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Identification of Stable Rice Genotypes Using WAASB and MTSI Indices

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ABSTRACT

Confronting the challenges of climate change, population expansion, and food security in Bangladesh demands the development of high-yielding, resilient rice varieties adapted to various agro-ecological zones. This study aimed to identify superior rice genotypes with consistent performance during the dry season (November-May) under irrigated condition using multi-environment trials (METs) at ten locations. Seven genotypes, along with a control variety, were evaluated for grain yield and agronomic parameters, including plant height, growth duration, panicle number, filled spikelets per panicle, and thousand-grain weight (TGW). The genotype-by-environment interaction (GEI) was analyzed, and stability was assessed using Weighted Average of Absolute Scores with Yield (WAASBY) and Multi-Trait Stability Index (MTSI) metrics. Results revealed significant GEI effects, with genotype BR(Bio)9777-116-12-2-5 demonstrating the highest yield and stability across environments. Grain yield showed strong positive correlations with most traits except TGW. WAASBY analysis identified BR(Bio)9777-116-12-2-5 as top-performing and stable genotypes, whereas others, such as BR(Bio)9777-84-4-1-1 and BR(Bio)9777-123-4-6-1 were less productive and unstable. MTSI further confirmed the exceptional performance of BR(Bio)9777-116-12-2-5, highlighting its suitability for varied agro-ecological zones. These outcomes underscore the significance of combining yield and stability metrics in breeding programs providing a valuable framework for developing climate-resilient rice varieties to enhance productivity and ensure food security in Bangladesh. This research offers valuable guidance for addressing emerging agricultural challenges and promoting sustainable food systems in the face of global environmental and population pressures.

1. INTRODUCTION

Rice (*Oryza sativa*) serves as the principal source of calories for over half of the global population, underpinning food security in many developing countries, including Bangladesh (Khush, 2005; Hussain, 2012; Maclean et al. 2013). In Bangladesh, where rice accounts for 70% of the daily caloric intake, its cultivation plays a crucial role in ensuring national food security (BRRI, 2020; FAO, 2020). However, the challenges posed by increasing population pressure, climate change, and shrinking arable land necessitate the development of high-yielding, stable rice genotypes that exhibit consistent performance across diverse environments (Lobell et al. 2008; IRRI, 2018).

One of the major challenges in developing such genotypes is the strong influence of genotype-by-environment interaction (GEI) on yield and other agronomic traits. GEI complicates the process of selecting stable and broadly adaptable genotypes because genotypes may perform well in one environment but not as well in another (Yan and Kang, 2003; Kulsum et al., 2018; Akter et al., 2018). Multi-environmental trials (METs) are frequently used to evaluate genotypes under diverse agro-climatic conditions, allowing breeders to assess both stability and yield performance simultaneously (Gauch et al., 2008; Crossa, 1990). Beyond yield, these trials also consider additional agronomic characters, such as plant height, maturity, and grain quality, which are essential for ensuring overall adaptability and market acceptability (Annicchiarico, 2002; Mohammadi et al. 2012; Mohammadi et al. 2023).

Recent advancements in statistical tools have improved the efficiency of analyzing MET data. The Weighted Average of Absolute Scores with Yield (WAASBY) index is a powerful method for combining yield and stability metrics, helping to identify genotypes that excel across environments (Olivoto et al. 2019; Nataraj et al. 2021; Lee et al. 2023; Dyulgerova and Dyulgerov, 2024). Similarly, the Multi-Trait Stability Index (MTSI) facilitates the evaluation of genotypes on basis of multiple traits, offering a holistic approach to genotype selection (Olivoto et al. 2019; Zuffo et al. 2020; Yue et al. 2022; Sampaio Filho et al. 2023). These tools have been successfully applied to various crops, including green gram (Aruna et al., 2024), black bean (Ambrósio et al., 2024), and sugar beet (Taleghani et al., 2023), to address the complexity of multi-trait and multi-environment selection.

In this study, we conducted a MET during the boro season across ten diverse locations in Bangladesh, assessing the performance of seven rice genotypes and a check variety. The objectives were to: (i) analyze the genotype-by-environment interaction and its impact on grain yield and other agronomic traits, (ii) evaluate the stability of genotypes using WAASBY and MTSI indices, and (iii) identify promising genotypes for breeding programs. By employing these advanced statistical methods, the study aims to identify rice genotypes with high yield potential and stability, contributing to the development of resilient varieties suitable for Bangladesh's diverse agro-ecological zones.

