

Research article

Selection of Stable Rice Genotypes through WAASB and MTSI Indices

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Abstract

The cultivation of high-yielding and stable rice varieties is essential for ensuring food security in Bangladesh. To achieve this, breeders often conduct multilocal trials to evaluate genotype performance across diverse environments. During the Aman rice season, six rice genotypes and three check varieties across nine locations were investigated in this study using a randomized complete block design. The primary aim was to identify superior genotypes using the Multi-Trait Stability Index (MTSI). Both mixed and fixed effect models were utilized in this study to achieve accurate and reliable results. The mean performance and stability (MPS) were effectively represented by the WAASBY (Weighted Average of Absolute Scores + Yield) biplot, which served as the superiority index in the analysis. The Likelihood Ratio Test (LRT) showed that genotype by environment interaction (GEI) and genotype had a substantial impact. Key findings showed that genotype-by-environment interaction (GEI) significantly influenced grain yield and related traits. While most traits positively correlated with yield, Thousand Grain Weight (TGW) did not. The WAASBY biplot effectively assessed performance and stability. Some genotypes, such as BRRI dhan33, BRRI dhan39, were stable but low yielding. Conversely, BRRI dhan49 and BR9786-BC2-119-1-1 were highly productive but less stable. Notably, BR9786-BC2-132-1-3 delivered the highest yield but exhibited moderate stability, making it promising yet sensitive to environmental changes. This study highlights BR9786-BC2-132-1-3 as a potential candidate for further evaluation due to its productivity, with ongoing research needed to improve its adaptability and resilience across diverse conditions.

Keywords: multi-environmental trials; multi-trait stability index; Metan; WAASB; rice; stability

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1. Introduction

Rice is a staple food for much of the global population, with approximately 90% of production occurring in Asia. In Bangladesh, rice is the primary crop and dietary staple, making the country the third-largest global rice producer, cultivating 11.69 million hectares with an average yield of 4.89 tons per hectare in 2022 (Food and Agriculture Organization, 2022). To meet the growing demand, rice yields must rise from 5.90 to 7.17 tons per hectare by 2030 (Kabir et al., 2021; Rabbi et al., 2021), necessitating high-yielding, seasonally adaptable varieties. Rice yield is a complex trait, determined by factors like spikelets per panicle, panicle counts per unit area, and grain weight (Sakamoto & Matsuoka 2008), is influenced by genotype-environment interactions (GEI), which can cause variability in yield and quality (Kang, 1998). Modern breeding focuses on developing stable, high-yielding varieties resilient to climate variability while maintaining commercial value like 'yield' (Peng et al., 1999; Hall & Richards, 2013; Hickey et al., 2019; Li et al., 2019).

Consequently, examining diverse genotypes across various environments is crucial for identifying stable and adaptable rice varieties (Sharifi et al., 2020). A clear understanding of GEI and crop stability aids in selecting superior varieties and screening breeding lines during variety development (Yan & Kang, 2003). Multi-environment trials (MET) play a vital role in rice breeding by evaluating genotype performance, stability, and adaptation under varying environmental conditions, ensuring efficient selection and resilience to environmental stress (Malosetti et al., 2013).

Various statistical methods, including analysis of variance (ANOVA) (Eberhart & Russel, 1966), best linear unbiased prediction (BLUP), additive main effects and multiplicative interaction (AMMI) (Gauch, 1992), joint regression analysis, and genotype plus the genotype-environment interaction (GGE) biplots (Yan & Kang, 2003), are commonly used to assess genotype stability and adaptability. Among these, AMMI and BLUP are effective but lack integration with linear mixed-effect models (LMM). To address the challenges of random GEI, novel approaches like the Weighted Average of Absolute Scores (WAASB) and WAASBY (WAASB + yield), introduced by Olivoto et al. (2019a), provide a balanced evaluation of stability and performance. These metrics combine AMMI and BLUP features, leveraging complete interaction principal components for better analysis of GEI in multi-environment trials (METs), as demonstrated in studies on stable and productive genotypes. Santos & Marza (2020) employed these metrics to choose genotypes of fodder oats that were more stable and productive.

Genotype selection based on multiple traits is challenging due to environmental impacts on phenotypic traits. The concept of a plant "ideotype," combining desirable traits, simplifies this process and enhances understanding of GEI in METs. Olivoto et al. (2019b) introduced another model named Multi-Trait Stability Index (MTSI), integrating fixed and mixed models to prioritize mean performance across environments (MPE) for multi-trait selection. The MET analysis (METAN) method, facilitating the all-inclusive selection of multiple traits into a unified index, offers a distinctive approach to selection (Olivoto & Lúcio, 2020). This approach, applied successfully in crops like soybean (Zuffo et al., 2020), *Brassica* (Bocianowski et al., 2019) and sweet potato (Alam et al., 2024). This study aimed to identify the most stable and high-yielding rice genotypes under diverse environmental conditions using advanced tools like MTSI and WAASBY, ensuring a balanced evaluation of performance and stability.

