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Evaluation of Advanced Boro Rice Lines for Yield Improvement and Breeding Potential in Bangladesh

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Abstract

Improving *Boro* rice productivity is critical for food security in Bangladesh. This study evaluated 63 advanced breeding lines and three BRRI check varieties for 13 agro-morphological and yield-related traits to identify superior genotypes and key selection criteria. Genotypic differences were highly significant for all traits, indicating substantial exploitable variability. V57 produced the highest grain yield (8.60 t ha^{-1}), followed by V32 (8.36), V40 (8.23), V54 (8.21), and V44 (8.14 t ha^{-1}), compared with 6.92–7.14 t ha^{-1} for the check varieties. V57 also combined the highest total and effective tiller numbers (16.50 and 14.10), 92.09% spikelet fertility, 176.70 filled grains $panicle^{-1}$, and only 15.17 unfilled grains $panicle^{-1}$. Unfilled grains $panicle^{-1}$ showed the highest GCV and PCV (18.06 and 18.61%), followed by length–breadth ratio (11.86 and 12.52%) and grain yield (10.21 and 10.77%). Broad-sense heritability was high for all traits (72.35–94.18%); grain yield exhibited 89.82% heritability and 19.92% genetic advance as percentage of the mean, indicating good selection potential. The first two principal components explained 70.7% of total phenotypic variation. Grain yield was strongly and positively correlated with effective tiller number (r = 0.96), total tiller number (r = 0.96), fertility percentage (r = 0.82), thousand-grain weight (r = 0.70), and filled grains $panicle^{-1}$ (r = 0.61), but negatively with unfilled grains $panicle^{-1}$ (r = −0.78). MGIDI identified V38, V35, V31, V47, V8, V54, V5, V63, V62, and V17 as desirable multi-trait genotypes with complementary strengths. These lines, together with the highest-yielding genotypes, represent promising parental and breeding materials, but require multi-environment validation for yield stability, adaptation, grain quality, and stress resilience.

Keywords Boro rice · yield improvement · genetic variability · heritability · multivariate analysis · MGIDI · genotype selection

1 Introduction

Rice (*Oryza sativa* L.), a dominant cereal crop of the Poaceae family, constitutes the primary staple food for more than half of the global population [1, 2]. Worldwide rice demand has increased substantially, with consumption rising by approximately 19%, from 437.18 million metric tons in 2008–2009 to 520.4 million metric tons in 2022–2023 [3]. Rice consumption is particularly concentrated in Asia, Sub-Saharan Africa, and South America, where it forms a central component of daily caloric intake [4].

In Bangladesh, rice holds unparalleled agronomic, economic, and food-security significance [5, 6]. It dominates both domestic production and consumption and occupies nearly 78% of the country's total cultivated land [7–9]. Rice cultivation in Bangladesh spans three distinct seasons: Aus, Aman, and *Boro* with national production overwhelmingly driven by the *Boro* season [1, 4, 10]. During the 2021–22 fiscal year, total rice production reached 38.15 million tons from 11.69 million hectares, of which *Boro* rice alone contributed 20.19 million tons from 4.82 million hectares, accounting for approximately 53% of total national output [11]. Consequently, the stability of Bangladesh's rice supply and food security is intrinsically linked to the productivity and sustainability of the *Boro* rice [9, 12].

The *Boro* season, extending from December to May, is characterized by a dry winter climate and complete reliance on irrigation [9, 13]. These conditions provide a unique opportunity to exploit genetic yield potential under controlled water management, making *Boro* rice a strategic focal point for productivity enhancement [9, 10]. Despite this advantage, Bangladesh's average rice yield (3.20 t ha^{-1}) remains substantially lower than yields achieved in leading rice-producing countries such as Japan (5.0 t ha^{-1}) and China (4.74 t ha^{-1}) [13, 14]. Bridging this yield gap is becoming increasingly urgent as arable land continues to decline due to rapid urbanization and industrial expansion [1, 15, 16]. Under such constraints, sustainable yield improvement must rely on enhancing per-unit land productivity and increasing cropping intensity rather than horizontal expansion [4, 16].

The adoption of high-yielding varieties (HYVs) has been instrumental in boosting rice production in Bangladesh [9, 17]. In addition to superior yield potential, HYVs generally exhibit improved efficiency in water and nutrient utilization compared with traditional landraces, resulting in higher economic returns for farmers [17–19]. Moreover, the deployment of short-duration cultivars is particularly advantageous in intensively cultivated systems, as it enables multiple cropping cycles and maximizes land-use efficiency [1, 4, 6].

Alongside productivity, grain size and shape have emerged as an important determinant of varietal acceptance and market value [20, 21]. With rising income levels and increasing health consciousness, consumers are placing greater emphasis on rice grain-quality attributes such as grain size, shape, and

weight; the specific attributes addressed in this study through thousand-grain weight and length-breadth ratio [20, 22]. Therefore, modern rice improvement programs must effectively balance yield enhancement with desirable morpho-physiological and grain-quality traits [23].

Although numerous high-yielding varieties (HYVs) have been released for the *Boro* season in Bangladesh, comprehensive and comparative evaluations of their morpho-physiological traits and yield components under local agro-ecological conditions remain limited [10, 13]. In particular, there is a lack of systematic studies linking growth characteristics, yield-contributing traits, and overall productivity of widely cultivated HYVs relative to standard check varieties during the *Boro* season [6, 13]. Addressing this knowledge gap is essential for identifying superior genotypes and guiding future breeding and varietal deployment strategies tailored specifically to Bangladeshi conditions [12, 15].

The successful breeding of high-yielding varieties necessitates a comprehensive elucidation of the genetic basis of yield components and their associations with grain yield [15, 24]. In this context, determining genotypic and phenotypic coefficients of variation (GCV and PCV) allows for the precise partitioning of variability into heritable and non-heritable components [13, 25]. Although heritability estimates provide insight into transmission efficiency, they are most effective for predicting selection response when coupled with genetic advance [26–28]. Concurrently, genotypic evaluation and correlation analysis serve as robust tools for identifying superior genotypes and establishing trait-yield relationships [29–31]. Moreover, to overcome the limitations of univariate analysis, multivariate approaches such as Principal Component Analysis (PCA) are essential [32–34]. These techniques reveal complex data structures and visualize the diversity among grain yield and its contributing traits, ensuring a rigorous and accurate selection process [15, 35]. Despite the release of numerous high-yielding *Boro* rice varieties, few studies have systematically integrated morpho-physiological performance with quantitative genetic and multivariate evaluations of advanced breeding lines under local agro-ecological conditions [6, 10, 13]. Genetic variability was assessed using genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance to determine the selection potential of key traits [25, 27, 36] while principal component analysis, hierarchical clustering, and a multi-trait genotype-ideotype distance index (MGIDI) were employed to elucidate trait relationships, quantify genetic diversity, and classify promising genotypes [15, 35, 37, 38]. Therefore, this study aimed to evaluate the growth, yield, and yield-contributing traits of selected advanced lines relative to standard check varieties and to identify superior genotypes and priority traits for the sustainable genetic improvement of *Boro* rice in Bangladesh.

2 Materials and methods

2.1 Plant materials and experimental sites

The experiment was carried out during the *Boro* season of 2025-2026 at a farmer-managed research field in Gazipur, Bangladesh. The experimental site is located in a tropical agro-climatic zone and is characterized by non-calcareous, dark gray sandy clay soil. Geographically, the area belongs to the Madhupur Tract, classified as Agro-Ecological Zone 28 (AEZ 28) (**Fig. 1**). Meteorological conditions prevailing throughout the crop growing period are presented in Supplementary Table 1. To ensure optimal crop growth under field conditions, recommended fertilizer doses were applied following standard agronomic practices. A total of 63 advanced rice lines (V1–V63), developed at ACI Seed Limited, Gazipur, Bangladesh, were evaluated in this study. The widely cultivated rice varieties BRRI dhan71 (BR71), BRRI dhan75 (BR75), and BRRI dhan87 (BR87) were used as check varieties and were obtained from the Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh. The names and sources of the germplasm are presented in Table 1.

2.2 Experimental design and agronomic management practices

The experiment was conducted during the *Boro* season using a randomized complete block design with three replications. Sixty-three advanced breeding lines (V1–V63) and three check varieties (BR71, BR75, BR87) were randomly assigned within each block. Each genotype was grown in a 10 m² plot, with 0.50 m between plots and 1.0 m between blocks. Pre-germinated seeds were raised in a puddled nursery, and 40-day-old seedlings were transplanted at 25 × 15 cm spacing, maintaining one seedling per hill. Missing hills were replanted within 7 days of transplanting.

Fertilizers were applied following the Bangladesh Agricultural Research Council recommendation for irrigated *Boro* rice. Urea, triple superphosphate, muriate of potash, gypsum, and zinc sulphate were applied at 300, 112, 127, 75, and 11 kg ha^{-1}, respectively. The full doses of all fertilizers except urea were incorporated during final land preparation. Urea was applied in three equal splits at approximately 15, 35, and 55 days after transplanting. Uniform irrigation, drainage, weeding, and integrated pest and disease management were maintained across all plots. Irrigation was discontinued 10–15 days before harvest. Each genotype was harvested separately when approximately 80% of the grains had turned golden yellow. Border rows were excluded, and grain yield was recorded from the net plot area, adjusted to 14% moisture content, and converted to tonnes per hectare. The experimental design followed standard rice evaluation procedures described in the supplied methodology. The weather conditions during the experimental period are presented in supplementary **Table 1**.

2.3 Measurement of morpho-physiological and yield traits

Data were recorded for 13 morpho-physiological and yield-related traits: total tiller number, effective tiller number, plant height, days to 10% heading, days to 80% heading, panicle length, filled grains per panicle, unfilled grains per panicle, spikelet fertility or fertility percentage, grain moisture percentage, thousand-grain weight, grain length-to-breadth ratio, and grain yield per hectare. Unless otherwise stated, plant-based observations were recorded from 10 randomly selected hills in the non-border rows of each plot, and the mean value was used for statistical analysis. The acronyms and units of measurement of the studied traits are presented in Table 2

2.3.1 Total and effective tiller numbers

Total tiller number was determined by counting all tillers, including the main culm, produced by each sampled hill at the maximum tillering stage. Effective tiller number was recorded at maturity as the number of panicle-bearing tillers per sampled hill.

2.3.2 Plant height

Plant height was measured in centimetres from the soil surface to the tip of the tallest panicle, excluding awns. Measurements were obtained from 10 randomly selected plants in each plot at physiological maturity.

2.3.3 Days to heading

Days to 10% heading and days to 80% heading were recorded as the number of days from sowing until approximately 10% and 80% of the plants within each plot, respectively, had visibly emerged panicles.

2.3.4 Panicle and grain characteristics

Panicle length was measured in centimetres from the basal node of the rachis to the tip of the panicle. Ten representative panicles were randomly collected from each plot. Filled grains per panicle and unfilled grains per panicle were separated manually and counted individually. Their respective plot means were used in the analysis.

Spikelet fertility percentage was calculated as:

$$\text{Spikelet Fertility (\%)} = \left(\frac{\text{Number of Filled Spikelets}}{\text{Total Number of Spikelets}} \right) \times 100$$

2.3.5 Grain moisture, weight, and dimensions

Grain moisture percentage was measured immediately after threshing using a calibrated digital moisture meter. Thousand-grain weight was determined by counting and weighing 1,000 clean and well-developed grains from each plot and was expressed in grams.

Grain length and breadth were measured from a representative sample of fully developed grains using a digital calliper. The length-to-breadth ratio (LBR) was calculated as:

$$\mathbf{LBR} = \mathbf{Mean\ grain\ length}/(\boldsymbol{Mean\ grain\ width})$$

2.3.6 Grain yield

Grain yield was determined from the harvested net plot area after threshing and cleaning. The observed grain weight was corrected to 14% moisture content.

2.4 Genetic analysis

Genotypic variance (σ^2g) and phenotypic variance (σ^2p) were determined following established methodologies outlined by Acquaah [39].

$$\text{Genotypic variance } (\sigma 2g = (MSg - MSe)/r$$

Where MSe is the mean square of the error, MS_g is the mean square of genotypes, and "r" is the number of replications

$$\text{Phenotypic Variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Here, σ^2p is phenotypic variance, σ^2g is genotypic variance, and σ^2e is environmental variance [40].

The genotypic and phenotypic co-efficient of variations were calculated according to the formula given by Singh and Chaudhary [41].

$$\text{Genotypic co} - \text{efficient of variation (GCV)} = \sqrt{\sigma 2g}/\bar{x} \times 100$$

Here,

σ^2_g = Genotypic variance; and

$\bar{x}$ = Population mean

$$\text{Phenotypic co} - \text{efficient of variation (PCV)} = \sqrt{\sigma 2p}/\bar{x} \times 100$$

Here,

σ^2_p = Phenotypic variance; and

$\bar{x}$ = Population mean

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were categorized as low (0–10%), moderate (10–20%), and high (≥20%), following the classification proposed by Burton and DeVane [42].

Broad-sense heritability (h^2_β) is defined as the proportion of genetic variance ($\sigma^2 g$) relative to the total phenotypic variance ($\sigma^2 p$), in accordance with the definition of Falconer [43], and was calculated using the following equation:

$$h\text{^}2\ b\ (\%) = \sigma 2g/\sigma 2p \times 100$$

Heritability estimates were categorized as low (0–30%), moderate (30–60%), and high (≥60%), following the classification proposed by Robinson et al. [44].