2. MATERIALS AND METHODS

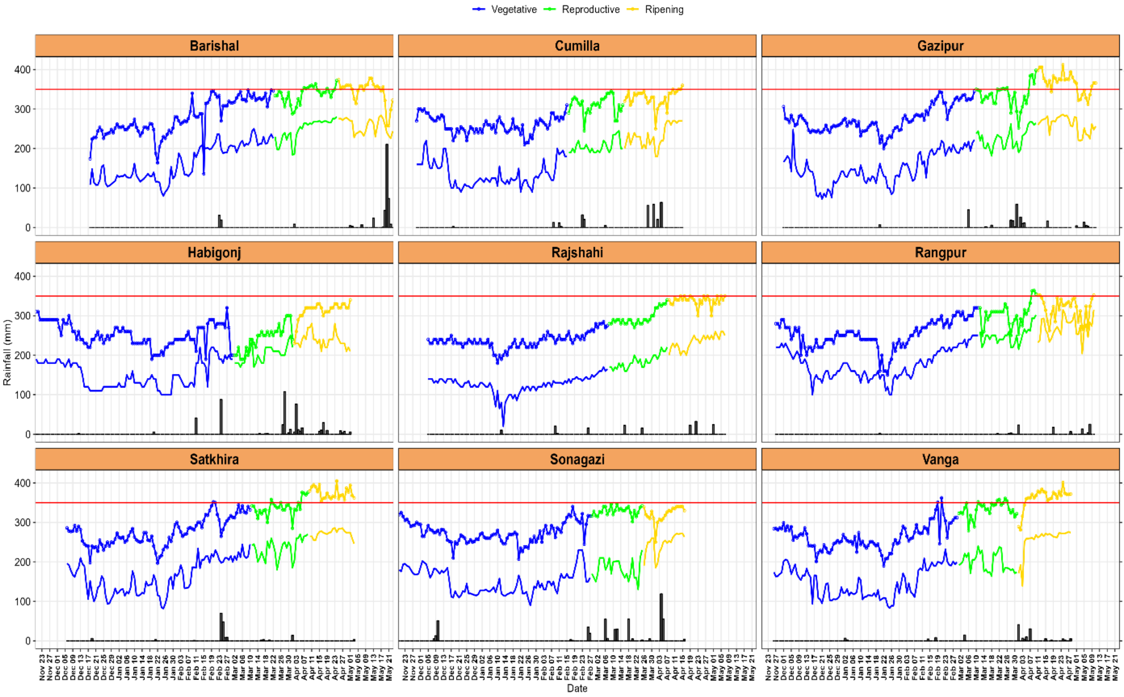
Experimental Design and Study Sites

The study was conducted during the boro season using a multi-environmental trial (MET) to evaluate seven rice (*Oryza sativa*) genotypes along with a check variety. Trials were laid out at ten diverse locations across Bangladesh Vanga, Barishal, Cumilla, Gazipur, Habigonj, Kustia, Rajshahi, Rangpur, Satkhira and Sonagazi, representing a wide range of agro-ecological conditions. The geographical locations were selected to capture significant environmental variation, including differences in soil type (Table 1), temperature, and water availability, typical of the rice-growing regions in the country with an elevation difference of 10 m (Coastal South) to 105 m (North) above sea level. It is situated between latitudes 23.6850° N and longitudes 90.3563° E. The weather data was shown in Figure 1. These data were collected from the websites of the Bangladesh Rice Research Institute (BRRI) and the Bangladesh Meteorological Department (BMD).

The experiment followed a randomized complete block design (RCBD) with three replications at each site. Each plot consisted of five rows, each 5 meters in length, with a row-to-row spacing of 20 cm. Standard agronomic practices, including irrigation, fertilization, and pest management, were followed as recommended by BRRI to ensure uniform crop management across locations.

Plant Material

The experimental material comprised seven advanced rice breeding lines BR(Bio)9777-116-12-2-5, BR(Bio)9777-124-1-1-2, BR(Bio)9777-116-12-2-2, BR(Bio)9777-123-4-6-1, BR(Bio)9777-84-4-1-1, BR(Bio)9777-117-4-5-3, BR(Bio)9777-116-2-4 and one check variety (BRRI dhan29) (Table 2). These lines were developed by crossing BRRI Dhan29 and FL378. BRRI Dhan29 is a widely cultivated, long-duration, high-yielding rice variety of Bangladesh (www.brri.gov.bd), whereas FL378 is recognized for its salt tolerance, derived from the salt-tolerant landrace Pokkali. The primary aim of the crossing was to develop salt tolerant lines. Fortunately, some of the lines performed well in non-saline conditions as well. These genotypes were selected based on their high yield potential in observational yield trials (non-replicated) followed by a Preliminary yield trial (Replicated). Transplanting was conducted from the first to the third week of January, depending on the seedling age and the suitability of the particular area (Table 3).



Note: Bar graph represent the rainfall and line graph with and without dot represent the maximum and minimum temperature respectively. Addithonally, the red line indicates critical maximum temperature (35 degree celcious) for rice production

Figure 1. Weather data (Maximum temperature, Minimum temperature and rainfall) of the whole growing season across ten locations

Table 1. Description of soil characteristics and weather in nine locations

Environment ID	Locations	Soil Characteristics
L1	Vanga	Silty Clay Loam, (pH-5.8), (OM-1.6%)
L2	Habigonj	Clay Soil (pH 4.5-5.5)
L3	Barishal	Silty Clay-Loam
L4	Rangpur	Sandy Loam, Slight Acidic (pH6.4),
L5	Kustia	Light Textured Sandy-Loam to Loam
L6	Cumilla	Sandy Clay Loam to Loam, (pH 5.8,)
L7	Rajshahi	Calcareous Loamy Soil (pH8.0-8.5)
L8	Gazipur	Clay Loam
L9	Satkhira	Silty-Loam, (pH 8.0)
E10	Sonagazi	Sandy-Clay Loam (pH 7)

Data Collection

The crop was harvested when it reaches maximum maturity. Yield was calculated from 10 m² (252 plants), leaving the guard rows on both sides of the plot. Rice grain yield adjustments made to accommodate a 14% moisture content on a sundry basis and yield 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) was counted at the time of harvesting. The 1000-grain weight (TGW) was measured after sun drying, when the moisture content reached 14%.

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

SL No.	Genotype ID	Genotype designation	Pedigree	Parent
01	G1	BR(Bio)9777	116-12-2-5	
02	G2	BR(Bio)9777	124-1-1-2	
03	G3	BR(Bio)9777	84-4-1-1	♀BRRI dhan29
04	G4	BR(Bio)9777	116-12-2-4	×
05	G5	BR(Bio)9777	116-12-2-2	♂ FL378
06	G6	BR(Bio)9777	117-4-5-3	
07	G7	BR(Bio)9777	123-4-6-1	
08	G8	BRRI dhan29 (Ck)		

BR=Short form of BRRI, Bio=Biotechnology division

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

Location ID	Location	Date of Seeding	Date of Transplanting
L1	Vanga	26/11/15	07/01/16
L2	Habigonj	20/11/15	02/01/16
L3	Barishal	18/12/15	20/01/16
L4	Rangpur	27/11/15	07/01/16
L5	Kustia	04/12/15	18/01/16
L6	Cumilla	29/11/15	31/12/15
L7	Rajshahi	05/12/15	10/01/16
L8	Gazipur	01/12/15	10/01/16
L9	Satkhira	06/12/15	18/01/16
E10	Sonagazi	20/12/15	06/01/16

Statistical Analysis

Analysis of Variance (ANOVA)

A combined ANOVA was conducted to assess the main effects of genotype (G), environment (E), and the genotype × environment interaction (GEI). The likelihood ratio test (LRT) was performed to test the significance of GEI and its impact on grain yield and other traits.

