ESTIMATION OF GENETIC VARIABILITY IN DIFFERENT MORPHOLOGICAL AND BIOCHEMICAL TRAITS IN BANGLADESHI *AMAN* RICE GENOTYPES

M. N. Sharker[1], M. M. Rana[1], T. K. Roy[2], M. G. Aziz[3] and A. K. Hasan[1*]

[1]Department of Agronomy, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh
[2]Entomology Division, Bangladesh Rice Research Institute (BRRI), Gazipur-1701, Bangladesh
[3]Department of Food Engineering and Technology, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh
[*]Corresponding author's email: akhasan@bau.edu.bd

ABSTRACT

This study comprehensively evaluates the morphological, biochemical, and grain quality of traditional *aman* rice landraces to understand their genetic variation and breeding potential. Twenty-four rice genotypes, including 23 landraces from different agro-ecological zones and one modern check (BRRI dhan87), were cultivated under randomized complete block design during the 2023 *aman* season at Bangladesh Agricultural University. Morphological traits such as plant height, tiller number, panicle length, grain weight, and yield components exhibited significant variations, with some landraces like Tulshimala and Bashful showing notably high performance. Biochemical analysis revealed considerable divergence in amylose and amylopectin contents, influencing grain texture and cooking quality; for instance, BRRI dhan87 had high amylose (24.09%) and low amylopectin, while landraces like Ashini and Binni showed opposite patterns, indicative of suitability for sticky rice. Grain color parameters assessed via CIE Lab colorimetry demonstrated wide variability, with light and dark grains distributed across genotypes, affecting consumer preferences and marketability. The evaluation of cooking and eating qualities, including elongation ratio, cooking time, water absorption, and alkali spreading value, highlighted diverse culinary attributes among landraces. Genetic analysis through variance components, heritability, and genetic advance indicated high heritability for key traits such as amylose content, sterile spikelets, and grain yield, suggesting their potential for improvement. Multivariate analyses, including PCA and cluster analysis, revealed large genetic diversity and grouped genotypes into five distinct clusters, with inter-cluster distances indicating significant genetic divergence. Clusters III and V, containing Kachamota, Isnishona, Binni, Moirul, and Sishumoti had the highest mean yield and quality attributes. Overall, the findings highlight the rich genetic reservoir of traditional rice landraces, emphasizing their value for breeding programs aimed to improve yield and grain quality.

Keywords: Rice germplasm; amylose; elongation ratio; heritability; genetic diversity; genetic coefficient of variation.

https://doi.org/10.36899/JAPS.2026.4.0094

INTRODUCTION

Rice (*Oryza sativa* L.) is the most dominant crop in Bangladesh and one of the most delicate agricultural products for both the domestic and international markets. Rice is a staple food, and its per capita consumption in Bangladesh is 114.50 kg (Yunus *et al*., 2019). Since rice is a tropical crop, it is grown extensively throughout the country with three distinct growth seasons; *aus, T. aman* and boro. Among these, *T. aman* rice covers most area under cultivation, with a production of 15426 thousand MT by covering 5725.91 thousand hectares of land annually (BBS, 2023).

Landraces of *T. aman* rice are crucial for local foods security and the agricultural sustainable development. The local rice cultivars are cultivated in varied regions of the country, which exhibit remarkable fineness, taste, aroma, high protein content and good cooking quality (Ahmed *et al.,* 2019; Siddique *et al.,* 2025). Unfortunately, the total number of landraces and the area they cultivated in Bangladesh is steadily declining (Hossain *et al*., 2012; BBS, 2023) due to introduction of new varieties. However, numerous traditional rice varieties still remain highly valued by both farmers and consumers due to their unique agronomic and quality traits. Hossain and Jaim (2009) confirm that farmers in Bangladesh continue to cultivate more than 1,000 traditional rice varieties and landraces, which represent invaluable genetic resources. Many of these landraces possess important traits, including resistance to biotic stresses such as bacterial leaf blight, blast disease and insect pests, as well as tolerance to abiotic stresses such as submergence, salinity, drought and cold. Furthermore, several landraces are rich in nutritional attributes including zinc, iron and antioxidant compounds, and exhibit superior grain quality and cooking properties, particularly aroma and premium eating quality (Siddique *et al*., 2025). These diverse genetic traits highlight the significance of traditional landraces as a vital reservoir of allelic variation that for future crop improvement initiatives and breeding programs.

