showed resistance to BB and blast both. Based on SNP genotyping and screening result different combinations of pyramided lines were identified. Those lines will be the potential donors for further breeding program. The genotypes BR11866-5R-277, BR11867-5R-118, BR11867-5R-331, BR12125-6R-6, BR12450-4R-108, and BRRI dhan101 could be promising candidates for breeding program targeting high yield, stability, superior quality, and durable disease resistance. The BR11866-5R-277 and BR11867-5R-331 line would be selected for further trial and variety release for bacterial blight (BB) and tungro (RTV) resistance, respectively.

1. Introduction

Rice (*Oryza sativa* L.) is an important staple food for over half of the global population and plays a vital role in food security and nutrition, especially in Asia (Fukagawa et al., 2019). In Bangladesh, food and nutritional security are synonymous to rice production. However, rice production is continually

threatened by several types of biotic stresses, particularly bacterial blight (BB), blast, and rice tungro disease, which collectively account for significant yield losses in many rice-growing areas.

Bacterial blight, spread by *Xanthomonas oryzae* pv. *oryzae* (Xoo), is one of the most detrimental rice

* Corresponding author at: Principal Scientific Officer, Plant Breeding Division, Bangladesh Rice Research Institute (BRRI), Gazipur-1701
E-mail: mahmuda.breeding@gmail.com (M Khatun)

diseases, causing 50% yield losses in epidemic condition (Iqbal et al., 2023; Fiyaz et al., 2022). *Magnaporthe oryzae* is the cause of blast disease, which is similarly deadly. It attacks crops at any growth stages, but most detrimental at flowering to early maturity. In a favorable environment, it causes even 100% yield loss in susceptible varieties (Pedrozo et al., 2025; Wang et al., 2014). Tungro disease, caused by a complicated combination of *rice tungro bacilliform virus* (RTBV) and *rice tungro spherical virus* (RTSV), is an additional limitation in tropical Asia, that leads to stunted growth and significant yield reductions (Dey et al., 2024; Bunawan et al., 2014). Significant progress has been achieved in disease resistance breeding by discovering and deploying of resistance genes like *Xa21*, *Xa5* and *Xa13* for BB; *Pi9*, *Pita* and *Pb1* for blast; and *TSV1* & *TBV1* for tungro (Fiyaz et al., 2022; Latif et al., 2025; Widiarta et al., 2025). Nevertheless, the durability of resistant genotypes is hampered by the evolution of noble isolates of the pathogen and climate change by the overcoming of the resistance (Michelmore et al., 2013).

Therefore, the modern disease resistance breeding strategies must be prioritized, combining higher yield potentials and broad-spectrum resistance to BB, blast, and tungro across diverse environments. Such integrated breeding strategies must be tested in multiple environments for improving yield, resilience and protecting rice from diverse biotic challenges.

Genotype-environment interaction (GEI) has a considerable impact on the performance and stability of each of the production and resistance traits, challenging the selection process in breeding programs (Egea-Gilabert et al., 2021). GEI represents the genotype-environment reaction in terms of adaptation. Cross-environment stability enables breeders to find out resilient cultivar that performs consistently in

diverse environments, specially having the potentiality to adapt in climate change (Justo et al., 2024).

GGE biplot analysis is one of the typical statistical methods to detect GEI of target traits across multiple environments. GGE biplots graphically represent the GEI of numerous environments that facilitate quick and easier evaluation of genotypes. GGE biplots illustrate the first and second principal components by single value decomposition of environment-centered multiple environment trial data to evaluate genotypes and mega-environment identification (Yan et al., 2000). A newer technique called WAASB is used to assess quantitative genotypic stability, the weighted average of absolute scores from the singular value decomposition of the matrix of best linear unbiased predictions (BLUP), for GEI effects obtained in a linear mixed model (LMM) (Olivoto et al., 2019).

In this context, the current study seeks to assess the stability and adaptation of rice genotypes with major diseases, particularly bacterial blight, blast & tungro, and high yield potential across multi-environmental conditions. The study also sheds light on the interactions between genotype, environment, and resistance expression, which will aid in the development of robust rice varieties that contribute to food security for sustainable agriculture.

2. Materials and methods

2.1. Plant materials

A total of 17 rice genotypes including, three check varieties, were used for field experiments. The complete set and details of genotypes used in the study are summarized in Table 1.

Table 1

Status and designation of the advanced breeding lines and check varieties of rice.

Genotypic code	Designation	Parentage	Remarks
G1	BR11866-5R-277	HHZ23-DT16-DT1-DT1/BP10620F-BB-4-17-BB8	Advanced Line
G2	BR11867-5R-118	BRRI dhan75/BP10620F-BB-4-17-BB8	Advanced Line
G3	BR11867-5R-119	BRRI dhan75/BP10620F-BB-4-17-BB8	Advanced Line
G4	BR11867-5R-331	BRRI dhan75/BP10620F-BB-4-17-BB8	Advanced Line
G5	BR11869-5R-148	BR8938-19-4-3-1-1/Habataki	Advanced Line
G6	BR12125-6R-149	BRRI dhan63*3/IR93323//IRBB60/N22	Advanced Line
G7	BR12125-6R-6	BRRI dhan63*3/IR93323//IRBB60/N22	Advanced Line
G8	BR12125-6R-79	BRRI dhan63*3/IR93323//IRBB60/N22	Advanced Line
G9	BR12437-4R-109	BRRI dhan58*2/IRBB60	Advanced Line
G10	BR12437-4R-164	BRRI dhan58*2/IRBB60	Advanced Line
G11	BR12450-4R-108	BRRI dhan29/IRBL9-W(RL)(Pi9)	Advanced Line
G12	BR12450-4R-24	BRRI dhan29/IRBL9-W(RL)(Pi9)	Advanced Line
G13	BR13790-5R-216	BRRI dhan29*3/Pb1 [US]	Advanced Line
G14	BR13796-5R-102	BRRI dhan64*2/pi21 [US]	Advanced Line
G15	BRRI dhan101		Resistant check
G16	BRRI dhan88		Susceptible & Standard check
G17	BRRI dhan89		Susceptible & Standard check

2.2. Locations and field experimental design

Seventeen rice genotypes were evaluated at the Regional Stations, namely, Rajshahi, Rangpur, Kushtia, Cumilla, Bhanga, Sonagazi, Satkhira, Habiganj, and Gazipur in Bangladesh Rice Research Institute (BRRI) (Table 2). The areas were chosen specifically because of their excellent potential for rice cultivation and the field trial was conducted in Boro season, 2023-24. The studies in all locations were set up in a randomized complete block design (RCBD) with two replications. The plot dimensions were 5 m × 2 m, with plants spaced 20 cm apart in rows and plant to plant.

Seedlings were transplanted 30-40 days after sowing, with one seedling per hill to maintain the line purity. Gap filling was carried out within two weeks after transplanting, to ensure homogeneous growth of the crop. Fertilizer was applied at the BRRI recommended rate (three instalments as top dressing). The first and second applications were completed during the tillering and booting stages, respectively. Weed, insect, and disease control were implemented as advised for the crop, utilizing an integration of chemical and cultural approaches. During crop development, additional irrigation was applied to maintain enough soil moisture in each plot.

Table 2

List of experimental locations with assigned environmental codes.

Locations	Locations/Environmental code
Satkhira	E1
Sonagazi	E2
Bhanga	E3
Cumilla	E4
Gazipur	E5
Habiganj	E6
Kushtia	E7
Rajshahi	E8
Rangpur	E9

2.3. Measurement of the traits

Three yield and yield attributing traits, namely plant height (PH; cm), growth duration (GD; days), and grain yield (YLD; t/ha), were measured across all location environments. PH was determined by

measuring upper ground height of 10 plants and measured mean plant height in centimeters (cm). The entire plot in each replication was harvested to determine grain yield (YLD), which was expressed in t/ha. The distribution patterns of collected data are shown in Fig. 1.