Estimating the WAASB and WAASBY Indices

The Weighted Average of Absolute Scores (WAASB) index, based on the Singular Value Decomposition (SVD) of BLUP (Best Linear Unbiased Prediction) 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 kth interaction principal component axis (IPCA) and ($IPCA_{ik}$) is the score of the ith genotype (or environment) in the kth 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 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 ith genotype. In our study, we assumed that θ_Y and θ_S are the weights for the response variable and stability (WAASB) (Olivoto et al., 2019b)[19], which are 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 ith 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)[19]:

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

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

Multi-Trait Stability Index (MTSI)

The multi-trait stability index (MTSI) (Olivoto *et al.,* 2019b)[19] was analyzed using following formula:

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

Where F_{ij} is the jth score of the ith genotype, F_j is the jth score of the ideotype, and MTSI is the multi-trait stability index for the ith genotype. Therefore, the genotype with the lowest MTSI is more ideotype-like and has a high MPE for every variable examined in every location.

Steps followed to calculate the MTSI are:

1. Define the ideotype by specifying the traits to be maximized or minimized. Factor analysis of WAASBY is performed, followed by calculating the Euclidean distance between genotypes 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 the desirable traits.

Software and Tools

All statistical analyses were conducted using R software, incorporating packages such as *metan* for stability analysis, *agricolae* for ANOVA, and *ggplot2* for data visualization. The WAASBY and MTSI indices were computed using custom scripts within the R framework, following the methods described by Olivoto et al. (2019) and Resende et al. (2014).

3. RESULTS AND DISCUSSION

The present study employed the Weighted Average of Absolute Scores from BLUP (WAASB) and the Multi-Trait Stability Index (MTSI) to evaluate the stability and performance of rice genotypes under diverse environmental conditions. These complementary approaches provided insights into both the adaptability and multi-trait performance of the tested genotypes.

Table 4. Analysis of Variance (ANOVA) for yield and agronomic traits across genotypes and environments P Values

	P Values					
Source	**GY**	**PH**	**GD**	**PN**	**SPN**	**TGW**
ENV	2.01e-61***	2.47e-65***	2.14e-153***	3.10e-41***	2.49e-32***	1.34e-06***
REP(ENV)	4.30e-02*	4.81e-06***	1.21e-02*	2.93e-02*	3.52e-01	1.74e-01
GEN	2.22e-04***	3.72e-15***	4.22e-42***	1.33e-13***	7.27e-21***	4.90e-104***
GEN:ENV	1.08e-01	1.03e-12***	2.41e-45***	2.60e-02*	2.20e-03*	1.57e-08***

GY= Grain Yield, PH= Plant Height, GD= Growth Duration, PN= Panicle Number, SPN= Spikelets per panicle, TGW= Thousand Grain Weight, *** Significant at 0.001% level, * Significant at 0.05% level

The ANOVA results revealed that environmental factors (ENV) had the strongest influence on traits such as Growth Duration (GD) and Plant Height (PH), aligning with Yan et al. (2007) and Yue et al. (2022), who reported substantial environmental effects on phenological traits. Genotypic effects (GEN) were highly significant for all traits, especially Thousand Grain Weight (TGW), confirming strong genetic control as noted by Gauch et al. (2008). Genotype-by-environment interactions (GEN × ENV) were generally minor, particularly for Grain Yield (GY), indicating stable performance across environments (Eberhart & Russell, 1966), though significant interactions for GD and TGW suggest some differential genotypic responses. These findings reinforce the importance of multi-environment testing to select broadly adapted and stable genotypes.

Table 5. Deviance analysis, genetic parameters and variance components of nine rice genotypes studied in nine locations

SL No.	Parameters	GY	PH	PN	SPN	TGW
1	Phenotypic variance	0.19	10.46	0.56	51.73	1.72
2	Heritability	0.08	0.16	0.18	0.55	0.93
3	$GEIr^2$	0.08	0.43	0.11	0.11	0.03
4	h^2mg	0.70	0.73	0.84	0.96	1.00
5	Selection accuracy	0.84	0.86	0.92	0.98	1.00
6	r_{ge}	0.09	0.51	0.14	0.24	0.40
7	CV_g	1.73	1.24	2.83	4.49	5.62
8	CV_r	5.42	2.00	5.57	3.55	1.16
9	CV ratio	0.32	0.62	0.51	1.26	4.85

Where GY: Grain Yield, PH: Plant Height, GD: Growth Duration, PN: Panicle Number, SPN: Spikelets per panicle, TGW: Thousand Grain Weight,,PV: phenotypic variance, GEI r2: GEI coefficient of determination, h2mg: heritability of genotypic mean, Acc: accuracy of genotype selection, rge: association among genotypic values across environments, CVg: genotypic coefficient of variation, CVr: residual coefficient of variation, CV ratio: coefficient of variation ratio

Genetic parameter estimates identified Thousand Grain Weight (TGW) as the most promising trait, with the highest heritability (0.93), genotypic mean heritability (h²mg = 1.00), selection accuracy (1.00), and genetic variability (CVg = 5.62), indicating strong genetic control and selection potential. Spikelet Number per Panicle (SPN) also showed moderate heritability (0.55), high selection accuracy (0.98), good environmental stability, and a favorable CV ratio (1.26), supporting reliable genetic gains, consistent with Huang et al. (2011), Sasaki et al. (2021), and Lu et al. (2022). In contrast, Grain Yield (GY), Plant Height (PH), and Panicle Number (PN) exhibited low heritability (0.08–0.18) and poor genotypic stability, reflecting strong environmental influence and limited direct selection efficiency, as reported by Unnati et al. (2017) and Moumeni et al. (2018). These results highlight TGW and SPN as key traits for genetic improvement, with yield gains depending on integrated genetic and environmental management strategies.

