



Diversity Analysis of Rice Genotypes Collected from Six Southern Districts of Bangladesh Based on Agro-Morphological Traits

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Abstract: Rice serves as a staple food for millions around the globe, and its productivity is heavily influenced by environmental factors, especially in the southern regions of Bangladesh. This study aimed to assess the agro-morphological diversity of forty local and modern rice genotypes to identify promising cultivars for improved yield and adaptability. The experiment was conducted at the Regional Station of the Bangladesh Rice Research Institute, Gopalganj, using a randomized complete block design (RCBD) with three replications. Significant variations were observed in key traits such as panicle length, filled and unfilled grains per panicle, grain length, grain breadth, 1000-grain weight, and grain yield per hill. Genotypes ASS22, ASS17, and ASS14 exhibited superior agronomic performance, demonstrating longer panicles, higher 1000-grain weight, and greater grain yield per hill. Principal Component Analysis (PCA) and correlation analysis identified grain length, grain breadth, and 1000-grain weight as the major contributors to genetic variability. Cluster analysis grouped the genotypes into three distinct clusters, with six top-performing genotypes (ACC4, ACC8, ACC24, ACC37, ACC6, and ACC16) exhibiting desirable traits for potential breeding programs. These findings highlight the importance of genetic diversity in rice improvement, particularly in southern environments. The identified high-performing genotypes would serve as valuable genetic resources for developing resilient and high-yielding rice genotypes based on their agro-morphological traits.

Keywords: Rice Genotypes; Morphological Traits; Principal Component Analysis; Cluster Analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is an essential food crop for the global population. It is essential to ensuring global food security both now and in the future. Maize and wheat contribute 19% and 5% of the world's dietary energy, respectively, whereas rice contributes 20% (BBS, 2021). According to this, rice is the most important strategic crop for ensuring the food and nutritional security of the world. The majority of the world's rice is produced in Asian nations, and it is the most important staple food in Bangladesh (Salam *et al.*, 2019). Approximately 75–80% of the land is under cultivation, depending on the season and agro-ecological zone (FAO, 2015). The need for production is rising along

with the population, and there is less land available for cultivation. The farmed kinds must be sophisticatedly dragonized for notable improvement in order to meet the consumptive measures and the individuals engaged with the processing, marketing, and distribution with the limited land and resources (Rahayu *et al.*, 2020).

All of Bangladesh's rice comes from just three genotypes: *Aus*, *Aman*, and *Boro*. Broadcast and transplanted *Aman* are usually cultivated in December and January, *Boro* from March to May, and *Aus* in July and August. The most significant of these new crops, *aman*, took up around 46% of the land used for rice cultivation (Islam *et al.*, 2018; Rahman *et al.*, 2024; Howlader *et al.*, 2024).

Rice germplasm diversity is significant to give information for plant breeding programmes; agromorphological characterization of germplasm genotypes is essential (Lin, 1991; Nascimento *et al.*, 2011). The requirement for developing new rice landraces with superior quality and adaptability is knowledge of diverse rice genotypes. The mix of many traits, such as panicle size, percentage of filled spikelets, and grain weight, results in the complex attribute known as rice grain yield (Madhubabu *et al.*, 2020). The panicle and its related characteristics are thought to be the most proactive component of rice, controlling both its yield and quality (Lei *et al.*, 2018; Sultana *et al.*, 2025).

Therefore, describing the rice panicle trait in connection to agricultural output and genetic diversity has long been an important study topic. The length of the panicle and the quantity of grains, which vary by genotype, are characteristics of the panicle trait (Nascimento *et al.*, 2011). This contributes to the variations across different types of germplasm. To build a strong and comprehensive breeding program to boost rice's grain output, it is essential to assess the genotypic genotype of panicle traits in different rice genotypes (Lei *et al.*, 2018).

Furthermore, in a genotype of environmental conditions, the morphological characteristics of germplasm resources are comparatively more stable. As a result, numerous research studies have assessed the classification, relationships, and genotype of rice landraces using scientific and efficient sampling utilizing mathematical statistical methods on morphological attributes of reproductive organs (Kumbhar *et al.*, 2015).

Germplasm utilization is commonly used by breeders in any rice improvement operation (Alexandratos and Bruinsma, 2012). In addition to being crucial for using the right attribute-based donors, systematic research and characterization of such germplasm is also necessary in the modern era to preserve the distinctive rice. Therefore, it is necessary to gather, utilize, and assess the untapped germplasm (Parikh *et al.*, 2012). Because it may directly provide information on germplasm richness and provide vital information for farmers or breeders, especially when the resource population is large, using morphological traits to analyze genetic diversity is considered to be a very simple

and economical way. Thus, this conventional approach is still widely used in the assessment of germplasm resources (Lei *et al.*, 2018). Bangladesh is enriched with many diversified landraces with 8000 registered rice germplasm in the BRRI gene bank (Akter *et al.*, 2018). Previously, many studies were done based on the various rice cultivars cultivated in mainstream production.

Our study focuses on the detailed characterization of 40 native genotypes collected from six distinct southern regions of Bangladesh. These genotypes are part of a germplasm repository housed at the regional BRRI branch in Gopalganj. The main objective is to assess the agronomic and quality traits of these cultivars to identify the top-performing local genotypes across the six districts of southern Bangladesh. This evaluation aims to provide farmers in the region with valuable insights into selecting the most suitable genotypes based on their morphological characteristics.

MATERIALS AND METHODS

Experimental Site and Setup

The experiment took place in the field as part of the Bangladesh Rice Research Institute's "Collection, Morphological Characterization, Rice (*Oryza sativa* L.) Genotype" study, located in Gopalganj, Bangladesh. Geographically, it lies between latitudes 83.54° and 85.56° and longitudes 26.12° and 26.39° North (UNDP, 1988). The soil exhibited a pH of 6.7 and a silty loam texture, and the study was conducted in a subtropical environment. The timeframe for this research project spanned from July to December 2022. Forty rice genotypes were evaluated in this study using seeds collected from the Bangladesh Rice Research Institute in Gopalganj. The collected rice genotypes (ACC) were used for categorization. In this research, the experiment followed the Randomized Complete Block Design (RCBD) with three replications and involved a total of 90 plots, each containing five plants of a single genotype. The properties of the experimental field at BRRI, Gopalganj, are detailed in Table 1. Genotypes were collected from BRRI, Gopalganj; additionally, they are provided in Table 2.