2. Materials and Methods

2.1 Description experimental sites

The study was conducted during the T. aman (transplanted aman) growing season of 2016 across nine locations in Bangladesh: Barishal, Cumilla, Gazipur, Habigonj, Kustia, Rajshahi, Rangpur, Satkhira, and Sonagazi. These sites were selected for their suitability as prime rice-growing zones with favorable agro-ecological conditions. The study area spans elevations from 10 m (Coastal South) to 105 m (North) above sea level and is located between 23.6850° N latitude and 90.3563° E longitude. The soil characteristics are summarized in Table 1, while weather data for the study zones are illustrated in Figure 1. Weather and soil data were obtained from the Bangladesh Rice Research Institute (BRRI, 2023) and Bangladesh Meteorological Department (BMD, 2023).

Table 1. Description of soil characteristics of nine locations

Location ID	Locations	Soil Characteristics
E1	Barishal	Silty Clay-Loam
E2	Cumilla	Sandy Clay Loam to Loam, (pH 5.8,)
E3	Gazipur	Clay Loam
E4	Habigonj	Clay Soil (pH 4.5-5.5)
E5	Kustia	Light Textured Sandy-Loam to Loam
E6	Rajshahi	Calcareous Loamy Soil (pH8.0-8.5)
E7	Rangpur	Sandy Loam, Slight Acidic (pH6.4),
E8	Satkhira	Silty-Loam, (pH 8.0)
E9	Sonagazi	Sandy-Clay Loam (pH 7)

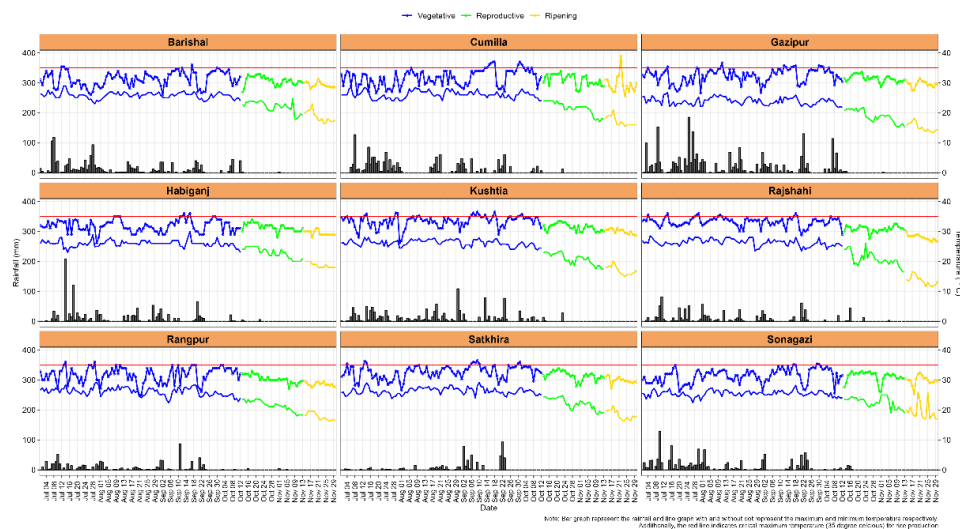


Figure 1. Rainfall, high temperature and low temperature throughout the whole crop growing season at nine different locations

2.2 Experimental design, materials, and cultural practices

Six potential rice genotypes (Table 2) along with three check varieties—BRRI dhan33, BRRI dhan39, and BRRI dhan49—were evaluated using a randomized complete block design with three replications. Two seedlings per hill were transplanted with a spacing of 20 cm × 20 cm in a 20 m² (5 m × 4 m) plot. Transplanting was conducted from the last week of July to mid-August (Table 3). The recommended fertilizer doses included triple super phosphate (44 kg/ha), muriate of potassium (52 kg/ha), and urea (96 kg/ha). Phosphorus and potassium, along with 50% of the total urea, were applied during transplanting. The remaining urea was split and top-dressed at 25 and 55 days after transplanting. Weed control was carried out manually three times, and disease and pest management were implemented as required, following guidelines from the Bangladesh Rice Knowledge Bank (2023).

Table 2. Description of rice genotypes used in this study with their pedigrees

Genotype designation	Pedigree	Parent
BR(Bio)9786	BC ₂ -124-1-2	♀BRRI dhan29 × ♂IRGC 103404 (<i>O. rufipogon</i>)
BR(Bio)9786	BC ₂ -119-1-1	
BR(Bio)9786	BC ₂ -132-1-3	
BR(Bio)9786	BC ₂ -2-1-1	
BR(Bio)9786	BC ₂ -139-2-3	
BR(Bio)9786	BC ₂ -124-1-5	

BR=Short form of BRRI, Bio=Biotechnology division, BC= backcross

Table 3. Detailed times of sowing and transplanting at nine locations

Location	Date of Seeding	Date of Transplanting
Cumilla	08/07/15	08/08/15
Habigonj	13/07/15	13/08/15
Kustia	02/07/15	30/07/15
Rangpur	01/07/15	28/07/15
Sonagazi	14/07/15	14/08/15
Satkhira	08/07/15	08/08/15
Rajshahi	05/07/15	04/08/15
Barishal	17/07/15	15/08/15
Gazipur	01/07/15	27/07/15

2.3 Data collection

The crop was harvested when it reached maximum maturity. Yield was calculated from 10m² (252 plants), leaving the guard rows on both sides of the plot. Rice grain yield adjustments were made to accommodate a 14% moisture content on a sundry basis and yield was converted into ton/hectare. The growth duration (GD) was recorded at the time of 80% crop maturity. Plant height (PH), filled spikelets/panicle (SPN) and panicle number (PN) were counted at the time of harvesting. The 1000 grain weight (TGW) was measured following sun drying and when the moisture content reached 14%.

