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Rice Genotypes' Yield Consistency and Adaptability in the Diverse Environment of Bangladesh

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Abstract

A rice genotype's stability and adaptability are necessary for its commercial adoption as a variety under a wide range of growing environments. This study aimed to evaluate the Genotype × Environment (GE) interaction and to find a stable rice genotype for varietal development. Utilizing additive main effects and multiplicative interaction (AMMI) and genotype main effect and genotype by environment interaction effects (GGE) analyses, three rice genotypes were studied for grain yield stability across seven environments. The GGE and AMMI studies showed strong GE interactions, showing variability in genotype and environment. The genotype RM-LD-1 was selected as the top performer for the trait, grain yield, according to AMMI1 and AMMI2 biplot models. The genotype RM-LD-1 had the highest yield and the most stability, according to a GGE biplot study (mean vs. stability). According to the genotype ranking graph, the genotype RM-LD-1 was determined as the best genotype for grain yield, followed by BAU-3 and BRRI dhan28. The genotype RM-LD-1 performed better in the environments Chapainawabganj, Rangpur, Sunamganj, and Mymensingh, according to the GGE biplot-polygon analysis. The genotype RM-LD-1 might be considered as a variety based on yield and wide environmental adaptation.

Keywords: Environment, Interaction, Multiplicative Rice, Yield

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Introduction

Rice is the staple meal of more than 3.5 billion people worldwide, accounting for 35–80 percent of total calorie uptake (Wassmann et al., 2009). By 2050, the world's population will reach nine billion people, necessitating a 60–110 percent increase in rice production over current levels (Ray et al., 2013). According to recent climate change predictions, high-temperature occurrences might harm 20 M ha of rice-growing land in Asian countries, reducing production by 14% in South Asia, 10% in East Asia and the Pacific, and 15% in Sub-Saharan Africa (Senguttuvel et al. 2021).

Rice is the main staple food for many Bangladeshi people. Stable and predictable rice yields are essential for maintaining food security and preventing food shortages in Bangladesh. Yield consistency is crucial for new rice variety development programs because it ensures a stable and reliable food supply. Consistent yields of an advanced rice line help farmers manage risks associated with fluctuating weather patterns, pest outbreaks, and market prices, leading to improved livelihoods and food security for the country.

For sustainable rice production, stable and broad adaptable cultivars are needed to assure improved yield and quality performance over various environmental conditions (Snowdon et al. 2021). The stability of a quantitative trait like yield potential is the consequence of several interactions between the variety's genetic makeup and the growing environment (Sserumaga et al., 2018). Furthermore, rice grain yield is a polygenic trait strongly affected by biotic and abiotic factors such as rainfall, temperature, moisture, and other biotic and abiotic factors (Raza et al., 2019). Thus, it's essential to understand the genotype-environment interaction before launching a crop variety for mass production (Chairi et al., 2020). A multi-environment trial (MET) is essential for determining a stable genotype across several settings or the best environment for a specific genotype (Pour-Aboughadareh et al., 2022). Plant breeders need to know about GE interactions to release the best variety for commercial production. The additive main effects and multiplicative interaction (AMMI) model is an effective statistical tool for the analysis of the above-mentioned issues (Gauch et al., 2006; Zobel et al., 1988; Gauch et al., 2008).

AMMI identifies the significant effects (additive effect) and the non-additive residual effect using analysis of variance (ANOVA) and principal component analysis to determine the GE interaction (Fana et al., 2019; Krishnamurthy et al., 2021). GGE biplots exhibit both genotype and genotype by environment variations (Xiao et al., 2019). The stability and adaptability of a specific advanced line can be detected by studying the G×E interaction analyzed with AMMI and GGE biplot models (Rani et al., 2021). Therefore, this study aimed to apply the AMMI model to evaluate the magnitude of the effect of GEI and the stability of grain yield of the advanced rice line tested in different locations.