Table 1. The soil properties in investigation field

Soil Property	Description	Citation
Soil Texture	Predominantly clayey or silty clay loam; fine particles with good water retention but poor drainage.	FAO (1988), BRRI (2015)
Soil pH	Moderately acidic to neutral, ranging from 5.5 to 6.8. Alkalinity may occur in waterlogged areas.	BRRI (2015), Rahman <i>et al.</i> , (2022)
Organic Matter Content	Low to medium, generally 1.5% to 2.5%. Organic residues from rice cultivation can improve this over time.	BRRI (2015), GOB (2012)
Nitrogen (N)	Often deficient due to continuous cropping; requires nitrogen supplementation via fertilizers.	(Rahman <i>et al.</i> , 2022), BRRI (2015)
Phosphorus (P)	Moderately available; often requires phosphate fertilizer applications for optimal crop growth.	GOB (2012), BRRI (2015)

Soil Property	Description	Citation
Potassium (K)	Generally adequate, but intensive farming can deplete reserves over time.	Rahman <i>et al.</i> , (2022), BRRI (2015)
Micronutrients	Possible deficiencies in zinc (Zn) and boron (B), critical for rice and other crops.	FAO (1988), GOB (2012)
Water Retention	High water-holding capacity due to clay-rich soils.	BRRI (2015), Rahman <i>et al.</i> , (2022)
Drainage	Poor drainage in low-lying areas, making them prone to waterlogging.	FAO (1988), GOB (2012)

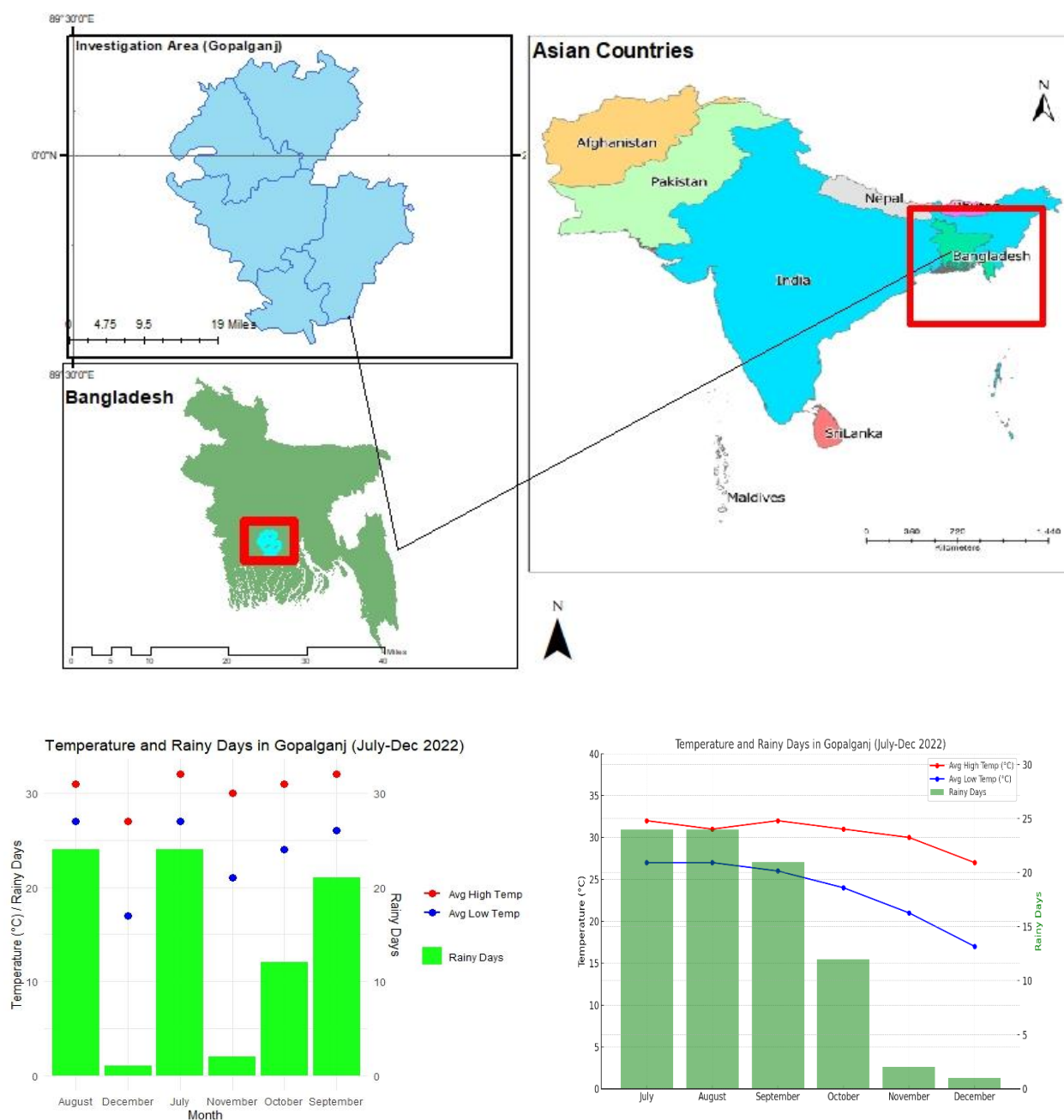


Figure 1. a) Investigation area of the Bangladesh and 2) The amounts rainfall and temperature during the studies.

Table 2. Different rice Genotypes with their location and special characteristics of Southern Area of Bangladesh.

Association	Genotype	Location	Special Traits
ACC01	Sissumoti	Kashiani, Gopalganj	Distinct fragrance, flavor.
ACC02	Debmani	Kashiani, Gopalganj	Low-input agricultural systems and produces high-quality grains.
ACC03	Modhushail	Kashiani, Gopalganj	Delicate grain structure and a light, airy texture.
ACC04	Lalzira	Tungipara, Gopalganj	Reddish or reddish-brown grains.
ACC05	Jabra	Tungipara, Gopalganj	Rich in carbohydrates, vitamins, and minerals.
ACC06	Laldigha	Kashiani, Gopalganj	Reddish or reddish-brown grains.
ACC07	Nazirshail	Kashiani, Gopalganj	Delightful and unique fragrance.
ACC08	Lokkhidigha	Gopalganj Sadar, Gopalganj	Robustness against pests, diseases, and environmental difficulties.
ACC09	Nonakachi	Shoronkhola, Bagherhat	Slender grain.
ACC10	Balam	Shoronkhola, Bagherhat	Slight reddish or brownish hue.
ACC11	Sadamota	Shoronkhola, Bagherhat	Moderate number of tillers.
ACC12	Lalmota	Shoronkhola, Bagherhat	Submergence tolerance.
ACC13	Chinikani	Shoronkhola, Bagherhat	Superior taste and cooking quality.
ACC14	Joyna	Mollahat, Bagherhat	White or light golden color grains.
ACC15	Nazirshail	Mollahat, Bagherhat	Delightful and unique fragrance that amplifies the taste of meals.
ACC16	Bashiraj	Mollahat, Bagherhat	High yield.
ACC17	Jabra	Mollahat, Bagherhat	High market price.
ACC18	Sada Jabra	Gopalganj Sadar, Gopalganj	Easy to sell.
ACC19	Jabra	Gopalganj Sadar, Gopalganj	More tillers (vigor).
ACC20	Lal digha	Gopalganj Sadar, Gopalganj	Consistent yields.
ACC21	Digha boro	Madhukhali, Faridpur	High yield.
ACC22	Jabra choto	Madhukhali, Faridpur	Pleasant and distinct aroma.
ACC23	Lal balam	Pirojpur, Pirojpur	Fodder for livestock.
ACC24	Tepadhan	Mollahat, Bagherhat	Elegant shape grains.
ACC25	Sadamota	Bagherhat Sadar, Bagherhat	Resilience to pests and diseases.
ACC26	Lalmota	Bagherhat Sadar, Bagherhat	Submergence tolerance.
ACC27	Badshavog (lal)	Bagherhat Sadar, Bagherhat	High yield.
ACC28	Hugli Dhan	Pirojpur Sadar, Pirojpur	Brownish hue.
ACC29	Kala Digha	Alfadanga, Faridpur	Rich in antioxidants.
ACC30	Khaiyamotor	Alfadanga, Faridpur	High milling recovery.
ACC31	Sadaboro	Alfadanga, Faridpur	High-yielding hybrid.
ACC32	Boro digha	Alfadanga, Faridpur	Awnless grains.
ACC33	Swarnadhan	Alfadanga, Faridpur	Strong and resilient straw.
ACC34	Lalboro	Alfadanga, Faridpur	Good taste.
ACC35	Malabhog	Vanga, Faridpur	Traditional aromatic rice.
ACC36	Laxmidigha	Naria, Sariatpur	High yield.
ACC37	Boro digha	Sadarpur, Faridpur	More tillers (vigor).
ACC38	Nayanmoni	Sadarpur, Faridpur	Good for rice products.
ACC39	Malaamon	Vanga, Faridpur	Fodder for livestock.
ACC40	Debmani	Boalmari, Faridpur	Shorter duration.