2.4 Statistical analysis

The following statistical analyses were carried out with the help of R software using "metan" package (Olivoto & Lúcio, 2020).

2.4.1 Estimating the WAASB and WAASBY indices

The Weighted Average of Absolute Scores (WAASB) index, based on the Singular Value Decomposition (SVD) of BLUP interaction effects for the i th genotype or environment, was calculated using the formula (Olivoto et al., 2019a):

$$WAASB_i = \frac{\sum_{k=1}^p |IPCA_{ik} \times EP_k|}{\sum_{k=1}^p EP_k}$$

Where, EP_k is the portion of variation explained by the k th IPCA, and interaction principal component axis ($IPCA_{ik}$) is the score of the i th genotype (or environment) in the k th IPCA. The WAASBY index combines grain yield (Y) and stability (WAASB) into a single metric to identify superior genotypes (Olivoto et al., 2019a). It was calculated using the following equation:

$$WAASBY_i = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$$

The weights between performance and stability are represented by $WAASBY_i$, which stands for the superiority index for the i th genotype. In our study, we assumed that θ_Y and θ_S , are the weights for the response variable and the stability (WAASB) (Olivoto et al., 2019b) supposed to be 50 and 50, indicating that grain yield and stability are equally weighted. Furthermore, twenty-one situations with different θ_Y and θ_S (100/0, 95/5, 90/10, ..., 0/100) were organized. The values of grain yield and WAASB for the i th genotype are G_i and W_i . The rescaled values (0-100) for the response variable (rG_i) and WAASB (rW_i) are as follows. Since the maximum and lowest values for grain yield and WAASB are the ideal values, the adjustments were performed using the following equations (Olivoto et al., 2019b):

$$rG_i = \frac{100 - 0}{G_{max} - G_{min}} \times (G_i - G_{max}) + 100$$

$$rW_i = \frac{0 - 100}{W_{max} - W_{min}} \times (W_i - W_{max}) + 0$$

2.4.2 Multi-Trait Stability Index (MTSI)

The Multi-Trait Stability Index (MTSI) (Olivoto et al., 2019b) was analyzed using the following formula:

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

Where F_{ij} is the j th score of the i th genotype, F_j is the j th score of the ideotype, and MTSI is the Multi-Trait Stability Index for the i th genotype. Therefore, the genotype that has the lowest MTSI is more ideotype-like and has a high MPE for every variable that was looked at in every location. Steps followed to calculate the MTSI are:

Steps for calculating MTSI:

1. Define the ideotype, specifying traits to be maximized or minimized. Factor analysis of WAASBY is performed, followed by calculating the Euclidean distance between genotype and the ideotype.
2. Assign weights, prioritizing traits such as grain yield (GY) and stability.
3. Compute the WAASBY index using the `waasb()` function in the *metan* package.
4. Use the `mtsi()` function to identify genotypes most similar to the predefined ideotype, emphasizing desirable traits.

3. Results and Discussion

Multi-environment trials (METs) are essential for evaluating crop yield and adaptability across diverse conditions (Malosetti et al., 2013). These trials improve genotype selection precision by analyzing genotype-by-environment interaction (GEI) using tools like mega-environment analysis, performance assessment, and stability analysis (Yan et al., 2007; Olivoto et al., 2019a). GEI, caused by differing genotype responses to environmental changes, is influenced by environmental diversity (e.g., location, climate, altitude) and genetic variability, often resulting in significant interactions crucial for genotype evaluation.

In this study, the nine trial locations exhibited substantial environmental variability. Soil properties varied (Table 1), with Kustia and Rangpur showing less-than-ideal conditions for rice compared to other sites. While clay loam, silty clay, or clay soil are optimal for rice, differences in texture and climate affected performance. Higher temperatures were observed in Kustia, Rajshahi, and Satkhira, while rainfall varied significantly, with Kustia, Rajshahi, Barishal, and Sonagazi receiving the least (Figure 1). These variations highlight the importance of diverse environmental conditions in METs. Genotype stability, linked to consistent phenotypic performance across environments, remains a key factor in evaluating adaptability (Becker & Léon, 1988).

3.1 Genetic parameters and mean performance evaluation

The LR test revealed significant genotype-environment interactions (GEI) for all studied traits ($p < 0.05$, Table 4). Restricted maximum likelihood analysis showed that 46.34% of phenotypic variation was due to genotypic variance, 26.77% to environmental effects, and 17.28% to GEI, with 8.04% attributed to residual variance (Table 5). Genotypic variance exceeded environmental, residual, and GEI variance for all traits (Figure 2). In the random-effects model, phenotypic variation was partitioned into components of environmental, environmental/block, GEI, and residual (error) variance, with genotypic variance treated as a random effect.