Method and Materials

During the dry season (Boro) of 2020-21, three rice genotypes were evaluated in seven different environmental conditions at different districts of Bangladesh: Chapainawabganj (E1; AEZ 26), Gopalganj (E2; AEZ 14), Rangpur (E3; AEZ 3), Barishal (E4; AEZ 13), Magura (E5; AEZ 11), Sunamganj (E6; AEZ 21), and Mymensingh (E7; AEZ 9). A stable rice genotype (RM-LD-1) and two released varieties (BAU-3 and BRRIdhan-28) were used in this study. The total experimental plot number was 168, with an individual plot size was 3m x 4m following RCBD design. Thirty-five-day-old single seedlings were transplanted in 20 cm x 20 cm spacing. Fertilizers were applied at the rate of 130:50:80: 30:2.5 kg ha^{-1} Urea, TSP, MP, gypsum, and ZnSO4, respectively, as per the fertilizer recommendation manual of Bangladesh Rice Research Institute (BRRI). Required weed management and plant protection measures were taken for healthy crop production during the whole growth period. To reduce the border impacts, two border rows were employed. The yield and yield contributing characters were recorded for statistical analysis.

Statistical Analysis

The statistical program R-Studio was used to create the AMMI and GGE biplots (R Studio, 2020; R Studio Team, 2020), along with all descriptive analysis and graphical presentations.

Results and discussion

Phenotypic performances of rice genotypes

Table 1 presents the mean data of different parameters as a result of genotype and location interaction. Among the genotypes, BAU-3 was the longest plant of all, having a height of 146.8cm, and RM-LD-1 was the shortest, having 83 cm in height. Average days to maturity ranged from 139 (RM-LD-1) days to 150 (BAU-3) days. In the case of the number of effective tillers, BRRI dhan28 possessed a higher value (13) than RM-LD-1 & BAU-3 (12). The longest panicle length (27.23cm) was produced by BAU-3, and the shortest (19.53 cm) by RM-LD-1. The highest yield (8.5 t ha^{-1}) was from the genotype RM-LD-1, and the lowest (6.24 t ha^{-1}) was from BAU-3.

Table 1. Phenotypic performance of the selected genotypes of rice in different locations

Location	Genotype	Plant height(cm)	Days to maturity (days)	Effective tillers/plant	Panicle length(cm)	Yield (ton/ha)	Filled grain/panicle	Thousand-seed weight (g)
	RM-LD-1	86.87lm	147e	13c-f	20.60j-l	7.25cd	151.33a-c	24.67ab
E1	BRRIdhan-28	103.20h	160a	15b	23.03fg	6.26jk	143.33b-e	21.83g-i
	BAU-3	123.57b	156b	12g	27.73a	6.24k	133e-g	22.67df
	RM-LD-1	90.87jk	132l	11h	19.70kl	6.66f-j	131.67e-g	23.37cd
E2	BRRIdhan-28	118.60cd	140ij	13d-g	24.43c-e	6.74e-h	135.33d-g	21.23i
	BAU-3	125.27b	145fg	12e-g	25.0b-e	6.32h-k	133.67e-g	22.17e-h
	RM-LD-1	88.10l	143gh	11h	19.93kl	8.1ab	162a	24.67ab
E3	BRRIdhan-28	120.57c	148e	13c-e	24.27de	6.67f-j	149.67a-c	21.73g-i
	BAU-3	124.47b	153c	12fg	25.30b-d	6.41h-k	127.33fg	21.9f-i
	RM-LD-1	78.27n	131l	9i	19.53l	7.8b	148.33a-d	24.87a
E4	BRRIdhan-28	91.17j	136k	9i	21.70h-j	6.43h-k	122.33gh	22.3e-h
	BAU-3	106.90g	139j	9i	25.77b	7.33c	150a-c	22.07e-h
	RM-LD-1	84.83m	142hi	12e-g	21.13ij	7.13-e	122.33gh	23.93bc
E5	BRRIdhan-28	109.23f	144g	12e-g	24.10ef	7.2cd	133e-g	22.77de
	BAU-3	116.70de	151d	12fg	24.47c-e	6.92c-f	108.67h	21.67hi
	RM-LD-1	63.33o	140j	14cd	20.80jk	8.31a	155.33ab	24.73ab
E6	BRRIdhan-28	99.40i	146ef	14c	22.20g-i	6.31i-k	130.67e-g	22.5e-g
	BAU-3	115.33e	157b	13c-e	27.00a	6.86d-g	131e-g	22.27e-h
	RM-LD-1	88.77ckl	136k	16a	22.40gh	8.5a	158a	24.6ab
E7	BRRIdhan-28	102.50h	147e	15b	25.40bc	6.47g-k	132.67e-g	22.5e-g
	BAU-3	146.80a	152cd	15b	27.23a	6.69f-i	140c-f	22e-i

