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Dissecting Genotype x Environment Interaction and Adaptability for Grain Yield in Irrigated Rice Systems

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ABSTRACT

Rice cultivation is widely adapted across diverse agro-climatic zones and serves as a global staple food, supplying up to 75% of caloric intake for nearly 3 billion people worldwide. In Bangladesh, evolving climate patterns are increasingly threatening rice productivity across diverse agro-ecological regions. Therefore, identifying stable, high-yielding genotypes across agro-climatic zones in Bangladesh is essential for sustaining national food security. This study evaluated the yield stability of 10 advanced inbred lines with 2 HYV as checks across 10 diverse agro climatic zones using AMMI and GGE models. Eight yield-related traits were analyzed, including days to maturity, plant height, number of effective tillers, panicle length, number of filled grains, percent spikelet sterility, 1000-grain weight, and grain yield. Combined ANOVA revealed significant effects of genotype, environment, and GEI on all traits, which were significantly associated with yield. The first two PCs explained 29.8% and 23.5% of variation in AMMI, and 30.66% and 22.79% in GGE. Among the studied genotypes, we found genotype G6 (NGR750-1) was the most stable comparable to the check HYV BRRI dhan89. Stability analysis showed that GEI strongly affects grain yield and the selection of stable genotypes across environments. Further investigation is required to elucidate the adaptive mechanisms of the identified genotype, focusing on physiological and molecular determinants of grain yield across diverse environments. The identified genotype could be used further within the framework of the rice improvement program or released as a high-yielding cultivar following multi-location evaluation.

1. Introduction

Rice (*Oryza sativa* L.) is a cereal crop of global significance, and as a major food source, it provides 35-75% of the calories consumed by over 3 billion people worldwide (Yu et al., 2012; Biswas et al., 2024). Global annual rice production exceeds 800 million metric tons, with cultivation spanning approximately

160 million hectares worldwide (FAOSTAT, 2024). It is grown under a variety of agro climatic conditions. Plant breeders frequently use yield performance and phenotypic expression to screen and select rice cultivars in test environments. Their efforts are more effective and successful as a result of these methods, to

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the point where their decisions provide a complete understanding of the environmental influences on the associated mechanisms and the phenotypic expression of such influences. As a result, the majority of crop technology efforts are focused on reducing risk, increasing yield stability, lowering costs, and increasing high returns (Oladosu et al., 2016). The rapid growth of world population, climate change, and limited arable land are expected to increase the production of cereal crops such as rice, wheat, and maize (Kang and Priyadarshan, 2007; Cordero-Lara, 2020). Rice production and productivity are hampered by a variety of factors, including a lack of improved varieties, diseases, and pre-and post-harvest machinery (MoARD, 2010).

In Bangladesh, rice is the staple food crop and plays a central role in food security and the national economy. The enormous area of over 11.46 million hectares helps Bangladesh to produce about 40.46 million tons of rice, placing the country as the third largest rice-producing in the world (BBS, 2025; FAOSTAT, 2025). The average yield of clean rice is just 3.55 tha⁻¹, which is significantly less than the potential yield of the widely used cultivated rice varieties. The main cause of the lower average yield is the variety's poor performance in various environments. New cultivars with high production potential and broader adaptability should be developed to cope with the continuously growing population. Yield is a complex trait that is largely influenced by genetic and environmental factors. It also depends on numerous traits. An ideal crop genotype should have a high mean yield and yield stability when grown in a diverse environment. Plant breeding programs and the introduction of new crop cultivars depend on the G x E interactions (McLaren and Chaudhary, 1994; Prasad and Singh, 1990).

The interaction between genotype and environment is a major concern of breeders. A genotype's stability performance is a trait that is genetically impacted (Patra and Mohanty, 1987). Wider adaptability and stability are crucial for developing an efficient breeding program. Determining a genotype's performance in various environments requires examining G x E interactions. This experiment examined certain progressive breeding lines and varieties as checks across various environments to identify the best and most stable genotypes.

