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Selection of Stable High-yielding Fine Grain Rice (*Oryza sativa* L.) Genotypes Using AMMI, WAASB, and Multi-Trait Stability Indices

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ABSTRACT

Fine-grain rice is highly preferred by consumers due to its superior cooking quality and higher market price. Consequently, the Bangladesh Rice Research Institute (BRRI) has developed several fine-grain rice genotypes through its breeding programs. This study evaluated the yield performance and stability of nine advanced fine-grain rice lines along with two local cultivars and five released varieties across ten agro-ecological zones during the 2023–24 Boro season. Genotype–environment interaction (GEI) for grain yield (GY) and yield-related traits was analyzed using the Additive Main Effects and Multiplicative Interaction (AMMI) model, the Weighted Average of Absolute Scores and Yield (WAASBY) index, and the Multi-Trait Stability Index (MTSI). Combined analysis of variance revealed that genotype, environment, and GEI significantly influenced grain yield and its components. Most traits exhibited moderate to high heritability (0.74–0.97) with selection accuracy above 80%, indicating strong genetic control. Among the tested genotypes, BR17-23-8-2-7B (G6) recorded the highest mean yield, while Bhanga, Faridpur (E3) was identified as the most favorable environment. Stability analyses indicated that G6 ranked highest based on WAASBY (91.45), whereas BRH11-7-17-10B (G7) and BRH9-3-2B (G8) were identified as the most stable genotypes according to MTSI. Overall, G6, G7, and G8 showed superior performance compared with the local and released varieties, suggesting their potential for cultivation and use in breeding programs targeting diverse agro-ecological environments.

1. Introduction

Fine-grain rice (*Oryza sativa* L.) plays an important role in global rice production, particularly in Asia, where it is highly valued for its aesthetic appearance, cooking quality, and suitability for regional dietary preferences (Custodio et al., 2019). These varieties are characterized by slender grains and relatively high amylose content, producing long and non-sticky cooked rice, which is widely preferred in many South

Asian countries, including Bangladesh (Custodio et al., 2016; Alam et al., 2024). Due to their superior grain quality and higher market value, the demand for fine-grain rice is steadily increasing in both domestic and international markets. Consequently, rice breeding programs are increasingly focusing on improving not only grain quality but also yield potential.

However, rice production in Bangladesh faces

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significant challenges due to climate change. Rising temperatures and irregular precipitation patterns are expected to adversely affect rice productivity, particularly through heat and drought stress during critical growth stages (Rahman et al., 2024). These stresses can severely reduce crop yield and threaten national food security. To address these challenges, the Bangladesh Rice Research Institute (BRRI) has played a leading role in developing climate-resilient and high-yielding fine-grain rice varieties. Between 2002 and 2022, several improved fine-grain rice varieties were released, including BRRI dhan81, BRRI dhan88, and BRRI dhan104.

Despite these advances, the performance of rice genotypes often varies considerably across different environments due to genotype $\times$ environment interaction (GEI). Variations in soil properties, climate, and management practices across regions can significantly influence yield performance and stability. Therefore, multi-environment trials (METs) are essential for evaluating genotype adaptability and identifying stable and high-performing cultivars across diverse agro-ecological conditions.

Several statistical approaches have been widely used to analyze GEI and genotype stability in METs. Among them, the Additive Main Effects and Multiplicative Interaction (AMMI) model, the Weighted Average of Absolute Scores Biplot (WAASB), and the Multi-Trait Stability Index (MTSI) are commonly applied to evaluate genotype performance and stability across environments (Gauch, 1992; Gauch and Zobel 1996; Olivoto et al., 2019). While AMMI and WAASB primarily focus on yield stability, MTSI enables simultaneous selection of genotypes based on multiple traits, thereby improving the efficiency and accuracy of genotype selection in breeding programs.

Although several fine-grain rice varieties have been developed in Bangladesh, limited studies have

comprehensively evaluated the stability and multi-trait performance of newly developed advanced lines across diverse agro-ecological zones. A clear understanding of genotype stability and adaptability under different environmental conditions is essential for identifying superior genotypes suitable for large-scale cultivation.

Therefore, the present study aimed to evaluate advanced fine-grain rice genotypes developed by the Bangladesh Rice Research Institute (BRRI) across multiple agro-ecological zones in Bangladesh during the 2023–2024 Boro season. Specifically, the study sought to assess genotype–environment interactions for grain yield and related traits and to identify stable and high-performing genotypes suitable for diverse environments.

2. Materials and methods

2.1. Experiment sites

The field experiment was conducted at ten locations representing major rice-growing regions of Bangladesh during the 2023–24 Boro season. The experimental sites were selected collaboratively by researchers from the Adaptive Research Division (ARD) and regional stations of the Bangladesh Rice Research Institute (BRRI). The geographical distribution of the study locations is presented in Fig. 1, which was prepared using QGIS version 3.38.3. Information on latitude, longitude, soil texture, and elevation of the experimental sites is provided in Table 1. Meteorological data, including average maximum temperature, relative humidity, and total rainfall during the growing period, were obtained from the Plant Physiology Division of the Bangladesh Rice Research Institute (BRRI) and the Bangladesh Meteorological Department (BMD). These climatic variables are illustrated in Fig. 2.

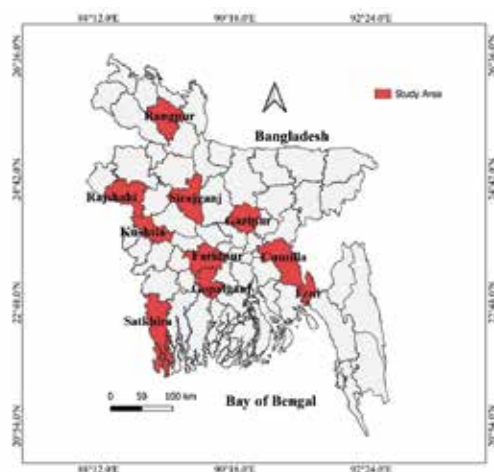


Fig. 1. Location of the study area in different districts of Bangladesh.

Table 1

Geographical, soil, and climatic characteristics of the ten environments used for multi-location trials of fine-grain rice during the 2023-24 Boro season.

Locations	Codes	Latitude	Longitude	Elevation (m)	Soil texture
Paba, Rajshahi	E1	24°43'57"N	88°66'22"E	17	Loam- clay
Sadar, Kushtia	E2	23°91'52"N	89°09'65"E	27	Clay-loam
Bhanga, Faridpur	E3	23°39'79"N	89°99'12"E	11	Clay loam-sandy loam
Kamarkhanda, Sirajganj	E4	24°39'42"N	89°63'74"E	13	Clay loam
Sadar, Satkhira	E5	22°73'07"N	88°98'69"E	3	Silty clay
Debidwar, Cumilla	E6	23°61'23"N	90°97'02"E	14	Grey loam - dark grey clay
Mithapukur, Rangpur	E7	25°52'13"N	89°30'19"E	34	Loam- clay loam
Sonagazi, Feni	E8	22°82'49"N	91°39'50"E	5	Silty loam-Clay loam
Sadar, Gopalganj	E9	22°96'08"N	89°82'15"E	3.1	Clay loam-sandy loam
Gazipur	E10	23°99'17"N	90°40'18"E	34	Silty clay loam