E1=Chapainawabganj, E2=Gopalganj, E3=Rangpur, E4=Barishal, E5=Magura, E6=Sunamganj, and E6=Mymensingh.

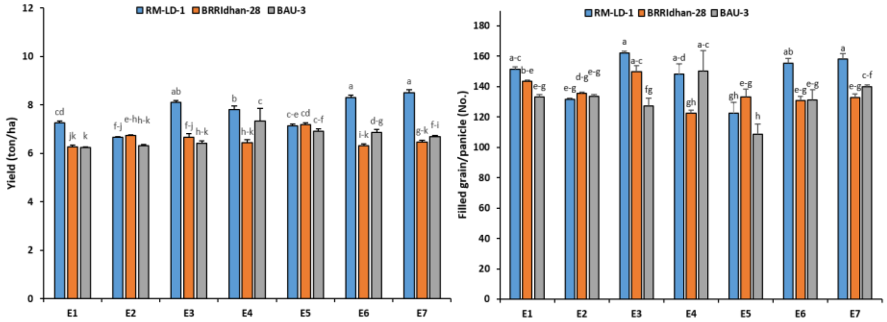


Fig. 1. Bar diagram showing the yield of rice genotypes at different locations

The yield of genotypes was the highest at E7 (Mymensingh) for RM-LD-1 (8.5 t ha^{-1}) followed by the yield of RM-LD-1 (8.31 t ha^{-1}) at location E6, though they are statistically similar. Statistically dissimilar closely produced yields are obtained by location E3 (8.1 t ha^{-1}) and E4 (7.8 t ha^{-1}). Interestingly, RM-LD-1 yielded better than other varieties over the locations than other genotypes. Filled grain/panicle is an important parameter that affects yield. The higher value tends to produce a higher yield of a certain plant. RM-LD-1 at E3 produced the highest (162) number of filled grain/panicles, followed by RM-LD-1 at E7 (158). Panicle length was the highest of BAU-3 (27.73 cm) at E1 and shortest panicle length was of RM-LD-1 (19.53 cm) at E4 (Figure 2a). Filled grain panicles-1 of genotypes varied among the locations. In every situation, RM-LD-1 showed better results in terms of filled grain (Figure 1). The 1000-seed weight is an important indicator of yield. In our experiment, this parameter was topped by RM-LD-1 across all locations (Figure 2b), indicating its superiority as a variety. The number of effective tillers per plant is a yield-contributing character that influences the yield of a genotype. More effective tillers indicate a better genotype. The highest number of effective tillers was recorded by RM-LD-1 (16) at E7, and the lowest was shown by RM-LD-1 (9) at E4. All the values of effective tillers/plants were significantly different from each other, statistically.

The plant height of BAU-3 (146.8 cm) was the highest at E7, and RM-LD-1(78.27 cm) recorded the shortest height among all genotypes across all seven locations. Semi-dwarfism increases yield in some rice plants, as suggested by previous experiments. Days to maturity of these rice genotypes was highest for BRRI dhan-28 (160 days) at E1 and lowest for RM-LD-1(131 days) at E4. The less time the genotype takes to mature, the better the genotype is for cultivation.