Thirty-eight-day-old seedlings were chosen for transplantation, and essential cultural practices were adhered to throughout the crop-growing season. Fertilizer was applied at rates of 260 kg/ha for urea, 100 kg/ha for TSP, 120 kg/ha for MOP, 110 kg/ha for gypsum, and 10 kg/ha for ZnSO₄ (Reference??). The final stage of land preparation included applying all fertilizers except urea. At 15 days after transplanting (DAT), 35 DAT, and just before flowering, three equally spaced applications of urea were administered.

Additionally, appropriate cross-cultural protocols and pest control methods were implemented as needed.

Data Collection

During the experiment, the plants under examination provide essential data on key characteristics. The following outlines the data recording procedures for each parameter.

A representative sample of rice panicles was selected from the plot to estimate the number of grains per panicle.

Each panicle was carefully hand-threshed to separate the grains, ensuring that none were lost. If a seed counter was available, it was used to efficiently count the grains; otherwise, manual counting was performed. The average grain count per panicle was determined by dividing the total number of grains by the number of sampled panicles.

To measure panicle length, a representative sample of panicles was chosen. Using a ruler scale, the length was measured from the base of the panicle, where it attaches to the stem, to its tip. The length of each panicle was recorded individually and expressed in millimeters.

A representative selection of rice panicles was randomly collected from different field locations. Each panicle was carefully hand-threshed to separate the grains, ensuring all grains were accounted for. If available, a seed counter was used to facilitate the counting process; otherwise, grains were counted manually. The average number of grains per panicle was obtained by calculating the mean across all sampled panicles.

The grain dimensions were determined with individual grains placed lengthwise on a flat surface and measured using a digital caliper. The average grain length and width were calculated by summing the measurements of multiple grains and dividing the total by the number of grains tested. The length and width of defective grains were measured using a digital caliper and recorded in millimeters.

The thousand-seed weight was measured by exactly 1000 seeds were counted and placed on a digital scale. The total weight was recorded in grams.

The yield per hill was calculated using an appropriate method and recorded in grams.

$$\text{Yield Per Hill} = \frac{\text{Total Grain Weight from Sampled Hills}}{\text{Number of Hills Sampled}}$$

Statistical Analysis

SPSS version 30 and STATISTIX version 10 software were used to statistically analyses the data. Analyses of variance (ANOVA), Principal component analysis, cluster analysis, correlation analysis were performed on each variable using the F test. To determine the statistical significance of the difference between means at the 5% and 1% levels of probability, a group researcher employed the LSD test in their investigation.

The formula proposed by the Genotypic Coefficient of Variation was used to determine the Phenotypic Coefficient of Variation.

Similarly, the following formula was used to determine the phenotypic coefficient of variation.

$$\text{Phenotypic Co-efficient of Variation (PVC)} = \sqrt{\frac{\sigma_{2ph}}{x}} \times 100$$

$$\text{Phenotypic Correlation (r}_{pxy}) = \frac{\sigma_{pxy}}{\sqrt{\sigma_{2px}\sigma_{2py}}}$$

Where, σ_{gxy} = Phenotypic Co-variance between the traits X and Y, σ^2_{px} = Phenotypic Variance of the trait X, σ^2_{py} = Phenotypic variance of the trait y.

RESULTS

Panicle Length

Statistically significant variance occurred in panicle length. The panicle length varied substantially among the genotypes, with a mean value of 17.83 cm to 29.83 cm. The highest panicle length (29.23 cm) was observed in ASS22, followed by 27.83 cm in ASS36, while the lowest panicle length, 17.83 cm, was observed in ASS15, followed by 18.02 cm in ASS09, respectively (Table 3).

Filled Grains Panicle⁻¹

Statistically significant differences were noted in the number of filled grains per panicle across various genotypes, with mean values ranging from 82.00 to 184.00. ASS37 recorded the highest number of filled grains per panicle at 184.00, followed by ASS13 with 135.00. Conversely, ASS18 and ASS29 had the lowest counts at 82.00, with ASS33 slightly lower at 56.00 (Table 3).

Unfiled Grains Panicle⁻¹

The number of unfiled grains per panicle was significantly different. The average number ranged from 8.00 to 66.00, showing a big difference between genotypes. Table 3 shows that ASS14 had the most unfiled grains per panicle (66.00), followed by ASS06 with 62.00. The fewest unfiled grains were in ASS31 with 8.00, followed by ASS08 and ASS28 with 11.00.