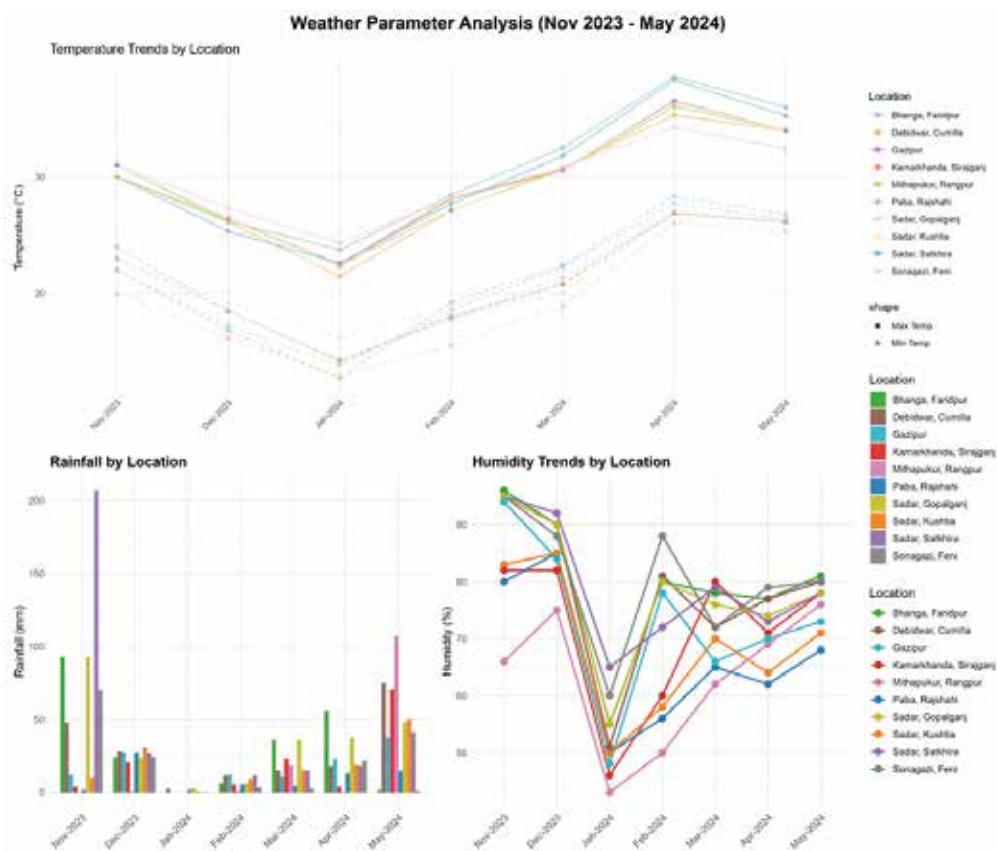


Fig. 2. Weather conditions of the selected regions during 2023-24 Boro season (a) Temperature OC; (b) Total rainfall (mm); (c) Relative humidity (%).

2.2. Plant materials

Seeds of the genotypes along with their chemical and physical properties were received from the Plant Breeding Division (PBD), BRRI for evaluating yield

potentiality and adaptability at farmers' field in different agro-ecological zones. Chemical and physical properties of the selected genotypes were analyzed except G4 and G14 at the Grain Quality and Nutrition (GQN) division, BRRI which are given in the Table 2.

Table 2

Chemical and physical properties of the genotypes.

Genotypes code	Alkali spreading value	Amylose content%	Protein content%	Elongation ratio	Imbibition ratio	Milling outturn%	Head rice yield%	L/B ratio	Size & shape
G1	6.9	25.7	8.1	1.5	3.9	70	57	3.3	LS
G2	3.2	25.0	8.1	1.5	4.8	70	56	3.3	LS
G3	7.0	25.4	8.0	1.7	4.8	69	61	3.4	LS
G4	-	-	-	-	-	-	-	-	MS
G5	5.2	24.0	7.1	1.4	3.9	71	56	3.6	MS
G6	4.1	19.2	8.2	1.5	4.3	72	60	3.0	MB
G7	3.7	19.1	7.7	1.4	3.9	72	60	3.0	MB
G8	3.6	19.0	7.6	1.4	4.3	72	62	3.1	MS
G9	3.7	19.1	7.3	1.5	4.5	72	59	3.0	MB
G10	3.1	25.4	7.7	1.4	4.3	70	61	3.1	LS
G11	3.6	25.0	8.1	1.6	4.8	62	60	2.8	SB
G12	7.0	27.0	9.0	1.4	4.3	62	43	3.3	LS
G13	7.0	27.1	8.6	1.4	3.9	70	56	4.5	Ex-LS
G14	-	-	-	-	-	-	-	-	LS
G15	4.8	26.0	9.8	1.3	4.5	71	60	3.1	LS
G16	4.2	25.6	9.0	1.4	4.7	69	43	3.4	LS

L/B Ratio: Length/Breadth Ratio, LS: Long Slender, Ex-LS: Extra-Long Slender, MS: Medium Slender, MB: Medium Bold, SB: Short Bold, G1: BR10645-6-4-8-1-2, G2: BR10646-3-2-2-4-3, G3: BR10648-12-1-3-4-1, G4: BRH15-24-7B, G5: BR9392-1-7-5B, G6: BR17-23-8-2-7B, G7: BRH11-7-17-10B, G8: BRH9-3-2B, G9: BRH13-9-5-2B, G10: Zira, Nachol, G11: Katari, Shibganj, G12: BRRI dhan104, G13: BRRI dhan107, G14: BINA dhan25, G15: BRRI dhan 88, G16: BRRI dhan81.

2.3. Experimental design and crop management

The field experiment was laid out as a randomized complete block design (RCBD) with three replications, resulting in 48 plots per site. Each plot measured 20 m² (4 m × 5 m). For the trial, 300 g of seeds from each genotype were sown in seedbeds, and 35–40-day-old seedlings were manually uprooted and transplanted into the main plots between the second and last week of November 2023. Plant spacing was maintained at 25 cm within rows and 15 cm between rows, with 2–3 seedlings per hill.

Experimental fields were plowed mechanically and prepared following recommended cultivation practices of the Bangladesh Rice Research Institute (BRRI) throughout the growing season (Bangladesh Rice Knowledge Bank, n.d.). Fertilizers were applied at the rate of 138 (300 kg Urea): 20 (100 kg TSP): 83 (165 kg MP): 20 (112 kg Gypsum): 4 (11 kg Zn SO4) kg/ha

NPKSZn in the trial. All phosphorus, potassium, sulfur, and zinc were applied during final land preparation, while nitrogen was split into three equal applications at 10, 30, and 40–50 days after transplanting (DAT). Irrigation was applied as needed, and weeds, insects, and other pests were controlled using recommended herbicides, insecticides, and pesticides.

2.4. Assessed traits

Data for the assessed traits were collected at flowering, maturity, and harvest stages. The dates of seeding, transplanting, 50% flowering, and 80% maturity were recorded to calculate the growth duration (GD). Plant height was measured from the soil surface to the tip of the panicle on 10 randomly selected plants per plot, and the values were averaged. The crop was harvested from a 3 m × 3 m area in the center of each plot, excluding border rows, after

approximately 80% of the grains had matured. Grain yield (GY) was adjusted to 12% moisture content and converted to tons per hectare (t/ha).

For the estimation of panicle per square meter (PPM), a 1m × 1m area was marked, and the number of panicles was counted within the marking. Ten panicles were randomly selected outside the marking area for GY, and the number of filled and unfilled grains was counted. The average number of filled and unfilled grains was calculated for each panicle. Thousand-grain weight (TGW) was determined in gm by counting and weighing 1000 grains (manually or automatic counting machine). Sterility percentage (STR) was calculated using the formula: STR = (Total unfilled grains / (Total filled grains + Total unfilled grains)) × 100.