The widespread adoption of high-yielding varieties (HYVs), which formed the backbone of the Green Revolution, has played a significant role in the erosion of landraces and wild relatives (Deb, 2021). However, landraces maintain their distinctiveness due to their historical origins, morphological uniqueness, and adaptation to local environments. In fact, allele richness in landraces is approximately 30% greater than that found in improved rice cultivars (Kovach and McCouch, 2008; Zhang *et al*., 2009).

Sustaining food production with limited cultivable land is a major challenge in Bangladesh. This challenge is exacerbated by rapid population growth. In these circumstances, the development of high yielding rice varieties that can adapt to diverse and adverse environments is essential. Rice grain quality is a complex trait that encompassing nutritional value, visual appearance and cooking and eating qualities.

Genetic parameters like genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance are crucial for assessing the magnitude and nature of variability among rice genotypes. These estimates help distinguish genetic variation from environmental effects, thereby identifying the potential to effective selection and improvement (Terfa and Gurmu, 2020). Traits exhibiting high GCV, heritability and genetic advance are largely governed by additive action of gene, while large differences between PCV and GCV highlights strong environmental influence on expression, therefore analysis of genetic parameter is fundamental for identifying superior genotypes and optimizing selection strategies (Thuy *et al*., 2023).

Despite extensive research on rice in Bangladesh, limited attention has been focused to integrated evaluation of morphological, biochemical, and grain quality traits of traditional *T. aman* rice landraces. In particular, studies rarely combine morphological variation with biochemical properties such as amylose and amylopectin content, which strongly influence cooking and eating quality. Furthermore, traditional landraces from diverse ecosystems, including haor, coastal saline, floodplain, and upland areas remain underexplored. Understanding this variability is essential for identifying valuable traits for breeding programs and for conserving genetic resources. Therefore, the present study was undertaken to address this gap by evaluating morphological diversity, biochemical composition, cooking and eating quality and grain appearance of T. *aman* rice landraces. This integrated approach aims to elucidate the extent of genetic diversity and identify promising germplasm for future rice development programs.

MATERIALS AND METHODS

Experimental site and agro-climatic conditions: The field experiment was carried out during *aman* season (July-December 2023) at the Agronomy Field of Bangladesh Agricultural University (BAU), Bangladesh (24°25' N latitude and 90°50' E longitude; 18 m above sea level). The site belongs to the Old Brahmaputra Floodplain (AEZ-9) characterized by non-calcareous dark grey floodplain soil under the Sonatola series. The soil had a silt loam texture, near-neutral pH (6.8), with low organic matter content and moderate fertility status (Supplementary Table 1). The experimental area weather was under the sub-tropical climatic zone, with high rainfall (annually 2200 mm; from April to September) during the *kharif* seasons and relatively dry conditions during the latter growth stages. During the cropping period the temperature ranged between 20 and 35 °C with high relative humidity. The detailed climatic condition during the period of experiment have been presented in Supplementary Table 2.

Experimental design, layout and planting materials: The experiment assessing genotype performance was conducted using a Randomized Complete Block Design (RCBD) with three replications. A total number of 24 rice genotypes were evaluated, comprising 23 traditional landraces collected from the different agro-ecological zones of Bangladesh and one modern variety (BRRI dhan87) used as a check (Table 1). Thus, a total of 72 plots, each measuring 3 m × 2 m, were established, covering an overall transplanting area of 550 m², including plot spacing. The source of collected seeds was from local farmers, research institute and were carefully labeled and preserved prior to sowing.

Crop Husbandry: Seedbeds were prepared by ploughing, puddling and leveling. The whole field for seedbeds was divided into 24 plot to fit the different rice genotypes and a 60 cm gap maintained to avoid overpopulation from one seedbed to another. Collected rice seeds were cleaned, and fully sundried for 24 hours. After-then, seeds were soaked in water for 24 hours and then incubated in moist gunny bags for another 48 hours to facilitate sprouting. After sprouting of seeds, they were sown in the previously prepared seedbeds. The experimental field was ploughed using a tractor followed by laddering to ensure fine tilth on 8 August 2023 and the layout of the field was done on the following day. A 25 days old seedling were transplanted into the main field on 9 August 2023. Transplanting was done with 2-3 seedling hill^{-1} by maintain spacing 20 cm × 15 cm and 60 cm spacing between plots. Fertilizers were applied as basal at rates of 115 kg ha^{-1} P_2O_5 (triple superphosphate), 125 kg ha^{-1}, K_2O (Muriate of potash), 100 kg ha^{-1} gypsum and 12 kg ha^{-1} zinc sulfate before transplanting. Nitrogen (200 kg ha^{-1}) was applied as urea in three equal splits at 15, 20 and 45 days after transplanting (DAT). Through-out the crop's growth period, standard cultural practices were maintained. Weed control was initiated three days after transplanting with Pendimethalin (Panida 33 EC) at 5 mL per liter of water, followed by hand weeding at 30 and 45 DAT. To control insects, Suntap Plus 50WP (Cartap hydrochloride 47.5% + Fipronil 2.5%) was applied twice, and brown spot disease was managed with Tilt 250EC. The field was irrigated with floodwater to a depth of about 5 cm during transplanting, with no additional irrigation needed due to reliance on monsoon rains.