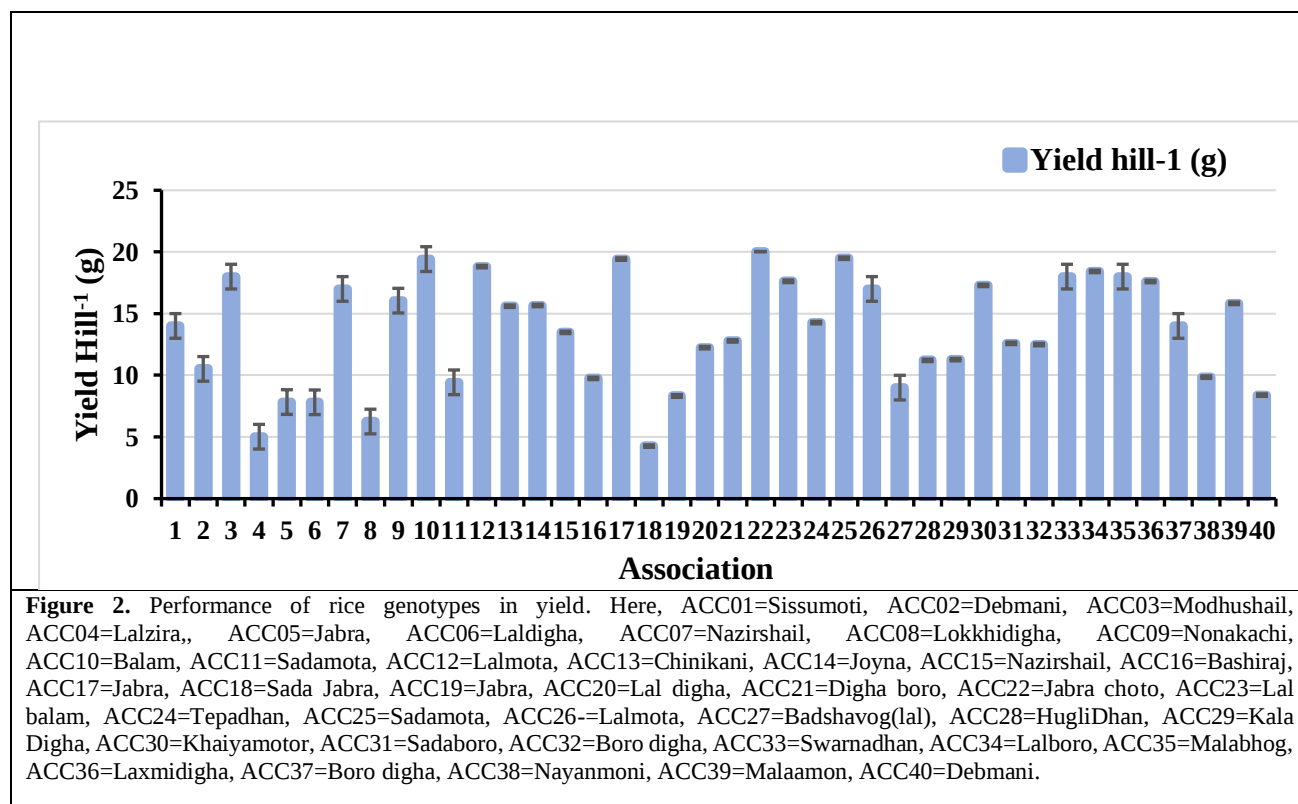


Table 3. Performance of rice genotypes in panicle length, filed grain, unfiled grain, grain length and grain breadth.

Association	Panicle Length (cm)	Filed Grains Panicle ⁻¹	Unfiled Grains Panicle ⁻¹	Grain Length (mm)	Grain Breadth (mm)
1	24.62j	118.00h	35.00h	8.86ef	3.14fgh
2	23.31o	119.00h	37.00f	8.72fgh	2.85klm
3	18.83b	127.00e	27.00m	8.85ef	3.14f-i
4	27.01d	110.00i	39.00d	5.85q	1.85s
5	22.43r	101.00m	26.00n	7.63l	2.98ijk
6	22.82q	85.00r	62.00b	7.84jk	2.92jkl
7	24.23l	92.00o	53.00c	8.87ef	2.43pq
8	23.62n	111.00i	11.00x	6.14p	2.12r
9	18.02c	127.00e	19.00r	7.91j	3.27def
10	20.63x	107.00j	13.00v	7.43m	3.23efg
11	19.23a	103.00l	17.00t	7.63l	3.28c-f
12	24.42k	86.00qr	12.00w	8.67gh	3.15fgh
13	26.24e	135.00c	24.00o	8.87ef	3.23efg
14	24.63j	108.00j	66.00a	8.30i	3.24efg
15	17.83d	90.00p	24.00o	8.92e	3.54a
16	26.02f	103.00l	18.00s	6.60n	3.21efg
17	23.63n	132.00d	33.00j	8.77efg	3.17e-h
18	25.02i	82.00s	22.00q	9.15d	2.39q
19	23.24o	85.00r	18.00s	9.26bcd	2.55op
20	22.23s	101.00m	22.00q	7.92j	3.23efg
21	20.83w	87.00q	38.00e	8.20i	3.46ab
22	29.23a	90.00p	34.00i	9.26bcd	3.56a
23	25.63h	86.00qr	27.00m	8.72fgh	3.33b-e
24	21.24v	104.00kl	23.00p	6.37o	2.34q
25	25.85g	140.00b	17.00t	9.33bc	2.64no
26	19.83y	83.00s	23.00p	8.77efg	3.40a-d
27	25.63h	75.00u	12.00w	9.84a	2.82klm
28	24.63j	77.00t	11.00x	8.57h	2.85klm

29	19.63z	82.00s	28.00l	7.45m	3.16fgh
30	22.02t	121.00g	19.00r	7.73kl	3.13f-i
31	23.02p	82.00s	8.00y	7.88jk	2.81lm
32	25.82g	125.00f	36.00g	8.75fg	3.44abc
33	21.83u	56.00v	14.00u	7.81jk	3.21efg
34	23.82m	96.00n	17.00t	9.27bcd	3.02hij
35	24.42k	118.00h	31.00k	9.39b	2.80lm
36	27.83b	124.00f	19.00r	8.79efg	2.43pq
37	25.62h	184.00a	18.00s	7.43m	2.63no
38	22.02t	105.00k	12.00w	8.76fg	2.73mn
39	23.63n	90.00p	22.00q	9.21cd	2.63no
40	27.22c	122.00g	36.00g	8.29i	3.08ghi
Level of significance	**	**	**	**	**
LSD _(0.05)	0.13	1.18	0.98	0.16	0.16
LSD _(0.01)	0.17	1.56	1.19	0.2	0.21
CV (%)	0.33	0.69	2.16	1.17	3.34

**= 1% level of significance, *= 5% level of significance

Table 4. Performance of rice genotypes in 1000 grain weight, defective grain length, defective grain breadth and grain yield per hill.