2.5. Statistical analyses

Statistical analysis was conducted using Statistics 10 and RStudio console with R version 4.4.1 (R Core Team, 2020). Combined ANOVA analysis and mean separation for genotypes, environments, and genotype-environment interactions (GEI) were performed using Statistics 10. The least significant difference (LSD) test was measured to distinguish mean values at a significance level of $p < 0.05$. Genetic parameters were calculated using the “metan” package in R statistical software. Principal component analysis (PCA) was computed to identify interrelationships among the study traits using the “factoextra” and “FactoMineR” packages in R. Additive main effects and multiplicative interaction (AMMI), Weighted Average of the Absolute Scores biplot (WAASB) and superiority index WAASBY statistical analyses and the Multiple trait stability index (MTSI) analysis were carried out in R software 4.4.1 using the “metan” package (Team, 2020; Olivoto et al. 2019).

AMMI was used to decompose GEIs into principal components, with the analysis performed according to the following equation:

$$y_{ij} = \mu + \alpha_i + \tau_j + \sum_{k=0}^p \lambda_k a_{ik} t_{jk} + \rho_{ij} + \varepsilon_{ij}$$

where, y_{ij} is GY response of the i -th genotype in the j -th environment; μ is grand mean; α_i and τ_j represent genotype effect i -th and the environment effect j -th; $\sum_{k=0}^p \lambda_k a_{ik} t_{jk} + \rho_{ij} + \varepsilon_{ij}$ is model of multiplicative genotype × environment interaction effect, which λ_k is singular value for the k -th interaction principal component axis (IPCA), a_{ik} is i -th genotype eigenvector for axis k , t_{jk} is the j -th environment eigenvector for axis k ; ρ_{ij} stands for the residual not explained by the

IPCA used in the model; and ε_{ij} is error relevant to the model (Olivoto et al., 2019).

The function `waasb()` computes the Weighted Average of the Absolute Scores considering all possible IPCA from the Singular Value Decomposition of the BLUPs for genotype-vs-environment interaction effects obtained by an Linear Mixed-effect Model (Olivoto et al., 2019), as follows:

$$WAASBi = \sum_{k=1}^p |IPCA_{ik} \times EPk| \sum_{k=1}^p |EPk|$$

where $WAASBi$ is the weighted average of absolute scores of the i th genotype; $IPCA_{ik}$ is the scores of the i th genotype in the k th IPCA; and EPk is the explained variance of the k th PCA for $k = 1, 2, \dots, p = \min(g-1, e-1)$.

The `waasby` index is used for genotype ranking considering both the stability (`waasb`) and mean performance (y) based on the following model (Olivoto, Alessandro D. C. Lúcio, et al., 2019).

$$waasby_i = [(rY_i \times \theta Y) + (rW_i \times \theta W)] / (\theta Y + \theta W)$$

where `waasbyi` is the superiority index for the i -th genotype; rY_i and rW_i are the rescaled values (0-100) for the response variable (y) and the stability (WAAS or WAASB), respectively; θY and θW are the weights for mean performance and stability, respectively.

The third and last step was the estimation of the multi-trait stability index (MTSI), according to Equation (Olivoto et al., 2019):

$$MTSI_i = [\sum_{j=1}^f (F_{ij} - F_j)^2]^{0.5}$$

where the MTSI is the multi-trait stability index for the i th genotype, F_{ij} is the j th score of the i th genotype, and F_j is the j th score of ideotype. The genotype with the lowest MTSI is then closer to the ideotype and therefore presents a high MPE for all analyzed variables.

3. Results

3.1. Analysis of variance

A combined analysis of variance (ANOVA) was performed for seven agronomic traits of sixteen genotypes evaluated across ten environments during the 2023–24 Boro season (Table 3). The results revealed highly significant variation ($p \leq 0.001$) among replications (R), genotypes (G), environments (E), and genotype × environment interactions (GEI) for all traits. This indicates that genetic, environmental, and their interaction effects significantly influenced grain yield and its related traits.

Table 3

Combine ANOVA of yield and its contributing traits on the basis of mean sum of squares of sixteen genotypes during the Boro 2023-24 season.

Source of variation	df	Mean sum of squares						
		GY	GD	PHT	TGW	PPM	GPP	STR
R	2	0.1035***	1.2***	43.21***	2.1143***	630***	1419.7***	54.222***
G	15	4.67***	328.13***	2295.44***	94.3428***	15944***	8968.3***	818.248***
E	9	24.1025***	1940.71***	1691.7***	36.2097***	111944***	20299.5***	655.815***
GEI	135	1.2359***	53.45***	76.12***	6.3023***	6968***	1508.4***	145.884***
Error	318	0.2038***	0.28***	8.72***	1.0027***	353***	264.6***	26.223***
Total	479							

R: Replication, G: Genotype, E: Environment/ locations, GEI: Genotype-environment interaction, *** significant at 0.1% level of probability, df: Degrees of freedom, GY: Grain yield, GD: Growth duration, PHT: Plant height, TGW: Thousand grain weight, PPM: Panicle per m², GPP: grains per panicle, STR: sterility percentage. *** indicates significance at $p \leq 0.001$.

3.2. Mean performance of yield and its attributing traits of all rice genotypes

The violin plot (Fig. 3) illustrated the variation in grain yield (GY) across genotypes and environments. Among the sixteen fine-grain rice genotypes, G6 recorded the highest mean GY (7.44 t/ha), followed closely by G9 (7.33 t/ha), G8 (7.27 t/ha), and G7 (7.24 t/ha), which were statistically similar. Growth duration (GD) ranged from 144 days (G15 and G16) to 156 days (G13), while plant height (PHT) varied between 91 cm (G5) and 128 cm (G14). Thousand

grain weight (TGW), an indicator of grain size, was highest in G13 (24.98 g), whereas the finest grains were observed in G6 (17.92 g). For other yield-contributing traits, the highest panicle number per m² (PPM) was recorded in G4 (342), and the highest grains per panicle (GPP) were observed in G8 (161). Sterility percentage (STR) ranged from 16.88% (G11) to 32.67% (G8). Overall, G6, G7, G8, and G9 combined high grain yield with favorable yield-related traits, indicating their potential for cultivation across diverse environments (Table 4).

Table 4

Mean values of yield and its attributing traits of sixteen fine grain rice genotypes.

Genotypes	GY (t/ha)	GD (days)	PHT (cm)	TGW (g)	PPM	GPP	STR
G1	6.86E	153D	106D	21.46BCD	272GH	124DE	17.06HI
G2	6.49FG	153CD	111B	21.939B	285EF	105G	21.94F
G3	6.02H	149G	106D	21.06DE	276FGH	114FG	17.35HI
G4	7.02CDE	149G	92I	18.84GH	342A	122DE	26.45DE
G5	6.96DE	149G	91I	20.06F	334A	117EF	26.21DE
G6	7.44A	148H	97G	17.92I	323B	139C	29.48BC
G7	7.24ABC	149G	99F	19.01G	322B	151B	28.34CD
G8	7.27AB	150F	99F	18.56GH	322B	161A	32.67A
G9	7.33AB	149F	99F	18.40HI	311C	150B	32.01AB
G10	6.48FG	150E	102E	21.08DE	310C	112FG	19.21GHI
G11	6.38G	154B	108C	20.60E	298D	128D	16.88I
G12	6.93DE	154B	99F	21.70BC	317BC	106G	21.59FG
G13	7.11BCD	156A	105D	24.98A	293DE	110FG	21.27FG
G14	6.61F	153C	128A	21.02DE	268H	142C	25.62E
G15	6.99DE	144I	95H	21.31CD	310 C	115EF	19.53FGH
G16	6.57FG	144I	98F	21.64BC	278FG	127D	21.36FG
CV%	6.58	0.35	2.89	4.86	6.18	12.85	21.74
LSD _{0.05}	0.23	0.27	1.5	0.51	9.54	8.26	2.6