The Additive Main Effects and Multiplicative Interaction (AMMI) model is a hybrid model that separates the additive variance from the interaction portion and then uses Principal Component Analysis (PCA) to generate a new set of coordinate axes that better explains the interaction pattern (Islam et al., 2014; Khatun et al., 2026). The AMMI analysis and the biplot facility were used to analyze the promising rice yield data in order to identify high yielding and stable genotypes that are adapted to various production environments, to determine the nature and size of G x

E interaction effects on grain yield in diverse production environments, and to identify the regions where rice genotypes would be adapted and produce competitive yields on a cost-benefit basis.

The study aimed to analyze the promising rice yield data in order to identify high yielding and stable genotypes that are adapted to various production environments. It also aimed to ascertain the nature and size of G x E interaction effects on grain productivity under diverse agro-climatic conditions and to pinpoint the regions where rice genotypes would be adapted and produce competitive yields based on a cost-benefit analysis.

2. Materials and method

2.1. Study area, Plant materials, Experimental design and Procedures

The study was carried out at nine BRRI regional stations and the headquarter of BRRI, viz., Barishal (E1), Rangpur (E2), Gazipur (E3), Bhanga (E4), Cumilla (E5), Gopalganj (E6), Habiganj (E7), Kushtia (E8), Rajshahi (E9), and Sonagazi (E10) of Bangladesh during the Boro season 2021-22. The trials were carried out under irrigated conditions. The study included ten rice genotypes, including two standard checks, viz., NGR 414-1(G1), NGR 418-1(G2), NGR 467-2(G3), NGR 521-2(G4), NGR 522-1(G5), NGR 750-1(G6), NGR 796-2(G7), NGR 1161-3(G8), NGR 1255-1(G9), NGR 1308-2(G10), BRRI dhan58 (G11), and BRRI dhan89 (G12). The experiment was set up at each location using a randomized complete block design with three replications. Thirty-five-days-old seedlings were planted at 2-3 seedlings with a spacing of 20 cm x 20 cm. The unit plot size was 10.8 m². Inorganic fertilizers were applied @ 260:100:120: 110:10 kg urea, triple super phosphate (TSP), muriate of potash (MoP), gypsum and zinc sulphate per hectare, respectively. Urea was applied in three equal splits at 15 days interval starting from 12 days after transplanting. Total amount of TSP, two-thirds of MoP, gypsum and zinc sulphate were applied at final land preparation. Rest one-third of MoP was applied with the third top dressing of urea. Crop management practices were done as and when necessary.

2.2. Site Characterization and Weather Condition

A panel of twelve advanced rice lines was cultivated in 10 different environments covering 9 out of 30 agro ecological zones determined on the basis of physiographic, hydrology, cropping pattern, season, soil types, and tidal activity of Bangladesh. The range of the average temperature during the cropping period (Nov. to May) was 22.55 to 26.130C. The highest degree of average temperature was observed in Cumilla, followed by Sonagazi (24.560C), Gazipur (24.480C) and Barishal (24.080C), and the average temperature found in Rangpur. The highest average

relative humidity prevailed in Barishal (80.83%), whereas the lowest average was found in Rangpur (67.79%). During the cultivated period, the average precipitation rate ranged from 4.99 mm in Habiganj followed by Cumilla (2.82 mm), Sonagazi (2.61 mm), and Rangpur (2.15 mm) to 0.48 mm in Rajshahi. The highest average sunshine period was recorded in Kushtia (6.93 hrday⁻¹) and the lowest average was calculated in Rangpur (5.01 hrday⁻¹).

2.3. Data collection

Five representative plants for each genotype in each replication were randomly selected to record data on eight different yield and yield contributing traits such as days to maturity (days), plant height (cm), effective tillers per hill (no.), panicle length (cm), filled grains per panicle (no.), spikelet sterility (%), 1000-grain weight (g), and grain yield (tha⁻¹).

2.4. Data analysis

The aggregated information from different environments was used to perform an analysis of

variance (ANOVA), boxplots of yield and yield component traits, GGE biplots for discrimination and representativeness, GGE biplots (which-won-where pattern), and Multi-trait Stability Index (MTSI) analysis using an R package for multi-environment trial analysis (Olivoto and Lúcio, 2020).