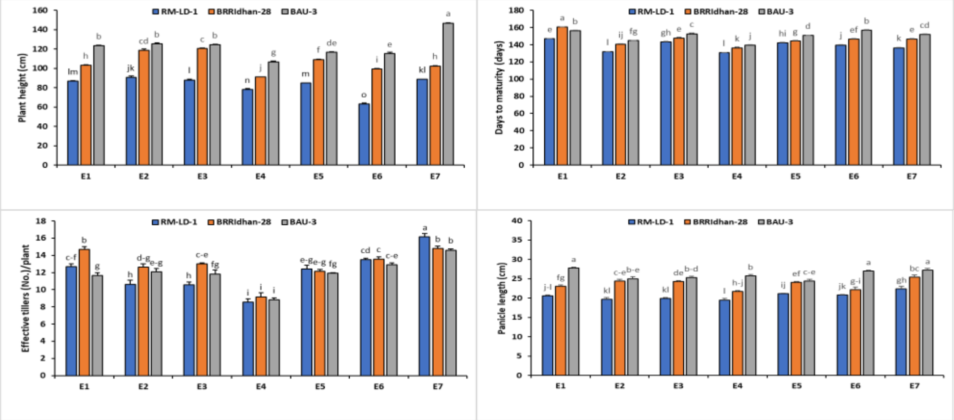


Fig. 2 (a). Bar diagram showing the effects of genotype: location Interaction on different parameters of rice

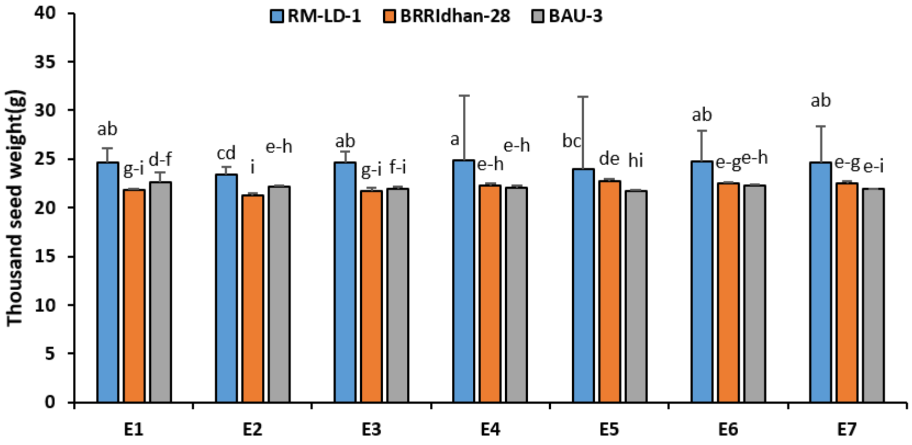


Fig 2 (b). Bar diagram showing 1000-seed weight of rice genotypes at different locations

Our experimental findings corroborated that the agronomic traits of rice significantly influence yield, consistent with several prior studies (Fageria et al., 2011; Qian et al., 2016; Zeng et al., 2017; Zhang et al., 2017). Filled grain is the product of the multiplication of grain per panicle (GPP) and seed setting. The quantity of GPP is primarily influenced by panicle architecture, encompassing panicle length and the quantity and length of primary, secondary, and tertiary branches (Kovi et al., 2011). If the number of filled grain/panicle is higher in a genotype, it is supposed to yield higher (Li et al., 2019). Filled grain/panicle of RM-LD-1 at all locations proved that it is a superior genotype.

The quantitative feature of TGW is influenced by grain size and grain filling rate, defined by the three dimensions of grain length, breadth, and height (Xie et al., 2015). Grain weight is primarily determined by genetic variables, but the grain filling rate is influenced by external environmental conditions (Li et al., 2019). Results from the study also support this statement. Panicle length of RM-LD-1 is smaller than others, but the number of spikelets is greater than other cultivars, which supports a higher filled grain/panicle of the present experiment.