Genetic parameters and mean performance evaluation

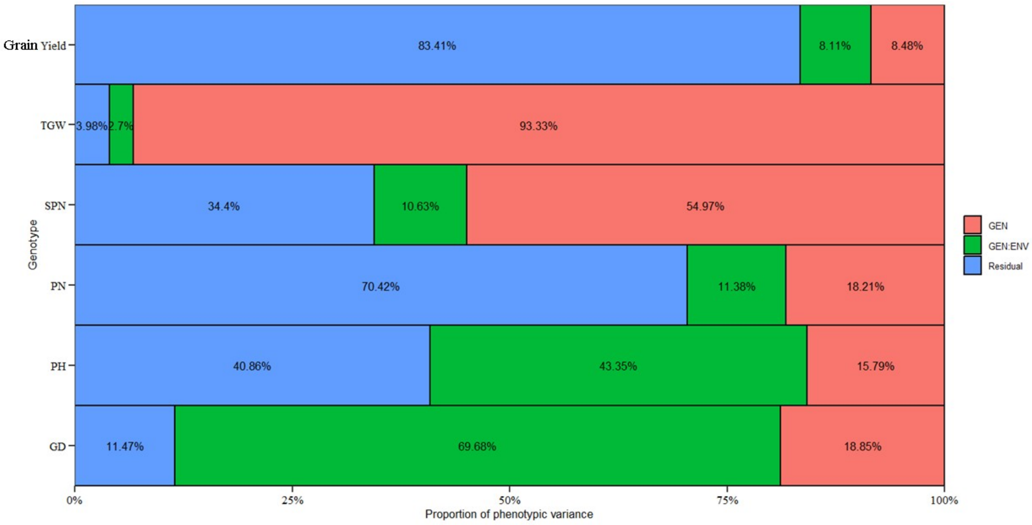


Figure 2. Assessment of rice trait variability across ten diverse environments: Exploring the proportion of phenotypic variance in seven genotypes and a check variety. Where GY: Grain Yield GD: Growth Duration, PH: Plant Height, SPN: Filled Spikelets/Panicle, PN: Panicle Number, TGW: 1000 grain weight

Partitioning of Phenotypic Variance

Phenotypic variance partitioning in rice traits highlights contrasting genetic and environmental influences (Figure 2). Grain yield showed low genetic contribution (8.48%) and dominant residual effects (83.41%), indicating strong environmental influence. In contrast, thousand-grain weight (TGW) had a predominantly genetic basis (93.33%) with minimal genotype-by-environment (GXE) interaction (2.7%), making it highly stable, as found by Chen et al. (2021). Filled spikelets per panicle (SPN) exhibited a moderate genetic influence (54.97%) and a significant G×E interaction (34.40%), reflecting sensitivity to factors like nutrient availability and water stress previously stated by Rang et al. (2011). Panicle number (PN) and plant height (PH) showed moderate genetic contributions (18.27% and 15.79%) but high residuals for PN (70.42%) and substantial GXE effects for PH (43.35%). Soil fertility and temperature variability might be responsible for this variability (Nishad et al. 2019). Growth duration (GD) was highly environment-sensitive, with GXE contributing 69.68%, which aligns with similar findings by Hossain et al. (2021). These findings emphasize targeting stable genetic traits like TGW for breeding while enhancing environmental adaptability for traits like GD and PH as suggested by Saud et al. (2022) and Wang et al. (2024).

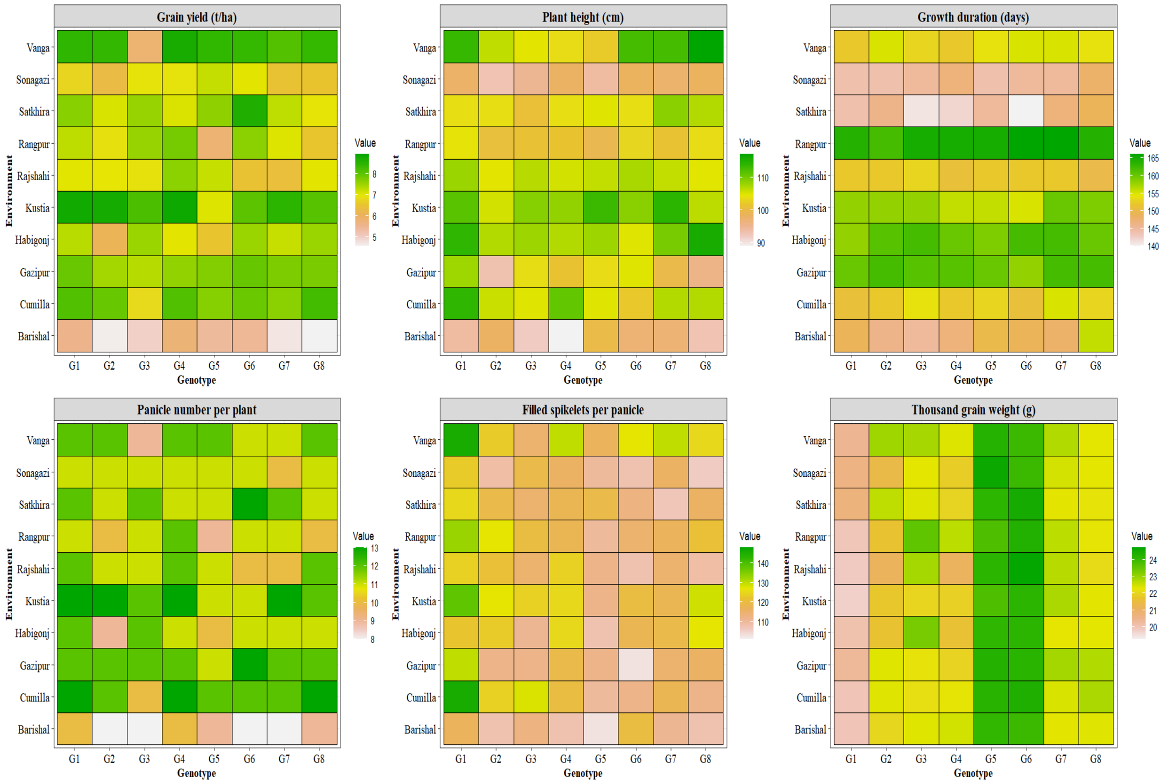


Figure 3. Average Yield, PH, GD, TN, SPN and TGW of eight rice genotypes across ten locations