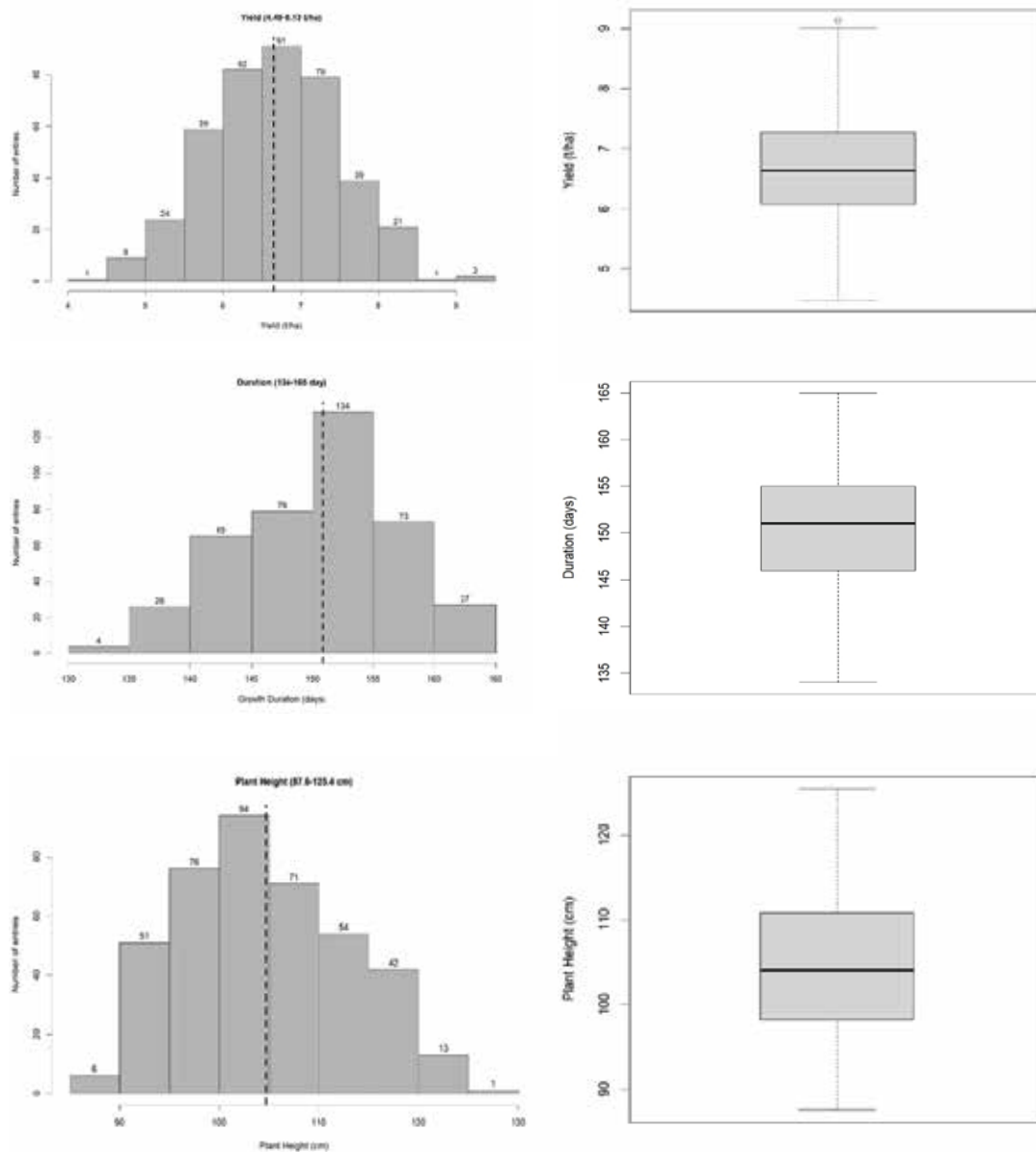


Fig. 1. Histogram and boxplot of grain yield, growth duration and plant height. Dot vertical line in histogram represent population mean and bold horizontal line in boxplot represent the population mean.

2.4. Statistical analyses

All statistical analyses were done by using R Studio version 2024.12.0. Utilizing the 'Agricolae' program, a combined ANOVA was performed to investigate the presence of GEI employing a complete dataset of studies across nine environments (Mendiburu, 2020). Agronomic performance of each genotype in each environment and combine performance was calculated in the best linear unbiased estimation model (BLUE) and predicted performance was calculated in best linear unbiased prediction model (BLUP) using R package lmerTest (Kuznetsova et al., 2017), emmeans (Lenth, 2025), pbkrtest (Halekoh & Højsgaard, 2014). Correlation of yield and yield contributing traits and the environment were calculated using the metan package (Olivoto & Lúcio, 2020). Principal component analysis was done using the factoextra package (Kassambara & Mundt, 2017).

Adaptability of genotypes and mega-environments (MEs), a group of environments that share the same winning genotypes, in the nine different environments, trials were evaluated using genotypic main effect plus GEI (GGE) biplot analysis (Yan et al., 2002), using the 'metan' package (Olivoto & Lúcio, 2020). Environments were evaluated using the 'discriminateness vs. representativeness' view of the GGE biplot. MEs and winner genotypes in a given set of environments were identified using a 'which-won-where' GGE biplot. Adaptability of genotypes to multi-environments was evaluated using

a 'ranking genotypes' GGE biplot, comparing the ideal genotypes, which were defined as showing the highest performance in all environments. To evaluate the yield stability of genotypes across environments a mean vs stability GGE biplot was created. For calculating the multi-trait stability index, the WAASBY index (Olivoto et al., 2019), a superiority index that allows weighting between performance and stability (WAASB), was calculated to identify genotypes that combined high agronomic value with stability. Multitrait Genotype-Ideotype Distance Index (MGIDI) was calculated using "metan" package for selecting Ideal genotype (Debnath et al., 2024).

3. Results

3.1. Variation and agronomic performance of grain yield and its components for multiple environments

In Regional Yield Trial (RYT), 17 rice genotypes were investigated across nine agro-climatic zones in Bangladesh to identify suitable genotype adaptation for yield, plant height, growth duration and disease resistance. Temperature, relative humidity, and precipitation varied significantly throughout the test sites. ANOVA revealed extremely significant main effects of genotype (G), environment (E), and genotype-by-environment interaction (GEI) for all evaluated traits (Table 3). The replication effects were non-significant for the variables except growth duration.

Table 3

Combined Analysis of Variance of yield and yield contributing characters.