Moderate plant height generally supports higher yields, while both excessive dwarfism and excessive height can reduce yield due to impacts on plant architecture, lodging resistance, and grain development. The significance of plant height on yield differs among rice ecotypes. In indica inbred and hybrid varieties, taller plants are generally thought to yield higher, whereas in Japonica hybrids, an increase in plant height may lead to a reduction in yield (Li et al., 2019).

In our experiment, plant height is negatively correlated (Figure 3) with yield, indicating that semi-dwarf varieties like RM-LD-1 produced better yield.

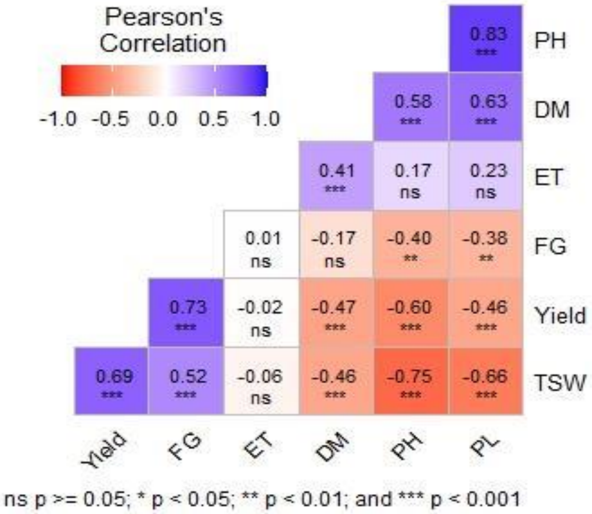


Fig. 3. Pearson's correlation coefficient of different parameters under study (FG=Filled grain/panicle, DM=Days to maturity, ET=Effective tiller/panicle), PH=Plant height, PL=Panicle length

The correlation plot reveals that days to maturity is highly significant with yield, but inversely. That means the less time it takes to mature, the higher the yield would be of that particular genotype for these genotypes. It also reveals that plant height is negatively correlated to yield. A similar scenario was observed for the character panicle length. But an effective tiller was insignificantly correlated. Filled grain/panicle is positively and highly correlated with yield. Thousand seed weight is highly and positively correlated with yield (Figure 3).

Table 4. Analysis of variance of grain yield for rice genotypes evaluated at seven environments

Source	Df	Sum Sq	Mean Sq	Explained SS (%)
Environment	6	4.27	0.71***	16.82
Genotype	2	15.43	7.23***	45.62
Environment × Genotype	12	8.69	0.72***	34.40
Replication	2	0.03	0.02	0.51
Error	40	0.841	0.06	2.65
Total	62	31.696		

NB. ** indicates significant at $p<0.001$ probability level

The genotype (45.62%), environment (16.82%), and G×E interaction (34.40%) all had a significant impact on the yield, according to the ANOVA. The significant mean sum of squares for genotypes shows a difference in the studied lines/varieties (Xu et al., 2014). The significant G×E interaction effect supports the genotypes' diverse responses to varying environmental conditions (Jadhav et al., 2019).

3.1 AMMI and GGE analysis of variance

Table 5: Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of rice genotypes across seven environments