The procedures described by Assefa et al. [45] were employed to estimate the expected genetic advance (GA) and genetic advance as a percentage of the mean (GAM), assuming a selection intensity (K) of 5%. Subsequently, following the classification proposed by Johnson et al. [40], genetic advance was categorized into low (0–10%), moderate (10–20%), and high (>20%) classes.

$$GA = K\ \times\ \sqrt{}\sigma 2p \times h\text{^}2\ b$$

$$GAM = K \times \sqrt{}\sigma 2p/\bar{}x$$

In this context, K denotes the selection intensity constant, h^2_β represents broad-sense heritability, X indicates the trait mean, and P corresponds to the phenotypic standard deviation, with K fixed at 5%.

2.5 Multi-trait genotype-ideotype distance index (MGIDI) analysis

The Multi-Trait Genotype–Ideotype Distance Index (MGIDI) analysis was performed in R version 4.3.3 using the metan package version 1.18.0 [46], following the MGIDI methodology of Olivoto and Nardino [38]. Before calculating the index, all traits were rescaled to a common 0–100 range to standardize variables measured in different units and facilitate direct comparison. An ideotype was then defined by assigning desirable target values to each trait according to the breeding objectives, and the distance between each genotype and the predefined ideotype was calculated to quantify the degree of similarity to the desired multi-trait profile.

2.6 Statistical analysis

Treatment means were compared using the Least Significant Difference (LSD) test at the 5% level of significance. Additionally, multivariate analyses were conducted using the R statistical program

(version 4.3.3). ANOVA and correlation analysis were conducted using the 'metan' and 'ggplot2' packages in R, while clustering, PCA, and radar plot were performed with the 'FactoMineR', 'factoextra', and 'ggplot2' packages. Significance levels for correlation coefficients are denoted as *, **, and *** for $p<0.05$, $p<0.01$, and $p<0.001$, respectively.

3 Results

The analysis of variance revealed highly significant differences ($p < 0.001$) among the studied genotypes for all yield and yield-contributing traits (**Table 3**), which indicate the presence of substantial variability among the breeding materials, providing considerable scope for the selection of superior genotypes. Such variability is particularly valuable in breeding programs, as it facilitates the identification and utilization of promising genotypes for the improvement of yield and associated agronomic traits.

Significant variation was observed among the genotypes for all evaluated agro-morphological and yield-related traits (**Table 4**). Considerable differences were evident in tillering ability, with the check varieties BR75 and BR87 recording 15.00 total tillers and 12.60 effective tillers, whereas BR71 produced 14.77 and 12.37, respectively. Several advanced breeding lines (ABLs) surpassed these values, particularly V57, which recorded the highest total and effective tiller numbers (16.50 and 14.10), followed by V32 (16.17 and 13.77), V40 (16.00 and 13.60), V27 and V54 (15.80 and 13.40), and V44 (15.77 and 13.37). These genotypes therefore exhibited comparatively strong tillering capacity, with a high proportion of productive tillers.

Plant height and heading behaviour also varied markedly among the evaluated materials. The check varieties were relatively short, ranging from 100.50 to 101.17 cm, and several advanced lines, including V17 (100.13 cm), V20 and V36 (101.10 cm), V21 (101.53 cm), and V4 (101.97 cm), showed comparable stature. In contrast, V35 (147.77 cm), V42 (136.97 cm), and V53 (135.20 cm) were substantially taller. For phenological traits, BR75 and BR87 reached 10% and 80% heading at 68.00 and 74.00 days, respectively, while BR71 required 72.00 and 78.00 days. V8 and V17 were the earliest advanced lines, reaching 10% and 80% heading at 67.67 and 73.67 days, respectively, whereas V34 and V53 were the latest, requiring 90.00 and 96.00 days. The observed variation indicates substantial scope for selecting genotypes with contrasting plant stature and crop duration according to specific production environments.

Variation in panicle architecture and grain formation was similarly noticeable. The check varieties had panicle lengths ranging from 25.83 to 26.20 cm, while several ABLs produced distinctly longer panicles, where V40 and V47 (30.33 cm), V38 (30.17 cm), V54 (29.17 cm), V52 (28.83 cm), V37

(28.67 cm), and V57 (28.50 cm). A number of these lines also exhibited superior grain-bearing capacity. Filled grains panicle^{-1} were highest in V27 (176.80), V57 (176.70), V32 (174.57), V44 and V54 (172.50), exceeding the check values of 165.47–169.50. In parallel, low numbers of unfilled grains were observed in V8 (14.17), V57 (15.17), V17 (15.27), V63 (15.47), and V10 and V27 (15.50), compared with 16.83–19.50 in the checks. Consequently, genotypes such as V57 and V27 combined high filled-grain numbers with low unfilled-grain numbers, indicating particularly favourable grain-filling performance. The trend in grain filling was further supported by differences in fertility percentage. The check varieties ranged from 89.45% in BR71 to 90.97% in BR87, whereas V57 recorded the highest fertility (92.09%), followed by V27 (91.94%), V63 (91.74%), V10 (91.65%), V62 (91.55%), V17 (91.51%), and V8 (91.50%). Conversely, relatively low fertility was recorded in V53 (84.58%), V23 (85.10%), V13 (85.36%), and V48 (85.38%). Thus, several high-performing lines combined reduced unfilled-grain numbers with high fertility, reflecting efficient reproductive performance.

Moisture percentage, thousand grain weight, and grain shape also showed substantial diversity. Grain moisture in the check varieties ranged from 17.80% to 20.00%, while relatively low values were recorded in V16 (18.00%) and V27 (18.03%), whereas V58, V60, and V32 showed comparatively higher moisture contents. Thousand grain weight varied widely, with V32 recording the highest value (30.67 g), followed by V40 (30.46 g), V50 (30.27 g), V35 (30.02 g), V38 (29.88 g), V31 (29.75 g), V51 (29.59 g), and V46 (29.58 g), all exceeding the check range of 25.64–26.11 g. Grain shape also differed markedly, as reflected by the length–breadth ratio. The highest ratios were observed in V52 (5.22), V54 (5.11), V45 (5.05), V31 (4.71), V22 (4.70), and V37 (4.68), indicating comparatively elongated grains, whereas V27 (2.91), V20 (3.11), and V57 (3.22) exhibited relatively broader grain types.

Grain yield per hectare showed clear differentiation among genotypes. The check varieties produced 6.92 t ha^{-1} in BR71, 7.11 t ha^{-1} in BR75, and 7.14 t ha^{-1} in BR87. Several ABLs markedly exceeded these values, with V57 recording the highest yield (8.60 t ha^{-1}), followed by V32 (8.36 t ha^{-1}), V40 (8.23 t ha^{-1}), V54 (8.21 t ha^{-1}), and V44 (8.14 t ha^{-1}). Other high-yielding lines included V63 (7.92 t ha^{-1}), V62 (7.90 t ha^{-1}), V34 (7.85 t ha^{-1}), V47 (7.81 t ha^{-1}), and V27 and V38 (7.75 t ha^{-1} each), whereas comparatively low yields were recorded in V18 (5.55 t ha^{-1}), V13 (5.61 t ha^{-1}), V23 (5.70 t ha^{-1}), and V19 (5.87 t ha^{-1}). Overall, the superior yield performance of V57, V32, V40, V54, V44, V63, V62, and V27 was associated with favourable combinations of several yield-contributing traits rather than superiority in a single character. V57 combined the highest grain yield with the highest total and effective tiller numbers, high fertility, high filled-grain number, and low unfilled-grain number. V32 and V40 combined high yield with exceptionally high thousand grain weight, while V54 exhibited a

favourable combination of high yield, long panicles, high filled-grain number, low unfilled-grain number, and an elongated grain type. V27 was distinguished by high filled-grain number, low unfilled-grain number, high fertility, relatively low grain moisture, and comparatively early heading. These genotypes therefore represent promising materials for further multi-environment evaluation to assess yield stability, adaptation, and grain-quality performance before advancement in the breeding program.

Genotypic and phenotypic coefficients of variation differed considerably among the studied traits (**Table 5**). In general, PCV values were slightly higher than the corresponding GCV values for all traits, indicating some environmental influence on trait expression; however, the relatively narrow differences between GCV and PCV for most characters suggest that phenotypic variation largely reflected underlying genotypic differences. Moderate GCV and PCV values were recorded for unfilled grains panicle^{-1} (18.06 and 18.61%), followed by length–breadth ratio (11.86 and 12.52%), and yield hectare^{-1} (10.21 and 10.77%), whereas the remaining traits exhibited comparatively low coefficients of variation. Among all traits, unfilled grains panicle^{-1} showed the highest GCV and PCV, indicating comparatively greater variability and wider scope for improvement through selection. In contrast, fertility percentage (GCV = 2.18%; PCV = 2.27%) and filled grains panicle^{-1} (GCV = 3.61%; PCV = 3.81%) exhibited the lowest relative variability, suggesting comparatively stable expression of these traits within the evaluated materials.

Broad-sense heritability was high for all studied traits, ranging from 72.35% for moisture percentage to 94.18% for unfilled grains panicle^{-1}. Particularly high heritability was observed for unfilled grains panicle^{-1} (94.18%), fertility percentage (92.49%), panicle length (90.37%), yield ha^{-1} (89.82%), length–breadth ratio (89.71%), filled grains panicle^{-1} (89.68%), total tiller number (87.84%), and effective tiller number (87.76%). Plant height (85.08%), thousand grain weight (81.62%), 10% heading days (77.54%), 80% heading days (77.39%), and moisture percentage (72.35%) also showed high heritability (**Table 5**). These estimates indicate that a large proportion of the observed phenotypic variation was attributable to genotypic differences, suggesting that phenotypic selection may be effective for several of these traits.

Genetic advance as a percentage of the mean (GAM) varied markedly among traits. High GAM was recorded for unfilled grains panicle^{-1} (36.11%) and length–breadth ratio (23.14%), while yield hectare^{-1} (19.92%) and plant height (18.85%) exhibited moderate GAM values. Moderate GAM was also observed for panicle length (14.64%), thousand grain weight (14.40%), 10% heading days (13.13%), moisture percentage (12.45%), 80% heading days (12.16%), effective tiller number (12.15%), and total tiller number (10.19%). In contrast, filled grains panicle^{-1} (7.03%) and fertility percentage (4.32%) exhibited low GAM despite their high heritability (**Table 5**).

The combination of high heritability and high GAM observed for unfilled grains panicle^{-1} and length–breadth ratio suggests a substantial contribution of additive genetic effects and indicates that direct phenotypic selection for these traits could be effective. Yield hectare^{-1} exhibited moderate GCV (10.21%) and PCV (10.77%), high broad-sense heritability (89.82%), and a GAM of 19.92%, indicating substantial genetic control and good potential for improvement through selection (**Table 5**). Plant height, panicle length, and thousand grain weight also combined high heritability with moderate GAM, suggesting reasonable prospects for genetic improvement. Conversely, filled grains panicle^{-1} and fertility percentage showed high heritability but low GAM, indicating that high heritability alone may not necessarily translate into large expected gains from selection. Overall, the observed variability, high heritability, and favourable genetic advance for several traits indicate substantial scope for selecting superior lines and improving important agro-morphological and yield-related characteristics in the evaluated breeding materials.

The scree plot illustrates the first principal component (PC1) accounted for 44.0% of the total variation, followed by PC2 (26.7%), together, the first two principal components explained approximately 70.7% of the total phenotypic variation (**Figure 2**).

Four major genetic clusters were formed where each represented by distinct colors and confidence ellipses. Cluster 1**,** predominantly positioned in the lower region of the PCA plot and characterized mainly by negative PC2 scores, included V1, V2, V4, V5, V7, V8, V9, V14, V17, V20, V21, V24, V25, V33, and V36, together with the parental genotypes BR71, BR75, and BR87. Cluster 2, located primarily on the left side of the plot with negative PC1 scores, comprised V10, V27, V31, V32, V34, V35, V37, V38, V40, V44, V47, V50, V51, V54, V57, V61, V62, and V63. Cluster **3**, positioned on the right side with positive PC1 scores, consisted of V3, V6, V11, V12, V13, V15, V16, V18, V19, V22, V23, V26, V28, V29, and V30, showing clear differentiation from Cluster 2 along PC1. Cluster 4, situated mainly in the upper region with positive PC2 scores, encompassed V39, V41, V42, V43, V45, V46, V48, V49, V52, V53, V55, V56, V58, V59, and V60. Some overlap among the clusters near the origin suggested shared genetic backgrounds (**Fig. 3**).

The variable PCA revealed that traits such as YPH, ET, TN, and UFGPP contributed strongly to Dim1, as indicated by their long vectors extending along the horizontal axis and high contribution values, while FGPP had a minimal contribution due to its shorter vector length near the center. Traits including 80HD, 10HD, MP, PH, and LBR aligned more closely with Dim2, highlighting their primary influence along the vertical axis, with 80HD and 10HD exhibiting particularly strong contributions and associations among them. TGW and PL displayed similar directions in the upper-left quadrant,

reflecting a close association, whereas FP extended prominently into the lower-left quadrant, contributing substantially to both dimensions (**Fig. 4**).

The PCA biplot of traits and genotypes exhibited Cluster 1, located in the lower quadrant with negative PC2 values, showing slight association with FP. Cluster 2 displaying strong associations with YPH, ET, TN, FGPP, TGW, PL, and FP. Cluster 3, exhibiting negative associations with the yield-related traits located on the left axis. Cluster 4, showing closely linked with 80HD, 10HD, MP, PH, and LBR. The trait UFGPP displaying very close link with V48 (**Fig. 5**).