Sources of variation	Df	YLD		PH		GD	
		MS	Pr(> F)	MS	Pr(> F)	MS	Pr(> F)
REP	2	0.11	0.52 ^{NS}	7.72	0.07 ^{NS}	68.83	3.837e-15 ***
GEN	16	2.42	< 2e-16 ***	860.57	< 2e-16 ***	363.22	< 2.2e-16 ***
ENV	8	13.26	< 2e-16 ***	795.34	< 2e-16 ***	1194.60	< 2.2e-16 ***
GEN: ENV	128	0.75	< 2e-16 ***	59.35	< 2e-16 ***	13.34	< 2.2e-16 ***
Residuals	253	0.17		2.95		1.81	

GEN = Genotypes, ENV = Environment, GEN: ENV = Genotype-environment interaction, REP = Replication, YLD = Grain Yield (t/ha), PH = Plant Height (cm), GD = Growth Duration (days)

*** = 0.1% level of significance, ** = 1% level of significance, * = 5% level of significance

The average grain yield varied from 4.56 to 8.71 t/ha, with a least significant difference (LSD, $p < 0.05$) of 0.51 t ha⁻¹. Using both best linear unbiased estimates (BLUE) and best linear unbiased predictions (BLUP), genotypes G1, G2, and G15 consistently performed well. Rangpur and Bhanga were identified as the most favorable environments, producing

average yields 13.38% and 10.6% higher than the grand mean, respectively (Table 4). The other agronomic traits, such as growth duration and plant height, are favorable, indicating its potential as a promising line for use as a parent or variety (Table S1 & Table S2).

Table 4

Best Linear Unbiased Estimation (BLUE) and Best Linear Unbiased Prediction (BLUP) Based Yield (t/ha) performance of tested genotype.

Gen	E1	E2	E3	E4	E5	E6	E7	E8	E9	pBLUE	pBLUP	rel
G1	6.79	6.34	8.59	6.54	5.92	6.05	7.24	5.92	7.91	6.81	6.72	0.67
G2	6.63	7.49	8.71	4.92	7.44	6.48	6.59	7.44	7.64	7.04	6.87	0.67
G3	6.53	7.20	7.82	5.86	6.38	6.09	6.18	6.38	7.14	6.62	6.59	0.67
G4	6.67	6.57	7.12	6.33	6.62	5.64	6.23	6.62	8.43	6.69	6.64	0.67
G5	5.30	6.55	6.19	7.03	7.66	5.26	5.93	7.66	7.21	6.53	6.53	0.67
G6	5.60	6.65	5.44	5.73	5.30	4.88	7.39	5.30	7.70	6.00	6.17	0.67
G7	5.87	6.49	7.22	6.45	5.96	5.49	6.24	5.96	6.44	6.24	6.33	0.67
G8	6.17	6.13	7.35	5.45	5.53	6.76	6.76	5.53	7.99	6.41	6.45	0.67
G9	5.85	6.70	6.32	6.54	5.82	6.06	7.03	5.82	6.96	6.34	6.40	0.67
G10	6.58	5.87	8.08	5.77	7.25	6.76	6.54	7.25	7.14	6.80	6.71	0.67
G11	5.76	6.26	7.41	6.62	5.92	5.91	6.59	5.92	7.22	6.40	6.44	0.67
G12	6.19	6.98	7.00	6.79	5.66	5.04	6.39	5.66	6.09	6.20	6.31	0.67
G13	6.19	6.23	6.86	5.44	6.35	7.12	6.80	6.35	7.96	6.59	6.57	0.67
G14	4.56	5.92	6.63	6.05	5.91	4.66	5.90	5.91	6.24	5.75	6.01	0.67
G15	6.75	6.59	7.43	6.65	7.78	6.24	6.86	7.78	7.65	7.12	6.91	0.67
G16	5.87	6.35	6.51	6.48	6.78	6.41	6.38	6.78	7.19	6.48	6.50	0.67
G17	5.63	6.75	7.46	6.06	5.71	7.18	6.81	5.71	8.33	6.49	6.51	0.67
Avg	6.06	6.53	7.19	6.16	6.35	6.00	6.58	6.35	7.37	6.50	6.51	
h2b	0.91	0.34	0.91	0.67	0.61	0.85	0.30	0.61	0.82	0.19		
SE	0.12	0.29	0.23	0.23	0.48	0.28	0.32	0.48	0.19	0.26		
LSD	0.24	0.57	0.45	0.45	0.94	0.55	0.63	0.94	0.37	0.51		

*** Genotypes (GEN), Pooled Best Linear Unbiased Estimation (pBLUE), Pooled Best Linear Unbiased Prediction (pBLUP), reliability (rel), Average (Avg), Heritability (h2b), standard error (SE), Least Significance difference (LSD).
Satkhira (E1), Sonagazi (E2), Bhanga (E3), Cumilla (E4), Gazipur (E5), Habiganj (E6), Kushtia (E7), Rajshahi (E8), Rangpur (E9)

3.2. Inter-location correlation patterns across nine test environments

The correlation analysis of grain yield across the nine tested locations indicated substantial variability in inter-location associations (Fig. 2). Several location pairs showed substantial positive association ($p < 0.05$ – 0.001), indicating similarities in genotype in the case of yield performance under comparable environmental conditions. Notably, Habiganj exhibited strong positive associations with Rangpur ($r = 0.57$, p

< 0.001), Satkhira ($r = 0.52$, $p < 0.01$), and Bhanga ($r = 0.43$, $p < 0.05$). In addition, Rajshahi was positively correlated with Satkhira ($r = 0.52$, $p < 0.01$), while Satkhira displayed high correlations with both Bhanga ($r = 0.59$, $p < 0.001$) and Rangpur ($r = 0.47$, $p < 0.01$). In contrast, certain pairs, such as Kushtia–Habiganj ($r = 0.10$) and Cumilla–Rajshahi ($r = -0.31$), exhibited weak or negative associations, indicating significant environmental diversity with distinct genotype-by-environment responses.

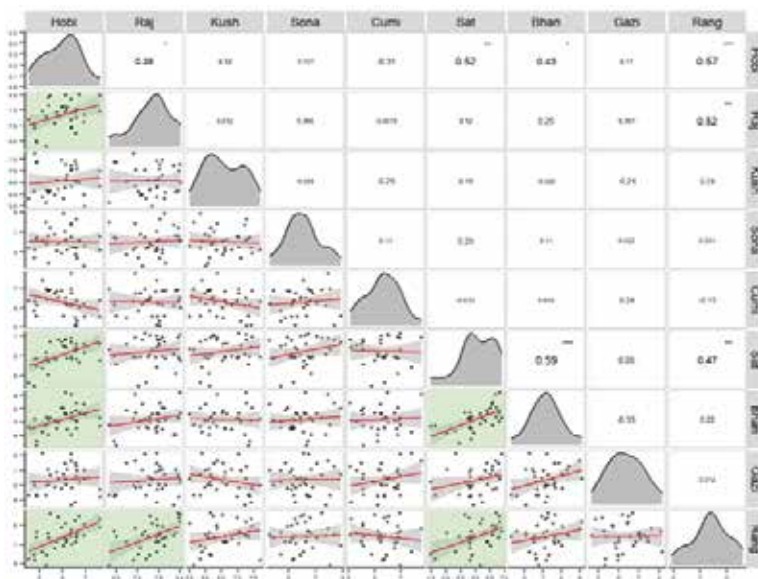


Fig. 2. Pairwise correlation matrix of grain yield across nine test locations (Habiganj, Rajshai, Kushtia, Sonagazi, Cumilla, Satkhira, Bhanga, Gazipur, and Rangpur). Diagonal panels show density plots, upper panels display correlation coefficients with significance levels * ($p < 0.05$), ** ($p < 0.01$), *** ($p < 0.001$), and lower panels present scatter plots with fitted regression lines.

Growth duration (GD) demonstrated a positive relationship ($p < 0.05$ - 0.001) across every location

pair (Fig. 3), illustrating similar maturity trends among genotypes in different environments.