3. Results and discussions

3.1. Yield and yield contributing traits

The boxplot revealed significant variability in yield-related traits such as plant height, effective tillers, filled grains, and grain yield across 12 genotypes and 10 environments. Average GY was significantly higher in E4 (Bhanga) than in other environments, whereas average plant height (PH), effective tillers per hill (ET), and filled grains per panicle (FG) were higher in E8 (Kushtia), E1 (Barishal), and E6 (Gopalganj) environments, respectively (Fig. 1).

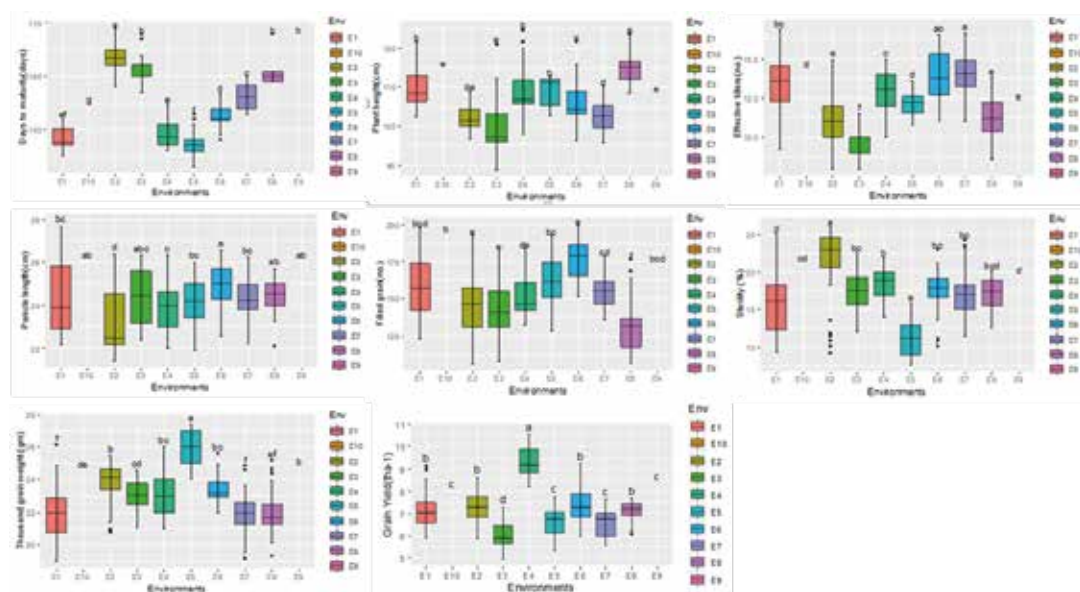


Fig. 1. Comparisons of yield-component traits and grain yield performance among ten environments. Boxplots with different lowercase letters indicate statistically significant differences (One-way analysis of variance followed by Scheffe's post hoc test; $P < 0.05$)

To quantify the interactions and describe the main effect among and within the sources of variations, a combined analysis of variance is used. Table 1 indicates the pooled analysis of variance. Days to maturity (days), plant height (cm), effective tillers per hill (no.), panicle length (cm), filled grain per panicle

(no.), spikelet sterility (%), thousand-grain weight (g), and grain yield (tha⁻¹) all showed significant differences ($P < 0.01, 0.05$). The percentage of variation for all traits is explained by the partitioning of the total sum of squares shown in Table 1. All traits showed significant variation due to environmental