Grain yield across locations ranged from 5.43 t/ha in Rajshahi to 4.35 t/ha in Habigonj, with the highest genotypic yield recorded for BR9786-BC2-132-1-3 (5.73 t/ha) and the lowest for BRRI dhan33 (4.19 t/ha) (Figure 3(a), 3(b)). Broad-sense heritability was high for most traits except panicle number per plant and spikelets per panicle, with genotypic selection accuracy (AS) ranging from 1 (GD) to 0.93 (TN & SPN) (Table 6). Coefficients of genotypic variation (CVg) were higher than residual variation (CVr) for all traits, with the highest CVg for yield (9.45) and the lowest for GD (4.07) (Table 7).

Plant height varied significantly among genotypes, with the tallest plants recorded in BR9786-BC2-132-1-3, followed by BR9786-BC2-119-1-1, and the shortest in BRRI dhan49. Growth duration was longest in BRRI dhan49 and shortest in BRRI dhan33, with three genotypes having 130 days and the remaining three 127 days of growth (Table 8).

The number of tillers per plant was highest in BR9786-BC2-132-1-3 and BRR1 dhan49, while BRR1 dhan33 had the fewest. BRR1 dhan49 also produced the highest spikelets per panicle, followed by BR9786-BC2-132-1-3 and BR9786-BC2-119-1-1. Thousand-grain weight was greatest in BR9786-BC2-124-1-2, BR9786-BC2-124-1-5, and BR9786-BC2-132-1-3, with BRR1 dhan49 having the lowest (Table 8).

Table 4. P-values for likelihood ratio test of the traits analyzed

	Yield	PH	GD	PN	SPN	TGW
GEN	3.77E-09	4.83E-13	9.43E-22	4.04E-09	2.73E-09	4.77E-54
GEN:ENV	2.35E-14	7.01E-36	8.42E-71	9.01E-11	9.66E-12	6.97E-05

Table 5. Percentage (%) of variation

Source	Yield	PH	GD	PN	SPN	TGW
ENV	28.13	45.77	53.96	20.01	12.55	0.22
REP(ENV)	1.95	0.38	0.06	4.85	1.80	0.33
GEN	33.69	35.09	37.90	34.61	40.46	96.31
GEN:ENV	24.42	15.97	7.71	25.20	28.78	1.57
Residuals	11.82	2.79	0.37	15.33	16.40	1.57

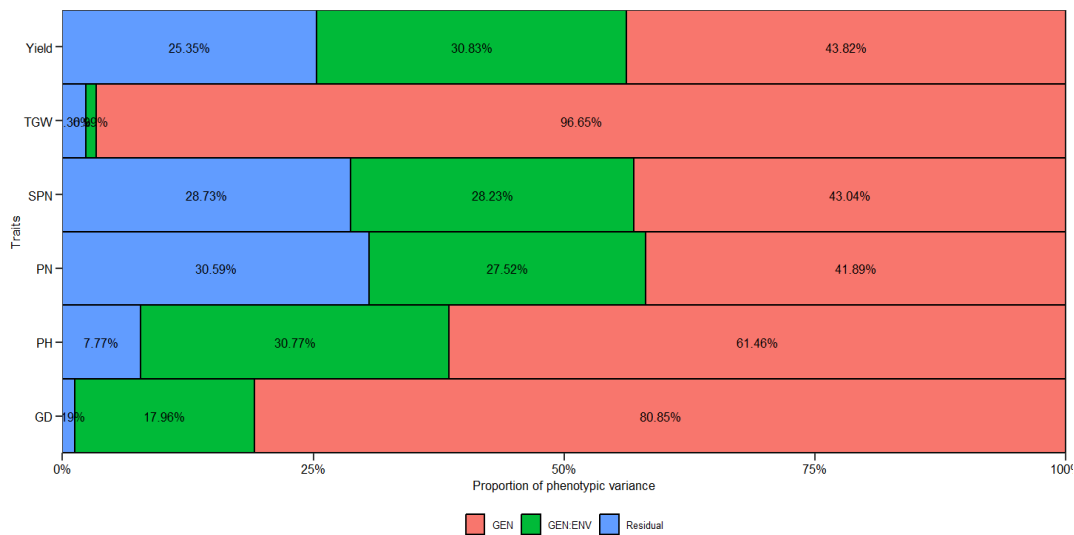


Figure 2. Assessment of rice trait variability across nine diverse environments: Exploring the proportion of phenotypic variance in six genotypes and three check varieties. Where GD: Growth Duration, PH: Plant Height, SPN: Filled Spikelets/Panicle, PN: Panicle Number, TGW: 1000 grain weight