The dendrogram depicted hierarchical clustering of the evaluated genotypes into four distinct clusters based on Euclidean distance (**Fig. 6**). Cluster I comprised 18 genotypes (V10, V62, V63, V38, V47, V40, V61, V27, V57, V50, V34, V51, V31, V35, V32, V54, V37, and V44), forming a distinct group that separated from the remaining clusters at a relatively large Euclidean distance. Cluster II encompassed 15 genotypes (V43, V53, V48, V49, V60, V58, V42, V39, V55, V52, V46, V56, V59, V41, and V45), forming a well-defined second group. Cluster III consisted of 15 genotypes (V22, V11, V15, V16, V26, V29, V3, V6, V28, V12, V23, V13, V18, V19, and V30) and showed the closest clustering relationship with Cluster IV. Cluster IV contained 18 accessions, comprising 15 genotypes (V36, V2, V33, V20, V21, V4, V14, V7, V25, V9, V24, V17, V8, V1, and V5) together with the three check varieties BR71, BR75, and BR87.

The Pearson's correlation coefficients revealed that grain yield hectare^{-1} (YPH) exhibited highly significant and very strong positive correlations with effective tiller number (0.96***) and total tiller number (0.96***), as well as fertility percentage (0.82***), thousand grain weight (0.70***), filled grain per panicle (0.61***), and panicle length (0.57***). In contrast, YPH displayed a highly significant and strong negative correlation with unfilled grain per panicle (−0.78***), along with non-significant associations with plant height (0.20 ns), 10HD (0.14 ns), 80HD (0.14 ns), and LBR (0.20 ns). Effective tiller number showed a perfect positive association with YPH (0.96***), FP (0.82***), FGPP (0.64***), TGW (0.57***), and PL (0.50***), alongside strong negative associations with UFGPP (−0.77***). FGPP was significantly and positively linked with YPH (0.61***) and FP (0.51***), but showed a negative association with UFGPP (−0.35*). Fertility percentage displayed an extremely strong positive correlation with YPH (0.82***) and TGW (0.49***). Phenological traits were positively interrelated, evidenced by a perfect positive correlation between 10HD and 80HD (1.00***), both of which showed moderate positive correlations with moisture percentage (0.57***) and plant height (0.50*** and 0.51***, respectively). Plant height exhibited strong positive associations with PL (0.41***), TGW (0.43***), and LBR (0.48***), but displayed non-significant correlations

with YPH, ET, TN, and grain filling traits. Thousand grain weight demonstrated significant positive correlations with YPH (0.70***) and LBR (0.31*) (**Fig. 7**).

The cluster heat map indicated that Cluster 1 (red bar), encompassing accessions such as V1, V4, V5, V7, V8, V9, V14, V17, V20, V21, V24, V25, V33, V36, BR71, BR75, and BR87, was primarily associated with lower values for heading traits (10HD, 80HD) alongside moderate-to-high expression of fertility percentage and grain yield. Check varieties BR75, BR87, and V8 recorded the lowest heading values, whereas V24 and V17 exhibited high FP. Cluster 2, comprising genotypes such as V10, V27, V31, V32, V34, V35, V37, V38, V40, V44, V47, V50, V51, V54, V57, V61, V62, and V63, was strongly linked with high tiller number (TN, ET), PH, FGPP, and YPH, with genotypes V32, V44, V57, and V61 showing the highest values for TN, ET, and YPH. Cluster 3 including V3, V6, V13, V15, V16, V18, V19, V22, V23, V26, V28, V29, and V30, exhibited pronounced low performance for yield components (TN, ET, FGPP, and YPH) but recorded higher UFGPP, with V13 and V18 displaying the highest UFGPP and lowest YPH. Cluster 4, encompassing V39, V41, V42, V43, V45, V46, V48, V49, V52, V53, V55, V56, V58, V59, and V60, was characterized by high phenological durations (10HD and 80HD), MP, and LBR, with V52 and V58 exhibiting the highest heading durations and V43 displaying elevated UFGPP and MP values (**Fig. 8**).

The radar plot provides an integrated comparison of scaled cluster mean values across multiple traits (**Fig. 9**). The graph showing MP, UFGPP, 80HD,10HD and PH are closely associated, where ET, TN, FP, PL, FGPP and YPH are strongly interlinked. The traits TGW, LBR, and UFGPP also linked extensively.

Based on the MGIDI ranking, ten genotypes (V38, V35, V31, V47, V8, V54, V5, V63, V62, and V17) formed a distinct, tightly clustered group at the low-distance (most desirable) end of the index beyond the selection threshold cut-off, well separated from the remaining non-selected genotypes (**Fig. 10**). The strengths-and-weaknesses decomposition of the selected genotypes showed that their ranking was driven by differing proportion contributions of the underlying trait factors (FA1–FA3), indicating that these accessions are not redundant but instead contribute complementary trait profiles for use as parental material in breeding schemes (**Fig. 11**). For instance, genotypes such as V17, V8, and V5 exhibited high contributions from FA2, whereas accessions like V62, V63, and V54 were predominantly characterized by FA1, and V35 was uniquely marked by a higher proportion of FA3. This multi-trait differentiation confirms that selection based on MGIDI successfully captures genotypes with well-balanced, complementary agronomic attributes while minimizing common multi-collinearity trade-offs.

A regression-tree partitioning of yield hectare^{-1} ≥ 12 with higher tiller proliferation (TN ≥ 16) reached the highest predicted yield class (mean 8.4; n = 3, 5%), followed closely by those with TN between 15 and 16 (mean 7.8; n = 12, 18%), while genotypes with lower tillering capacity (ET < 11), shorter panicles (PL < 26 cm), and reduced grain weight (TGW < 24 g) formed the lowest-yielding class (mean 5.6; n = 3, 5%) (Fig. 12). Intermediate yield categories were predominantly delineated by panicle length and successive thresholds of effective tillers, where genotypes with ET < 11 but longer panicles (PL ≥ 26 cm) averaged 6.4 (n = 3, 5%), and those maintaining ET ≥ 11 achieved mean yields ranging between 6.6 and 7.3 (**Fig. 12**). A representative image of the experimental plot and V37 genotype is presented in Supplementary **Figure 1**.

4 Discussion

The analysis of variance revealed highly significant differences among the 66 *Boro* rice genotypes, comprising 63 advanced lines and three BRRI check varieties, for all 13 agro-morphological and yield-related traits (all p < 0.0001; Table 3). This substantial genotypic variability indicates considerable scope for selecting superior genotypes with desirable yield and component-trait combinations. Similar differentiation has been reported in advanced rice breeding materials and mutant populations, highlighting the value of ANOVA for identifying promising materials for yield improvement [15, 25, 47]. Thus, the observed variability can be effectively exploited in subsequent breeding and selection programs [47, 48].

Marked variation was observed among the genotypes for all agro-morphological and yield-related traits, confirming substantial diversity within the breeding population [15, 49]. Tillering ability varied considerably, with several advanced breeding lines outperforming the BRRI checks. V57 showed the strongest tillering capacity, followed by V32, V40, V27, V54, and V44, and these lines also produced high proportions of effective tillers, indicating efficient conversion of vegetative tillers into productive panicles. Productive tillering can increase panicle density and contribute substantially to grain yield when supported by adequate assimilate supply during reproductive development [12, 23]. Plant height and heading behaviour also varied markedly. V17, V20, V36, V21, and V4 had plant stature comparable to the relatively short check varieties, whereas V35, V42, and V53 were considerably taller. V8 and V17 were among the earliest advanced lines, while V34 and V53 were among the latest. Such variation provides opportunities to select genotypes with plant stature and maturity duration suited to specific *Boro* rice environments. Early heading may improve cropping-system efficiency and reduce exposure to late-season heat and water stress, whereas later materials may benefit environments where a longer growth period supports greater biomass accumulation and grain development [1, 4, 36].

Considerable diversity was also evident in panicle architecture and grain formation. V40, V47, V38, V54, V52, V37, and V57 produced longer panicles than the checks, while V27, V57, V32, V44, and V54 had particularly high numbers of filled grains per panicle. In contrast, V8, V57, V17, V63, V10, and V27 recorded relatively few unfilled grains. The combination of high filled-grain number and reduced sterility in V57 and V27 indicates favourable reproductive performance and efficient assimilate partitioning. These traits are important selection targets because panicle size and spikelet-filling efficiency directly influence grain productivity [12, 35].

Variation in fertility percentage further reflected differences in reproductive efficiency. V57, V27, V63, V10, V62, V17, and V8 showed comparatively high fertility, whereas V53, V23, V13, and V48 had lower values. Genotypes combining high fertility with fewer unfilled grains are likely to maintain more efficient fertilisation and grain filling under field conditions. Therefore, simultaneous selection for filled grains, spikelet fertility, and reduced sterility may be more effective than selection for a single reproductive trait [12, 47, 50, 51].

Grain moisture, thousand-grain weight, and grain shape also contributed to the observed diversity. V16 and V27 showed comparatively lower grain moisture, whereas V58, V60, and V32 had higher moisture levels. V32, V40, V50, V35, V38, V31, V51, and V46 produced heavier grains than the check varieties, indicating stronger grain-filling capacity. Thousand-grain weight is influenced by post-anthesis assimilate accumulation and remobilisation and is therefore an important component of grain productivity [52, 53]. Grain shape also differed, with V52, V54, V45, V31, V22, and V37 showing more elongated grains, whereas V27, V20, and V57 had comparatively broader grains, providing scope to incorporate grain-quality preferences into breeding objectives.

Grain yield clearly differentiated the genotypes, with several advanced lines substantially outperforming the checks. V57 was the most productive genotype, followed by V32, V40, V54, and V44, while V63, V62, V34, V47, V27, and V38 also showed strong yield performance. In contrast, V18, V13, V23, and V19 were comparatively low yielding. The superior performance of the leading genotypes resulted from favourable combinations of productive tillering, panicle development, filled-grain number, fertility, and grain weight rather than superiority in a single trait. V57 was particularly promising because it combined the highest grain yield with strong tillering, high fertility, numerous filled grains, and few unfilled grains. V32 and V40 combined high yield with high thousand-grain weight, whereas V54 combined high yield with long panicles, numerous filled grains, fewer unfilled grains, and an elongated grain type. V27 was distinguished by high filled-grain number, low unfilled-grain number, high fertility, relatively low grain moisture, and early heading. Similar variation in yield contributing traits were recorded by [15, 47].

Estimation of genotypic and phenotypic coefficients of variation provided insight into the genetic basis of trait expression [15, 25]. PCV values were slightly higher than the corresponding GCV values for all traits, indicating some environmental influence; however, the narrow differences between the two estimates for most characters suggest that much of the observed variation was associated with genotypic differences under the tested conditions [1, 12, 35]. The greatest variability was observed for unfilled grains panicle^{-1}, followed by length–breadth ratio and yield hectare^{-1}, whereas fertility percentage and filled grains panicle^{-1} were comparatively stable. Broad-sense heritability was high for all traits, particularly unfilled grains, fertility, panicle length, yield, grain shape, tillering, and filled grains, indicating a strong genotypic contribution to phenotypic variation and good prospects for phenotypic selection under similar environments [13, 15]. However, heritability should be interpreted together with genetic advance because high heritability does not always translate into a large selection response. Genetic advance as a percentage of the mean was highest for unfilled grains panicle^{-1} and length–breadth ratio, followed by yield hectare^{-1} and plant height, while panicle length, thousand-grain weight, heading traits, moisture percentage, and tillering showed moderate gains. In contrast, filled grains panicle^{-1} and fertility percentage exhibited low genetic advance despite high heritability, suggesting more limited progress through direct selection. Overall, combined consideration of GCV, PCV, heritability, and genetic advance provides a more reliable basis for identifying traits with the greatest breeding potential [1, 36, 47, 54]. The combination of high heritability and high GAM for unfilled grains panicle^{-1} and length–breadth ratio suggests strong genetic control and good prospects for direct selection. Yield hectare^{-1} also showed moderate GCV and PCV, high heritability, and relatively high GAM, while plant height, panicle length, and thousand-grain weight combined high heritability with moderate GAM, indicating useful opportunities for genetic improvement [47].