factors ranging from 9% to 77%. The majority of the variation in genotype performance is caused by a large difference in genotype mean between locations. In comparison, replication showed the least variation, ranging from 0.33% to 3.46%. Panicle length contributed the most to genotype effects (48.89%), while plant height and spikelet sterility percent showed similar variation due to genotype effects (16.88% and 15.97% of the total sum of squares, respectively). However, there was a small variation due to genotype effect in filled grain number per panicle and grain yield tons per hectare (4.96% and 4.33% of total sum of square, respectively). The total sum of squares for days to maturity, plant height in cm, effective tiller number, panicle length in cm, filled grain number per panicle, spikelet sterility percent, thousand grain weight in g, and grain yield tons per hectare accounted for 7.30%, 16.82%, 15.37%, 19.04%, 26.04%, 20.61%, 14.04%, and 21.92% of the total sum of squares. For days to maturity, the variation in environment (76.63%) indicated that the tested environments in this current study were diverse, with the greatest differences among environment effects causing the most variation in grain yields. The GE interaction explained 21.92% of the variation in yield tons per hectare. For the explained sum of squares of yield tons per hectare, the magnitude of the GE interaction was approximately five times that of genotypic variation. This demonstrated that genotype responses differed significantly across environments. According to Kang and Pham (1991), a large amount of GE interaction reduces genotype effectiveness by

confounding yield performance through the dissociation of phenotypic from genotypic value. The substantial degree of variance seen in this study's GE interactions concerning the G impact raised the prospect of various mega-environments with various genotypes that produce high yields (Yan and Kang, 2002). According to Freeman (1973), the main reason for genotype evaluation across a wide range of environments is to estimate adaptability and stability. The significant GE interaction effects demonstrated that genotypes responded differently to different environments or locations, emphasizing the importance of testing rice varieties at multiple locations. It also demonstrates the difficulties that rice breeders face when selecting the best varieties for release. When genotype-by-environment interaction is caused by predictable factor (environment) variation, rice breeders have the option of developing genotypes that perform well in multiple environments (Dehghani et al., 2006). The percentage of explained sum of squares values revealed that the highest proportion of DM variation (76.73%) was due to environment; the highest proportion of PH variation (41.09%); the highest proportion of ET variation (46.43%); the highest proportion of FG variation (26.83%) was due to environment; the highest proportion of ST variation (30.31%) was due to environment; and the highest proportion of TGW variation was due to environment. Genotype effects explained a large proportion of PL variation (48.89%). GY was more affected by the environment and GEI, accounting for 47.55% and 21.92% of total variation, respectively.

Table 1

Combined analysis of variance (ANOVA) of yield-component traits and grain yield.

Source	Df	DM	PH	ET	PL	FG	ST	TGW	GY								
		MS	%ESS	MS	%ESS	MS	%ESS	MS	%ESS								
E	9	1729.78**	76.63	994.11**	41.09	76.87**	46.43	6.67**	8.97	5743.43**	26.83	226.04**	30.31	51.25**	42.27	29.05**	47.55
Rep (E)	20	5.31*	0.52	19.89**	1.83	2.58**	3.46	0.15 ^{NS}	0.44	215.31*	2.24	9.35**	2.79	0.41 ^{NS}	0.76	0.09 ^{NS}	0.33
G	11	141.89*	7.68	334.12**	16.88	7.17**	5.30	29.76**	48.89	868.58**	4.96	97.43**	15.97	14.10**	14.22	2.17**	4.34
GEI	99	14.98**	7.30	36.99**	16.82	2.31**	15.37	1.29**	19.04	506.77**	26.04	13.98**	20.61	1.55**	14.04	1.22**	21.92
Residuals	220	0.52	0.56	6.48	6.55	0.95	14.07	0.11	3.62	121.67	13.89	2.96	9.71	0.73	14.67	0.10	3.93

E, environment; Rep (E), replication (environment); G, genotype; GEI, genotype-environment interaction; DM, days to maturity in days; PH, plant height in cm; ET, effective tillers number per hill; PL, panicle length in cm; FG, filled grain number per panicle; ST, spikelet sterility percent; TGW, thousand-grain weight in g; GY, grain yield ton per hectare; Df, degrees of freedom; MS, mean square; ESS (%), proportion of explained sum of squares; *, $p < 0.05$; **, $p < 0.01$; ns, not significant.