Association	1000-Grain weight (g)	Defective Grain Length (mm)	Defective Grain Breadth (mm)	Grain Yield hill ⁻¹ (g)
1	26.85j	6.26gh	2.62e-i	14.00i
2	27.84g	6.38efg	2.62e-i	10.52mn
3	26.34k	6.77abc	2.83bc	18.00cde
4	13.13c	4.19o	1.73r	5.02s
5	24.34rs	5.51kl	2.73c-f	7.83q
6	16.43a	5.51kl	2.57g-j	7.81q
7	28.53ef	6.53def	2.24no	17.00fg
8	23.84u	4.17o	1.89q	6.25r
9	24.43r	5.43l	2.72c-f	16.05gh
10	25.14op	5.02m	2.63d-h	19.42ab
11	21.13x	5.76j	2.75b-f	9.43o
12	28.65e	6.51def	2.76b-e	18.81bc
13	27.92g	6.57cde	2.75b-f	15.63h
14	29.45b	6.27g	2.84bc	15.66h
15	27.55h	6.51def	2.88b	13.48ij
16	17.55z	4.65n	2.77bcd	9.75no
17	25.23o	6.24gh	2.72c-f	19.42ab
18	24.25s	6.78abc	2.04p	4.26s
19	25.25o	6.64bcd	2.21o	8.33pq
20	26.34k	5.73j	2.85bc	12.24kl
21	24.02t	6.29g	2.85bc	12.79jk
22	29.25c	6.65bcd	3.29a	20.03a
23	30.83a	6.05hi	2.72c-f	17.62def
24	14.42b	4.65n	1.89q	14.27i
25	26.02l	6.71bcd	2.24no	19.49ab
26	26.25k	6.37efg	2.88b	17.00fg
27	22.83v	6.83ab	2.42j-m	9.00op
28	24.72q	6.21gh	2.49h-l	11.20m
29	23.83u	5.68jk	2.61f-i	11.27lm
30	26.25k	5.76j	2.65d-g	17.28ef
31	22.52w	5.73j	2.52g-j	12.59jk
32	29.02d	6.26g	2.64d-g	12.49k
33	28.45f	5.84ij	2.63d-h	18.00cde

34	28.65e	6.53def	2.51g-k	18.43cd
35	27.34i	6.93a	2.37k-m	18.00cde
36	25.85m	6.52def	2.02pq	17.63def
37	18.53y	5.51kl	2.48i-l	14.00i
38	25.43n	6.33fg	2.29mno	9.85no
39	25.73m	6.69bcd	2.34l-o	15.83h
40	25.02p	6.35fg	2.51g-j	8.39pq
Level of significance	**	**	**	**
LSD _(0.05)	0.15	0.21	0.15	0.98
LSD _(0.01)	0.19	0.28	0.19	1.3
CV (%)	0.37	2.19	3.55	4.44

**= 1% level of significance, *= 5% level of significance

Grain Length (mm)

Grain length varied significantly among genotypes, ranging from a mean of 5.85 mm to 9.84 mm. The longest grain length, 9.84 mm, was observed in ASS27, followed by 9.33 mm in ASS25. In contrast, the shortest grain lengths were recorded at 5.85 mm in ASS04 and 6.14 mm in ASS08, respectively (table 3).

Grain Breadth (mm)

The grain breadths varied significantly. Grain breadth varied significantly among genotypes, with a mean value ranging from 1.85 mm to 3.56 mm. The highest grain breadth (3.56 mm) was found in ASS22, followed by 3.54 mm in ASS15, and the narrowest grain breadth (1.85 mm) in ASS04, followed by 2.12 mm in ASS08 (table 3).

1000-Grain weight (g)

There was a highly significant variance in 1000-grain weight. The 1000-grain weight varied significantly between genotypes, with a mean of 13.13 g to 30.83 g. The longest 1000-grain weight was 30.83 g in ASS23, followed by 29.45 in ASS14, and the shortest 1000-grain weight was 13.13 g in ASS04, followed by 14.42 in ASS24 (table 4).

Defective Grain Length (mm)

Defective grain length showed statistically significant variation. The defective grain length varied significantly across genotypes, with a mean value ranging from 4.17 mm to 6.93 mm. The greatest faulty grain length (6.93 mm) was found in ASS35, followed by 6.83 mm in ASS27, and the shortest defective grain length (4.17 mm) was discovered in ASS08, followed by 4.19 mm in ASS04 (table 4).

Defective Grain Breadth (mm)

There was a statistically significant variance in faulty grain breadth. The defective grain breadth varied significantly between genotypes, with a mean of 1.73 mm to 2.88 mm. The greatest defective grain breadth (2.88 mm) was seen in ASS15 and ASS26, followed by 2.85 mm in ASS20 and ASS21, while the shortest defective grain breadth (1.73 mm) was observed in ASS04, followed by 1.89 mm in ASS08 (table 4).

Grain Yield hill⁻¹ (g)

Grain yield hill-1 indicated a statistically significant difference. The grain yield hill-1 differed significantly among genotypes, ranging from 4.26 g to 20.03 g. The largest grain yield hill-1 was 20.03 g in ASS22, followed by 19.49 in ASS25, and the smallest grain yield hill-1 was 4.26 g in ASS18, followed by 5.02 in ASS04 (table 4) and (figure 2).

In the scree plot (Figure 3a), the first two principal components (PC1 and PC2) accounted for 39.6% and 21.2% of the total variance, respectively, indicating their substantial contribution to the overall variability in the principal component analysis (PCA). The correlation analysis of various parameters across forty rice genotypes revealed significant relationships among them, with notable variations observed. Among all parameters, grain length and grain breadth exhibited the most significant results. Specifically, grain breadth showed a strong correlation with defective grain breadth, and grain length was significantly associated with defective grain length, as illustrated in Figure 3b. Additionally, Figure 3b highlights some less significant relationships among other parameters.

In the principal component analysis (PCA) of various rice genotypes, several parameters, including 1000-grain weight, defective grain length, grain length, and defective grain breadth, exhibited significant relationships and variations among the rice genotypes studied. Notably, accessions ACC24, ACC08, ACC04, and ACC37 showed significant negative associations, while ACC22, ACC32, ACC23, and ACC14 displayed significant positive associations across all rice genotypes, as illustrated in Figure 4a. Figure 4b highlights the performance of specific accessions in different regions: In the Gopalganj Division, ACC37, ACC06, and ACC08 demonstrated the highest performance. In the Bagerhat area, ACC24 and ACC16 stood out with superior performance among all genotypes. In the Faridpur area, ACC37 exhibited the highest performance. In contrast, genotypes from other areas showed comparatively lower performance than these selected accessions.

In cluster analysis using the Ward method, three distinct clusters were formed. Among these, one cluster demonstrated the highest performance. This cluster included six rice genotypes: ACC4, ACC8, ACC24, ACC37, ACC6, and ACC16. Based on the scatter diagram of 40 rice genotypes using PCA scores superimposed with clustering

from D² analysis, the best-performing genotypes are 4, 8, 24, 37, 6, and 16. These genotypes are positioned distinctly from others, indicating significant genetic diversity and potential agronomic superiority. Their placement suggests they exhibit desirable traits such as high yield potential and superior morphological characteristics against in the southern environment. The clear separation from other

clusters in the PCA plot further confirms their genetic distinctiveness, making them strong candidates for breeding programs and further research (figure 6a).