The multivariate analyses revealed substantial phenotypic differentiation among the evaluated genotypes. The first principal components captured most of the total variation, indicating that the major patterns of diversity could be explained primarily by yield formation, tillering ability, reproductive performance, phenology, and grain morphology. Yield hectare^{-1}, total tiller number, effective tiller number, and unfilled grains panicle^{-1} contributed strongly to the primary axis of variation, suggesting that productive tillering and grain-filling efficiency were major factors differentiating the breeding materials. Similar importance of tillering ability and spikelet-filling traits in explaining variation among rice genotypes has been reported previously [12, 15, 35]. The secondary principal component was mainly associated with heading behaviour, plant height, moisture percentage, and grain shape, representing a distinct axis of phenological and architectural variation. This differentiation is useful for

507 selecting genotypes with maturity duration and plant stature suited to specific production environments,
508 cropping systems, and adaptation needs [1, 4, 36].
509 The PCA biplot showed that grain yield was closely associated with effective and total tiller number,
510 filled grains panicle^{-1}, fertility percentage, thousand-grain weight, and panicle length, indicating that
511 yield improvement depends on coordinated enhancement of productive tillering, panicle development,
512 and grain-filling efficiency rather than any single trait. The close association between the two heading
513 traits confirms their common phenological basis, whereas the relationship between panicle length and
514 thousand-grain weight suggests their contribution to a related component of yield formation [12, 13].
515 The correlation analysis supported the patterns identified by the PCA. Grain yield was positively
516 associated with productive tillering, fertility percentage, grain weight, filled-grain number, and panicle
517 length, but negatively associated with unfilled grains panicle^{-1}. These associations indicate that
518 genotypes capable of producing more productive tillers and maintaining efficient reproductive
519 development are more likely to achieve higher grain yield. The correlation coefficients describe
520 association rather than causation, and the stability of these relationships should be confirmed across
521 environments [1, 35].
522 The heat-map and radar-plot analyses provided complementary evidence of the distinct trait profiles
523 of the genotype groups. The group containing the check varieties was generally associated with
524 comparatively early heading and moderate-to-high fertility, whereas the high-performing group showed
525 stronger expression of tillering, filled grains, and yield. Another group was characterized by reduced
526 yield-component expression and increased numbers of unfilled grains, while the late-maturing group
527 was associated with longer heading duration, higher moisture content, and greater grain elongation. The
528 consistency among the PCA, clustering, heat-map, and radar-plot results indicates that the observed
529 genotype groups were defined by meaningful combinations of agronomic and reproductive traits rather
530 than by isolated trait differences.
531 The MGIDI analysis identified V38, V35, V31, V47, V8, V54, V5, V63, V62, and V17 as desirable
532 genotypes based on their balanced performance across multiple traits. Their selection was supported by
533 complementary strengths and weaknesses across the underlying factors, indicating that the selected
534 genotypes were not phenotypically redundant. For example, some selected lines were distinguished by
535 reproductive and phenological attributes, whereas others contributed stronger yield-component or
536 grain-quality characteristics. This complementary diversity enhances their value as potential parents for
537 developing segregating populations with broad and balanced trait combinations [15, 25].
538 The regression-tree analysis further emphasized the importance of effective tillering, total tillering,
539 panicle length, and thousand-grain weight in differentiating yield performance. Genotypes with

stronger productive tillering and favourable panicle and grain characteristics were generally associated with the highest-yielding classes, whereas materials with weak tillering, shorter panicles, and lower grain weight tended to perform poorly. These findings reinforce the importance of selecting for coordinated source–sink development and efficient conversion of assimilates into harvestable grain [13, 36]. Because regression-tree groups may be influenced by population size and environmental conditions, the identified selection patterns should be validated through multi-environment testing. Overall, the multivariate results demonstrate that the breeding population contains useful diversity for improving yield, reproductive efficiency, maturity duration, plant stature, and grain characteristics.

5 Conclusion

The study revealed substantial genetic and phenotypic variation among the 66 *Boro* rice genotypes for all evaluated agro-morphological and yield-related traits. Several advanced lines outperformed the BRRI check varieties for important yield components and grain yield. V57 was the most promising genotype, followed by V32, V40, V54, V44, V63, V62, and V27. Their superior performance was associated with productive tillering, high fertility, efficient grain filling, favourable panicle traits, and greater grain weight. High heritability and favourable genetic advance for several traits indicated good prospects for phenotypic selection. Correlation, PCA, clustering, regression-tree, and MGIDI analyses identified productive tillering, fertility, filled grains, panicle development, and grain weight as important contributors to yield performance. The selected genotypes should be advanced as potential parents and breeding materials for developing high-yielding *Boro* rice varieties. Further multi-environment testing, stability analysis, grain-quality assessment, stress screening, and molecular validation are required before cultivar advancement.

6. Limitations

This study was conducted during a single *Boro* season at one location, limiting assessment of genotype × environment interactions and yield stability across environments. Pedigree information was unavailable, preventing evaluation of genetic relatedness and parental contributions among the advanced breeding lines. The study also lacked molecular-marker validation, so multi-environment testing and molecular characterization are needed before cultivar advancement.

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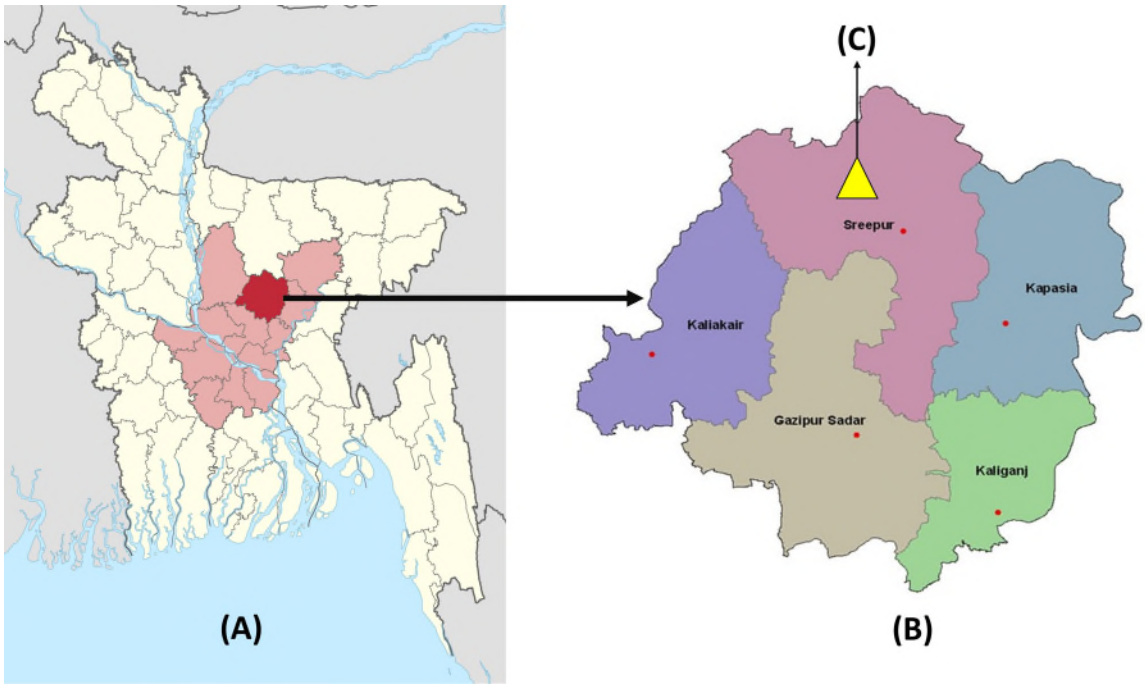


Figure 1. Geographical location of the experimental site in Gazipur, Bangladesh. (A) Map of Bangladesh highlighting the location of Gazipur district; (B) administrative map of Gazipur district showing its five upazilas; and (C) location of the experimental site in Sreepur Upazila, indicated by a yellow triangle.

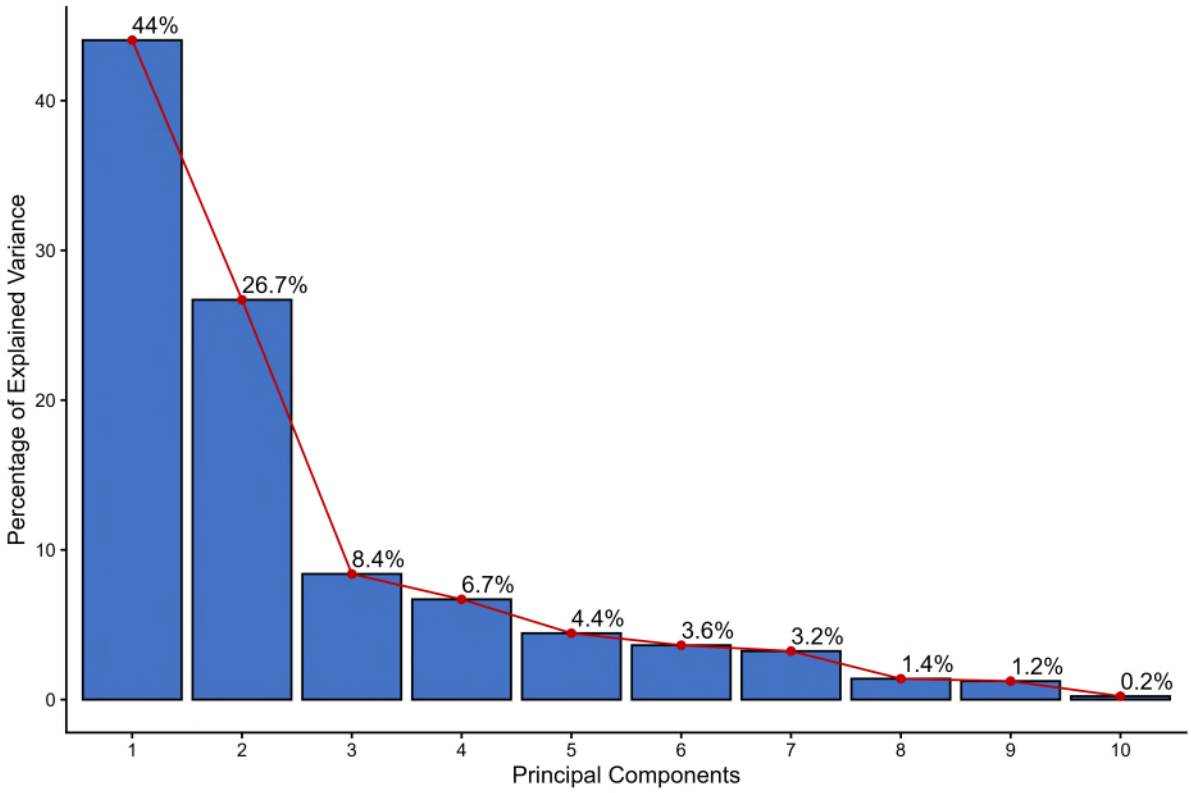


Figure 2. Scree plot showing the percentage of total variance explained by the first ten principal components (PCs) in the principal component analysis (PCA). The first two principal components (PC1 and PC2) explained 44.0% and 26.7% of the total variance, respectively, accounting for a cumulative variance of 70.7%. The blue bars represent the percentage of variance explained by each principal component, while the red line illustrates the decreasing trend in explained variance across successive components.

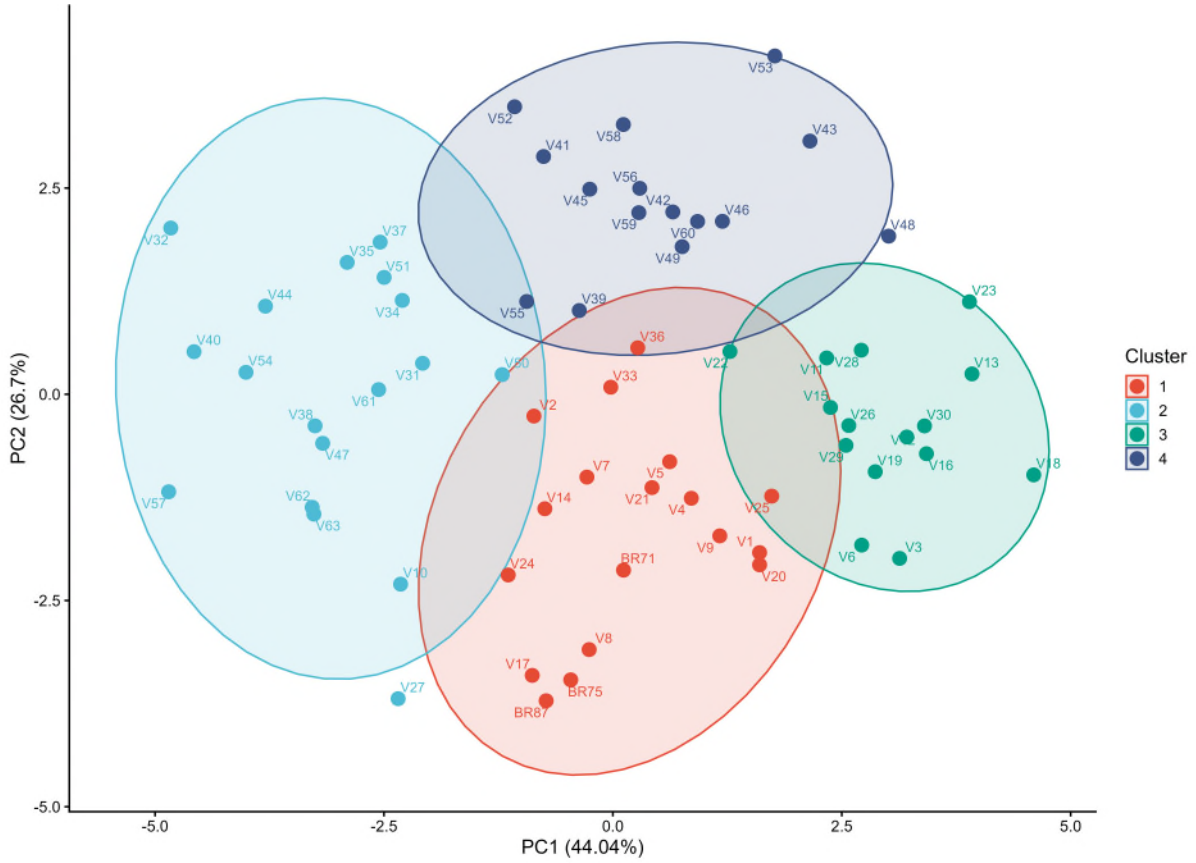


Figure 3. Principal component analysis (PCA)-based clustering of individual advanced breeding lines. The PCA score plot illustrates the distribution and grouping of advanced breeding lines into four distinct clusters based on their multivariate characteristics. The first two principal components, PC1 and PC2, explained 44.0% and 26.7% of the total variation, respectively, accounting for a cumulative variance of 70.7%. Different colors represent the four clusters, while the ellipses illustrate the dispersion and overlap of breeding lines within and among clusters.