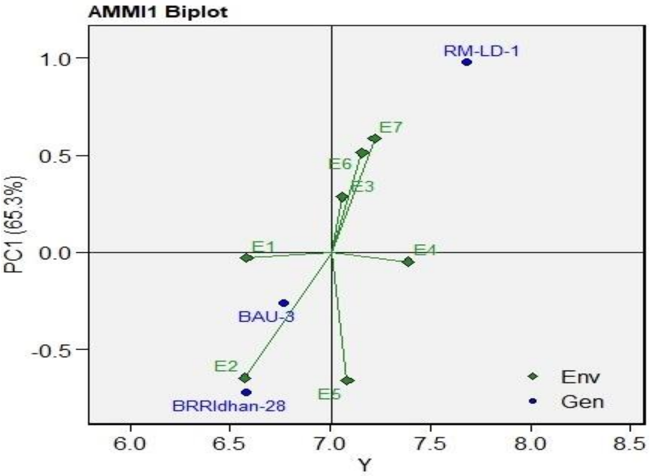
Source	Df	Sum Sq	Mean Sq	Explained SS (%)	Proportion	Accumulated
Environment	6	5.331	0.888***	12.51		
Replication	14	0.439	0.031	1.03		
Genotype	2	14.459	7.230***	33.94		
Genotype × Environment	12	10.905	0.909***	25.60		
PC1	7	7.125	1.018	16.73	65.3	65.3
PC2	5	3.779	0.756	8.87	34.7	100
Residuals	28	0.562	0.020	1.32		
Total	74	42.6	0.576			

NB. *** indicates significant at p<0.001 probability level

According to AMMI analysis, genotypes, environments, and their interaction contributed 33.95%, 12.51%, and 25.60% of the total sum of squares, respectively (Table 6), indicating diverse environments, likely due to variations in rainfall, temperature, and other biotic/abiotic factors (Zewdu et al., 2020). Significant genotype-by-environment (G×E) interaction was observed. The first two interaction principal component axes (IPCA1 and IPCA2) were significant ($p < 0.05$) and explained 65.3% and 34.7% of the G×E interaction, respectively, together accounting for 100% (Gauch & Kang, 1996). This suggests that the G×E interaction among the three genotypes can be reliably predicted using these two components (Susanto et al., 2015; Jadhav et al., 2019; Senguttuvel et al., 2021).

Stability analysis of genotypes for grain yield across the environment:

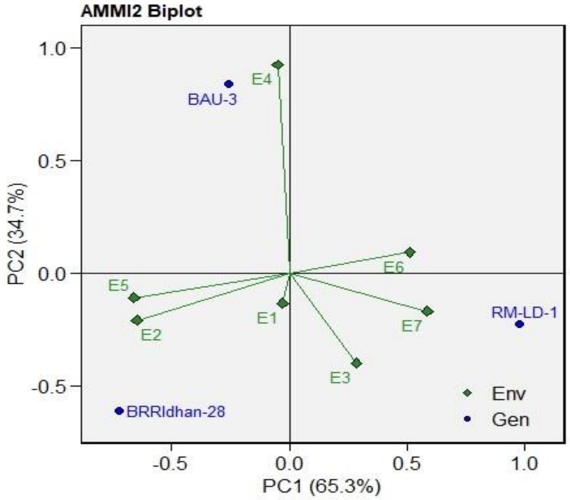
In the AMMI1 biplot, mean yield is on the horizontal axis and PC1 on the vertical (Ebdon & Gauch, 2002). Genotypes aligned horizontally have similar yields, while those aligned vertically share interaction patterns. RM-LD-1, located far right of the mean, showed the highest yield with strong additive effects (Fig. 4). Genotypes or environments with higher PC1 scores, positive or negative, have greater interaction effects. Low or near-zero PC1 scores indicate stability (Crossa et al., 1990). RM-LD-1, farthest from the origin, had the strongest interaction effect. BAU-3 and BRRI



Note: Chapainawabganj (E1), Gopalganj (E2), Rangpur (E3), Barishal (E4), Magura (E5), Sunamganj (E6), and Mymensingh (E7).

Fig. 4. AMMI1 biplot for grain yield of three rice genotypes and seven environments using genotypic and environmental IPCA scores.