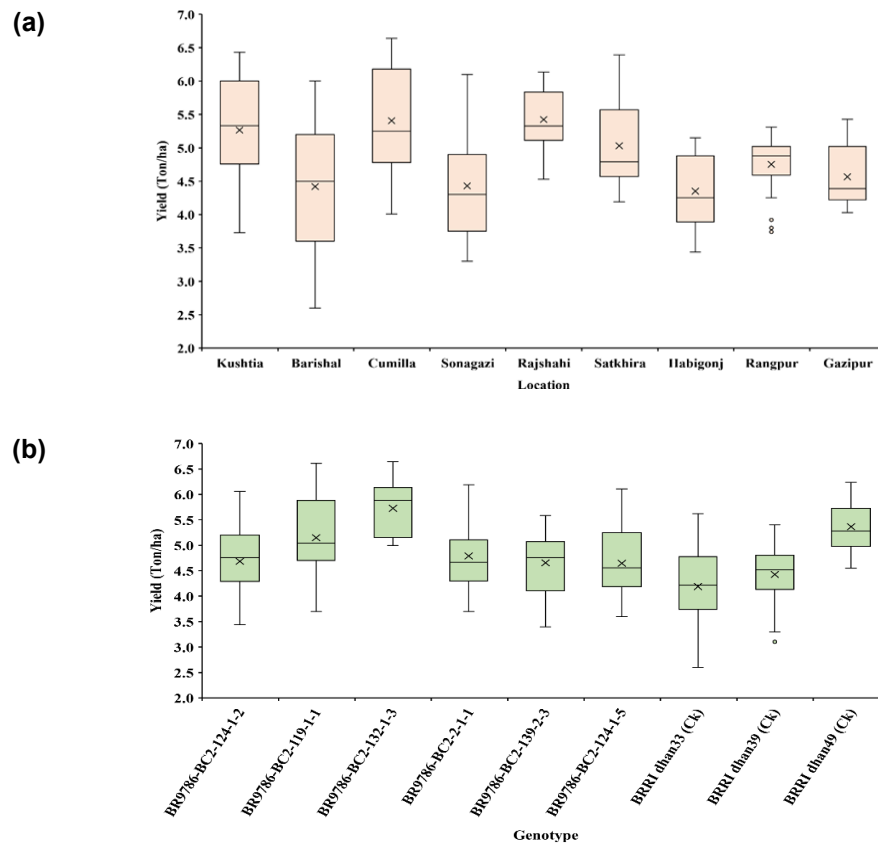


Figure 3. (a) Average locational grain yield (GY) of nine studied rice genotypes and (b) Average genotypic rice grain yield in nine studied locations

Table 6. Broad sense heritability (%) and selection accuracy (AS) of yield and yield related parameters in nine locations

ENV	Heritability (%)						AS				
	Yield	PH	GD	PN	SPN	TGW	Yield	PH	GD	PN	SPN
Barishal	86	93	99	75	91	100	0.93	0.96	1.00	0.87	0.95
Cumilla	85	98	100	88	78	100	0.92	0.99	1.00	0.94	0.88
Gazipur	99	99	100	100	98	99	0.99	1.00	1.00	1.00	0.99
Habigonj	97	99	100	100	95	100	0.99	0.99	1.00	1.00	0.98
Kushtia	91	97	100	80	78	97	0.95	0.99	1.00	0.89	0.88
Rajshahi	75	100	99	63	84	99	0.86	1.00	1.00	0.79	0.92
Rangpur	97	98	100	97	83	99	0.99	0.99	1.00	0.98	0.91
Satkhira	98	98	100	91	93	99	0.99	0.99	1.00	0.95	0.96
Sonagazi	88	46	99	90	88	99	0.94	0.68	1.00	0.95	0.94

Table 7. Deviance analysis, genetic parameters and variance components of nine rice genotypes studied in nine locations

Parameters	Yield	PH	GD	PN	SPN	TGW
Phenotypic variance	0.479	48.3	33.1	0.617	142	2.39
Heritability	0.438	0.615	0.808	0.419	0.43	0.967
GEI r^2	0.308	0.308	0.18	0.275	0.282	0.009
h^2mg	0.909	0.943	0.975	0.909	0.911	0.998
Selection accuracy	0.954	0.971	0.988	0.953	0.955	0.999
r_{ge}	0.549	0.798	0.938	0.474	0.496	0.294
CV _g	9.45	5.03	4.07	5.73	7.11	6.51
CV _r	7.19	1.79	0.494	4.89	5.81	1.02
CV ratio	1.31	2.81	8.23	1.17	1.22	6.4

Where PV: phenotypic variance, GEI r^2 : GEI coefficient of determination, h^2mg : heritability of genotypic mean, Acc: accuracy of genotype selection, r_{ge} : association among genotypic values across environments, CV_g: genotypic coefficient of variation, CV_r: residual coefficient of variation, CV ratio: coefficient of variation ratio

Table 8. Average PH, GD, TN, SPN and TGW of nine rice genotypes across nine locations

Genotype	PH (cm)	GD (Days)	PN (per plant)	SPN (per panicle)	TGW (gm)
BR9786-BC2-119-1-1	115.17	131	8.92	113.38	23.53
BR9786-BC2-124-1-2	107.23	127	8.56	105.83	24.61
BR9786-BC2-124-1-5	109.12	127	8.43	107.32	24.37
BR9786-BC2-132-1-3	119.51	130	9.75	113.64	24.31
BR9786-BC2-139-2-3	108.58	127	8.65	107.53	23.62
BR9786-BC2-2-1-1	104.19	130	8.89	110.63	22.83
BRRI dhan33 (Ck)	103.17	117	8.33	100.42	23.72
BRRI dhan39 (Ck)	105.80	122	8.60	103.48	23.60
BRRI dhan49 (Ck)	103.03	135	9.76	128.67	19.56
CV (%)	1.80	0.51	5.28	5.74	1.00
LSD _{0.05}	1.05	0.35	0.25	3.40	0.13

Where PH: Plant height, GD: Growth duration, PN: Panicle number per plant, SPN: Filled spikelets per panicle, TGW: Thousand grain weight

Genotypic yield variation, common in rice trials, has been reported by previous researchers. For example, Shrestha et al. (2021) observed yield variation across 12 rice genotypes under irrigated lowland and upland rainfed conditions. Locational yield variation can result from factors like temperature, rainfall, soil fertility, and differences in transplanting time. In this experiment, supplementary irrigation was provided, when necessary, but soil fertility status was not initially evaluated. Thus, temperature and transplanting time were likely contributors to yield differences across locations. Prior studies (Kabir et al., 2014; Nishad et al., 2019; Mann & Dhillon, 2021) have similarly shown that variations in these factors significantly impact rice yield.