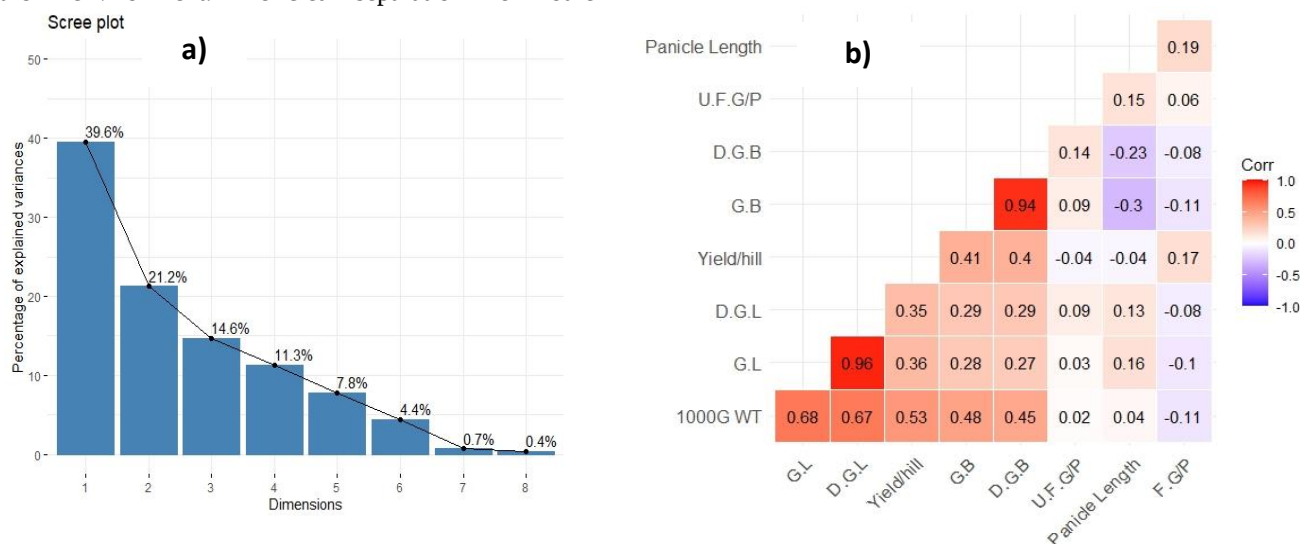


Figure 3. a) Scree plot of PCA analysis and **b)** correlation analysis among all variables in rice genotypes. Here, UFGP- Unfiled grain per panicle, DGB- Defective grain breadth, GB- Grain breadth, DGL- Defective grain length, GL- Grain length, 10000 WT- 10000 Grain weight. Here, the correlation matrix presents the relationship between different traits, with color intensity indicating the strength and direction of correlations (red for positive and blue for negative).

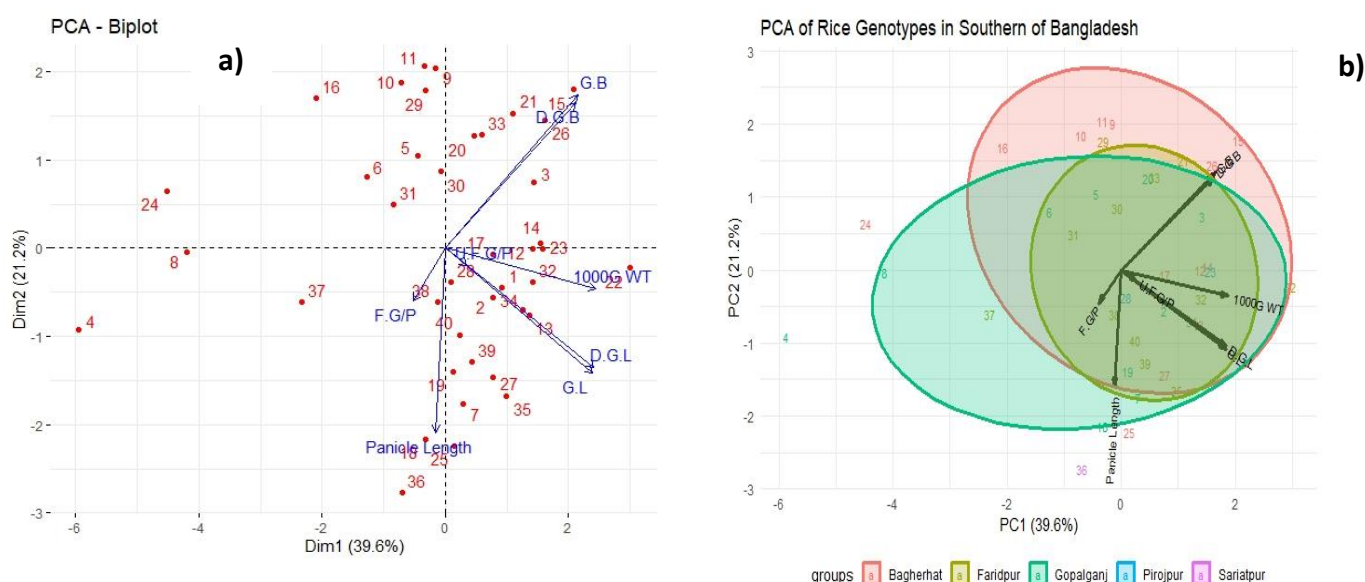


Figure 4. a) PCA analysis of rice genotypes and all parameters in rice genotypes and **b)** PCA analysis based on Southern area of Bangladesh. Here, UFGP- Unfiled grain per panicle, DGB- Defective grain breadth, GB- Grain breadth, DGL- Defective grain length, GL- Grain length, 10000 WT- 10000 Grain weight. Also, association (ACC)