The heatmap presents the performance of eight genotypes (G1 to G8) across ten locations (Vanga, Sonagazi, Satkhira, Rangpur, Rajshahi, Kushtia, Habigonj, Gazipur, Cumilla, and Barishal). The data cover six important traits: grain yield (t ha^{-1}), plant height (cm), growth duration (days), panicle number per plant, filled spikelets per panicle, and thousand-grain weight (g) (Fig. 3).Grain yield varied significantly, with G1 (Vanga) and G7 (Rajshahi) consistently performing well in locations like Rajshahi, Kushtia, and Gazipur, while G3 (Satkhira) and G6 (Cumilla) exhibited lower yields. G8 (Barishal) and G1 (Vanga) showed taller plants, potentially advantageous in certain environments but prone to lodging, whereas shorter genotypes like G3 and G4 (Rajshahi) might also benefit from high-density planting as suggested by Chand et al. (2019). G5 (Rangpur) and G7 displayed shorter growth durations, suitable for short cropping seasons, while G6 and G8 required longer durations, fitting longer growing seasons (Chen et al., 2022). High panicle numbers in G1 and G2 (Sonagazi) contributed to yield potential, with Vanga and Rangpur favouring this trait, while G4 and G7 showed fewer panicles (Khan et al., 2018). G1 and G7 excelled in filled spikelets, which are crucial for fertility, particularly in Vanga and Rajshahi, unlike G3 and G6, which had lower values, aligning with the findings of Shahidullah et al. (2010). Finally, G1 demonstrated the highest thousand grain weight, indicating superior grain quality, especially in Vanga and Rajshahi, compared to lower TGW in G2 and G6. Similar result was previously stated by Sadimantra et al. (2023).

The analysis of grain yield (t/ha) across eight rice genotypes (G1–G8) in multiple locations of Bangladesh revealed significant variability due to genotype-environment interactions (Figure 4). Locations like Cumilla and Vanga showed higher yields (over 8 t/ha), while Barishal recorded the lowest, particularly for G1 and G8, highlighting the role of environmental factors such as soil, rainfall, and temperature. Genotypes G5 and G6 excelled in Vanga and Rajshahi, indicating their adaptability to favorable conditions, while G1 and G8 showed lower yields but greater stability across locations, suggesting resilience to variable environments. The location-specific performance of G2 and G4 emphasizes the importance of multi-environment testing, as supported by Nafisah et al. (2020), Kumar et al. (2020) and Jutso et al. (2024), who highlighted the impact of environmental factors on rice stability and yield. These findings underscore the importance of selecting genotypes suited to specific agroecological zones. G5 and G6 are ideal for high-productivity regions like Rajshahi and Vanga, while G1 and G8 are better suited for marginal environments. Breeding programs should prioritize developing varieties that combine high yield with broad adaptability, as recommended by Rabbi et al. (2022) Tiwari et al. (2014), to enhance food security in Bangladesh.

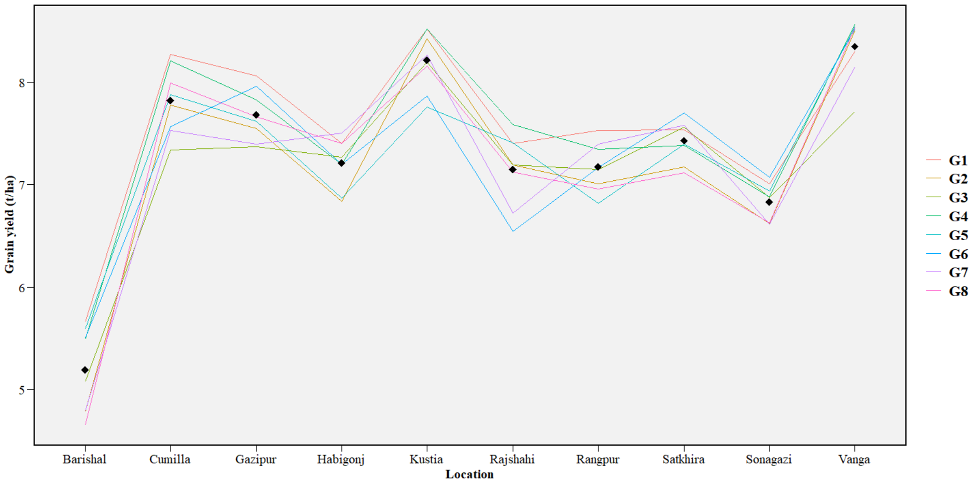


Figure 4. Grain yield (t/ha) variability eight rice genotypes (G1-G8) across ten locations (L1-L10) of Bangladesh

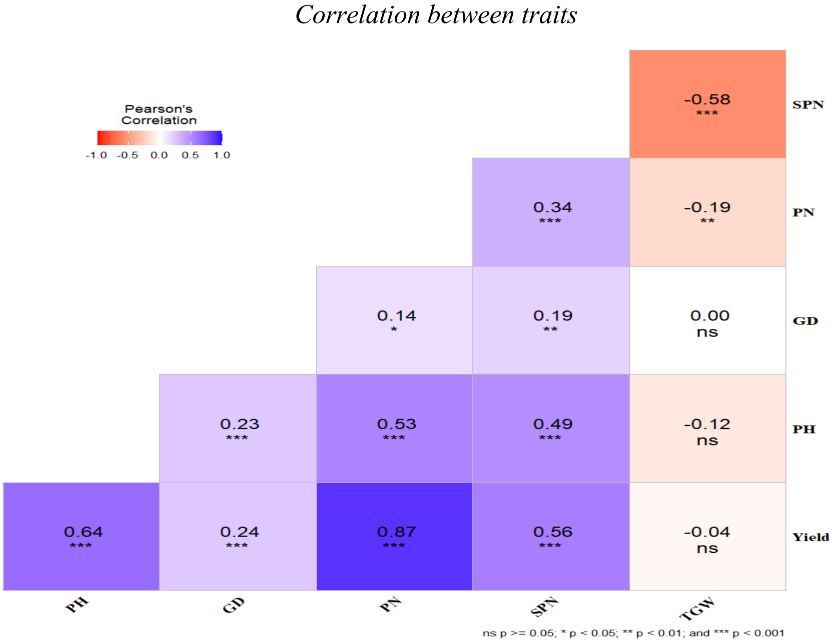


Figure 5. Pearson's correlation heatmap with coefficient values of different traits among eight rice genotypes evaluated in ten environments. PH=Plant Height, GD= Growth Duration, PN= Panicle Number, SPN= Spikelet per Panicle, TGW= Thousand grain weight, ns= non-significant, *= p<0.05, **= p<0.01 and ***= p<0.001