Analysis of variance revealed a significant effect of genotype on grain yield, while the notable impact of GEI highlighted differences in genotype performance across environments. This variance underscores the importance of conducting trials across multiple sites and growing seasons to improve genotype selection efficiency. Substantial GEI effects have been reported in various field crops, including rice, by Balakrishnan et al. (2016), Sharifi et al. (2017), Das et al. (2019), Huang et al. (2021), and Enyew et al. (2021). Instead of relying solely on the significance of GEI effects, we emphasized the application of multi-environment trial analytical techniques to better interpret genotype performance patterns. GGE biplot analysis proved valuable in identifying optimal test locations, defining mega-environments, and determining superior genotypes, all of which are crucial for guiding future breeding activities (Yan et al., 2000; Yan & Kang, 2003). Similar studies on rice have shown that environment, genotype, and GEI significantly influence yield, as demonstrated by Chandel et al. (2010), Suwanto and Nasrullah (2011), Akter and Hassan (2014), Rerkasem et al. (2015), Sharifi et al. (2017), Sadimantara et al. (2018), and Rahayu (2020).

3.2 Coefficient of correlation among traits of rice

In Figure 4, there was a positive significant correlation observed between PH and grain yield ($r=0.54$), GD and grain yield ($r=0.23$), PN and grain yield ($r=0.82$), SPN and grain yield ($r=0.74$), PN and PH ($r=0.42$), SPN and PH ($r=0.19$), TGW and PH ($r=0.27$), PN and GD ($r=0.26$), SPN and GD ($r=0.28$), SPN and PN ($r=0.45$). A significant negative correlation was found between TGW and grain yield ($r=0.18$), TGW and GD ($r=0.33$), TGW and PN ($r=0.33$), TGW and SPN ($r=0.53$). The results show that these traits were positively correlated with rice grain yield, making them crucial traits for introducing genetic improvement in rice. Plant breeders can also concentrate their efforts on the characteristics that are highly correlated with grain yields in order to create superior rice genotypes. Prior research has documented a strong association between GY and PH, PN, SPN, and GD (Li et al., 2019; Russinga, 2020; Hasan et al., 2022).

3.3 Selection of rice genotypes through WAASBY biplot

The WAASB index, which utilizes all significant principal components, ensures a comprehensive assessment of genotype stability while selecting high-performing and stable genotypes. The $GY \times$ WAASB biplot (Figure 5) effectively illustrates grain yield and stability simultaneously, facilitating the identification of genotypes with broad adaptability (Sharifi et al., 2020; Huang et al., 2021; Pour-Aboughadareh et al., 2021). Unlike the AMMI Stability Value (ASV), which may misrepresent stability under complex GEI patterns, WAASB provides a robust framework for classification and selection (Olivoto et al., 2019a).

The biplot highlights genotypic variation and is divided into four quarters. Genotypes in the first quarter, such as BRRI dhan33 and BRRI dhan39, showed high WAASB values, indicating instability but with potential for environment-specific adaptation (e.g., BRRI dhan39 with E9 and BR9786-BC2-139-2-3 with E7). These findings emphasize the importance of identifying location-specific genotypes to optimize production (Li et al., 2019; Zuffo et al., 2020). Genotypes in the third quarter, such as BR9786-BC2-2-1-1, had below-average yields but demonstrated high stability, reflecting the yield-stability trade-off crucial for breeding programs (Fischer et al., 2014; Bailey-Serres et al., 2019). In the fourth quarter, BRRI dhan49 and BR9786-BC2-119-1-1 combined high productivity with excellent stability, making them prime candidates for broad adaptability under changing climates.

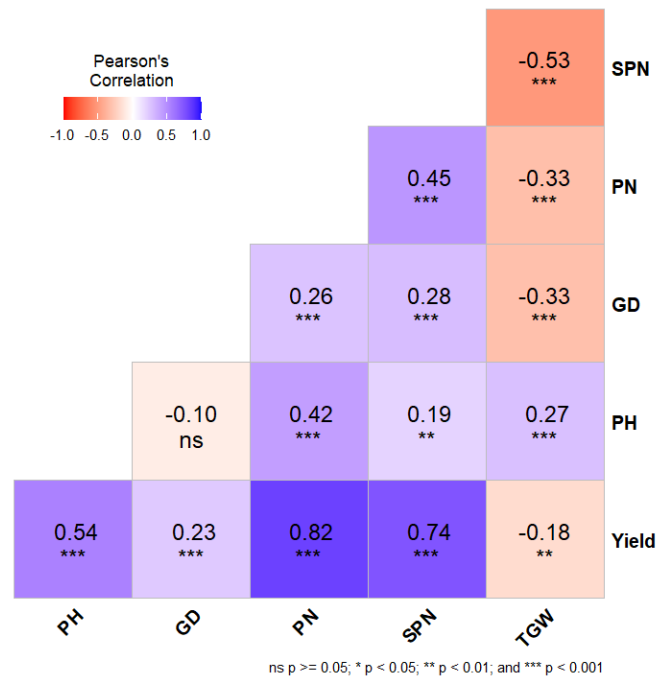


Figure 4. Pearson's correlation heatmap with coefficient values of different traits among nine rice genotypes evaluated in nine environments