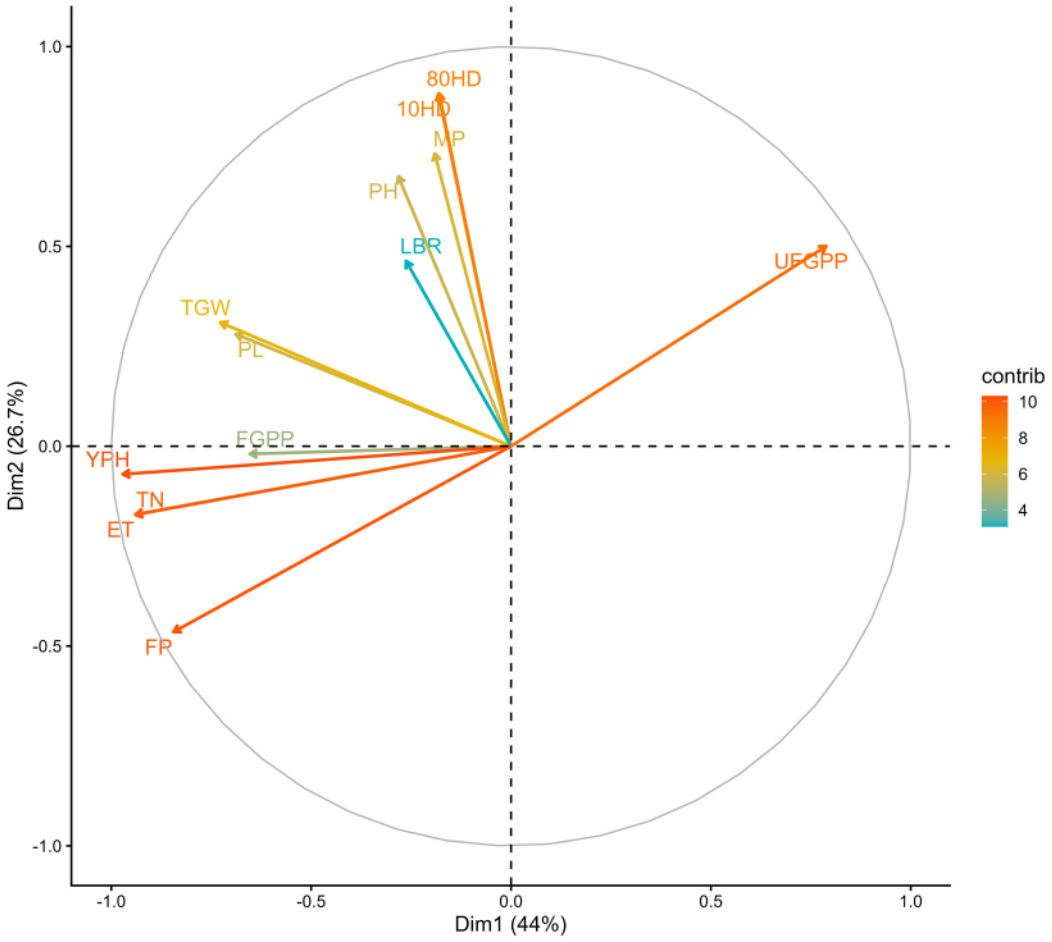


Figure 4. Principal component analysis (PCA) variable correlation plot illustrating the relationships among the studied traits of advanced breeding lines. The first two principal components, PC1 (Dim1) and PC2 (Dim2), explained 44.0% and 26.7% of the total variation, respectively, accounting for a cumulative variance of 70.7%. The arrows indicate the direction and strength of association of individual traits with the principal components, while the angles between arrows reflect the correlations among traits. The color gradient represents the relative contribution of each trait to the principal components, with warmer colors indicating higher contributions.

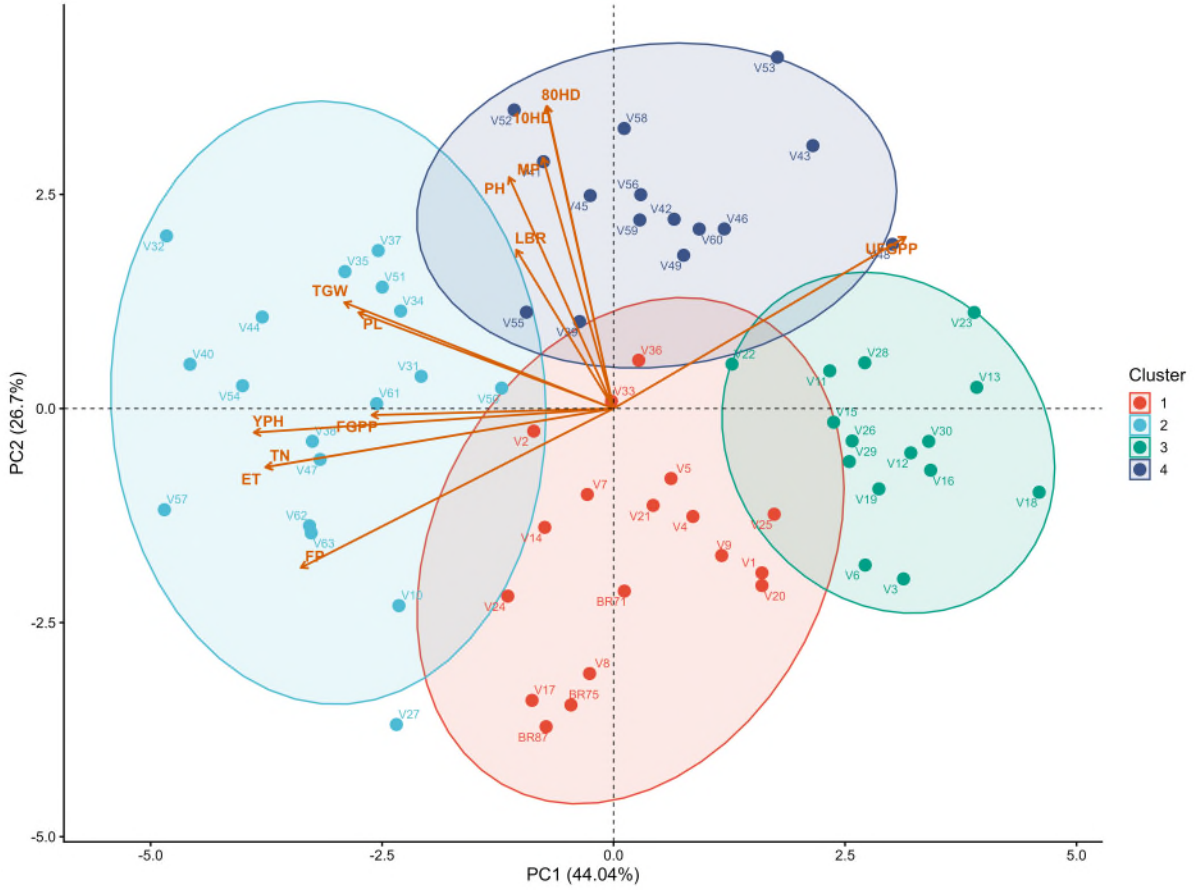


Figure 5. Principal component analysis (PCA) biplot illustrating the relationships between advanced breeding lines and studied traits. The biplot shows the distribution of advanced breeding lines into four clusters based on their multivariate characteristics and their associations with the studied traits. The first two principal components, PC1 (44.0%) and PC2 (26.7%), explained 70.7% of the total variation. Different colors represent the four clusters, while the ellipses illustrate their dispersion and overlap. The orange arrows represent the studied traits, with their directions and lengths indicating their associations with the principal components. The angles between trait vectors indicate the relationships among traits, while the positions of breeding lines relative to the vectors suggest their associations with specific traits.

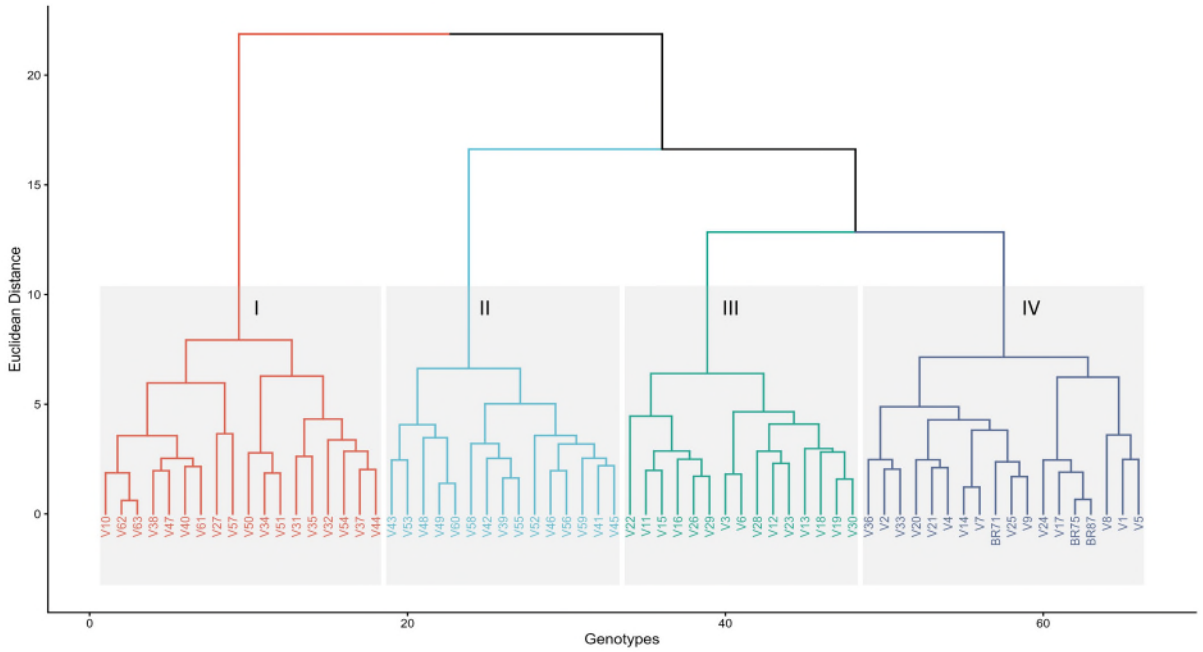


Figure 6. Hierarchical cluster analysis of the studied advanced breeding lines based on their phenotypic characteristics. The dendrogram illustrates the genetic divergence among the studied genotypes using Euclidean distance as a measure of dissimilarity. The genotypes were grouped into four major clusters (I, II, III, and IV), represented by different colors. The vertical axis indicates Euclidean distance, reflecting the degree of dissimilarity among genotypes, while the horizontal axis represents the individual genotypes. Genotypes grouped within the same cluster exhibited relatively greater similarity, whereas those belonging to different clusters showed greater divergence.

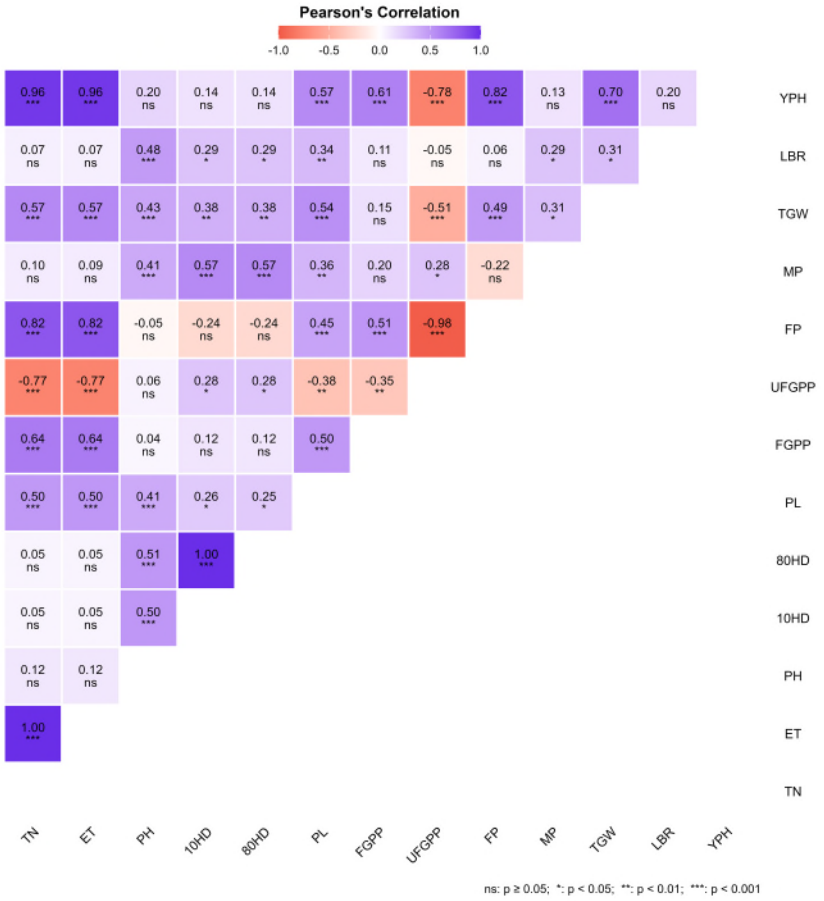


Figure 7. Pearson's correlation heatmap illustrating the relationships among 13 agro-morphological and yield-related traits of advanced Boro rice breeding lines. The heatmap presents the direction, strength, and statistical significance of pairwise correlations among the studied traits. The numerical values within each cell represent Pearson's correlation coefficients (r). Statistical significance is indicated by *, **, and *** at $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively, while ns denotes a non-significant correlation ($p \geq 0.05$).