LSD: Least significant differences among mean values at 5% level of significant, CV: Coefficient of variations, G1: BR10645-6-4-8-1-2, G2: BR10646-3-2-2-4-3, G3: BR10648-12-1-3-4-1, G4: BRH15-24-7B, G5: BR9392-1-7-5B, G6: BR17-23-8-2-7B, G7: BRH11-7-17-10B, G8: BRH9-3-2B, G9: BRH13-9-5-2B, G10: Zira, Nachol, G11: Katari, Shibganj, G12: BRRI dhan104, G13: BRRI dhan107, G14: BINA dhan25, G15: BRRI dhan 88, G16: BRRI dhan81, GY: Grain yield, GD: Growth duration, PHT: Plant height, TGW: Thousand grain weight, PPM: Panicle per m2, GPP: grains per panicle, STR: sterility percentage.

On the other hand, Table 5 exhibits the mean values of eight yield and yield-contributing traits across ten different locations during the Boro 2023-24 growing season. Fig. 3 displayed that the highest GY was recorded in E3 (Bhanga, Faridpur) at 8.29 t/ha. The second highest grain yield was found 7.49 t/ha in both E7 (Mithapukur, Rangpur) and E10 (West byde, BRRI, Gazipur) environments. The poorest performance was observed in E5 (5.81 t/ha) followed by E2 (6.20 t/ha) and E8 (6.14 t/ha) in terms of grain yield. The similar result also observed for growth duration. These two environments E2 and E8 also displayed the lowest growth duration 143 days and 144 days, respectively. While, the longest growth

duration was recorded in E4 (162 days) followed by E7 (157 days). The tallest PHT was observed in E1 (Paba, Rajshahi) at 112 cm, whereas E9 (Kamarkhanda, Sirajganj) recorded the shortest at 87.61 cm. In case of TGW, E4 (Kamarkhanda, Sirajganj) had the highest value at 21.67 g which was statistically similar to 21.49 g found at E5 (Sadar, Satkhira). The lowest TGW was observed in E1 region. E3 showed the highest PPM at 381, whereas E2 had the lowest at 264. E7 region had the highest GPP at 159 and the minimum result was found in E4 region. Furthermore, the highest STR was recorded in E1 at 30.86%, while E4 had the lowest at 19.17%.

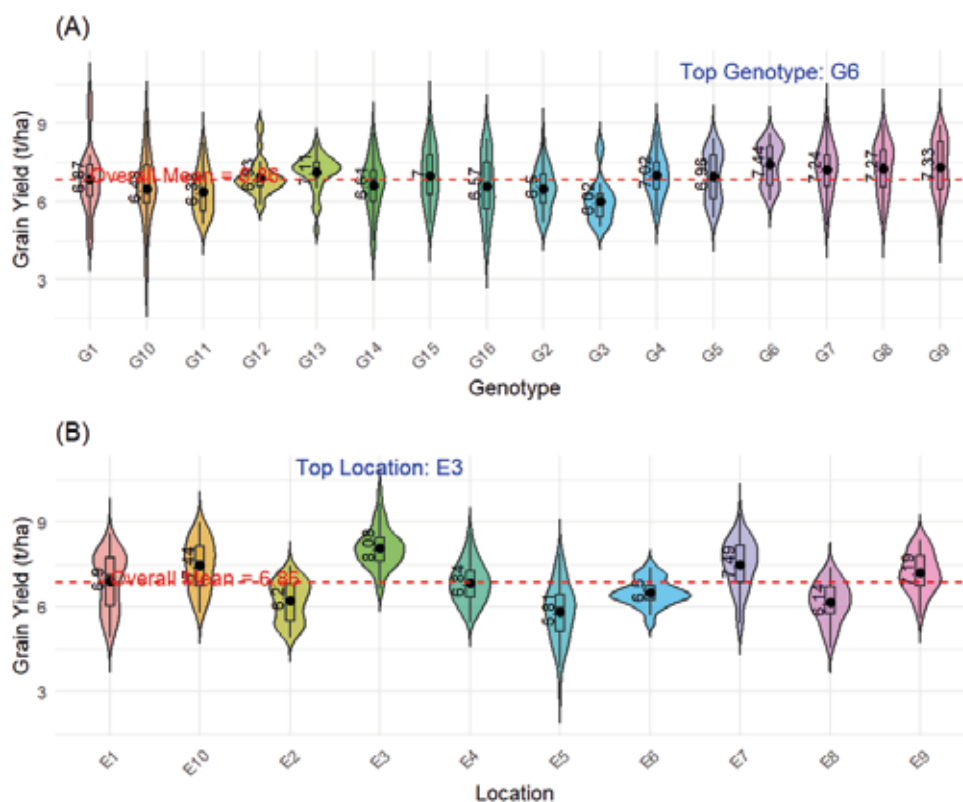


Fig. 3. Violin plots of mean grain yield results (A) Mean grain yield (t/ha) of the genotypes (B) Mean grain yield (t/ha) of all locations. G1: BR10645-6-4-8-1-2, G2: BR10646-3-2-2-4-3, G3: BR10648-12-1-3-4-1, G4: BRH15-24-7B, G5: BR9392-1-7-5B, G6: BR17-23-8-2-7B, G7: BRH11-7-17-10B, G8: BRH9-3-2B, G9: BRH13-9-5-2B, G10: Zira, Nachol, G11: Katari, Shibganj, G12: BRRI dhan104, G13: BRRI dhan107, G14: BINA dhan25, G15: BRRI dhan 88, G16: BRRI dhan81, E1: Paba, Rajshahi, E2: Sadar, Kushtia, E3: Bhanga, Faridpur, E4: Kamarkhanda, Sirajganj, E5: Sadar, Satkhira, E6: Debidwar, Cumilla, E7: Mithapukur, Rangpur, E8: Sonagazi, Feni, E9: Sadar, Gopalganj, E10: BRRI Westbyde, Gazipur.

Table 5

Locational mean values of yield and yield attributing traits of PQR genotypes during Boro 2023-24 season.

Environments	GY (t/ha)	GD (days)	PHT (cm)	TGW (g)	PPM	GPP	STR
E1	6.89D	149F	112A	19.56EF	283E	146B	30.86A
E2	6.20F	143J	103F	20.17CD	264F	115E	22.70DE
E3	8.08A	153D	107B	19.20F	381A	141BC	28.29B
E4	6.84D	162A	106C	21.67A	315C	101F	19.17F
E5	5.81G	152E	97H	21.49A	313C	128D	23.28CD
E6	6.50E	145H	95I	20.51C	217G	119E	20.73EF
E7	7.49B	157B	105D	21.27AB	276E	159A	22.36DE
E8	6.14F	144I	102G	21.28AB	315C	92G	25.19C
E9	7.19C	146G	92J	20.99B	371B	137C	19.70F
E10	7.44B	155C	104E	19.85DE	302D	128D	23.32CD
LSD _{0.05}	0.18	0.21	1.19	0.4	7.55	6.53	2.06

LSD: least significant differences among mean values at 5% level of significant, E1: Paba, Rajshahi, E2: Sadar, Kushtia, E3: Bhanga, Faridpur, E4: Kamarkhanda, Sirajganj, E5: Sadar, Satkhira, E6: Debidwar, Cumilla, E7: Mithapukur, Rangpur, E8: Sonagazi, Feni, E9: Sadar, Gopalganj, E10: BRRI Westbyde, Gazipur. GY: Grain yield, GD: Growth duration, PHT: Plant height, TGW: Thousand grain weight, PPM: Panicle per m², GPP: grains per panicle, STR: sterility percentage.