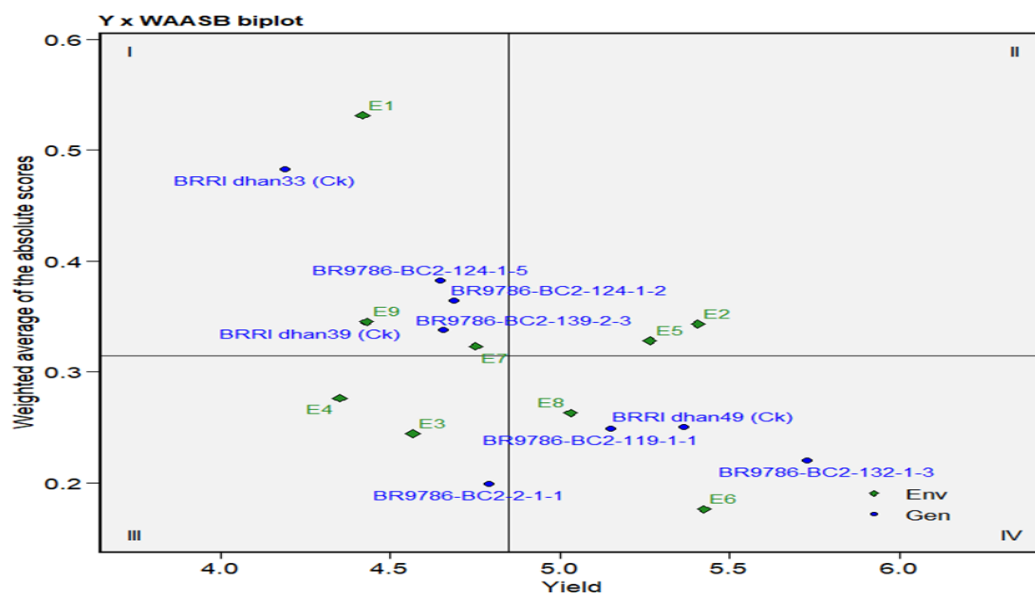


Figure 5. Weighted average of the absolute scores vs grain yield of nine rice genotypes studied in nine locations of Bangladesh

(Cairns et al., 2012). Of note, BR9786-BC2-132-1-3 achieved the highest yield but showed relatively lower stability, highlighting the need for targeted regional trials and stability improvement to unlock its potential (Zhao et al., 2017).

Environmentally, E6 emerged as the most stable, with a low WAASB index indicating consistent genotype performance. Such stable environments serve as benchmarks for evaluating genotypic adaptability and guiding breeding strategies in the face of GEI and climate variability (Gage et al., 2017; Olivoto et al., 2019a).

3.4 Ranking genotypes according to performance (grain yield) and stability weights

In plant breeding, balancing grain yield (GY) and stability (WAASB) is essential to identify genotypes that combine high productivity with resilience across diverse environments. Figure 6 illustrates the impact of these traits on genotype rankings and groups them into four distinct clusters: Cluster I: Includes BR9786-BC2-119-1-1, BR9786-BC2-2-1-1, and BRR1 dhan49, which are high-yielding but relatively unstable. Cluster II: Consists of BR9786-BC2-139-2-3 and BR9786-BC2-124-1-2, which exhibit moderate grain yields but superior stability. Cluster III: Features BR9786-BC2-124-1-5, BRR1 dhan33, and BRR1 dhan39, which are highly stable but below average in yield. Although reliable, these genotypes may require improvements to achieve competitive productivity. Cluster IV: Contains only BR9786-BC2-132-1-3, a genotype with the highest yield but poor stability. Its exceptional productivity makes it suitable for favorable and predictable environments, though it may underperform in variable conditions. This clustering approach, consistent with the methodology of Sharifi et al. (2020), provides breeders with a clear framework for selecting genotypes that align with specific breeding goals, whether the focus is on maximizing yield, ensuring stability, or achieving a compromise between the two.

3.5 Genotype selection through MTSI

Figure 7 shows the rankings of genotypes based on the Multi-Trait Stability Index (MTSI) and indicates BR9786-BC₂-132-1-3 as the selected genotype. According to Olivo et al. (2019b), the cutting point is shown by the red circle (MTSI=1.33). In addition, the index's result for grain yield was nearly identical to the WAASBY index's result (Figure 7).