Note: TN: Total tiller number; ET: Effective tiller number; PH: Plant height; 10HD: Days to 10% heading; 80HD: Days to 80% heading; PL: Panicle length; FGPP: Filled grains per panicle; UFGPP: Unfilled grains per panicle; FP: Fertility percentage; MP: Moisture percentage; TGW: Thousand-grain weight; LBR: Length-to-breadth ratio; YPH: Yield per hectare.

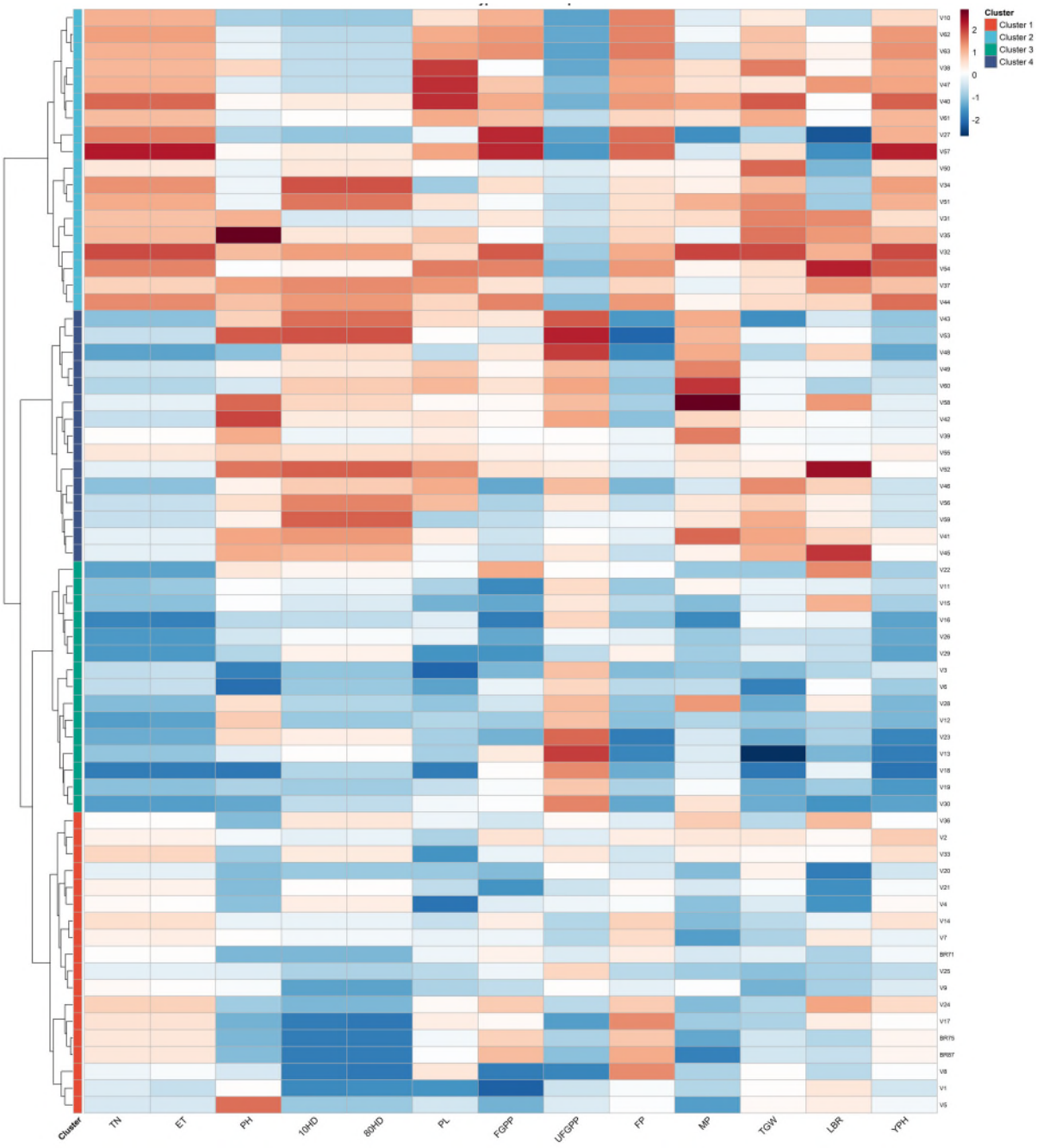


Figure 8. Hierarchical clustering heatmap illustrating the variation and relationships among advanced Boro rice genotypes based on 13 agro-morphological and yield-related traits. The heatmap displays the relative performance of the studied genotypes across different traits and their classification into four distinct clusters (Clusters 1–4). Each row represents an individual genotype, while each column corresponds to a studied trait. The color gradient indicates standardized trait values, with red representing relatively higher values, blue indicating relatively lower values, and white representing intermediate values. The dendrogram

on the left illustrates the hierarchical relationships among genotypes based on similarities in their multivariate trait profiles. The colored cluster annotations distinguish the four genotype groups, highlighting differences in their agro-morphological and yield-related characteristics.

Note: TN: Total tiller number; ET: Effective tiller number; PH: Plant height; 10HD: Days to 10% heading; 80HD: Days to 80% heading; PL: Panicle length; FGPP: Filled grains per panicle; UFGPP: Unfilled grains per panicle; FP: Fertility percentage; MP: Moisture percentage; TGW: Thousand-grain weight; LBR: Length-to-breadth ratio; YPH: Yield per hectare.

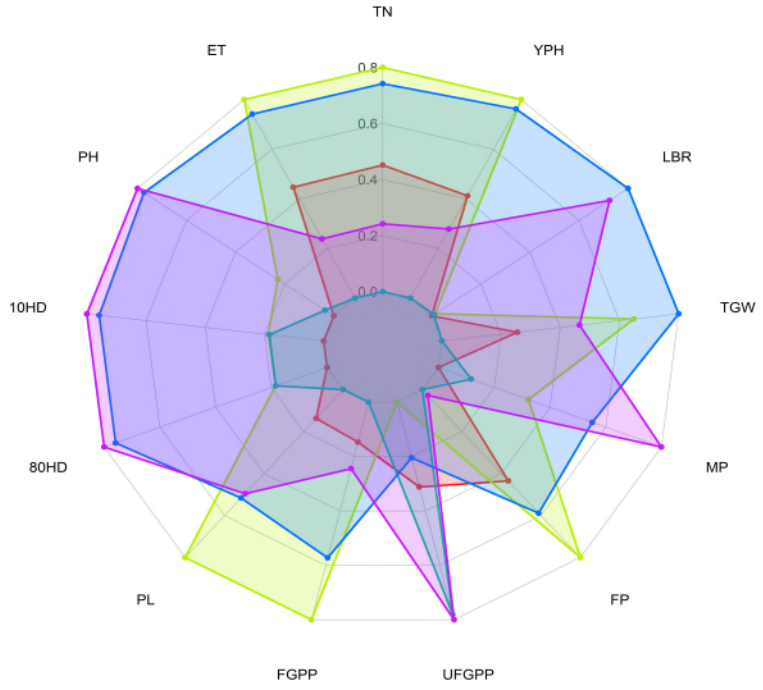


Figure 9. Radar plot illustrating the comparative distribution and variation of 13 agro-morphological and yield-related traits among the identified genotype clusters of advanced Boro rice breeding lines. The radar plot displays the relative performance patterns of the studied traits across the genotype clusters using standardized trait values. Each colored polygon represents a distinct cluster profile, while the radial axes correspond to individual traits. The distance from the center indicates the relative magnitude of each standardized trait value, with greater distances representing higher relative values. Differences in polygon shapes and sizes highlight variation in trait expression among the genotype clusters.

Note: TN: Total tiller number; ET: Effective tiller number; PH: Plant height; 10HD: Days to 10% heading; 80HD: Days to 80% heading; PL: Panicle length; FGPP: Filled grains per panicle; UFGPP: Unfilled grains per panicle; FP: Fertility percentage; MP: Moisture percentage; TGW: Thousand-grain weight; LBR: Length-to-breadth ratio; YPH: Yield per hectare.

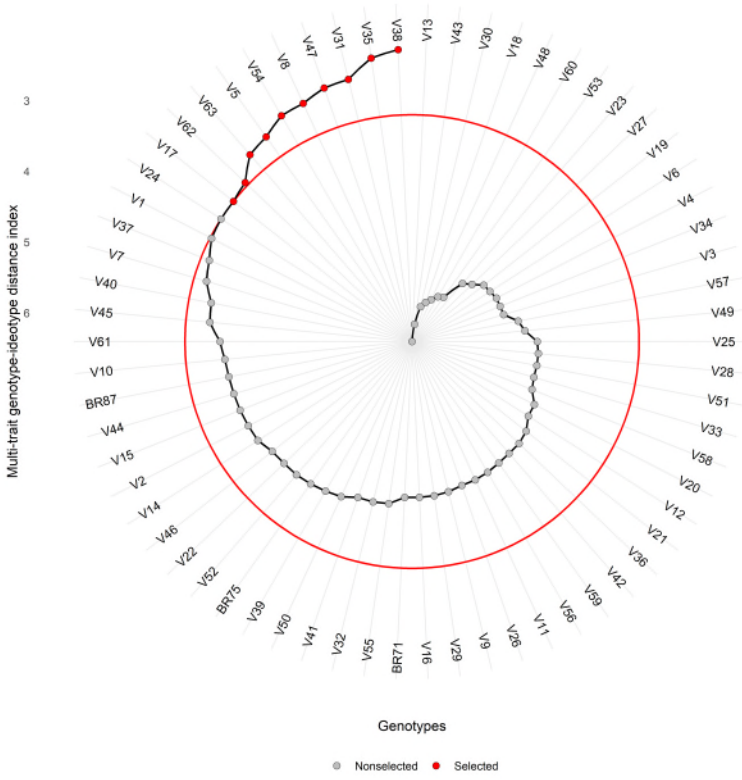


Figure 10. Ranking and selection of advanced Boro rice genotypes based on the multi-trait genotype–ideotype distance index (MGIDI). The circular plot illustrates the ranking of 66 rice genotypes according to their MGIDI values, reflecting their relative distances from the predefined ideal genotype (ideotype). Genotypes with lower MGIDI values are considered closer to the ideotype and therefore more desirable for simultaneous improvement of multiple traits. The red dots represent selected genotypes, whereas the gray dots indicate non-selected genotypes. The red circle represents the selection threshold determined by the predefined selection intensity. Genotypes falling within the selection threshold were identified as promising breeding materials based on their overall multi-trait performance.

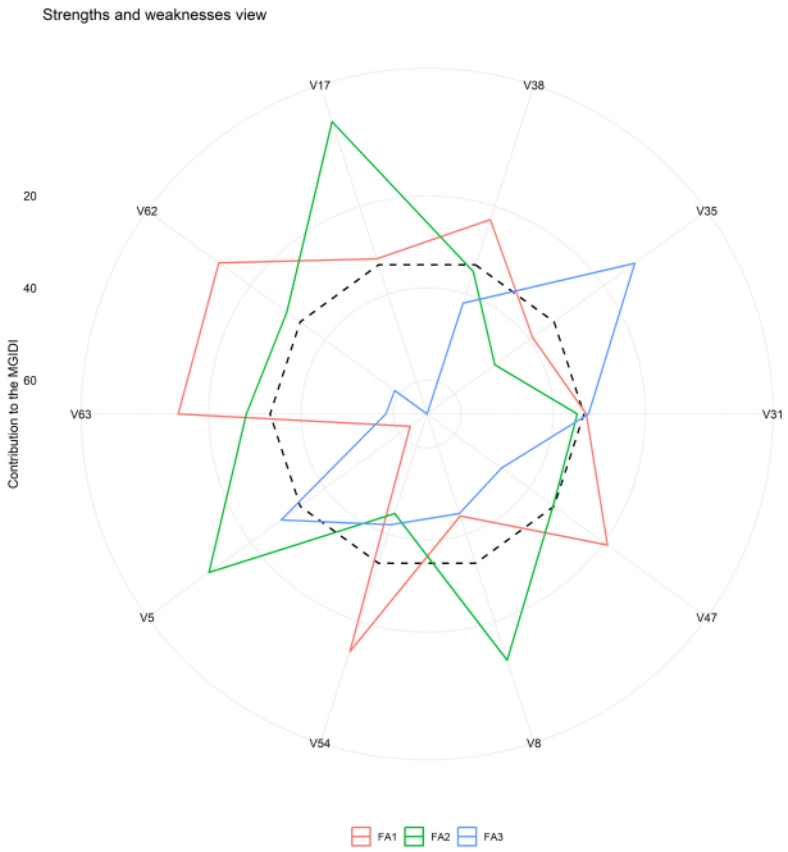


Figure 11. Strengths and weaknesses of selected advanced Boro rice genotypes based on the multi-trait genotype–ideotype distance index (MGIDI) analysis. The radar plot illustrates the relative contributions of three latent factors (FA1, FA2, and FA3) to the MGIDI values of the ten selected genotypes (V17, V38, V35, V31, V47, V8, V54, V5, V63, and V62). The red, green, and blue lines represent the contributions of FA1, FA2, and FA3, respectively, highlighting differences in the multi-trait profiles of the selected genotypes. The dashed black line indicates the average contribution of all factors and serves as a reference for identifying the relative strengths and weaknesses of individual genotypes. Lower factor contributions indicate relative strengths, whereas higher contributions indicate relative weaknesses in relation to the predefined ideotype.