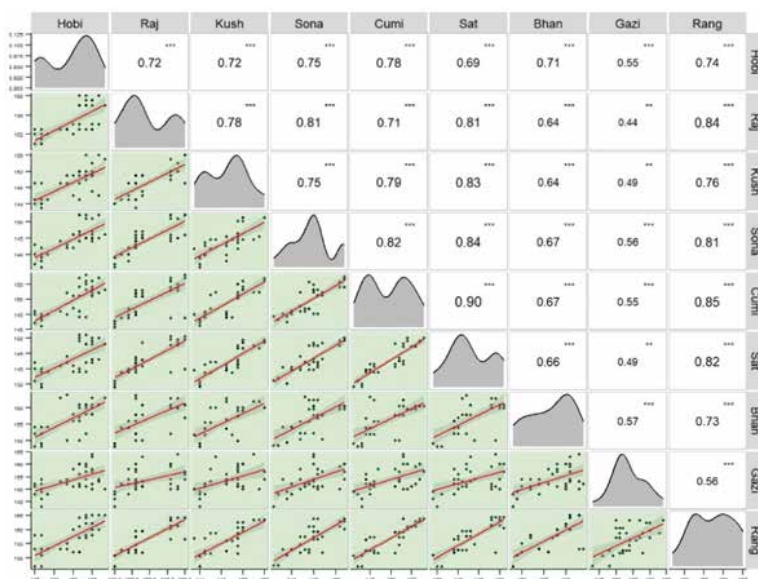


Fig. 3. Pairwise correlation matrix of rice growth duration (days) across nine test locations (Habiganj, Rajshai, Kushtia, Sonagazi, Cumilla, Satkhira, Bhanga, Gazipur, and Rangpur). Diagonal panels show density plots, upper panels display correlation coefficients with significance levels * ($p < 0.05$), ** ($p < 0.01$), *** ($p < 0.001$), and lower panels present scatter plots with fitted regression lines.

In addition, plant height (PH) revealed substantial positive associations across the locations ($p < 0.05-0.001$) (Figure 4), indicating uniformity in plant stature under different climatic conditions. Cumilla

was an exception, with four non-significant relationships with Habiganj, Kushtia, Bhanga, and Gazipur, demonstrating that plant height expression is influenced by environmental factors of this location.

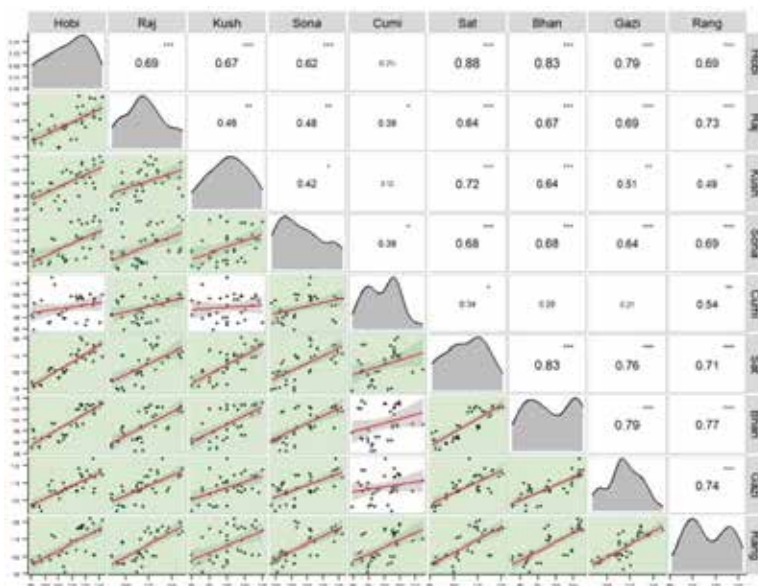


Fig. 4. Pairwise correlation matrix of plant height (cm) across nine test locations (Habiganj, Rajshai, Kushtia, Sonagazi, Cumilla, Satkhira, Bhanga, Gazipur, and Rangpur). Diagonal panels show density plots, upper panels display correlation coefficients with significance levels * ($p < 0.05$), ** ($p < 0.01$), *** ($p < 0.001$) and lower panels present scatter plots with fitted regression lines.

3.3. PCA-based assessment of genotype performance across diverse rice-growing environments

The PCA biplot (Fig. 5) shows the connections between 17 rice genotypes (G1-G17) and three traits viz. grain yield, growth duration, and plant height. The first two principal components, PC1 and PC2, explained 47.1% and 37.9% of total variation, respectively, and accounted for a total of 85.0% of the observed variance. PC1 was robustly and positively linked to grain yield and growth duration, as seen by their vectors near alignment, whereas PC2 was primarily connected with plant height. Genotypes positioned near specific traits on the biplot indicate

higher performance for those traits. For example, G1 and G2 were near the YLD vector, indicating better yield performance, whereas G4, G13, and G17 were closer to the GD vector, indicating a longer maturity period. G11 and G12 were situated closer to the PH vector, indicating higher plant height.

The genotypes (e.g., G9, G15) close to the origin performed averagely for the examined characteristics, whereas those (e.g., G7, G16) placed in opposite directions from the trait (YLD) vector likely performed worse. The large dispersion of genotypes across all quadrants indicates significant variation in trait combinations, implying that the examined lines exhibit a variety of adaptation strategies (Fig. 5).

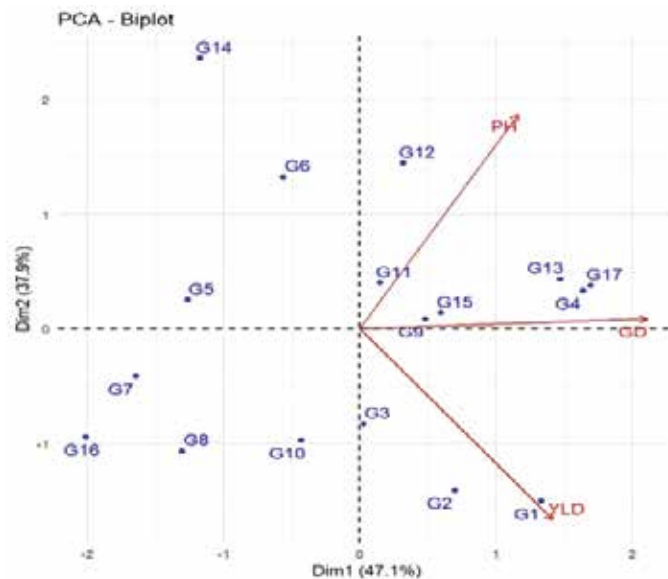


Fig. 5. Principal component analysis (PCA) biplot showing the relationship among 17 rice genotypes (G1–G17) and three traits—grain yield (YLD), growth duration (GD), and plant height (PH)—across environments.

3.4. Environmental evaluation and grain yield adaptability of the genotypes in specific environments

Evaluation of discriminativeness vs. representativeness was performed using GGE bi-plots. The biplot (Fig. 6) demonstrated that PC1 and PC2 explained 42.39% and 20.63% of the total variation, respectively. Environments E6, E9, E3, and E5 were the most discriminative, whereas E3 was also being

highly representative of the target environment (Fig. 6). E4 and E1 had moderate discriminative ability, but E4 showed low representativeness, while E8 and E2 were the least discriminative. Genotypes G8, G13, and G17 were closely associated with E6 and E9, suggesting broad adaptation, whereas G2 and G5 showed possible specific adaptation to E5 and E4, respectively.