3.3. Genetic parameters of studied traits

Genetic parameters for seven yield and yield-contributing traits of sixteen fine-grain rice genotypes across ten environments were estimated using a linear mixed model (Table 6). The phenotypic variance (σ_p^2) was highest for panicle number per m² (PPM, 2854), followed by grains per panicle (GPP, 927), indicating substantial variation among genotypes for these traits. Broad-sense heritability (h^2_b), which estimates the proportion of total phenotypic variance attributable to genetic factors, ranged from 0.11 (PPM) to 0.71 (plant height), while mean-based heritability (h^2_{mg}), calculated across environments, was higher, ranging from 0.56 to 0.97, reflecting strong genetic control for most traits.

The coefficient of determination of genotype $\times$ environment interaction effects (GEI r^2) varied between 0.22 and 0.77, suggesting that some traits

were more influenced by environmental interactions than others. Selection accuracy (SA) was generally high (>0.80) for all traits, except PPM (0.75), indicating reliable genotype selection. Genotype-environment correlation (r_{ge}) was strongest for growth duration (GD, 0.99) and PPM (0.86), while grain yield (GY) showed moderate correlation (0.62), highlighting the influence of environment on yield. The ratio of genotypic to residual coefficient of variation (CV_g / CV_r) ranged from 0.74 to 5.75, with the highest value observed for GD, indicating that genotypic variation was relatively greater than residual variation for certain traits.

Overall, the analysis indicates that traits such as plant height, thousand-grain weight (TGW), and GD are largely under genetic control, while traits like PPM and GPP are more affected by environmental interactions, providing useful insights for selection in multi-environment trials.

Table 6

Genetic parameters of yield and its attributing traits of sixteen fine grain rice genotypes studied under 10 locations in LMM.

Parameters	GY	GD	PHT	TGW	PPM	GPP	STR
σ_p^2 (%)	0.665	27.2	105	5.72	2854	927	87.9
h^2_b	0.17	0.34	0.71	0.51	0.11	0.27	0.26
GEI r^2	0.52	0.65	0.22	0.31	0.77	0.45	0.46
h^2_{mg}	0.74	0.84	0.97	0.93	0.56	0.83	0.82
SA	0.86	0.92	0.98	0.97	0.75	0.91	0.91
r_{ge}	0.62	0.99	0.73	0.63	0.86	0.62	0.61
CV_g	4.93	2.01	8.41	8.32	5.69	12.5	20.1
CV_r	6.65	0.349	2.83	4.91	6.14	12.8	21.4
CV ratio	0.74	5.75	2.97	1.69	0.93	0.98	0.94

σ_p^2 : Phenotypic variance, h^2_b : Broad sense heritability, GEI_{r2} : Coefficient of determination of the interaction effects, h^2_{mg} : Mean basis heritability, SA: Selection accuracy, r_{ge} : Genotype-environment correlation, CVg: genotypic coefficient of variation, CVr: residual coefficient of variation, CV ratio: ratio of CV_g and CV_r , GY: Grain yield, GD: Growth duration, PHT: Plant height, TGW: Thousand grain weight, PPM: Panicle per m^2 , GPP: grains per panicle, STR: sterility percentage.

3.4. Principal component analysis (PCA)

Principal component analysis (PCA) was conducted to explore patterns of variation and relationships among seven yield and yield-contributing traits by reducing data dimensionality. Seven principal components (Dim-1 to Dim-7) were initially identified, with Dim-1 and Dim-2 explaining the majority of the variance (49.1%; Fig. 4), indicating that two components capture nearly half of the variability among genotypes. In the PCA biplot, traits located close to each other reflect positive correlations, whereas traits positioned in opposite directions indicate negative correlations.

Dim-1 was primarily influenced by grain yield (GY), grains per panicle (GPP), panicles per m^2 (PPM), thousand grain weight (TGW), and sterility percentage (STR). The positive association of GY with PPM and GPP suggests that genotypes with more panicles and higher grain number per panicle tend to produce higher yields. Conversely, the negative correlation

between GY and TGW indicates a trade-off between grain size and overall yield under the tested environments. Dim-2 was mainly associated with plant height (PHT) and growth duration (GD), reflecting differences in vegetative growth patterns and maturity among genotypes. Genotypes with taller plants and longer growth duration tend to have different resource allocation strategies compared to early-maturing or shorter genotypes.

The color gradient in the biplot highlights trait contributions, with red representing the highest contribution (GD) and blue the lowest (PPM), further emphasizing that growth duration strongly differentiates genotypes along Dim-2, while yield components largely drive variation along Dim-1. These results indicate that selection for high-yielding genotypes should consider both panicle and grain number, while accounting for the negative association with grain size. Similarly, genotypes with favorable combinations of plant height and growth duration can be targeted for adaptation to specific environments.

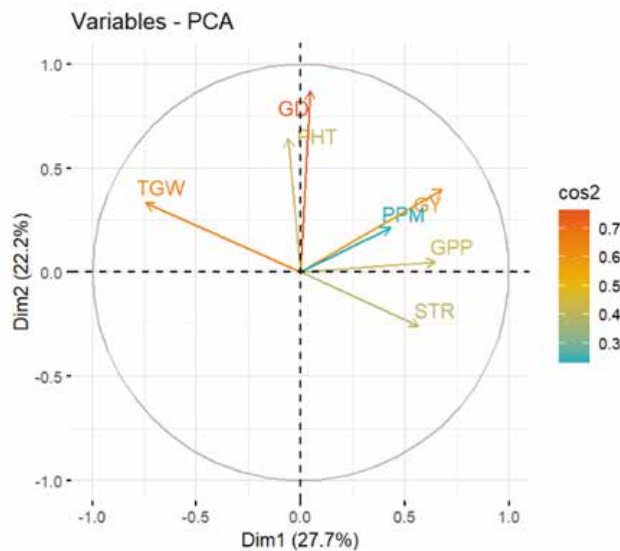


Fig. 4. Principal component analysis of yield and its attributing traits for Dim1 and Dim2.

3.5. Mean yield performance for GEI

Fig. 5 illustrates the GEI effects on GY using heatmap. The columns and rows represent the genotypes and environments, respectively. The color gradient ranging from purple to yellow indicating the lower to higher grain yield. Variability in GY is evident across E and G, with significant differences observed in

mean yield values. The highest GY was recorded in the E3 region for the G1 genotype, reaching 9.7 t/ha, followed by G7 at 8.7 t/ha in E7 region and G15 at 8.7 t/ha in E3 region. Conversely, the lowest yield was observed in G10, measuring 3.9 t/ha in the E5 region followed by G16 and G14 with 4.5 t/ha in the same environment.