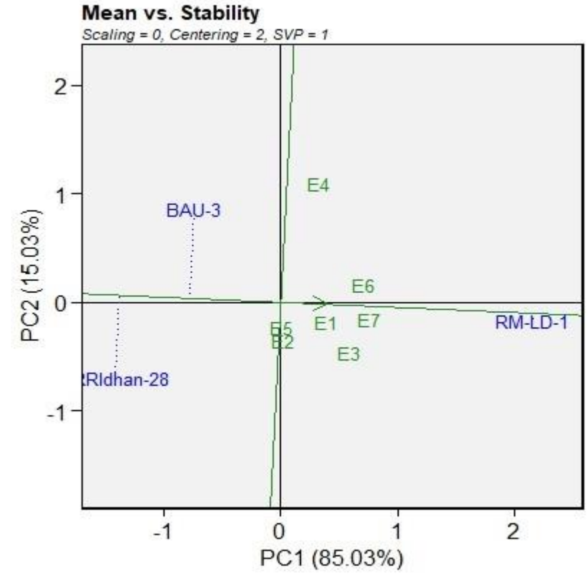
dhan28 showed lower-than-average yields and negative IPCA1 values, suggesting greater stability than RM-LD-1. In the AMMI2 biplot, environment points are connected to the origin. Short spokes (e.g., E1) indicate weak interactions, while long spokes (e.g., E2, E3) indicate stronger discriminating environments. Genotypes near the origin show low interaction; those farther away are more responsive to environmental changes. RM-LD-1, far from the origin, was the most sensitive. BAU-3 and BRRI dhan28 were also sensitive, but to a lesser extent. These findings align with earlier studies (Anandan et al., 2009; Crossa et al., 1990; Kempton, 1984).



Here,
E1= Chapainowabganj,
E2= Gopalganj,
E3= Rangpur,
E4= Borishal,
E5= Magura,
E6= Sunamganj and
E7= Mymensingh.

Fig. 5. AMMI2 biplot for grain yield showing the interaction of IPCA2 against IPCA1 scores of three rice genotypes in seven environments.

Mean vs. Stability



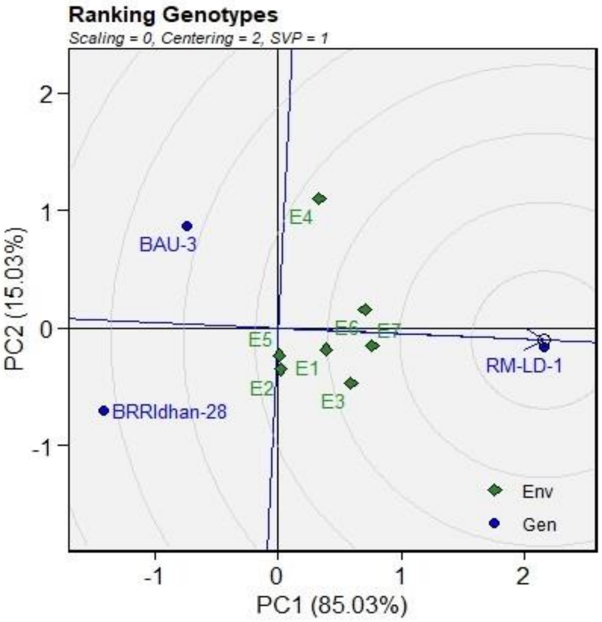
Note:
Chapainawabganj (E1), Gopalganj (E2), Rangpur (E3), Barishal (E4), Magura (E5), Sunamganj (E6), and Mymensingh (E7).

Fig. 6. The mean vs. stability view for grain yield showing the GGE interaction of three rice genotypes in seven locations.

In the mean vs. stability graph, the positive side of the mean line from the origin indicates a higher yield than the average, while the negative side indicates a lower yield than the average (Zulqarnain et al., 2017). The genotype with the highest yield was RM-LD-1, followed by BAU-3 and BRRIdhan-28. The genotype that is closer to the mean line is more stable than the average. The genotypes that are farthest from the mean line are less stable than the average. RM-LD-1 was the most stable of the three, followed by BRRIdhan-28 and BAU-3.