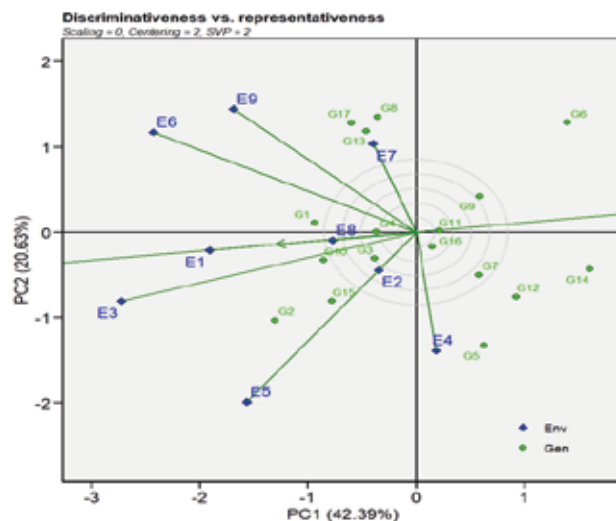


Fig. 6. Discriminativenss and representativeness GGE biplot for Evaluation of Environment.

Mega-environments have been identified employing the "which-won-where" pattern from the GGE biplot (Fig. 7). Perpendicular lines connecting the biplot origin to the polygon's sides split the environments into distinct sectors. The first mega

environment (ME) included E6, E9, and E7 genotypes, with G7 and G8 dominating the others. The second ME contained E1, E2, E3, E5, and E8, with G2 the winner. The third ME was made up only of E4, with G5 and G14 emerging as the best-performing line.

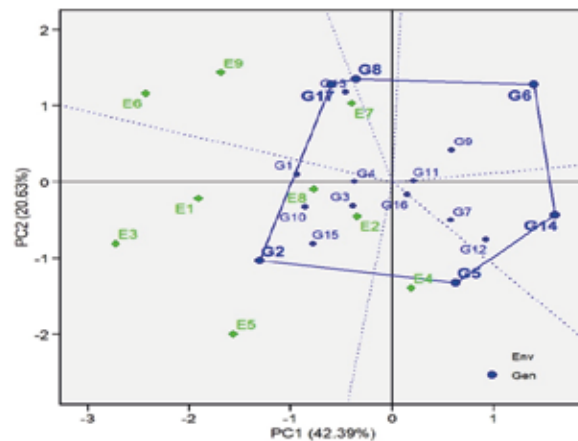


Fig. 7. GGE Biplot Showing "Which-Won-Where" Pattern of Rice Genotypes Across Test Environments for identification of Mega-Environment (ME) and location specific winning genotype.

3.5. Genotypic performance and stability based on gge biplot analysis

The genotypic performance and stability were analyzed using GGE biplot analysis from two perspectives: "Ranking Genotypes" and "Mean vs. Stability" as shown in the Figures 8 and 9, respectively. Both biplots had been generated using scaling = 0, centering = 2, and SVP = 2.

In the "Ranking Genotypes" biplot (Fig. 8), genotypes were ranked according to their proximity to the "ideal genotypes" defined as the genotype with the highest mean performance and the greatest stability. The genotypes G2, G15, G1, and G10 were closest to the optimal genotype position, indicating higher performance across contexts. The genotypes notably G6 and G14 were far from the AEC axis, implying poor performance.

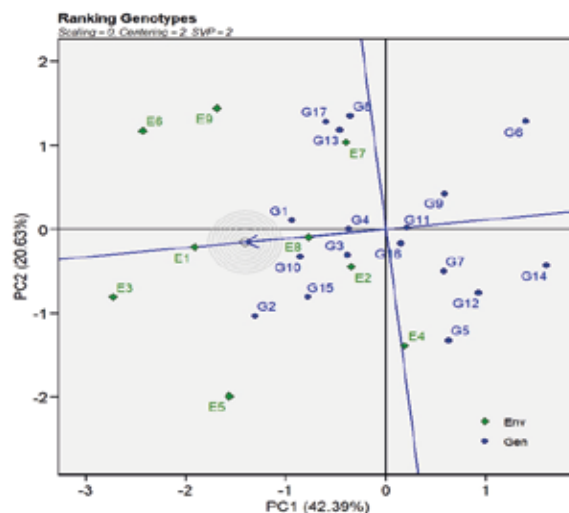


Fig. 8. GGE Biplot Ranking of Rice Genotypes for Mean Yield and Stability across Environments.

The "Mean vs. Stability" biplot (Fig. 9) offered additional details by extracting genotypic performance and stability. The genotypes G2, G15, G1, and G10 were found around the AEC abscissa, indicating higher average performance; however, only G1 and G10 had extremely short projections onto the coordinate, showing high mean performance and stability. G3 and G4 performed similarly to the mean, with very good

stability, owing to their short expansions from the AEC coordinate. Overall, these analyses proved G1 and G10 as the most preferable genotypes, integrating high yield performance with greater stability, making them an excellent choice for selection in breeding programs aimed at broad adaptation. Other genotypes, such as G2, G3, G4, and G15, had a favorable profile that warranted additional investigation.

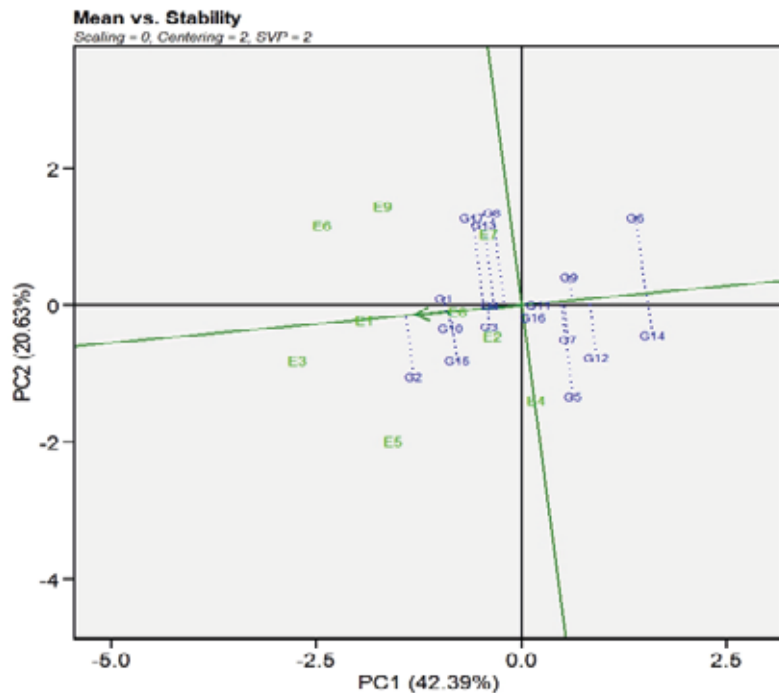


Fig. 9. Mean vs. Stability Biplot Depicting Genotypic Performance across Multi-Environment Trials.

3.6. Multi-trait selection and stability assessment using MGIDI

The Multi-trait Genotype-Ideotype Distance Index (MGIDI) approach was used to find superior genotypes based on various variables (yield, plant height, and growth duration) while taking into account both performance and stability. The first panel (left) exhibits the multi-trait stability index, which ranks genotypes according to their MGIDI scores (Fig. 10). A lower MGIDI number suggests greater proximity to the ideotype, and thus better performance across attributes. Based on a specified selection criterion (horizontal line), seven genotypes-G1, G8, G16, G15, G4, G7, and G11 were recognized as selected (highlighted in blue), while the others were classed as non-selected (red). The second panel (center) shows the impact of each genotype to the MGIDI index, proving that selected genotypes consistently have

shorter distances to the ideotype, indicating greater multi-trait performance (Fig. 10). Among the genotypes, G1, G17, and G4 had the lowest MGIDI scores, indicating that they are the most promising candidates for advancement. The third panel (right) shows the strengths and weaknesses view, with the top-performing genotype G1 alongside G4 and G17 for comparison reasons. The polygon depicts each genotype's proportionate contribution to the main factor (FA1), with G1, G4, and G17 having a well-balanced and narrow polygon shape, indicating more consistent performance across traits and fewer deficiencies (Fig. 10). Overall, the MGIDI analysis effectively integrated multi-trait information, allowing for the selection of genotypes with superior and stable performance profiles such as G1, G17, and G4, resulting in more informed selection decisions in breeding programs.