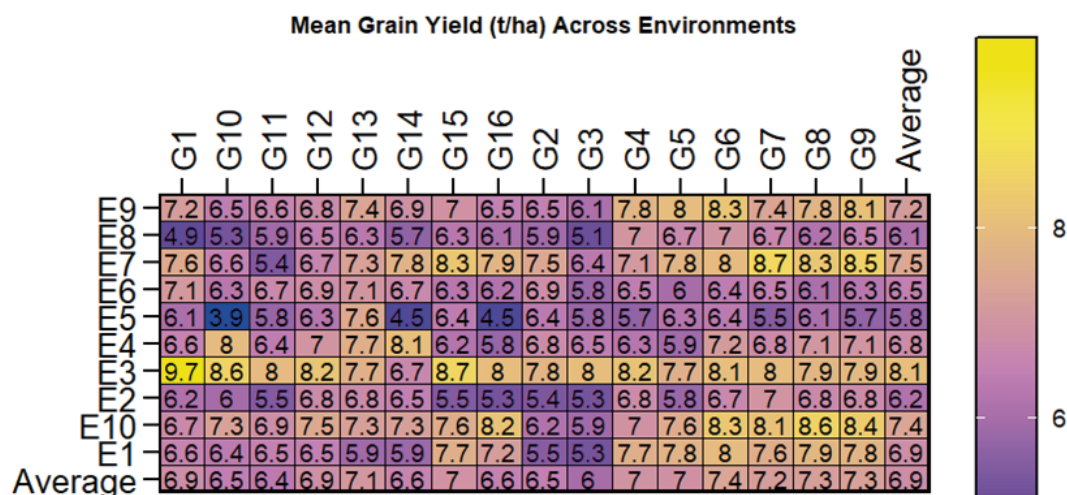


Fig. 5. The mean performance of grain yield (t/ha) of studied sixteen (16) rice genotypes across ten (10) environments during the 2023-24 Boro season. G1: BR10645-6-4-8-1-2, G2: BR10646-3-2-4-3, G3: BR10648-12-1-3-4-1, G4: BRH15-24-7B, G5: BR9392-1-7-5B, G6: BR17-23-8-2-7B, G7: BRH11-7-17-10B, G8: BRH9-3-2B, G9: BRH13-9-5-2B, G10: Zira, Nachol, G11: Katari, Shibganj, G12: BRRI dhan104, G13: BRRI dhan107, G14: BINA dhan25, G15: BRRI dhan 88, G16: BRRI dhan81, E1: Paba, Rajshahi, E2: Sadar, Kushtia, E3: Bhanga, Faridpur, E4: Kamarkhanda, Sirajganj, E5: Sadar, Satkhira, E6: Debidwar, Cumilla, E7: Mithapukur, Rangpur, E8: Sonagazi, Feni, E9: Sadar, Gopalganj, E10: BRRI Westbyde, Gazipur.

3.6. AMMI analysis of variance

Table 7 presents the AMMI ANOVA, highlighting the contributions of different sources of variation to the total sum of squares (TSS) observed in the selected genotypes dataset for GY. The analysis of variance revealed that GY was significantly affected by E, G and GEI, with a p-value less than 0.001. The majority of the

total sum of squares (TSS) in the model was attributed to E (216.98), followed by GEI (166.89) and G (70.01). The interaction of the first two principal components (PCs) accounted for approximately 61% of the variance. Among the PCs of the AMMI ANOVA, the first six PCs were significant at ≤ 0.01 probability, contributing to a total of 95.9% of the variance.

Table 7

AMMI analysis of variance of rice grain yield (GY) (t/ha) for sixteen rice genotypes studied under 10 locations during 2023-24 Boro season.

Source	Df	TSS	MSS	Proportion	Accumulated
E	9	216.98	24.11***	-	-
R (E)	20	2.69	0.13	-	-
G	15	70.01	4.67***	-	-
GEI	135	166.89	1.24***	-	-
PC1	23	63.03	2.74***	37.8	37.8
PC2	21	38.69	1.84***	23.2	61.0
PC3	19	26.87	1.41***	16.1	77.1
PC4	17	17.64	1.04***	10.6	87.6
PC5	15	7.67	0.51**	4.6	92.2
PC6	13	6.16	0.47**	3.7	95.9
PC7	11	3.70	0.34	2.2	98.1
PC8	9	2.43	0.27	1.5	99.6
PC9	7	0.69	0.10	0.4	100
Residuals	300	62.34	0.21	-	-
Total	614	685.79	1.12	-	-

E: Environment/ location, R: Replication, G: Genotype, GEI: Genotype-environment interaction, *** significant at 0.001% level of probability, ** significant at 0.01% level of probability, df: Degrees of freedom, TSS: Total sum of square, MSS: Mean sum of square, PC: Principal component.

3.7. Additive main effects and multiplicative interaction (AMMI1 & AMMI2) biplot

Additive main effects and multiplicative interaction 1 (AMMI 1) depicts the biplot abscissa and ordinate illustrating the first principal component analysis (PCA1) and main effects of Grain yield (GY) (Figure 6). The first PCA scores were plotted against the second PCA scores to generate the biplot for the environments and genotypes when compared (Figure 6). The AMMI 2 revealed the importance of PCA2 scores along the first PCA in explaining the complexity of GEI involving significant multi-environments and identifying the adaptation of genotypes. The 16 accessions tested in the ten environments allowed us to understand the GEI using AMMI through the trait of GY. Similarities and dissimilarities among the 16 accessions were observed on the basis of the GEI study. In this study, the PCA values interactions accounted for 61% of the $G + G \times$

E interaction variation for the GY, shown in the AMMI2 biplot. The genotypes were closer to origin indicating zero scores; at the same time, those placed at the right side of the center of the axis had higher performance than the accessions found at the left-hand side. It appears that genotypes G4, G14 were closer to the origin in AMMI1 biplot, but genotypes G3, G9, G13, and G16 were far from the origin. In Figure 5, G6, G7, G8, G9, G12 and G13 located on the right side of the center of the axis had higher yields than G2, G3, G10, G11 and G16. On the other hand, in AMMI 2 biplot, G12 was close to the origin, while G5, G8, G13 and G14 were far from the center. Environment E3, E6 and E7 had practically low contribution on the first PCA1, while E4, E5 and E10 had a high score on the first and second PCAs for grain yield. For grain yield, it was observed that genotypes G8 and Environments E7 and E10 had a significant effect on the GE interaction.

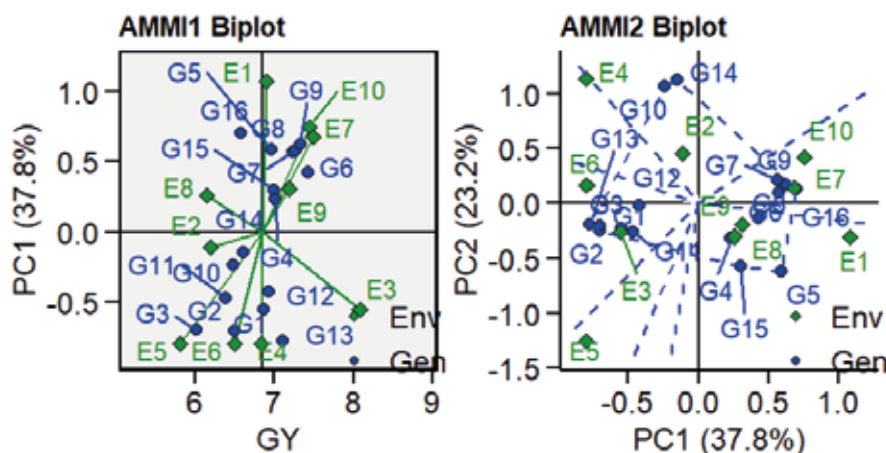


Fig. 6. Additive main effects and multiplicative interaction (AMMI) 1 & 2 biplots based on PC1 and PC2 illustrating $G \times E$ interactions of the 16 fine grain rice accessions under ten sites for GY. PC1: Principal Component 1, PC2: Principal Component 2.