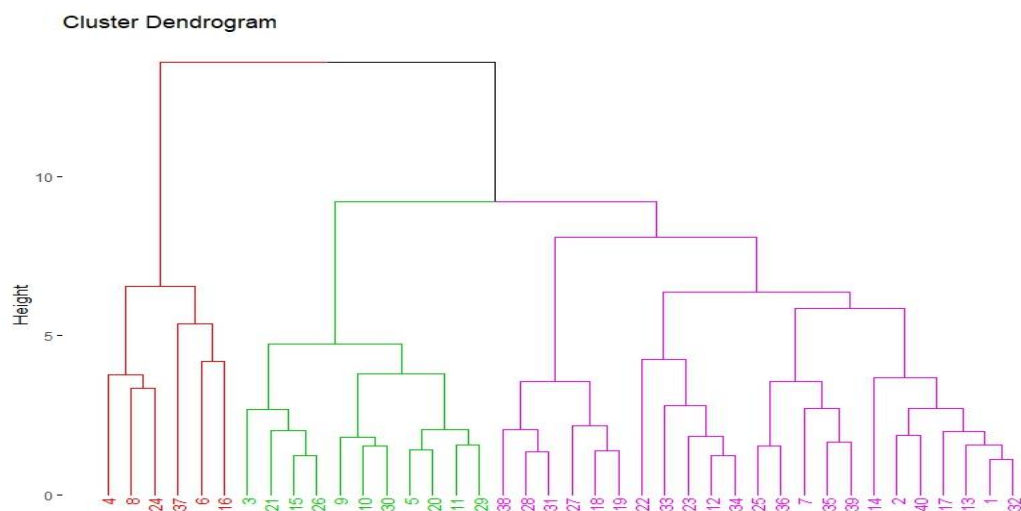
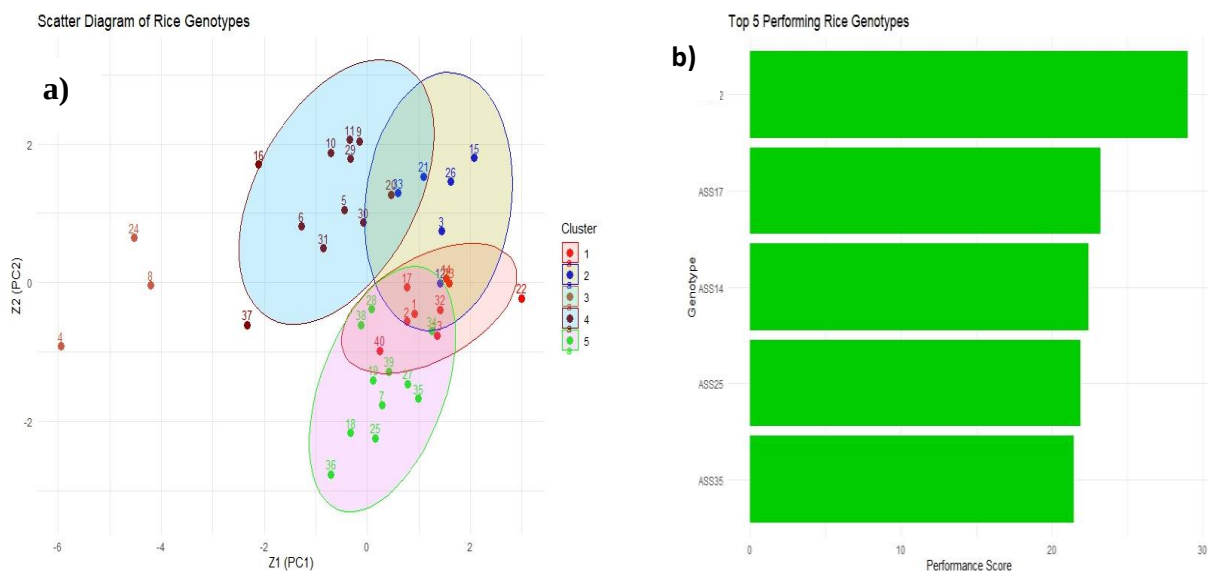


Figure 5. Cluster analysis of forty rice genotypes in southern part of Bangladesh. Figure. 5. Cluster analysis of forty rice genotypes in southern part of Bangladesh. Here, ACC01=Sisumoti, ACC02=Debmani, ACC03=Modhushail, ACC04=Lalzira,, ACC05=Jabra, ACC06=Laldigha, ACC07=Nazirshail, ACC08=Lokkhidigha, ACC09=Nonakachi, ACC10=Balam, ACC11=Sadamota, ACC12=Lalmota, ACC13=Chinikani, ACC14=Joyna, ACC15=Nazirshail, ACC16=Bashiraj, ACC17=Jabra, ACC18=Sada Jabra, ACC19=Jabra, ACC20=Lal digha, ACC21=Digha boro, ACC22=Jabra choto, ACC23=Lal balam, ACC24=Tepadhan, ACC25=Sadamota, ACC26=Lalmota, ACC27=Badshavog(lal), ACC28=HugliDhan, ACC29=Kala Digha, ACC30=Khaiyamotor, ACC31=Sadaboro, ACC32=Boro digha, ACC33=Swarnadhan, ACC34=Lalboro, ACC35=Malabhog, ACC36=Laxmidigha, ACC37=Boro digha, ACC38=Nayanmoni, ACC39=Malaamon, ACC40=Debmani



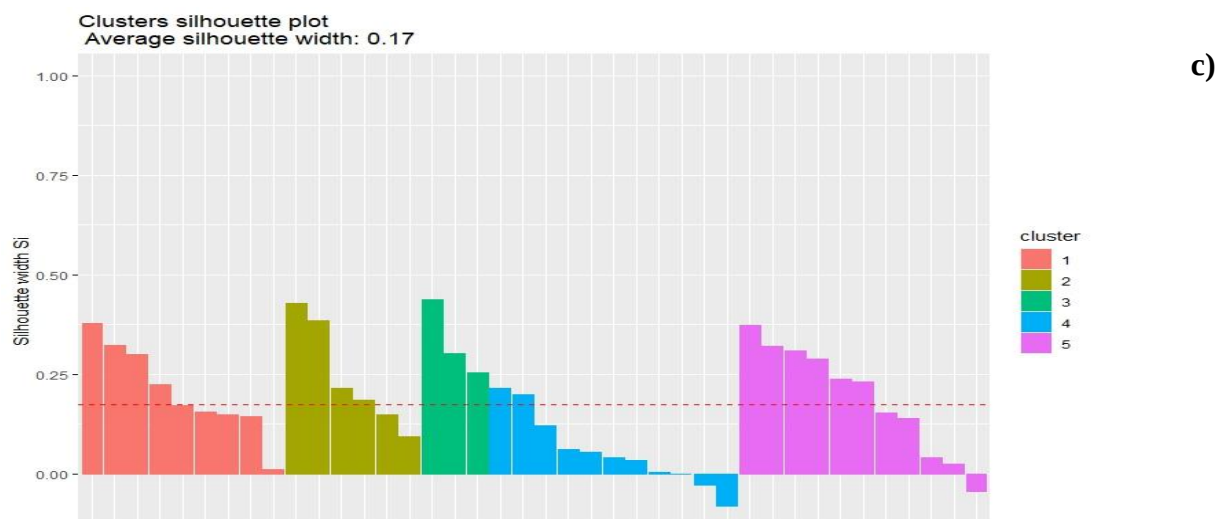


Figure 6. a) Scatter diagram of 40 rice genotypes based on PCA scores superimposed with clustering from D2 analysis, **b)** five best performing genotypes based on their distance among 40 genotypes, **c)** Cluster silhouette plot and their contributions among 40 rice genotypes.