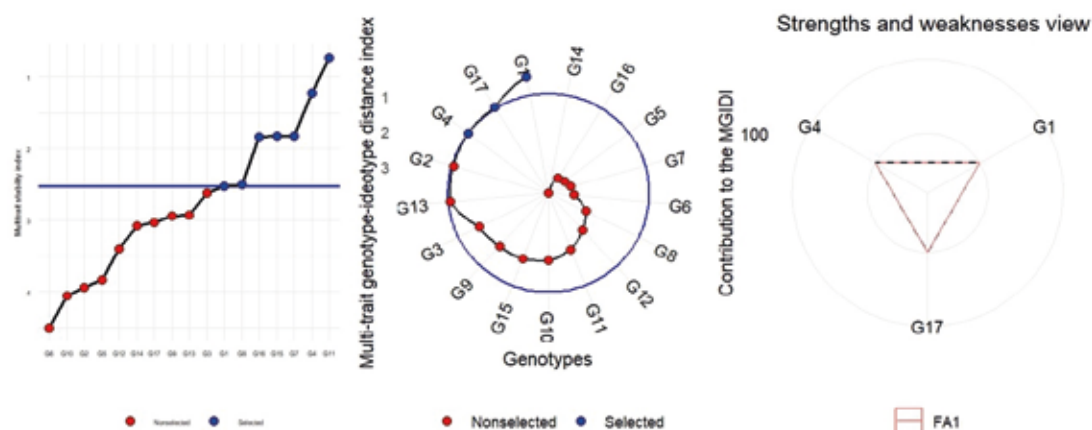


Fig. 10. Multi-Trait Genotype-Ideotype Distance Index (MGIDI) Analysis Showing Genotype Selection, Contribution to Ideotype, and Strengths-Weaknesses Profile.

3.7. Grain quality assessment of rice genotype

To access the grain quality, seventeen rice genotypes were tested for milling quality, grain physicochemical parameters, and cooking properties (Table 5). Milling outturn (%MOT) was attractive in all entries, above the desired criterion of 60%, ranging from 66.9% in G1 (BR11866-5R-277) to 73.0% in G5. Head rice recovery (%HRR) denotes post-milling grain integrity and should be greater than 50% to meet market standards. G3 obtained the highest %HRR (70.0%), followed by G17 (61.7%), G4 (61%), G1 (57.7%), and G10 (57.5%). On the contrary, G11 obtained the lowest %HRR (20.9%).

Grain length and breadth express the significant variation among the genotype which varies from 5.5 mm (G14) to 6.6 mm (G2) and 1.9 mm (G6, G12, G14) to 2.5 mm for grain length and breadth, respectively. The tested genotypes were classed into three groups based on grain size and shape (S&S), i.e., six genotypes long-bold (LB), nine medium-bold (MB), and two long-slender (LS). The alkali spreading value (ASV) denotes the gelatinization temperature, which ranges from 3.1 (G14) to 7.0 (G2, G11). Amylose content (%A) measures the stickiness or non-stickiness of

cooked rice, which should be greater than or equal to 24% to meet the national preference of Bangladesh. Amylose content (%A) of tested genotypes ranges from 16.8% (G14), and 27.5% (G17), and thirteen out of seventeen genotypes fulfill the amylose content criteria. Protein content added nutritional value to rice, which spanned from 7.5% (G17) to 10.5% (G14) in the tested genotypes. Cooking time is another quality property as the short of the cooking time, the greater the ability to save national energy which varies between 12.3 min (G12) and 19.3 min (G17). The elongation ratio denoted the length expansion after cooking, which ranges from 1.3 to 2.4, and G7 (BR12125-6R-6) displaying the most expansion during cooking. Imbibition ratio (IB) measures water absorption during cooking, which ranging from 2.6 (G2) to 4.5 (G7, G16) in the tested genotypes.

Overall, genotypes G1, G2, G4, G5, G10, G13, G15, G16, and G17 demonstrated adequate quality parameters at the national preference criterion, making them promising candidates for varietal release and breeding. On the other hand, G3, and G14, despite of good milling output and head rice recovery, were rejected from selection because their amylose content was below the desired range.

Table 5

Grain quality parameters of 17 rice genotypes evaluated for milling, cooking, and physicochemical traits.

GEN	%MOT	%HRR	L	B	S&S	ASV	%A	%P	CT	ER	IB
G1	66.9	57.7	6.2	2.5	LB	3.2	26	8.3	16.3	1.3	2.7
G2	69.7	51.5	6.6	2.4	LB	7	25	8	14.3	1.3	2.6
G3	70	51.6	5.9	2.5	MB	5	20.9	9	18	1.4	4.1
G4	70.6	61.0	5.9	2.5	MB	3.6	25.6	7.9	17	1.4	3.4
G5	73	53.6	6.4	2.5	LB	3.4	26.2	9.2	18	1.4	3.7
G6	71.8	38	6.2	1.9	LB	4.4	24	9.4	14.30	1.5	3.2
G7	69.5	51.6	6.3	2.1	LB	4.7	23.1	8.9	15.30	2.4	4.5
G8	70	51.5	5.8	2.2	MB	4.4	24	9.4	14.30	1.5	3.2
G9	68.9	47.6	6.1	2.4	LB	3.8	17.7	8.2	14.30	1.3	4
G10	68.6	57.5	6	2.4	MB	4.6	25.7	7.7	13.30	1.4	4.3
G11	69.9	20.9	5.9	2.5	MB	7	25.7	8.8	13	1.4	4.3
G12	70.6	22.5	6.2	1.9	LS	6	26.3	8.6	12.30	1.6	4.3
G13	71.1	70	5.6	2.1	MB	4.2	25.1	8.5	13	1.3	3.3
G14	67.4	61.7	5.5	1.9	MB	3.1	16.8	10.5	13.30	1.3	3.5
G15	69	55.8	6.5	2.3	LB	3.9	26.8	9.8	16.30	1.4	4.3
G16	71.2	59.7	6.2	2	LS	4.8	26	9.8	17.3	1.3	4.5
G17	70	61.7	5.7	2	MB	4.3	27.5	7.5	19.3	1.4	3.5

Here, Milling out-turn (%MOT), head rice recovery (%HRR), Grain length in milli-meter (L), Grain breadth in milli-meter (B), size and shape (S&S), Alkali spreading value (ASV), Amylose content in percentage (%A), Protein content in percentage (%P), cooking time in minutes (CT), Elongation ratio (ER), Imbibition ratio (IB).