The MTSI index provides an efficient method for selecting rice genotypes that balance both performance and stability, utilizing multi-trait data from multi-environment trials (Olivoto et al., 2019b). In the face of large genotype-environment interactions (GEI), breeders must prioritize genotypes that perform well across a range of conditions, especially given the challenges posed by climate change. This is crucial for ensuring food security in an era of shifting weather patterns (Bailey-Serres et al., 2019; Zuffo et al., 2020). The ability of MTSI to incorporate key yield components, such as panicle number (PN), spikelets per panicle (SPP), and thousand-grain weight (TGW), ensures a more holistic assessment of genotypic performance. This method aligns with the growing demand for breeding strategies that prioritize resilience and sustainability without compromising productivity (Fischer et al., 2014; Gage et al., 2017). Notably, the consistency between MTSI and WAASBY results underscores the robustness of this genotype selection process. BR9786-BC2-132-1-3, with its shorter growth duration and strong grain yield potential, is an excellent candidate for further yield trials and breeding programs.

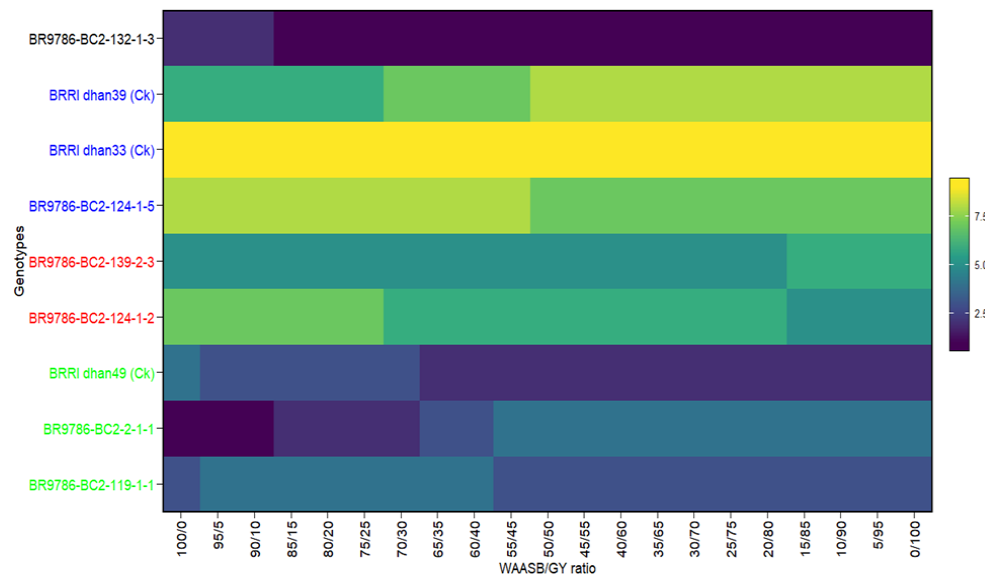


Figure 6. Based on yields and stability, nine rice genotype rankings are shown, each with a different weight. The four clusters correspond to four genotype classifications: (1) productive but unstable genotypes, (2) stable but low productive genotypes, (3) low productive and unstable genotypes, and (4) highly productive and stable genotypes.

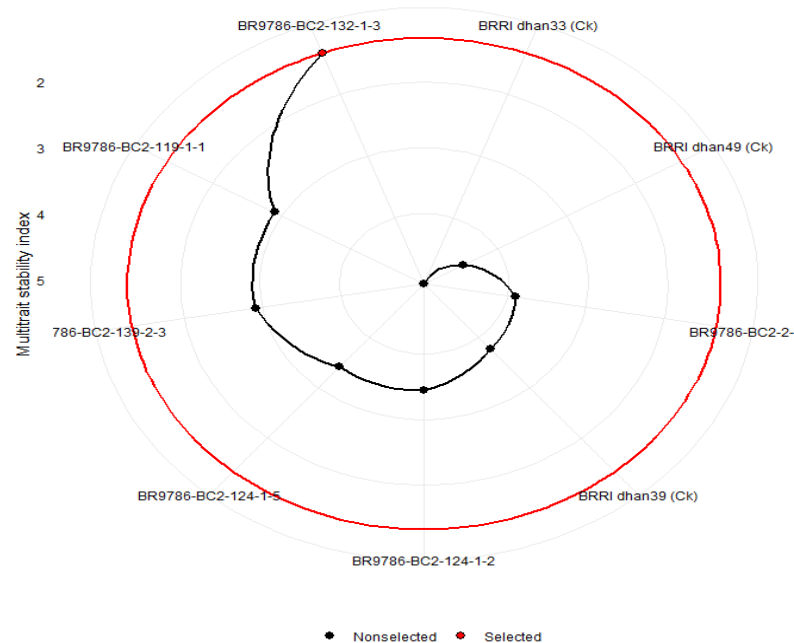


Figure 7. Ranking of rice genotypes based on the Multi-Trait Stability Index (MTSI)

4. Conclusions

The combined use of the WAASBY and MTSI methods highlights their effectiveness in identifying promising genotypes like BR9786-BC2-132-1-3, which showcases exceptional grain yield potential and a shorter growth duration compared to the high-yielding check variety BRRI dhan49. Despite its relatively low stability, these advanced selection methods underscored its adaptability and strong performance in specific regions. To fully harness its potential, further regional trials and stability evaluations are essential. With enhanced stability, this genotype could become a cornerstone in breeding next-generation, high-yielding Aman rice varieties, significantly contributing to future rice production and food security advancements.

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6. Conflicts of Interest

The authors declare no conflicts of interest.

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