Genotype Ranking

Using the genotype ranking biplot, we can determine an ideal genotype compared to the other genotypes studied. RM-LD-1 may be deemed the best leading genotype due to its closeness to the arrowhead in the circle for yield. In most circumstances, an optimal genotype is found towards the head of the arrow in the circular ring's center, in the innermost circle. In comparison to the genotypes in the outside circle, the genotype in the inner circle is extremely preferred. An ideal genotype should have high mean and stability qualities for successful selection (Yan, 2006). The genotype RM-LD-1 was ranked first, followed by BAU-3 and BRRIdhan-28, based on the optimal genotype for yield. Oladosu et al. (2017) also found similar findings.

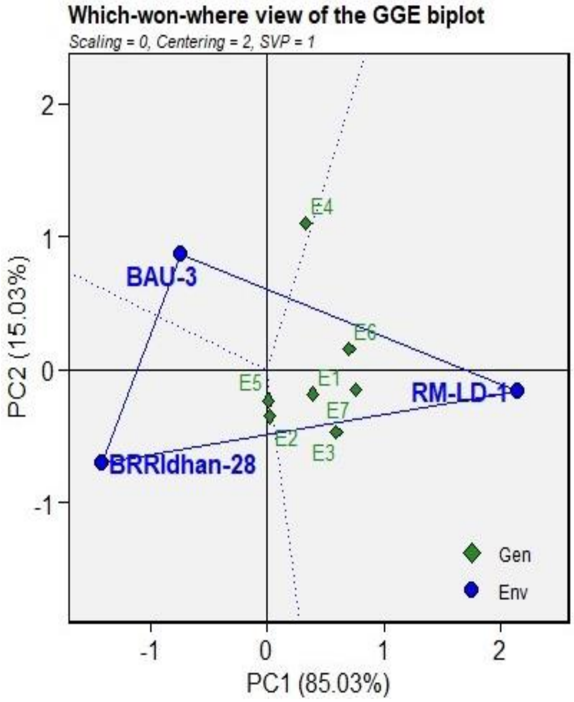


Note: Chapainawabganj (E1), Gopalganj (E2), Rangpur (E3), Barishal (E4), Magura (E5), Sunamganj (E6), and Mymensingh (E7).

Fig. 7. Ranking of genotypes relative to an ideal genotype on the basis of grain yield.

Which-won-where view

Representing the who-won-where pattern is essential for determining whether or not distinct mega-environments (ME) exist in a given location (Oliveira 2021). The which-won-where pattern is explicitly displayed in the polygon view of a GGE-biplot, making it a concise summary of the GEI pattern. The best genotypes in each environment and combination of habitats are indicated by the GGE biplot's polygon view (Zhou M, 2021). A GGE-polygon view biplot explicitly exhibits the which-won-where pattern and provides a concise description of the GEI pattern. The GGE biplot's polygon view shows the best genotypes in each environment and collection of environments (Yan and Hunt, 2002). RM-LD-1, BAU-3, and BRRIdhan-28 were the vertex genotypes used in this study. Each sector's vertex genotype is the one that



Note: Chapainawabganj (E1), Gopalganj (E2), Rangpur (E3), Barishal (E4), Magura (E5), Sunamganj (E6), and Mymensingh (E7).

Fig. 8. Polygon views of the GGE biplot based on symmetrical scaling for ‘which-won-where’ pattern of rice genotypes in seven environments showing genotype performed the best in particular environment.

produced the maximum yield for the environment within that sector. It also indicates environmental clustering, implying the existence of many mega-environments. As a result of the biplot analysis of data from various environments, three mega-environments exist. The first mega-environment consists of environments E1, E3, E6, and E7, with genotype RM-LD-1 as the winner; the second mega-environment consists of environments E2 and E5, with genotype BRRIdhan-28 as the winner; and another mega-environment consists of environments E4, with genotype BAU-3 as the winner.

Conclusion

The genotype RM-LD-1 produced the maximum yield in most environments, of where Chapainawabganj, Rangpur, Sunamganj, and Mymensingh providing the best environments. The advanced line RM-LD-1 is a prominent and potential new variant and could be introduced as a variety in Bangladesh.

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