3.8. Genomic trait value evaluation by SNP based trait genotyping and screening for bacterial blight and rice leaf blast

Molecular markers were utilized to evaluate the presence of key resistance and quality-related genes across 17 rice genotypes (Table 6). All the tested genotypes carried the *Wax-A* gene, which suggests a link between higher amylose production and maintaining desirable grain quality for national preferences. Twelve among the tested genotypes contained one or more disease resistance genes, that mean more than 70% population already have different levels of resistance against major diseases. Five tested lines have one or more bacterial blight resistance genes i.e., *Xa21*, *Xa4* and *Xa7*, that's about one-third of the tested population. Notably, G2 had

Xa21 in combination with *BADH2* genes. Besides, nine tested genotypes had one or more blast resistance genes (*Pi9*, *Pb1*, *pita*), which represented more than 50% population. Additionally, two (G11 & G12) among the nine blast resistant genotypes had three major blast resistance genes i.e. *Pi9*, *Pb1*, *pita*. The heat tolerance-associated QTL *qHTSF4.1* was identified in G7 and G8. The trait marker *TSV1* which is responsible for tungro resistance, was found in G4 and G13. The screening result demonstrated different level of reactions against BB and blast in artificial inoculation (Table 6). Among the genotypes G1, G3, G15 showed resistant (R) and G4 showed moderately resistant (MR) reaction for Bacterial blight. On the other side, genotypes G11, G12 showed resistant (R) and G2, G3, G7, G8, G15 demonstrated moderately resistant reaction against leaf blast. The genotypes G3 and G15 showed moderately resistant to resistant reaction against both BB and blast pathogen. In summary, different combinations of pyramided lines were generated along with good yield potential and grain quality, which will be used as potential donors for improving resilience against major diseases like bacterial blight, blast and tungro.

Table 6

Screening for Bacterial blight (BB) and Leaf blast along with gene composition in seventeen rice genotypes.

GEN	Lesion length (cm)		BB scoring (0-9)	Remarks	Blast Scoring (0-9)			Remarks	Gene (s)
	Iso#1	Iso#2			R1	R2	R3		
G1	1.5	1	1	R	NA	NA	NA	NA	<i>Wax-A, Xa21, Pb1</i>
G2	4	5	5	MS	4	4	4	MR	<i>Wax-A, Xa21, BADH2</i>
G3	1.5	2	1	R	4	4	3	MR	<i>Wax-A, Xa21, Pb1</i>
G4	1	3	3	MR	NA	NA	NA		<i>Wax-A, tsv1</i>
G5	5	6	5	MS					<i>Wax-A, Xa21, Pb1</i>
G6	NA	NA	NA	NA	4	5	5	MS	<i>Wax-A</i>
G7	NA	NA	NA	NA	3	3	3	MR	<i>Wax-A, Pi9, Pb1, qHTSF4.1</i>
G8	NA	NA	NA	NA	3	3	4	MR	<i>Pb1, qHTSF4.1</i>
G9	NA	NA	NA	NA	NA	NA	NA	NA	<i>Wax-A</i>
G10	NA	NA	NA	NA	NA	NA	NA	NA	<i>Wax-A, Pb1</i>
G11	NA	NA	NA	NA	0	0	1	R	<i>Wax-A, Pi9, Pita, Pb1</i>
G12	NA	NA	NA	NA	1	2	2	R	<i>Wax-A, Pi9, Pita, Pb1</i>
G13	NA	NA	NA	NA	5	5	5	MS	<i>Wax-A, Pb1, TSV1</i>
G14	NA	NA	NA	NA	5	5	5	MS	<i>Wax-A</i>
G15	1	1	1	R	3	3	3	MR	<i>Wax-A, Xa21, Xa4, Xa7</i>
G16	20	25	9	HS	NA	NA	NA	NA	<i>Wax-A</i>
G17	15	12	9	HS	NA	NA	NA	NA	<i>Wax-A</i>

4. Discussion

We tested 17 rice genotypes across nine agro-climatic zones of Bangladesh. The result reveals a significant level of genetic variability with substantial genotype-by-environment (GEI) effect on grain yield and other associated traits. The dominant significant effect of genotype, environment, and GEI demonstrated the importance of cross-environment trials for identifying stable genotypes to maintain across country yield performance. Nowadays most of scientists believe that yield does not rely only on the genotypes but also it is influenced by the environmental heterogeneity like edaphic factors (Mfupe et al., 2023; Huang et al., 2021). The current study demonstrated that the genotypes G1, G2, and G15 performed quite uniformly across all the environments for grain yield. Therefore, the genotypes might be declared as adaptable rice genotypes in case of yield performance (Sandhu et al., 2021). The superior performance of Rangpur and Bhanga suggests these sites provided optimal conditions for expression of yield potential, possibly due to favorable climatic and edaphic factor. To access the inter-location adaptability, the association among the environments was analyzed. The inter-location correlation analysis indicated that certain environments, such as Habiganj and Rangpur, exhibited strong positive associations. The findings suggest similar environmental selection pressures and similar adaptability of rice genotypes. Conversely, weak/poor or negative correlations were

demonstrated between the sites like Kushtia–Habiganj and Cumilla–Rajshahi. The findings reflect high environmental divergence, which can be exploited for identifying location-specific adaptation (Habib et al., 2024). The positive correlations were recorded for growth duration and plant height across the most environments which suggested less influence of those traits by environmental variability compared to grain yield.

PCA and GGE biplot analyses further clarified adaptation patterns of the genotypes. The genotypes G1, G2, G15, and G10 exhibited broad adaptability across the environments due to high mean performance and stability. Identified Mega-environments (ME) prove the heterogeneity of the nine agro-climatic zones and also support out breeding strategies. For example, G7 and G8 exhibited broad adaptation to the first ME (E6, E7, and E9), whereas G5 and G14 showed specific adaptation to E4. Such findings emphasize the potential for both wide and location-specific varietal recommendations, in line with the “which-won-where” concept (Ghazy et al., 2023).

As adaptability not only depends on a single trait like yield, though it's the prime criterion for farmers, and breeders to address the food security. For that's reason, we conducted a multi-trait stability index and Multi-trait Genotype Ideotype distance index (MGIDI) to select the best adaptable line. In the current study, MGIDI provided a holistic evaluation by integrating yield, growth duration, and plant height performance

with stability. The selected genotypes G1, G4, and G17, as closest to the ideotype, indicate their potential for improvement of multiple traits without major complications. This approach enhances selection efficiency by durable productivity with agronomic suitability (Pallavi et al., 2024; Palaniyappan et al., 2024; Al-Mamun et al., 2024).

Stable performance is not enough for a long time adaptation to a variety without attending to the preferences of consumers by maintaining grain quality. That's why grain quality assessment is done to select the best adaptable lines. The results revealed that the most genotypes met or exceeded the national standards of Bangladesh for milling outturn standard (>60%), head rice recovery (>50%), and amylose content (>24%). Genotypes G1, G2, G4, G5, G10, G13, G15, G16, and G17 combined superior milling quality with favorable cooking properties, supporting their dual suitability for market and breeding purposes. Notably, some high-yielding genotypes, such as G3 and G14, were excluded from selection due to suboptimal amylose content, highlighting the need to integrate quality traits into varietal development pipelines.

Nowadays, molecular techniques have become a more reliable approach by discovering high-throughput genotyping for trait selection. The SNP based trait genotyping emerges as a quick and reliable method for different stress breeding like disease resistance. The SNP-based genotyping of current genotypes revealed the successful pyramiding of resistance genes against multiple biotic stresses, including BB (*Xa21*, *Xa4*, *Xa7*), blast (*Pi9*, *Pita*, *Pb1*), and tungro (*TSV1*), along with heat tolerance QTL (*qHTSF4.1*). The combined effect of those genes improves broad-spectrum durable resistance and reduces reliance on chemicals for disease management (Fiyaz et al., 2022). Screening for BB and blast resistances demonstrate range of reactions against BB and blast which support the genotyping results. From screening and genotyping result, it should be concluded that G2, G3 and G15 might be potential elite parents with multiple resistance genes and higher yield for the bacterial disease resistance breeding program. However, the durability of resistance genes remains a challenge due to pathogen evolution, the need for continuous monitoring, and strategic deployment of R-gene combinations (Michelmore et al., 2013).