Figure 5 shows the correlation analysis, which highlights key rice traits influencing yield, with Panicle Number (PN) showing the strongest positive correlation with grain yield (0.87***), emphasizing its critical role in enhancing productivity (Yano et al., 2019). Spikelet Number per Panicle (SPN) also contributes significantly to grain yield (0.56***), although it negatively correlates with Thousand Grain Weight (TGW) (-0.58*), indicating a trade-off between grain number and size (Li et al. 2021, Parida et al. 2022 and Wang et al. 2023) implying that in this population, heavier grains do not necessarily translate to higher yields, likely because yield depends more on panicle and spikelet numbers. While there is a fundamental biological relationship often a trade-off between spikelet number per panicle and thousand grain weight, this relationship is significantly modulated by environmental conditions (Sheehy et al., 2001; Liu et al., 2024). Plant Height (PH) positively correlates with grain yield (0.64*), likely due to its support for more panicles and spikelets (Saran et al. 2023 and Banjare et al. 2023), while Growth Duration (GD) shows a weaker positive correlation (0.24*), suggesting its effect varies by environment (Vegara et al. 1966). PN and TGW exhibit a moderate negative correlation (-0.19), indicating a challenge in balancing grain size and number. Breeding strategies should prioritize increasing PN while managing trade-offs with TGW and SPN to optimize both yield and quality.

Genotype Selection through WAASB method

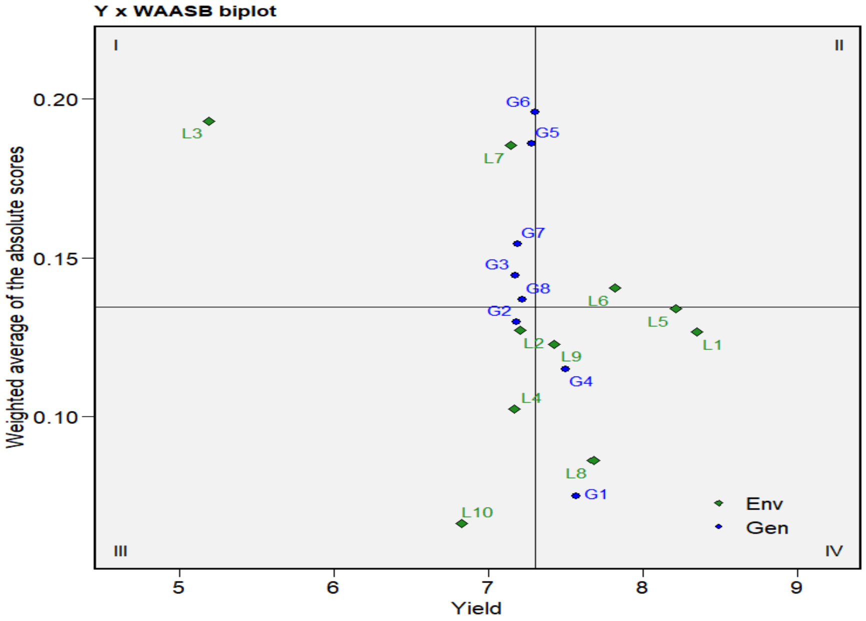


Figure 6. Weighted average of the absolute scores vs grain yield of eight rice genotypes studied in ten locations of Bangladesh.

The biplot analysis using the Weighted Average of Absolute Scores (WAASB) methodology effectively evaluates yield performance and stability across diverse environments, enabling the identification of broadly adaptable genotypes. Genotype G1 emerged as the most promising candidate due to its high yield and low WAASB value indicating high stability, as reflected by its position in Quadrant IV of the biplot (Figure 5). Its minimal environmental interaction effects indicate suitability for large-scale adoption, aligning with findings by Olivoto et al. (2020), Huang et al. (2021) and Ghazy et al. (2023), which confirm WAASB's reliability in balancing productivity and stability. In contrast, genotypes like G6 and G5, which exhibit high yields but lower stability, may perform well in specific favorable environments, whereas low-yield, unstable genotypes like G3 and G7 are less desirable. Moderately stable genotypes, such as G4, near the plot center, perform consistently in average conditions but lack the yield advantage of G1. These results align with those of Sharifii et al. (2020) and Huang et al. (2021), highlighting the importance of genotypes that balance yield and stability, particularly in resource-constrained environments.

Environmental factors also significantly influence performance. For instance, environment L1 supports high-yielding, stable genotypes like G1, while L3 exhibits poor adaptability. Conversely, environments like L8 and L10, with high stability but low productivity, may suit marginal conditions. These findings are consistent with Lata et al. (2010) and Misra et al. (2021), emphasizing stable environments' role in genotype evaluation.

Overall, G1 is the superior genotype due to its high yield, stability, and adaptability, making it ideal for diverse agroecological zones. This aligns with Hirawati et al. (2021) and Malosetti et al. (2013), who emphasize integrating yield and stability in genotype selection. The WAASB methodology, combined with biplot analysis, provides a robust framework for identifying genotypes that maximize productivity and resilience, ensuring economic and agronomic sustainability.