3.2. Environmental evaluation and adaptability in specific environments

View of GGE biplot (Discrimination and representativeness)

GGE biplots were used to compare discriminativeness and representativeness (Fig. 2). The lengths of environment vectors from the biplot origin are proportional to the standard deviation within each environment, representing the environments' discriminating ability. Among the ten environments, environmental conditions (E1) demonstrated the greatest discriminating ability for ET and PL, while environmental conditions (E2) demonstrated the

greatest discriminating ability for FG, ST, and TGW and environmental conditions (E10) demonstrated the greatest discriminating ability for DM and PH. (Fig. 2). Discriminating ability was ranked as follows for the term GY: $E9 > E1 > E2 > E3 > E7 > E4 > E5 > E10 > E6 > E8$. The angle formed by the environment line and the average environment axis (AEA), which runs through the average environments and biplot origin, indicates how representative each environment is. E2 was more representative than the other environments for DM, ST, and TGW, exhibiting a smaller angle with the AEA line. E7 was the most representative of ET and GY. Environmental condition E1 was the most representative for PH; E9 was the most representative for PL; and E4 was the most representative for FG.

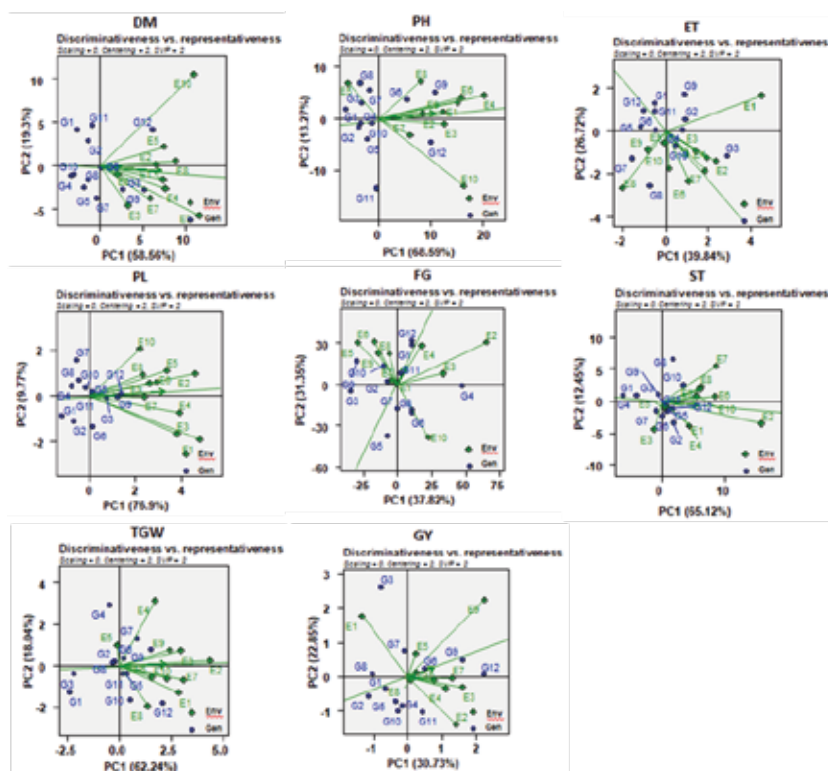


Fig. 2. Discrimination and representativeness view of the genotypic main effects plus genotype by environment interaction (GGE) biplots based on yield-component traits and grain yield data of 12 genotypes in ten environments. Green diamonds represent individual trials in 10 different environments. The average environment for each plot is indicated with a green arrow. The average-environment axis (AEA) is indicated with a thick green line passing through the biplot origin and the average environment arrow. Blue circles show individual genotypes. DM, days to maturity; PH, plant height in cm; ET, effective tillers number; PL, panicle length in cm; FG, filled grain number per panicle; ST, spikelet sterility percent; TGW, thousand-grain weight in g; GY, grain yield ton per hectare.