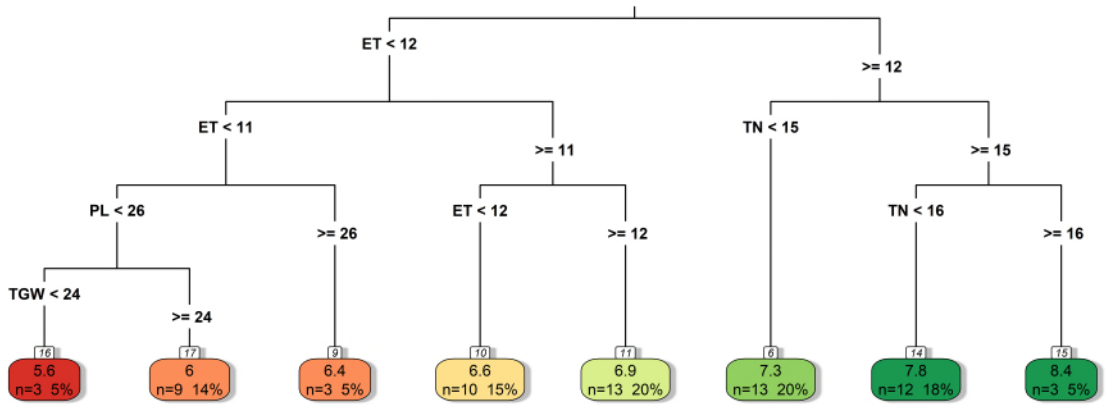


Figure 12. Regression tree analysis illustrating the influence of yield-contributing traits on grain yield (t ha^{-1}) in advanced Boro rice genotypes. The regression tree partitions the studied genotypes into eight terminal groups based on effective tiller number (ET), total tiller number (TN), panicle length (PL), and thousand-grain weight (TGW). Each branching point represents a threshold value of a trait used to divide genotypes into groups with different predicted grain yields. The terminal nodes display the mean predicted grain yield (t ha^{-1}), the number of genotypes (n), and their percentage of the total population. The predicted grain yield ranged from 5.6 to 8.4 t ha^{-1}, with the highest yield associated with ET ≥ 12 and TN ≥ 16. The color gradient from red to green represents increasing predicted grain yield, highlighting the importance of tillering ability and other yield-contributing traits in differentiating genotype performance.

Note: ET: Effective tiller number; TN: Total tiller number; PL: Panicle length; TGW: Thousand-grain weight; n: Number of genotypes within each terminal node; t ha^{-1}: Tonnes per hectare. The percentages indicate the proportion of genotypes represented by each terminal node.

Table 1. Name and sources of the germplasm

Genotype code/ Variety Name	Sources
V1	ACI-Plant Genetic & Development Centre (ACI-PGRDC), Hybrid Rice Genetics, ASRBC, ACI Seed Limited, Gazipur, 1706, Bangladesh
V2	
V3	
V4	
V5	
V6	
V7	
V8	
V9	
V10	
V11	
V12	
V13	

Genotype code/ Variety Name	Sources
V14	
V15	
V16	
V17	
V18	
V19	
V20	
V21	
V22	
V23	
V24	
V25	
V26	
V27	
V28	

Genotype code/ Variety Name	Sources
V29	
V30	
V31	
V32	
V33	
V34	
V35	
V36	
V37	
V38	
V39	
V40	
V41	
V42	
V43	

Genotype code/ Variety Name	Sources
V44	
V45	
V46	
V47	
V48	
V49	
V50	
V51	
V52	
V53	
V54	
V55	
V56	
V57	
V58	

Genotype code/ Variety Name	Sources
V59	
V60	
V61	
V62	
V63	
BR71	Bangladesh Rice Research Institute (BRRI), Gazipur-1701, Bangladesh
BR75	
BR87	

Note: The pedigree of the advanced breeding lines is not available due to variety release issue

Table 2. List of morphological and yield-related traits with their acronyms and units of measurement

Traits Name	**Acronym**	**Unit of measurement**
Total tiller number	TN	Count
Effective tiller number	ET	Count
Plant height	PH	cm
10% Heading days	10HD	Days
80% Heading days	80HD	Days
Panicle length	PL	cm
Filled grain panicle^{-1}	FGPP	Count
Unfilled grain panicle^{-1}	UFGPP	Count
Fertility percentage	FP	%
Moisture percentage	MP	%
Thousand grain weight	TGW	g
Length-breadth ratio	LBR	Ratio
Yield per hectare	YPH	ton ha^{-1}

Table 3. Analysis of Variance of yield and yield contributing traits of the studied genotypes

Traits	Replication MS (df = 2)	Genotype MS (df = 65)	Error MS (df = 130)	Genotype F-value	Genotype p-value
Total tiller number	0.0797 ns	1.8795***	0.0829	22.6648	<0.0001
Effective tiller number	0.0888 ns	1.8686***	0.0830	22.5155	<0.0001
Plant height	0.9252 ns	407.5066***	22.5065	18.1061	<0.0001
Days to 10% heading	3.9141 ns	107.1596***	9.4372	11.3550	<0.0001
Days to 80% heading	3.5909 ns	106.7450***	9.4730	11.2684	<0.0001
Panicle length	4.7588***	11.8208***	0.4053	29.1656	<0.0001
Filled grains per panicle	8.1554 ns	108.3632***	4.0013	27.0820	<0.0001
Unfilled grains per panicle	0.6438 ns	43.2867***	0.8730	49.5827	<0.0001
Fertility percentage	0.3161 ns	11.5267***	0.3036	37.9657	<0.0001
Moisture percentage	0.5256 ns	7.2337***	0.8172	8.8513	<0.0001
Thousand-grain weight	1.6155 ns	13.6814***	0.9555	14.3187	<0.0001
Length-to-breadth ratio	0.0889*	0.7088***	0.0261	27.1667	<0.0001
Yield per hectare	0.1073 ns	1.5677***	0.0571	27.4640	<0.0001

Here, MS, mean square; df, degrees of freedom. Significance levels: ns, not significant; *, $p < 0.05$; **, $p < 0.01$; and ***, $p < 0.001$. Significance symbols beside replication and genotype mean squares indicate the corresponding effects. All genotype effects were highly significant ($p < 0.0001$).

Table 4. Mean performance of the genotypes for the studied traits

Genotype	TN	ET	PH	10HD	80HD	PL	FGPP	UFGPP	FP	MP	TGW	LBR	YPH
V1	14.4 m-p	11.83 p-s	115.5 h-o	69 t-u	75.33 u-v	22.93 z-b	150.53 c	19 q-u	88.79 k-o	19.43 o-v	26.89 j-t	4.24 g-k	6.63 r-v
V2	14.9 i-m	12.47 k-o	113.43 j-r	77.67 j-r	84 j-s	24.57 t-x	166.7 e-m	19.7 m-s	89.43 h-l	21.3 d-n	27.63 g-p	4.1 h-l	7.53 e-k
V3	14.17 o-r	11.8 p-s	93.33 x-z	73 q-u	79 r-v	21.9 b	156.47 x-a	24.37 e-f	86.52 v-x	19 s-v	24.29 x-c	3.68 p-t	6.64 r-v
V4	14.8 j-n	12.33 l-p	101.97 t-x	81 g-m	87 g-n	22.17 b	161.83 p-v	20.43 l-r	88.79 k-o	18.97 s-v	25.86 o-y	3.27 u-v	7.07 k-r
V5	14.33 m-q	11.97 o-r	133.13 b-e	73.33 q-u	79.33 r-v	25.17 p-w	156.37 x-a	19.6 n-t	88.86 k-o	18.37 t-v	27.04 i-s	4.2 h-k	6.91 m-t
V6	14.17 o-r	11.8 p-s	91.07 z	73.33 q-u	79.33 r-v	23.33 y-a	162.5 n-u	23.5 f-h	87.37 q-v	19.63 m-u	22.74 b-c	4.06 i-n	6.32 u-y
V7	14.9 i-m	12.53 i-o	115.73 h-n	78.67 j-q	84.67 j-r	25.77 m-t	162.9 m-t	18.17 s-w	89.96 g-j	18.37 t-v	24.96 t-a	4.21 g-k	6.85 o-t
V8	14.57 k-o	12.27 l-p	109.9 n-u	67.67 u	73.67 v	26.97 h-m	152.47 b-c	14.17 a	91.5 a-b	19.37 p-v	26.92 j-t	3.7 o-t	6.98 l-s
V9	14.8 j-n	12.37 l-p	114.63 i-q	70.67 s-u	76.67 t-v	24.53 t-y	160.03 s-x	21.27 j-p	88.27 m-q	20.7 g-s	23.99 y-c	3.61 q-t	6.73 p-u
V10	15.5 c-h	13.1 c-i	104.53 r-w	73.33 q-u	79.33 r-v	27.13 g-l	170.13 c-g	15.5 z-a	91.65 a-b	20.17 k-t	27.45 g-q	3.68 p-t	7.42 f-l
V11	13.83 q-t	11.5 r-u	115.17 i-p	78 j-r	84.33 j-r	24.5 u-y	153.47 a-c	23.23 f-i	86.85 t-w	20.93 f-r	26.29 m-w	3.92 k-r	6.5 t-w
V12	13.5 t-v	11.13 t-w	123.4 f-i	73.33 q-u	79.33 r-v	24.63 s-x	158.13 v-z	24.27 e-g	86.69 u-x	19.5 n-v	24.53 w-b	3.64 p-t	6.12 w-z
V13	13.87 p-t	11.47 r-u	110.87 m-t	79.67 i-p	85.67 i-q	24.47 v-y	166.17 h-o	28.5 a-b	85.36 y-a	20.1 k-t	20.81 d	3.44 t-u	5.61 a
V14	15.1 g-k	12.7 g-l	112.3 k-s	78 j-r	84 j-s	25 q-w	165.8 h-p	18.03 s-w	90.19 e-i	18.87 s-v	25.15 s-z	3.93 k-q	7.33 h-n

Genotype	TN	ET	PH	10HD	80HD	PL	FGPP	UFGPP	FP	MP	TGW	LBR	YPH
V15	13.8 q-u	11.43 r-u	114.8 i-p	76.67 k-s	83 k-s	23.7 x-z	155.47 z-b	22.47 h-k	87.37 q-v	18.9 s-v	26.06 n-x	4.55 b-f	6.33 u-x
V16	13.27 u-v	10.87 v-w	106.17 o-w	75.33 l-s	81.33 m-u	25.5 o-v	152.57 b-c	23.33 f-i	86.73 u-x	18 u-v	26.64 k-u	3.95 k-p	5.94 x-a
V17	15.07 h-k	12.67 h-m	100.13 v-y	67.67 u	73.67 v	26.77 i-n	164.57 j-q	15.27 z-a	91.51 a-b	19.23 q-v	24.9 u-a	4.19 h-k	7.04 l-r
V18	13.2 v	10.8 w	92 y-z	74.67 n-t	80.67 o-u	22.43 a-b	164.17 l-r	26.23 c-d	86.22 w-y	20.17 k-t	22.61 c	3.96 k-p	5.55 a
V19	13.83 q-t	11.43 r-u	105.33 q-w	73.67 p-u	79.67 q-v	24.97 q-w	163.57 l-t	24.13 e-h	87.14 r-w	20.57 h-s	23.9 z-c	3.6 r-t	5.87 y-a
V20	14.47 l-o	12.07 n-q	101.1 u-x	73.33 q-u	79.33 r-v	24.23 w-y	156.8 w-a	21.37 j-n	88.01 o-s	18.9 s-v	27.27 g-r	3.11 v-w	6.62 r-v
V21	14.9 i-m	12.5 j-o	101.53 u-x	79.67 i-p	85.67 i-q	24.83 r-x	154.13 a-c	18.83 r-u	89.11 j-n	20.03 k-t	26.66 k-u	3.24 u-v	6.96 l-t
V22	13.53 s-v	11.13 t-w	119.73 f-m	80.33 h-o	86.33 h-p	26.07 l-r	170.37 c-f	21.37 j-n	88.86 k-o	19.1 s-v	24.64 v-a	4.7 b-c	6.36 u-x
V23	13.63 r-v	11.23 t-w	121.83 f-j	81 g-m	87 g-n	24.4 v-y	156.13 y-b	27.33 b-c	85.1 z-a	19.97 k-t	23.86 z-c	3.65 p-t	5.7 z-a
V24	15.23 e-j	12.83 e-l	103.7 s-w	72 r-u	78 s-v	26.43 j-o	168.5 d-j	18.23 s-w	90.24 d-i	18.87 s-v	25.12 s-z	4.6 b-f	7.4 f-l
V25	14.5 l-o	12.1 m-q	110.87 m-t	74.33 o-t	80.33 p-u	24.73 s-x	162.83 m-t	23.47 f-h	87.41 q-v	19.23 q-v	24.35 x-c	3.63 q-t	6.5 t-w
V26	13.47 t-v	11.07 u-w	109.1 n-v	79 i-q	85 i-r	25.73 m-u	155.47 z-b	20.7 k-q	88.25 m-q	19.13 r-v	25.39 r-z	3.75 n-t	5.99 x-a
V27	15.8 b-d	13.4 b-d	105.03 r-w	73 q-u	79 r-v	25.83 m-s	176.8 a	15.5 z-a	91.94 a-b	18.03 u-v	25.09 s-z	2.91 w	7.75 d-h
V28	13.77 q-u	11.37 s-v	120.57 f-l	74.67 n-t	80.67 o-u	24.13 w-y	160.83 q-v	24.47 e-f	86.8 t-x	22.63 b-f	23.88 z-c	4.2 h-k	6.11 w-z
V29	13.47 t-v	11.07 u-w	105.7 p-w	80.67 g-n	86.67 g-o	23 z-b	154.13 a-c	18.5 s-v	89.28 i-m	19.2 q-v	26.21 m-x	3.77 m-s	5.95 x-a