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

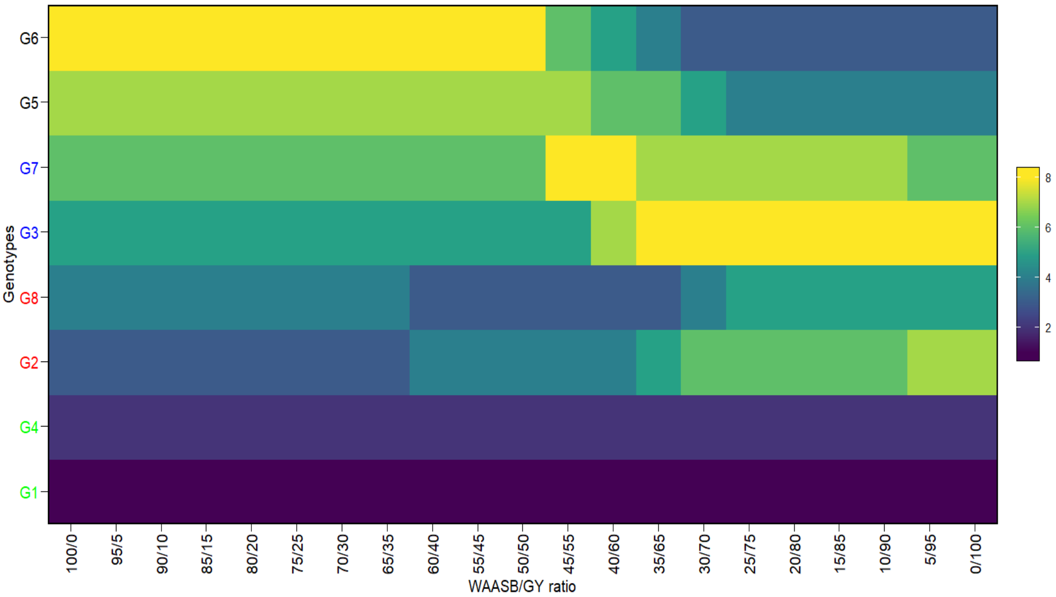


Figure 7. Based on yields and stability, eight rice genotype rankings are shown, each with a different weight. The four clusters correspond to four genotype classifications: (1) Productive but unstable genotypes, (2) Stable but low productive genotypes, (3) Moderately productive and medium stable genotypes, and (4) stable but poorly productive genotypes.

The heatmap illustrates the performance of eight genotypes (G1 to G8) across varying WAASB/GY ratios, representing trade-offs between stability (WAASB) and productivity (GY) (Figure 6). The horizontal axis displays ratios from 100/0 to 0/100, and the colour gradient, from dark blue (low) to yellow (high), reflects the magnitude of performance for each genotype under different scenarios. Genotype G6 consistently shows superior performance (yellow regions), indicating its adaptability across diverse ratios, while G5 and G7 perform moderately well under specific conditions. In contrast, G1 and G4 exhibit persistently low values (dark purple), suggesting poor adaptability but high productivity.

These results highlight the potential of genotypes like G6 and G5 for breeding programs targeting environments where both stability and yield are important, while G1 and G2 may lack the necessary versatility. Its exceptional productivity makes it suitable for favourable and predictable environments, though it may underperform in variable conditions. Multi-trait stability analysis is crucial for a more comprehensive investigation, particularly in capturing the complex interactions between traits under varying conditions. Further validation under real-world environments, considering additional traits such as stress tolerance, is needed to refine these findings. This study aligns with previous research emphasizing the importance of stability and adaptability indices, such as WAASB, in multi-environment trials and trait-based selection (Yan et al. 2007; Gauch 2018; Hongyu et al. 2014).

Genotype selection through MTSI index

The radial plot of the Multitrait Stability Index (MTSI) effectively evaluates genotype performance by combining productivity and stability across multiple traits. G1 emerges as the most promising genotype, positioned on the outermost edge of the red curve, signifying superior multitrait performance and stability (Figure 7). This highlights G1's potential for high yield and robust performance across diverse environments, aligning with findings from Olivoto et al. (2019) and Sharifii et al. (2021) on the importance of multitrait stability indices for sustainable crop production. In contrast, genotypes G3, G4, and G7, located closer to the plot's center, exhibit lower stability and weaker multitrait performance, making them unsuitable for recommendation. G5 and G6 show moderate multitrait performance but lack the overall stability of G1, limiting their suitability for broad cultivation. These observations are consistent with Poli et al. (2018) and Pradhan et al. (2024), which stress the need for genotypes that excel in both yield and multitrait stability for reliable performance in variable environments.

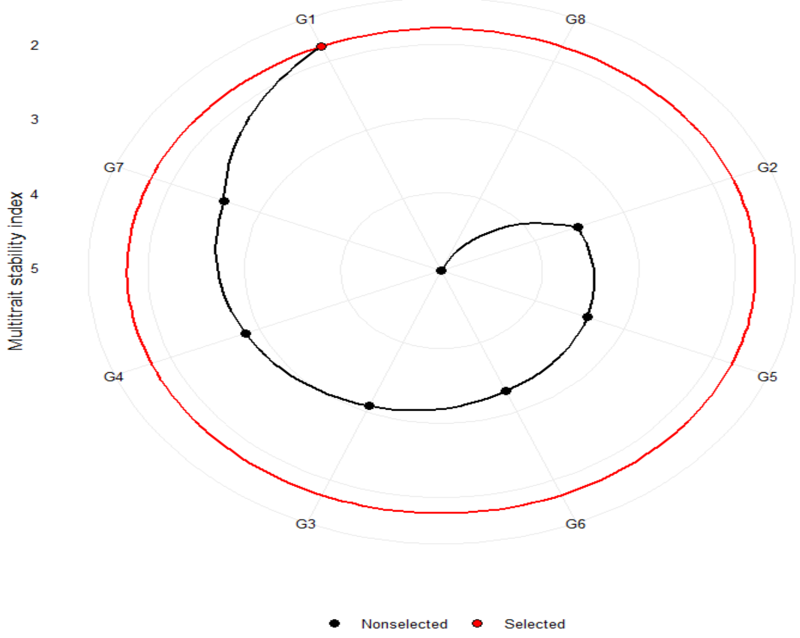


Figure 8. Ranking of rice genotypes based on the multi-trait stability index (MTSI).

The MTSI approach integrates multiple agronomic traits into a single framework, enabling breeders to identify genotypes that balance yield, resilience, and adaptability. This methodology, supported by studies like Zuffo et al. (2020), Yue et al., (2022) and Ponsiva et al. (2024), ensures effective selection for sustainable breeding programs. Based on above discussion, G1 stands out as the optimal genotype due to its high multitrait stability and performance, making it ideal for large-scale adoption and breeding programs. Future research should further assess G1 under specific biotic and abiotic stress conditions to validate its adaptability and contribution to sustainable agriculture.