3.8. Genotype Stability and Ranking Based on WAASB and WAASBY

In this study, the stability and performance of 16 rice genotypes across ten environments for the 2023–24 Boro seasons were also evaluated using Weighted Average of Absolute Scores from BLUPs (WAASB) and Weighted Average of Absolute Scores from the BLUPs and Yield (WAASBY) indices (Table 8). The WAASB index measures stability, with lower values indicating greater stability. While the WAASBY index combines both yield and stability, where higher

values are preferable. The WAASB biplots and WAASBY graphs (Fig. 7) illustrate the stability and performance of the selected genotypes across environments.

In the WAAS biplot, all entries were divided into four quadrants. The quadrant I considered unstable genotypes or environments with high discrimination ability, and with productivity below the grand mean. The second quadrant (II) consists of unstable but highly productive genotypes. Genotypes within quadrant III have low productivity, but can be considered stable due to the lower values of WAASB.

The genotypes within the quadrant IV are highly productive and broadly adapted due to the high magnitude of the response variable and high stability performance (lower values of WAASB). Genotypes G6, G4, G9, G8, G7, and G12 were positioned in Quadrant IV, indicating high discriminative ability and high representativeness, with WAASB values ranging between 0.24 and 0.32 (Table 8). Among them, G12 had the lowest WAASB value. Conversely, the highest WAASB score (0.47) was found for G10, which was positioned in Quadrant I along with G2 and G14, indicating poor and unstable performance. However, G13 displayed a high WAASB value (0.46), second only to G10, suggesting instability despite its high yield. Furthermore, G3 and G11 showed low discriminating

ability across locations and were positioned in Quadrant III.

The WAASBY plot (Fig. 7) ranked genotypes based on combined yield and stability, categorizing them as above-average (blue) or below-average (red) performers. From the figure 7B, it observed that 7 out of 16 genotypes performed above average. G6 ranked highest (WAASBY = 91.45), followed by G12, G4, G8, G9, and G7 (WAASBY ~80), demonstrating a strong balance of high yield and stability. In contrast, 9 genotypes fell below average, indicated lower suitability for broad adaptation. Genotypes G10 followed by G3, G2 remained lowest position in the below average in WAASBY rankings.

Table 8

Mean grain yield (t/ha), WAASB and WAASBY scores of genotypes under study: rRESP – genotype ranking based on grain yield, rWAASB – genotype ranking based WAASB, rWAASBY – genotype ranking based WAASBY.

Genotype	Mean grain yield (t/ha)	rResp	WAASB	rWAASB	WAASBY	rWAASBY
G1	6.87	10	0.44	14	35.02	11
G10	6.48	14	0.47	16	16.10	16
G11	6.38	15	0.36	9	35.94	10
G12	6.93	9	0.24	1	82.21	2
G13	7.11	5	0.46	15	40.88	9
G14	6.61	11	0.42	13	30.73	13
G15	7.00	7	0.34	7	61.14	7
G16	6.57	12	0.41	11	32.51	12
G2	6.50	13	0.41	12	28.49	14
G3	6.02	16	0.35	8	25.71	15
G4	7.02	6	0.26	2	80.64	3
G5	6.96	8	0.38	10	52.40	8
G6	7.44	1	0.28	3	91.45	1
G7	7.24	4	0.31	5	77.59	6
G8	7.27	3	0.30	4	80.32	4
G9	7.33	2	0.32	6	79.13	5

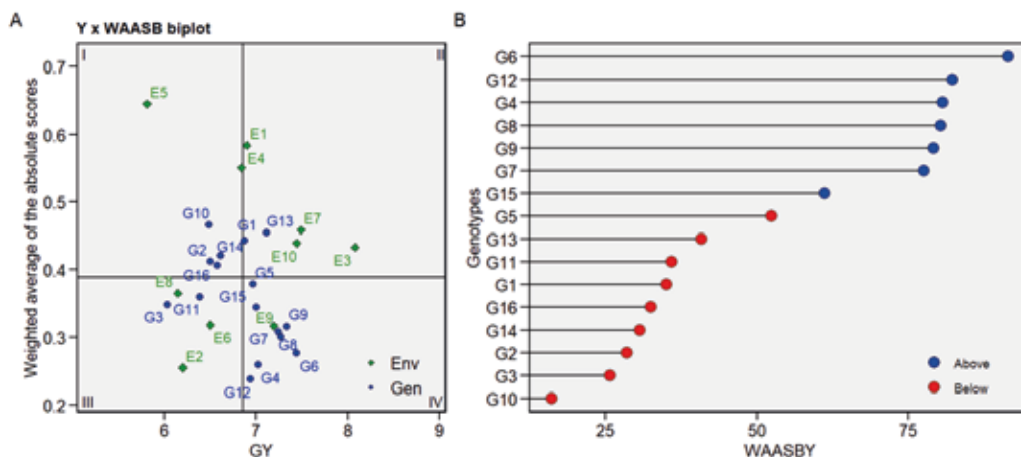


Fig. 7. WAASB statistic. A) Biplot of the mean grain yield and B) the weighted average of absolute scores for the best linear unbiased predictions of the genotype-vs.-environment interaction during 2023-24 season. WAASB: Weighted Average of Absolute Scores Biplot, WAASBY: Weighted Average of Absolute Scores Yield, G1: BR10645-6-4-8-1-2, G2: BR10646-3-2-2-4-3, G3: BR10648-12-1-3-4-1, G4: BRH15-24-7B, G5: BR9392-1-7-5B, G6: BR17-23-8-2-7B, G7: BRH11-7-17-10B, G8: BRH9-3-2B, G9: BRH13-9-5-2B, G10: Zira, Nachol, G11: Katari, Shibganj, G12: BRRI dhan104, G13: BRRI dhan107, G14: BINA dhan25, G15: BRRI dhan 88, G16: BRRI dhan81, E1: Paba, Rajshahi, E2: Sadar, Kushtia, E3: Bhanga, Faridpur, E4: Kamarkhanda, Sirajganj, E5: Sadar, Satkhira, E6: Debidwar, Cumilla, E7: Mithapukur, Rangpur, E8: Sonagazi, Feni, E9: Sadar, Gopalganj, E10: BRRI Westbyde, Gazipur.

3.9. Multitrait stability index (MTSI)

Table 9 displays the results of the factor analysis, which reveal the selection gain percentage (SG) (%), desired selection sense, and the achievement status of the goal based on factor analysis of selected rice genotypes using seven traits. The factor analysis revealed that contributing factors formed into three distinct groups consisting of eight traits under study. The desired selection sense was to increase for all traits. The goal was successfully achieved for four traits

(GY, PPM, GPP and STR). The goal of 3 traits such as PHT, GD and TGW was 0 as well as negative SG (%). Furthermore, the SG (%) for studied traits was ranged from 5.76 to 29.5%. The Fig. 8 illustrated the order of the most stable genotype determined by the multi-trait stability indexing (MTSI). Within this context, the red circle symbolizes the threshold for selecting the stable genotype. The genotype named G7 and G8 stands out as the most stable compared to other genotypes.

Table 9

Factor analysis of seven traits in sixteen fine grain rice genotypes for MTSI.