Table 1. Name of the landraces with ecosystem and source of collection

Sl. No.	Rice Germplasm	Source of Collection	Ecosystem	Sl. No.	Rice Germplasm	Source of Collection	Ecosystem
1	Biroi	Tangail	Charland	13	Binni	Barishal	Tidal
2	Shishumoti	Jashore	Plainland	14	Ashini	Barishal	Plainland
3	Isnishona	Shatkhira	Saline	15	Lal balam	Barishal	Tidal
4	Bashful	Shatkhira	Saline	16	Nazirshail	Dinajpur	Plainland
5	Champani	Khulna	Saline	17	Porajita	Sirajganj	Plainland
6	Tulshimala	Sherpur	Hill	18	Haloi	Jamalpur	Charland
7	Kachamota	Barishal	Tidal	19	Pakistani bashmoti	BRRI	Plainland
8	Malshira	Cumilla	Charland	20	Red rice	Mymensingh	Plainland
9	Moirul	Cumilla	Plainland	21	Indonesian black rice	BRRI	Plainland
10	Zirashail	Dinajpur	Plainland	22	Kasturi-68	Faridpur	Plainland
11	Sada pan kaich	Sunamganj	Haor	23	Bashiraj	Mymensingh	Plainland
12	Ganjia	Jamalpur	Charland	24	BRRI dhan 87	BRRI	Plainland

Crop harvest, yield assessment and data collection: The crop was harvested at physiological maturity, when approximately 90% of the grains turned golden yellow color, between 30 November and 15 December 2023. For the measurement of yield contributing traits, five hills were randomly selected from each experimental plot, excluding the border row hills. Subsequently, plants were harvested from the central 4 m^2 area (2 m × 2 m) of each plot. The harvested samples were bundled plot-wise, labeled properly and finally transported to the threshing floor. Grain and straw were separated and sun-dried individually. Finally, rice grain yield was adjusted to 14% moisture content and grain yield converted to t ha^{-1}. The following formulas were used to estimate biological yield and harvest index (Donald and Hamblin, (1976):

Biological yield (t ha^{-1}) = Grain yield (t ha^{-1}) + Straw yield (t ha^{-1})
Harvest index = (Grain yield (t ha^{-1}) ÷ Biological yield (t ha^{-1})) × 100

Grain color analysis using CIE l*a*b colorimeter: Grain color of both unhusked (paddy) and husked grains of rice was determined using a CIE L*a*b colorimeter under illuminant D65 with a 10° standard observer. Before measurement, all samples were equilibrated to room temperature to maintain uniform moisture content. For each collected germplasm, about 50 g of grain was collected and properly labeled. For unhusked (paddy) samples, twenty intact and clean grains were randomly selected for each replication. The grains were placed on the sample holder in such a way that the measurement port was completely covered, and the grains were oriented uniformly. For husked (milled) rice, whole kernels were selected and arranged in a Petri dish to form a single uniform layer that completely covered the measurement aperture. The aperture size was adjusted according to the grain size, and calibration was repeated whenever necessary to ensure stability. For each sample, five readings were taken from different positions of the sample surface to account for any variation in grain colour. Each reading provided values for L* (lightness), a* (red-green axis), and b* (yellow-blue axis).