DISCUSSION

The current study uncovered significant agro-morphological differences among the rice genotypes, and we evaluated, showcasing their morphological diversity and potential for enhancing crop yields. We observed notable variations in key traits like panicle length, the number of filled and unfilled grains per panicle, grain size, 1000-grain weight, and grain yield per hill. These differences point to a broad spectrum of adaptability and physiological efficiency among the genotypes. Panicle length, which ranged from 17.83 to 29.83 cm, is crucial for determining the number of spikelets and ultimately affects yield. The longest panicle we found in ASS22 suggests that it has effective mechanisms for spikelet initiation and elongation, likely due to its advanced vascular development and ability to transport nutrients (Pachauri *et al.*, 2017; Sow *et al.*, 2014; Ilieva *et al.*, 2019). On the other hand, the shorter panicles in ASS15 might indicate issues with nutrient distribution or weaker sink strength during the reproductive phase. The number of filled grains per panicle varied significantly, ranging from 82 to 184, reflecting differences in the relationships between sources and sinks, as well as photosynthetic efficiency. ASS37, which had the highest count of filled grains, likely shows strong partitioning of photosynthates and favorable floral structure. In contrast, genotypes like ASS18 and ASS29 had fewer filled grains, possibly due to pollen sterility, low spikelet fertility, or environmental stress during flowering (Sinha *et al.*, 2015; Tripathi *et al.*, 2013; Dikshit *et al.*, 2016). The count of unfilled grains per panicle, which ranged from 8 to 66, further emphasized the reproductive efficiency of the different genotypes. High numbers in ASS14 and ASS06 suggest potential spikelet abortion or incomplete fertilization, possibly due to abiotic stress or genetic limitations. In contrast, ASS31, with very few unfilled grains, indicates strong reproductive resilience and

better resource management in field conditions (Hasan *et al.*, 2025).

Grain dimensions—specifically length (ranging from 5.85 to 9.84 mm) and breadth (between 1.85 and 3.56 mm)—play a crucial role in agro-morphological traits that influence market value and consumer choices. Genotypes such as ASS27 and ASS25, known for their long and slender grains, are particularly sought after in premium markets, often linked to specific QTLs that relate to endosperm development (Miah *et al.*, 2025). On the other hand, the broader grains found in ASS22 and ASS15 might indicate a higher deposition of endosperm, while the narrower grains in ASS04 could be a result of limited grain filling due to developmental challenges (Sinha *et al.*, 2013; Karim *et al.*, 2024). The 1000-grain weight, which ranges from 13.13 to 30.83 g, is a key component of yield and showed significant variation among different genotypes. The heavier grains in ASS23 and ASS14 suggest that these varieties are effective at nutrient uptake and deposition during the grain filling process (Fatamatuzzohora *et al.*, 2024; Mia *et al.*, 2025). In contrast, the lower weights observed in ASS04 may point to issues like suboptimal grain filling or environmental stresses, such as high temperatures or water shortages during grain development. When it comes to defective grain dimensions, the reduced length (from 4.17 to 6.93 mm) and breadth (1.73 to 2.88 mm) indicate potential physiological or pathological issues during grain formation. Genotypes like ASS35 and ASS15 showed more defects, likely due to incomplete grain filling or biotic stress, while ASS08 and ASS04 displayed better grain integrity, hinting at superior stress tolerance (Sarwar *et al.*, 2015; Roy and Sharma, 2014).

The grain yield per hill ranged quite a bit, from 4.26 to 20.03 grams, showcasing the combined effects of various agro-morphological traits. Genotypes like ASS22 and ASS25, which boasted the highest yields, demonstrated a well-rounded performance in areas such as panicle morphology, grain filling, and overall biomass distribution

(Puranjoy and Paresh, 2023; Ali et al., 2025; Al Masum et al., 2025; Bashir et al., 2025; Haque et al., 2025). On the flip side, lower yields in ASS18 and ASS04 were linked to shorter panicles, lighter grain weight, and a higher number of unfilled grains, aligning with the research by Mehmood et al. (2021) and Yesmin et al. (2024). Principal Component Analysis (PCA) revealed that the first two principal components, PC1 and PC2, explained 39.6% and 21.2% of the total variance, respectively. Traits such as 1000-grain weight, grain length, and the breadth of defective grains played a significant role in contributing to genetic diversity (Akhtar et al., 2022; Kakar et al., 2021). This emphasizes the potential of these traits as crucial factors in selecting varieties. Cluster analysis further divided the genotypes into three distinct groups, with the top cluster—featuring ACC4, ACC8, ACC24, ACC37, ACC6, and ACC16—showing desirable characteristics like longer panicles, heavier 1000-grain weights, and fewer defective grains (Khan et al., 2023; Pathak, 2018; Howlader et al., 2025). These genetically superior genotypes are promising candidates for future breeding efforts, especially in areas like Gopalganj and Bagerhat, where ACC37 and ACC24 have demonstrated outstanding field performance. In summary, the observed diversity in agro-morphological traits highlights the significance of factors like panicle structure, grain filling ability, and grain weight in boosting rice yields. These insights provide a solid foundation for selecting parent genotypes in breeding programs aimed at improving yield and adapting to environmental challenges (Tefera et al., 2023; Saha et al., 2022; Umamaheswar et al., 2024; Maruf et al., 2024).

CONCLUSION

This study demonstrated significant genetic variability among rice genotypes for yield and quality traits, reflecting their potential for breeding programs. Genotypes such as ASS22, ASS17, and ASS14 excelled in traits like panicle length, grain yield per hill, and 1000-grain weight, while genotypes like ASS18 and ASS04 showed lower performance, emphasizing the influence of genetic and environmental factors. Principal Component Analysis (PCA) identified grain dimensions and 1000-grain weight as primary contributors to variability, with strong correlations observed among key traits. Cluster analysis grouped genotypes into three distinct clusters, with ACC4, ACC8, ACC24, ACC37, ACC6, and ACC16 forming the highest-performing cluster, indicating their potential for targeted breeding strategies. These findings offer valuable insights for developing high-yielding, adaptable rice genotypes suitable for diverse agro-climatic conditions.

DECLARATIONS

Author Contributions

Md. Saiful Islam Shumon: Conceptualizations, Investigation, Methodology, and Review; **Nayan Chandra Howlader:** Conceptualizations, Investigation, Methodology, Data Curation, Formal Statistical analysis, Writing-original draft, Review & Editing, Visualizations and

Data Interpretations; **Zilhas Ahmed Jewel:** Conceptualizations, Investigation, Supervision, Review & Editing, Funding Acquisition and Validations; **Md. Hasan Mia:** Formal Statistical analysis, Writing-original draft and Review; **Sarah Khan and Md. Nahidul:** Investigation and Methodology; **Md. Sohel Rana:** Writing-original draft and Review. **Mohammad Zahidul Islam:** Conceptualizations, Investigation, Validation, Review, Resource, Validations and Supervision.

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Conflicts of Interest

The authors declare they have no conflicts of interest.

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Data availability

The datasets used during the current study available from the corresponding author on reasonable request. No datasets were generated or analyzed during the current study.

Statement on collection of plant material

The collection of plant material for this study was conducted in accordance with relevant institutional, national, and international guidelines and legislation. All necessary permits and approvals were obtained from the Bangladesh Rice Research Institute (BRRI), Gopalganj, ensuring compliance with ethical and legal standards.

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