Genotype	TN	ET	PH	10HD	80HD	PL	FGPP	UFGPP	FP	MP	TGW	LBR	YPH
V30	13.5 t-v	11.1 u-w	98.7 w-z	75.33 l-s	81.33 m-u	26 l-r	164.13 l-r	26.43 c-d	86.13 w-y	21.43 d-m	23.93 y-c	3.27 u-v	5.96 x-a
V31	15.37 d-i	12.97 d-k	127.07 c-f	76.67 k-s	82.67 l-t	25.53 n-v	166.37 g-o	18.83 r-u	89.83 h-k	21.57 c-l	29.75 a-e	4.71 b	7.36 g-m
V32	16.17 a-b	13.77 a-b	125.53 d-g	86.33 a-h	92.33 a-h	27.33 f-k	174.57 a-b	17.37 u-y	90.95 b-g	23.63 a-b	30.67 a	4.55 b-f	8.36 a-b
V33	15.2 f-j	12.8 f-l	103.63 s-w	81.33 f-l	87.33 f-m	23 z-b	162.57 n-u	22.47 h-k	87.86 o-t	21.07 e-p	26.96 j-s	4.08 h-m	7.37 g-m
V34	15.73 b-f	13.33 b-f	113.2 j-r	90 a	96 a	24.33 v-y	167.03 e-l	19.17 q-u	89.71 h-k	21.07 e-p	28.7 b-j	3.63 q-t	7.85 c-f
V35	15.4 d-i	13 d-k	147.77 a	81.67 f-k	87.67 f-l	27.83 d-i	163.9 l-s	18.17 s-w	90.02 g-j	20.4 j-s	30.02 a-d	4.66 b-e	7.67 e-j
V36	14.77 j-n	12.37 l-p	101.1 u-x	81.67 f-k	87.67 f-l	25.83 m-s	160.83 q-v	21.6 i-l	88.16 n-r	21.8 c-k	25.24 s-z	4.5 b-g	7.02 l-r
V37	15.23 e-j	12.83 e-l	128.47 b-f	87.33 a-f	93.33 a-f	28.67 c-e	166.7 e-m	18.5 s-v	90.01 g-j	20.37 j-s	27.71 f-o	4.68 b-d	7.61 e-j
V38	15.47 c-h	13.07 c-j	121.97 f-j	75.33 l-s	81.33 m-u	30.17 a-b	163.83 l-s	15.83 y-a	91.18 a-e	21.5 d-l	29.88 a-d	4.1 h-l	7.75 d-h
V39	14.77 j-n	12.37 l-p	127.23 c-f	78.33 j-q	84.33 j-r	26.83 i-m	164.13 l-r	21.27 j-p	88.53 l-p	23 b-d	26.63 k-u	4.01 k-n	6.87 n-t
V40	16 b-c	13.6 b-c	116.03 h-n	81.33 f-l	87.33 f-m	30.33 a	170.47 c-e	16.27 x-z	91.29 a-c	22.4 b-g	30.46 a-b	4.08 h-m	8.23 a-c
V41	14.5 l-o	12.1 m-q	127.83 c-f	86.67 a-g	92.67 a-g	26.83 i-m	160.7 q-v	21.33 j-o	88.28 m-q	23.27 b-c	29.19 a-g	4.35 f-j	7.21 j-o
V42	14.23 n-q	11.83 p-s	136.97 b	81.33 f-l	87.33 f-m	27.17 g-l	164.5 k-q	25.43 d-e	86.61 u-x	21.67 c-k	27.23 h-r	4.04 j-n	6.79 o-u
V43	13.83 q-t	11.43 r-u	123.07 f-i	88.67 a-c	94.67 a-c	27.33 f-k	166.37 g-o	27.6 b-c	85.77 x-z	22.33 b-i	23.1 a-c	3.82 l-r	6.23 v-y
V44	15.77 b-e	13.37 b-e	124.67 e-h	86.67 a-g	92.67 a-g	27.5 e-j	172.5 b-c	16.5 w-z	91.27 a-d	20.93 f-r	27.91 e-n	4.37 e-i	8.14 b-d

Genotype	TN	ET	PH	10HD	80HD	PL	FGPP	UFGPP	FP	MP	TGW	LBR	YPH
V45	14.5 l-o	12.1 m-q	127.43 c-f	85 a-i	91 a-i	26 l-r	160.37 r-w	22.6 g-j	87.65 p-u	21 f-q	28.92 a-i	5.05 a	7.03 l-r
V46	13.8 q-u	11.4 r-v	117.87 g-n	83.67 b-j	89.67 b-j	28.33 c-g	155.47 z-b	24.47 e-f	86.4 v-x	20 k-t	29.58 a-f	4.39 d-h	6.6 r-v
V47	15.5 c-h	13.1 c-i	111.17 l-t	75.33 l-s	81.33 m-u	30.33 a	168.57 d-i	16.5 w-z	91.08 a-f	21.37 d-m	27.64 g-p	4.65 b-f	7.81 c-g
V48	13.57 s-v	11.17 t-w	102.1 t-x	82.67 d-k	88.67 d-l	24.83 r-x	166.5 f-n	28.5 a-b	85.38 y-a	22.37 b-h	25.09 s-z	4.39 c-h	5.98 x-a
V49	14.27 n-q	11.87 p-s	116.93 g-n	81.67 f-k	87.67 f-l	27.83 d-i	164.57 j-q	24.47 e-f	87.06 s-w	22.83 b-e	26.53 l-v	4 k-o	6.51 s-w
V50	15 h-l	12.6 h-n	112.23 k-s	81.67 f-k	87.67 f-l	26.33 j-p	162.37 o-u	19.57 o-t	89.24 i-m	20.97 f-q	30.27 a-c	3.46 s-u	7.35 g-m
V51	15.53 c-h	13.13 c-h	112.7 k-s	88.33 a-d	94.33 a-d	27.17 g-l	163.5 l-t	18.5 s-v	89.83 h-k	22.23 b-i	29.59 a-f	3.6 r-t	7.73 d-h
V52	14.5 l-o	12.1 m-q	132.9 b-e	89.33 a-b	95.33 a-b	28.83 c-d	166.73 e-m	22.37 h-k	88.17 n-r	21.23 d-o	27.35 g-r	5.22 a	7.06 l-r
V53	14.23 n-q	11.83 p-s	135.2 b-c	90 a	96 a	26.33 j-p	161.17 q-v	29.37 a	84.58 a	22.13 b-j	26.48 m-v	4.06 i-n	6.33 u-y
V54	15.8 b-d	13.4 b-d	115.13 i-p	80.33 h-o	86.33 h-p	29.17 b-c	172.5 b-c	16.57 w-z	91.23 a-d	20.93 f-r	27.88 e-n	5.11 a	8.21 a-c
V55	15 h-l	12.6 h-n	123.07 f-i	82.33 e-k	88.33 e-l	27.33 f-k	165.47 i-p	21.47 j-m	88.51 l-p	21.37 d-m	27.03 i-s	4.03 k-n	7.22 i-o
V56	14.23 n-q	11.83 p-s	121.07 f-k	87.67 a-e	93.67 a-e	28 c-i	158.8 u-z	22.47 h-k	87.6 p-u	21.27 d-n	28.19 d-m	4.16 h-k	6.65 q-v
V57	16.5 a	14.1 a	116.57 g-n	81.33 f-l	87.33 f-m	28.5 c-f	176.7 a	15.17 z-a	92.09 a	20 k-t	27.85 e-n	3.22 u-v	8.6 a
V58	14.5 l-o	12.1 m-q	133.83 b-d	83 c-j	89 c-k	26.43 j-o	164.5 k-q	24.5 e-f	87.04 s-w	25.1 a	26.51 l-v	4.66 b-e	6.79 o-u
V59	14.23 n-q	11.83 p-s	117.33 g-n	89.33 a-b	95.33 a-b	24.5 u-y	159.8 t-y	20.5 l-r	88.63 l-p	21.3 d-n	29.09 a-h	4.18 h-k	6.61 r-v

Genotype	TN	ET	PH	10HD	80HD	PL	FGPP	UFGPP	FP	MP	TGW	LBR	YPH
V60	14.07 o-s	11.67 q-t	109.57 n-v	83.67 b-j	89.67 b-j	28.17 c-h	166.7 e-m	25.33 d-e	86.81 t-x	23.8 a-b	26.57 k-v	3.63 q-t	6.61 r-v
V61	15.43 d-i	13.03 d-k	111.53 k-s	79.67 i-p	85.67 i-q	28.33 c-g	168.9 c-i	18.6 s-v	90.07 f-j	21.4 d-m	28.99 a-h	4.04 j-n	7.68 e-i
V62	15.63 b-g	13.23 b-g	111.57 k-s	75 m-t	81 n-u	28.33 c-g	171.5 b-d	15.83 y-a	91.55 a-b	20.53 i-s	28.52 c-k	4.07 h-m	7.9 c-e
V63	15.5 c-h	13.1 c-i	112.27 k-s	75.33 l-s	81.33 m-u	28.6 c-e	171.7 b-d	15.47 z-a	91.74 a-b	19.77 l-u	28.46 c-l	4.15 h-k	7.92 c-e
BR71	14.77 j-n	12.37 l-p	100.5 u-y	72 r-u	78 s-v	25.83 m-s	165.47 i-p	19.5 p-t	89.45 h-l	20 k-t	26.11 n-x	3.64 p-t	6.92 m-t
BR75	15 h-l	12.6 h-n	100.53 u-y	68 u	74 v	26 l-r	168.17 d-k	17.83 t-x	90.41 c-h	18.5 t-v	25.7 p-z	3.67 p-t	7.11 k-q
BR87	15 h-l	12.6 h-n	101.17 u-x	68 u	74 v	26.2 k-q	169.5 c-h	16.83 v-z	90.97 b-g	17.8 v	25.64 q-z	3.74 n-t	7.14 k-p
CV (%)	1.96	2.35	4.15	3.90	3.63	2.44	1.22	4.49	0.62	4.39	3.67	4.02	3.44

Note: Values represent trait means of three replications. Means followed by the same lowercase letter(s) within a column are not significantly different at $p < 0.05$ according to Duncan's Multiple Range Test (DMRT). Trait acronyms: TN, total tiller number (count); ET, effective tiller number (count); PH, plant height (cm); 10HD, days to 10% heading; 80HD, days to 80% heading; PL, panicle length (cm); FGPP, filled grains per panicle (count); UFGPP, unfilled grains per panicle (count); FP, spikelet fertility percentage (%); MP, grain moisture percentage (%); TGW, thousand-grain weight (g); LBR, grain length-to-breadth ratio; YPH, grain yield per hectare ($\text{t}\ \text{ha}^{-1}$); CV, coefficient of variation (%).

Table 5. Genotypic and phenotypic variance, GCV, PCV, heritability, and genetic advance for the studied traits

Traits	Genotypic Variance (σ^2g)	Phenotypic Variance (σ^2p)	GCV (%)	PCV (%)	Broad-sense Heritability (H^2%)	Genetic Advance	Genetic Advance as % of Mean (GAM%)
Total tiller number	0.60	0.68	5.28	5.63	87.84	1.49	10.19
Effective tiller number	0.60	0.68	6.29	6.72	87.76	1.49	12.15
Plant height (cm)	128.33	150.84	9.92	10.75	85.08	21.53	18.85
10% Heading days	32.57	42.01	7.24	8.22	77.54	10.35	13.13
80% Heading days	32.42	41.90	6.71	7.63	77.39	10.32	12.16
Panicle length (cm)	3.81	4.21	7.48	7.86	90.37	3.82	14.64
Filled grain panicle^{-1}	34.79	38.79	3.61	3.81	89.68	11.51	7.03
Unfilled grain panicle^{-1}	14.14	15.01	18.06	18.61	94.18	7.52	36.11
Fertility percentage	3.74	4.04	2.18	2.27	92.49	3.83	4.32
Moisture percentage	2.14	2.96	7.10	8.35	72.35	2.56	12.45
Thousand grain weight (g)	4.24	5.20	7.74	8.57	81.62	3.83	14.40
Length-breadth ratio	0.23	0.25	11.86	12.52	89.71	0.93	23.14
Yield ha^{-1}	0.50	0.56	10.21	10.77	89.82	1.39	19.92

Note: σ^2g and σ^2p represent genotypic and phenotypic variances, respectively. GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; H^2, broad-sense heritability; GAM, genetic advance as a percentage of the mean. Categorization followed standard descriptors: GCV and PCV as low (<10%), medium (10–20%), or high (>20%); broad-sense heritability (H^2) as low (<30%), medium (30–60%), or high (>60%); and GAM as low (<10%), moderate (10–20%), or high (>20%).

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