Overall, the integration of multi-environment yield evaluation, grain quality assessment, and genomic profiling in this study enabled the selection of both broad and specific adaptation of the selected genotypes. The genotypes G1, G10, G2, G15, G4, and G17 emerged as particularly valuable for breeding programs aiming to develop rice cultivars with stable high yield, desirable quality traits, and durable resistance to major diseases. Furthermore, G1 and G4 genotypes have the potential to be good performing genotypes for bacterial blight resistance. In future these genotypes should be incorporated for line

development using genomic selection models to accelerate genetic gain of the breeding programs.

References

- Al. Mamun, S. A., Ivy, N. A., Khan, M. A. I., Rehana, S., Sultana, M. S., Adhikary, S. K., & Islam, M. M. (2024). Genotype selection from azide-induced rice mutants using multitrait genotype-ideotype distance index (MGIDI): Unveiling promising variants for yield improvement. *Advances in Agriculture*, 2024(1), 5719580.
- Bunawan, H., Dusik, L., Bunawan, S. N., & Amin, N. M. (2014). Rice tungro disease: From identification to disease control. *World Appl. Sci. J.*, 31(6), 1221-1226.
- Debnath, P., Chakma, K., Bhuiyan, M. S. U., Thapa, R., Pan, R., & Akhter, D. (2024). A novel multi trait genotype ideotype distance index (MGIDI) for genotype selection in plant breeding: Application, prospects, and limitations. *Crop Design*, 3(4), 100074.
- Dey, S. R., Das, R., & De, M. (2024). A brief review on present status of rice tungro disease: types of viruses, vectors, occurrence, symptoms, control and resistant rice varieties. *Int. J. Adv. Life Sci. Res.*, 7, 15-23.
- Egea-Gilabert, C., Pagnotta, M. A., & Tripodi, P. (2021). Genotype $\times$ environment interactions in crop breeding. *Agronomy*, 11(8), 1644.
- Fiyaz, R. A., Shivani, D., Chaithanya, K., Mounika, K., Chiranjeevi, M., Laha, G. S., ... & Sundaram, R. M. (2022). Genetic improvement of rice for bacterial blight resistance: Present status and future prospects. *Rice Science*, 29(2), 118-132.
- Fukagawa, N. K., & Ziska, L. H. (2019). Rice: Importance for global nutrition. *Journal of nutritional science and vitaminology*, 65(Supplement), S2-S3.
- Ghazy, M. I., Abdelrahman, M., El-Agoury, R. Y., El-Hefnawy, T. M., El-Naem, S. A., Daher, E. M., & Rehan, M. (2023). Exploring genetics by environment interactions in some rice genotypes across varied environmental conditions. *Plants*, 13(1), 74.
- Habib, M. A., Azam, M. G., Haque, M. A., Hassan, L., Khatun, M. S., Nayak, S., ... & Sarker, U. (2024). Climate-smart rice (*Oryza sativa* L.) genotypes identification using stability analysis, multi-trait selection index, and genotype-environment interaction at different irrigation regimes with adaptation to universal warming. *Scientific Reports*, 14(1), 13836.
- Halekoh, U., & Højsgaard, S. (2014). A kenward-roger approximation and parametric bootstrap methods for tests in linear mixed models—the R package pbkrtest. *Journal of Statistical Software*, 59, 1-32.
- Huang, X., Jang, S., Kim, B., Piao, Z., Redona, E., & Koh, H. J. (2021). Evaluating genotype $\times$ environment interactions of yield traits and

- adaptability in rice cultivars grown under temperate, subtropical and tropical environments. *Agriculture*, 11(6), 558.
- Iqbal, J., Yousaf, U., Asgher, A., Dilshad, R., Qamar, F. M., Bibi, S., ... & Haroon, M. (2023). Sustainable rice production under biotic and abiotic stress challenges. In *Sustainable agriculture in the era of the OMICs revolution* (pp. 241-268). Cham: Springer International Publishing.
- Justo, S. B., Mkamilo, H. G., Danga, N. O., Huseni, R., Bakari, F. S. A., Mwakapala, R. A., Lee, S. B. et al. (2024). Genotype and genotype x environment interaction effects on the rice grain yield performance in different agro-ecologies in Tanzania.
- Kassambara, A., & Mundt, F. (2017). *Package factoextra: Extract and visualize the results of multivariate data analyses*. R package version 1.0.7. Foundation for Statistical Computing, Vienna, Austria.
- Kuznetsova, A., Brockhoff, P. B., & Christensen, R. H. (2017). lmerTest package: tests in linear mixed effects models. *Journal of statistical software*, 82, 1-26.
- Latif, M. A., Kayess, O., Hasan, R., & Rahman, L. (2025). Molecular marker assisted gene stacking for multiple diseases resistance in an elite rice cultivar, BRRI dhan48. *Plant Gene*, 42, 100505.
- Lenth, R. (2025). emmeans: Estimated marginal means, aka Least-Squares Means. R package (Version 1.11.2-00002).
- Mendiburu, FD. (2020). *Agricolae: Statistical Procedures for Agricultural Research*. R Package Version 1.3-3. 2020.
- Mfupe, B. P., Msolla, S. N., & Chilagane, L. A. (2023). Genotype and Environment Interaction for yield performance of 12 Advanced Tongil rice genotypes with Doubled Haploid Background under Salts stress conditions in Tanzania. *African Journal of Agricultural Research*, 19(8), 857-867.
- Michelmores, R. W., Christopoulou, M., & Caldwell, K. S. (2013). Impacts of resistance gene genetics, function, and evolution on a durable future. *Annual review of phytopathology*, 51(1), 291-319.
- Olivoto, T., & Lúcio, A. D. C. (2020). metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, 11(6), 783-789.
- Olivoto, T., Lúcio, A. D., da Silva, J. A., Marchioro, V. S., de Souza, V. Q., & Jost, E. (2019). Mean performance and stability in multi-environment trials I: combining features of AMMI and BLUP techniques. *Agronomy journal*, 111(6), 2949-2960.
- Palaniyappan, S., Arunachalam, P., Banumathy, S., & Muthuramu, S. (2024). Introspection of discriminate function analysis and MGIDI selection index for selection to improve yield in rice (*Oryza sativa* L.). *Indian journal of genetics and plant breeding*, 84(02), 202-208.
- Pallavi, M., Prasad, B. M., Shanthi, P., Reddy, V. L. N., & Kumar, A. N. (2024). Multi trait genotype-ideotype distance index (MGIDI) for early seedling vigour and yield related traits to identify elite lines in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 15(1), 120-131.
- Pedrozo, R., Osakina, A., Huang, Y., Nicolli, C. P., Wang, L., & Jia, Y. (2025). Status on genetic resistance to rice blast disease in the post-genomic era. *Plants*, 14(5), 807.
- Sandhu, N., Yadav, S., Catolos, M., Cruz, M. T. S., & Kumar, A. (2021). Developing climate-resilient, direct-seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Frontiers in plant science*, 12, 637488.
- Wang, X., Lee, S., Wang, J., Ma, J., Bianco, T., & Jia, Y. (2014). Current advances on genetic resistance to rice blast disease. *Rice-Germplasm, genetics and improvement*, 195-217.
- Widiarta, I. N., Firmansyah, F., Yunus, M., Apriana, A., Sisharmini, A., Santoso, T. J., ... & Hairmansis, A. (2025). Rice virus disease in Indonesia: epidemiology and varietal resistance. *Phytopathology Research*, 7(1), 11.
- Yan, W., Hunt, L. A., Sheng, Q., & Szlavniks, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop science*, 40(3), 597-605.
- Yan, W., & Kang, M. S. (2002). *GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists*. CRC press.