3.3. Polygon view of gge biplot (which-won-where pattern)

Based on 'which-won-where' patterns in GGE biplots (Fig. 3), environments were separated into prospective MEs. A polygon is formed by connecting the genotypes furthest from the biplot origin with straight lines, containing all other tested genotypes. Perpendicular lines drawn from the biplot's origin to each polygon's side divide the biplot into environment sectors. Genotypes were assigned genotype codes (G1-G12) to make them easier to identify in the plot. For DM, the ten environments were divided into two MEs: E2, E5, E8, and E10 in the first; and E1, E3, E4, E6, E7, and E9 in the second. The first sector's vertex genotype was G12 (BRRI dhan89), whereas the second sector's vertex genotype was G3 (NGR 467-2). The ten environments were separated into three MEs for PH. The first ME with E5 and G8 (NGR 1161-3) was the best-performing genotype. G9 (NGR 1255-1) was the winning genotype in the second ME, which included E1, E2, E4, E6, and E8. G12 (BRRI dhan89) was the winning genotype in the third ME, which included E3, E7, E9, and E10. For ET, G3 (NGR 467-2) and G8 (NGR 1161-3) genotypes performed best in the first ME (E1, E2, E3, E4, and E7) and second ME (E5, E6, E8, E9, and

E10), respectively. For PL, all environments encompassed in one sector (E1-E10) and genotypes G12 (BRRI dhan89) performed best. According to these findings, G12 (BRRI dhan89) was the winning genotype, with the longest panicle in all settings. For FG, the best-performing genotypes in the first ME (E1, E5, E6, E7, and E9), second ME (E4 and E8), third ME (E2 and E3), and fourth ME (E10) were G9 (NGR 1255-1), G1 (NGR 414-1), G4 (NGR 521-2), and G5 (NGR 522-1), respectively. For ST, the best-performing genotypes were G8 (NGR 1161-3), G10 (NGR 1308-2), and G2 (NGR 418-1) in the first ME (E7), second ME (E2, E6, E8, E9, and E10), and third ME (E1, E3, E4, and E5), respectively. For TGW, G4 (NGR 521-2) and G9 (NGR 1255-1) were the best-performing genotypes in the first ME (E4 and E5), second ME (E3 and E9), and third ME (E1, E2, E6, E7, and E8), respectively. The ten environments in GY's multiple environment trials were divided into two ME sectors. G3 (NGR 497-2) and G12 (BRRI dhan89) genotypes performed best in the first ME (E1, E5, and E6) and second ME (E2, E3, E4, E7, E8, E9, and E10), respectively. These results showed that G3 (NGR 497-2) and G12 (BRRI dhan89) were the winning genotypes, with the highest yield for the first and second MEs, respectively.

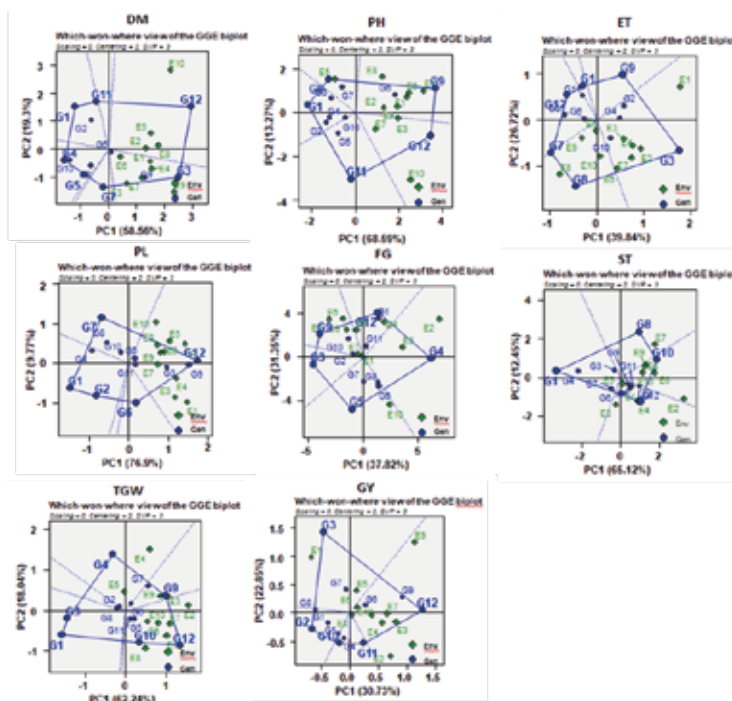


Fig. 3. DPolygon view of GGE biplot for 'which-won-where' analysis based on the yield-component traits and grain yield data of 12 genotypes in ten environments. Green diamonds represent individual trials in 10 different environments. Small and large green circles show individual genotypes and the genotypes with the highest performance, respectively. DM, days to maturity; PH, plant height in cm; ET, effective tillers number; PL, panicle length in cm; FG, filled grain number per panicle; ST, spikelet sterility percent; TGW, thousand-grain weight in g; GY, grain yield ton per hectare.