VAR	Factor	X _o	X _s	SD	SG (%)	Sense	Goal
GY	FA1	6.86	7.25	0.395	5.76	increase	100
PPM	FA1	304	322	18.6	6.12	increase	100
STR	FA1	23.6	30.5	6.95	29.5	increase	100
PHT	FA2	102	99.3	-2.97	-2.9	increase	0
GD	FA3	151	150	-1.04	-0.687	increase	0
TGW	FA3	20.6	18.8	-1.81	-8.8	increase	0
GPP	FA3	127	156	29.4	23.2	increase	100

X_o: Observed mean, X_s: Mean of selected genotypes, SG: Selection gain, FA: factor, GY: Grain yield, GD: Growth duration, PHT: Plant height, TGW: Thousand grain weight, PPM: Panicle per m², GPP: grains per panicle, STR: sterility percentage.

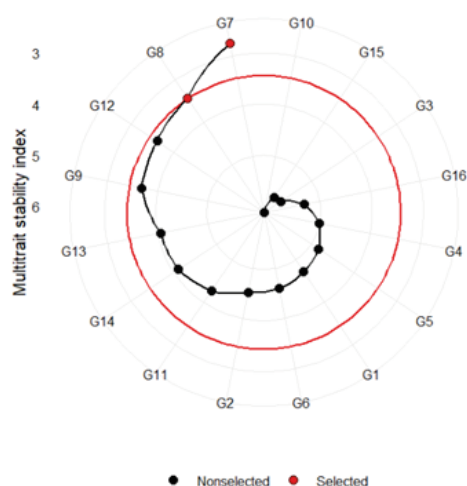


Fig. 8. Ranking of genotype stability based on MTSI index. MTSI: Multitrait stability index.

4. Discussion

This study aimed to evaluate the yield stability of 16 fine grain rice genotypes across ten diverse agro-ecological zones in Bangladesh. By conducting a comprehensive analysis of variance (ANOVA) for grain yield and its contributing traits, we observed significant effects of genotype, environment, and genotype-environment interaction (GEI), aligning with previous research findings (Akter et al., 2016; Huang et al., 2021). The detected profound differences among genotypes and environments can largely be attributed to variations in environmental conditions, the genetic diversity inherent in the studied genotypes, and the complex interactions between these two variables.

To select ideal genotypes for commercial application, it is essential for plant breeders to assess genetic parameters and stability of key traits. This study employed broad-sense heritability (h^2), coefficients of variation (CV), and selection accuracy (SA) to explore the genetic diversity among the genotypes (Dyulgerova and Dyulgerov 2024; Fellahi et al., 2020; Resende and Alves 2022). Our findings confirm that phenotypic variance exhibited sensitivity to environmental factors, with the GEI exerting the dominant influence on phenotypic variance in grain yield. This interaction resulted in lower heritability estimates, which ranged from 11% to 71% (Table 6), consistent with earlier observations (Dyulgerova and Dyulgerov 2024). An SA above 50% indicates this was acceptable for verifying the significance of genetic effects in the context of the heritability of the trait (h^2), genotypic correlation across environments (r_e), and the number of repetitions in multi-environment trials (Resende & Alves, 2022).

This analysis revealed high genetic diversity among genotypes, demonstrated by CV ratios, particularly for growth duration (GD), plant height (PHT), and thousand grain weight (TGW), all exceeding 1. The implications of this genetic diversity suggest a potential for selective breeding to enhance yield. However, variance component analysis alone cannot fully elucidate the complexities of GEI. Employing more advanced statistical models would be advantageous in providing deeper insights into the GEI (Mukul et al., 2025; Oladosu et al., 2017).

Through principal component analysis (PCA), GD and GY emerged as the most significant traits contributing to the overall agronomic performance, reinforcing the insight from previous studies (Chandra et al., 2021; Oladosu et al., 2018). These findings resonate with considerations of rice growth stage dynamics—an extended growth duration typically correlates with increased yields while plant height is also a crucial parameter (Biswash et al., 2023; Limbongan et al., 2024; Shrestha et al., 2021; Zhu et al., 2023; Ahmed et al., 2017; Chen et al., 2022; Shrestha et al., 2021). Interestingly, certain high-yield cultivars demonstrated optimal yield within shorter growth periods, suggesting that specific gene

expressions may enhance yield performance regardless of growing time (Wei et al., 2022).

Utilizing the additive main effects and multiplicative interaction (AMMI) model allowed for a more nuanced identification of superior lines compared to check varieties, offering enhanced accuracy over traditional ANOVA methods (Gauch and Zobel 1997). The results (Table 8) suggest that the first two PCs accounted for 61% of the variance, in alignment with previous work advocating for the use of fewer PCs in multi-environment trials (Mukul et al., 2025; Ahmed, 2025; Esan et al., 2023; Gauch and Zobel 1996). In the AMMI biplot, genotypes G6, G7, G8, and G9 exhibited the best yield performance, indicating their potential for broader adaptability.

Since breeders always prefer the yield performance with stability for varietal recommendations, so a mixed-effect model-based superiority index, WAASBY helps to identify the adaptability and productivity combining weighting between performance of response variable and WAASB stability score. The WAASB statistics were calculated based on mean GY and stability, integrating AMMI analysis and the BLUP model to examine the GEI effect (Olivoto et al., 2019). WAASB stability index has been employed in identification of stable genotypes in different economic traits such grain yield in rice (Hasan et al., 2025; Mukul et al., 2025; Hossain et al., 2023), grain yield in maize (Supriadi et al., 2024), yield performance of wheat (Al-Ashkar et al., 2023), grain yield in soyabean (Nataraj et al., 2021) and forage sorghum (Behera et al., 2024). In this study, G6 identified as the most outstanding genotype, combining the highest mean grain yield (7.44 t/ha) with strong stability (WAASB = 0.28), resulting in the highest WAASBY score (91.45). Similarly, G12, although slightly lower in yield (6.93 t/ha), demonstrated exceptional stability (WAASB = 0.24), leading to the second-highest WAASBY value (82.21). Genotypes G4, G8, and G9 also exhibited favorable combinations of high yield and moderate to high stability, ranking among the top five based on the WAASBY index. In contrast, G10, G3, and G2 showed poor performance in both yield and stability, making them less suitable for recommendation. The GY × WAASB biplot supported these findings by clearly positioning superior genotypes like G6 and G8 in the desirable quadrant of high yield and low instability.

Lastly, our findings reveal that the overall reliability of genotype recommendations significantly increases by taking into account both yield performance and stability across multiple traits. The positive correlation of yield efficiency with associated traits during growth further underscores the complexity of breeding decisions (Fageria, 2007). This study advocates for the implementation of multi-trait selection indices (MTSI) to enhance genotype evaluation. Key performers G7 and G8 excelled in all seven assessed traits, echoing the approaches previously adopted by researchers for comprehensive genotype assessments (Hasan et al., 2025; Habib et al.,

2024; Lee et al., 2023; Olivoto et al., 2019; Sruthi et al., 2024).

5. Conclusion

In conclusion, statistical approaches such as the AMMI and WAASB biplot revealed that four advanced genotypes (G6, G7, G8, and G9) demonstrated superior performance and adaptability across varied environments compared to the released check varieties. Additionally, the integration of multi-trait selection indices (MTSI) confirmed G7 and G8 as top performers across multiple traits, highlighting the importance of incorporating stability and multi-trait assessments into breeding programs. These findings will accelerate the development of climate-resilient rice varieties in Bangladesh, particularly focusing on the superior yield performance and stability of genotypes. Future investigations should evaluate these promising genotypes under specific stress-prone conditions, such as heat and drought during the reproductive stage, as well as in lowland and rainfed agro-ecological zones where environmental variability is highest. Such targeted trials, combined with advanced statistical approaches, will refine genotype recommendations and support the development of high-yielding, stress-resilient rice varieties suitable for Bangladesh's diverse rice-growing regions.

Conflict of Interest

"The authors declare no conflict of interest."

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