Strength and Weakness of the Genotype

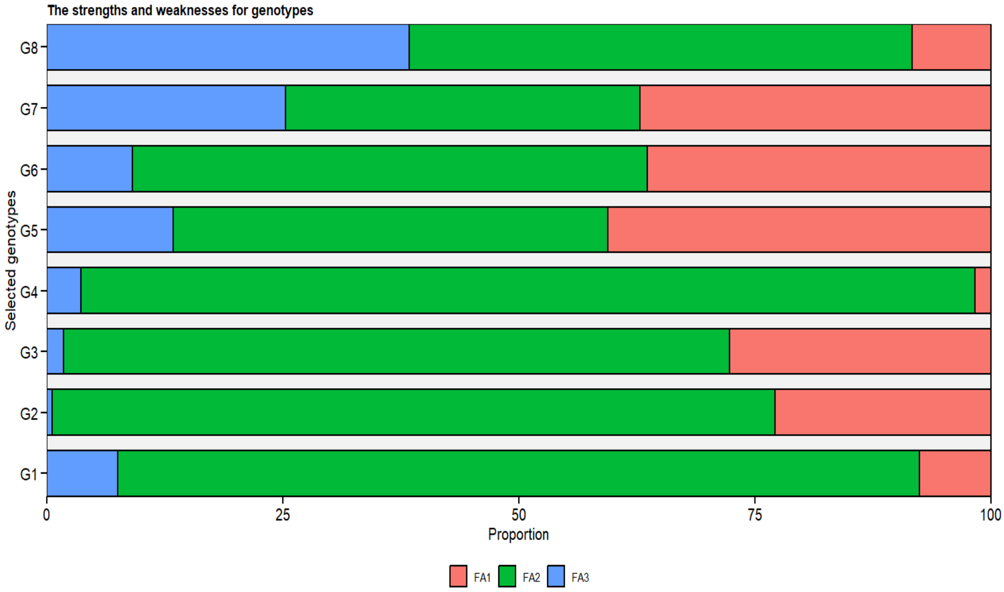


Figure 9. Strength and weakness of genotypes based on all traits

The data reveals key insights into the genetic potential and breeding opportunities for rice, focusing on three main factors: FA1 (Grain yield, panicle number [PN], and thousand grain weight [TGW]), FA2 (plant height [PH]), and FA3 (spikelet number [SPN] and growth duration [GD]) (Figure 8). For FA1, yield showed moderate variability, with a heritability of 0.70 and a selection gain of 2.53, indicating strong genetic influence and potential for improvement (Kanfany et al. 2021). PN, with a high heritability of 0.84 and a selection gain of 4.52, is an ideal target for breeding, as it directly impacts yield (Pallabi et al. 2024). However, TGW decreased, suggesting that while it is genetically stable (heritability of 0.99), the reduction may not be desirable unless it correlates with other improvements (Giri et al., 2018).

In FA2, PH showed a moderate increase, highlighting the need for a balanced approach to prevent lodging and optimize yield (Rani et al. 2017). FA3 revealed a significant increase in SPN, with a heritability of 0.96 and a selection gain of 11.28, indicating substantial potential for improving yield, as spikelet number directly influences grain count (Parida et al. 2022; Wang et al. 2023). GD showed a slight decrease, which may be a trade-off for other improvements, as growth duration often impacts yield and quality in complex ways (Kawano & Tanaka 1968). Overall, the findings suggest that prioritizing traits such as PN and SPN can lead to significant improvements in rice yield, thereby contributing to enhanced food security.

Winner Genotype

Table 6. Winner genotype selection for each trait (yield, plant height, panicle number, spikelet number per panicle, thousand grain weight, and growth duration) across different environments (L1 to L10)

SL. NO.	ENV	Yield	PH	PN	SPN	TGW	GD
1	L1	G4	G8	G2	G1	G5	G1
2	L2	G7	G8	G1	G1	G5	G1
3	L3	G1	G5	G1	G1	G5	G3
4	L4	G1	G8	G1	G1	G6	G2
5	L5	G4	G1	G1	G1	G6	G6
6	L6	G1	G1	G1	G1	G5	G1
7	L7	G4	G1	G1	G1	G6	G8
8	L8	G1	G1	G1	G1	G5	G6
9	L9	G6	G7	G3	G1	G5	G6
10	L10	G6	G1	G1	G1	G5	G1

The genotype selection across environments (L1 to L10) reveals significant variability in rice performance (Table 6). Genotype G1 consistently excels in panicle number, spikelet number per panicle, and growth duration, demonstrating adaptability and robust agronomic performance. Its moderate plant height balances high yield potential with resistance to lodging, aligning with Rani et al. (2017), who emphasized moderate plant height's role in crop management. G1’s dominance in panicle and spikelet numbers corroborates findings by Giri et al. (2021) and Wang et al. (2023), linking these traits to higher yields.

Genotypes G4, G6, and G7 perform strongly in terms of yield, especially in environments such as L1, L2, and L10, underscoring the importance of adaptability to diverse agroecological zones, as highlighted by Jing et al. (2010). Meanwhile, G5 excels in thousand grain weight, balancing grain size and yield, a trait Giri et al. (2018), Hasan-Ud- Daula and Sarker (2020) noted as complementary to productivity. However, trade-offs between grain size and yield require careful management.

G1’s ability to perform well across environments, including diverse growth durations, underscores its versatility, even in challenging conditions like shorter growing seasons or drought. In summary, G1’s superior performance and adaptability make it an ideal candidate for breeding programs aimed at improving rice productivity across agroecological zones.

4. CONCLUSION

This study highlights significant genetic and environmental influences on key rice traits across diverse environments. Genotype BR(Bio)9777-116-12-2-5 consistently outperformed others in yield, stability, and multi-trait performance, demonstrating strong adaptability across various agroecological zones. Traits like panicle number and spikelets per panicle were key contributors to yield, while trade-offs were noted between spikelet number and grain weight. BR(Bio)9777-116-12-2-5’s broad adaptability and robust performance make it an ideal candidate for breeding programs targeting high yield and resilience. These findings emphasize the importance of integrating genetic potential and environmental interactions to enhance rice productivity and food security.

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