3.4. Multi-trait stability index (mtsi) analysis

All yield and quality traits, including DM, PH, ET, PL, FG, ST, TGW, and GY, were used to calculate MTSI (Table 2). The Varimax rotation criterion was used to determine the final loadings. The communality ranged

from 0.746 for TGW to 0.979 for ET after Varimax rotation. The genotypes' MTSI values are displayed in Fig. 4. Based on their MTSI scores, the genotypes denoted by red color dots were selected. The order of the stable and selected genotypes was G6 (NGR 750-1), followed by G12 (BRRI dhan89) (Fig. 4).

Table 2

Communalities and selection differential of various characters based on MTSI.

Sl. No.	VAR	FA1	Communality	Uniquenesses	Xo	Xs	SD	SD (%)
1	DM	0.0118	0.853	0.147	47	59.4	12.4	26.3
2	PH	0.57	0.946	0.0543	46.7	65.9	19.2	41.0
3	ET	-0.119	0.979	0.0207	49.3	54.8	5.41	11.0
4	PL	-0.166	0.886	0.114	54.5	57.5	2.99	5.48
5	FG	0.337	0.837	0.163	44.6	64.4	19.8	44.3
6	ST	0.561	0.761	0.239	59.8	74.6	14.8	24.8
7	TGW	0.823	0.746	0.254	54.9	70.8	15.9	29
8	GY	0.891	0.856	0.144	51.7	73.6	21.9	42.4

Xo, mean of genotypes; Xs, mean of selected genotypes; SD, selection differential.

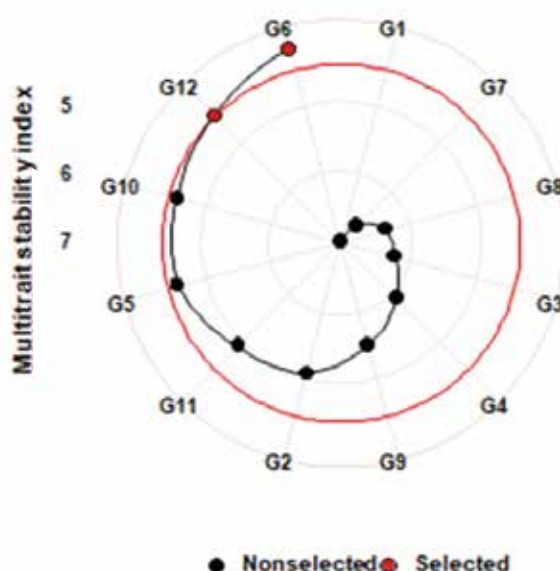


Fig. 4. Multi-trait Stability Index (MTSI) values of the genotypes.

4. Conclusions

The primary goal of plant breeders is to develop high yield potential varieties to sustain agricultural production. Such cultivars should also exhibit stable performance and broad adaptability across diverse environments. Combined ANOVA showed significant variation due to genotype, environment, and GEI for

all yield related traits, with environment contributing the largest share of total variance. Thus, the environment had a strong influence on the phenotypic expression of yield components and grain yield. The AMMI biplot showed PC1 explaining over 45% of variation for most traits (except yield at 29.8%), while PC2 accounted for less than 30% for all yield-related traits. Genotypes NGR750-1 and BRRI dhan89, with

near-zero scores, exhibited high stability across environments. The results indicate that the genotype NGR750-1 is stable and widely adaptable, making it a promising high yielding cultivar alternative to BRRI dhan89 for diverse agro-climatic zones of the country.

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