The mean values of L*, a*, and b* for each replication were calculated. From these values, chroma (C*) and hue angle (h°) were derived using the following equations (Loughrey, 2002):

$$\text{i.}C^* = \sqrt{(a^*)^2 + (= b^*)^2}$$

$$\text{ii.}h^\circ = \tan^{-1}\left(\frac{b^*}{a^*}\right)$$

Assessment of cooking and eating quality: The parameters related to cooking and eating quality were analyzed in the Food and Industrial Microbiology Laboratory, BAU. The calculation of elongation ratio was done by dividing the ratio of cooked rice length by the milled rice length (Juliano, 1971) using 10 intake kernels sample^{-1}. The absorption of water was determined by using the formula given below (Ranalli et al., 2003). 5 g rice sample was taken for this measurement.

$$\text{Water absroption (g)} = \frac{\text{Weight of cooked rice grain}}{\text{Weight of uncooked grains}}$$

Amylose (%) and Amylopectin content (%): From each germplasm, ten milligrams of rice flour were placed in 100-mL volumetric flasks, then 0.9 mL of NaOH and 1 mL of 95% ethanol were added. The contents were diluted to 100 mL after being boiled for 10 min in a boiling water bath. A 100 mL volumetric flask was filled with five milliliters of sample solution, 1.5 mL of iodine solution and 1 mL of acetic acid. By adding distilled water, the final volume was made to 100 mL, and the suspension was well stirred and kept for 20 min. At a wavelength of 620 nm, the samples were measured twice (Perez and Juliano, 1978). As starch basically consists of amylose and amylopectin, the amylopectin content was calculated by decreasing the starch content with amylose.

Alkali Spreading Value (ASV) test: The ASV was assessed by soaking six whole kernels of milled rice in a 10 mL volume of 1.7% KOH solution at 27–30 °C for 23 hours. After 23 hours, the degree of disintegration or spreading of the kernels was examined according to the standard reference table.

Statistical Analysis: Collected data were subjected to analysis of variance (ANOVA) using Statistix 10, considering genotypes as fixed effects and replications as random effects. Mean separation was performed by using Duncan's multiple range test (DMRT) at 5% probability level. Genetic parameters, including variance components, heritability, genetic advance, cluster formation, correlation coefficients, and principal component analysis were performed by using R studio software (version 2025.09.2+418) and "doebioresearch", "Ime4", "FactoMineR", "factoextra" and "cluster" package. Prior to analysis, comprehensive data management was conducted using Microsoft Office Excel. Subsequently, the data were analyzed using MS Excel for correlation analysis, BASICA for path coefficient and D^2 analysis, and STATGRAPHICS Plus for diversity, clustering, and dendrogram construction. These analytical tools facilitated robust statistical inference and meaningful interpretation of the results.

RESULTS

Morphological and yield-related traits: The mean performance of 24 *T. aman* rice varieties revealed highly significant differences for morphological and yield-contributing traits (Table 2). Plant height varied from 79.00 to 151.87 cm with Tulshimala (151.87 cm), Bashful (151.33 cm) and Haloi (150.20 cm) being tallest, while Pakistani Bashmoti (79.00 cm) exhibited shortest plant height. Whereas modern rice cultivar BRRI dhan87 demonstrated moderate plant height (102.00 cm). The number of productive tillers hill^{-1} also differed significantly among germplasm, varying from 5.93 to 10.80. Tulshimala produced the maximum number of productive tillers (10.80), closely followed by Malshira (10.60), Binni (10.47), Champani (10.33) and Bashiraj (10.20). In addition, the lowest number of productive tillers hill^{-1} was recorded in Sishumoti (5.93) followed by Kachamota (6.07), Mairul (6.13) and Ashini (6.60).

The longest panicle was observed in Biroi (23.79 cm), followed by Bashful (22.82 cm), Haloi (22.52 cm), Kasturi-68 (22.26 cm), Naizershail (22.11 cm), and BRRI dhan87 (22.05 cm). The shortest panicle was recorded in Ashini (18.54 cm), followed by Sada pan kaich (19.68 cm) and Isnishona (19.87 cm). The sterile spikelets number panicle^{-1} was exhibited maximum in Kachamota (46.10), followed by Naizershail (31.52), Kasturi-68 (30.27) and Indonesian black-ice (27.94), whereas sishumoti (12.93) produced the fewest sterile spikelets (Table 2). The number of grains panicle^{-1} was observed maximum in Porajita (131.12), followed by and Bashful (109.20), Tulshimala (106.14) and BRRI dhan87 (100.63). The lowest number of grains panicle^{-1} was recorded in Kachamota (26.20) followed by Isnishona (58.80), Ashini (61.79) and Indonesian black rice (64.11). Significant differences were also observed for 1000-grain weight, which ranged from 11.06 to 33.03 g. The highest 1000-grain weight was obtained from Sishumoti (33.03 g), followed by Haloi (30.93 g), Kachamota (29.53 g), Sada pan kaich (29.43 g), and BRRI dhan87 (28.13 g). In contrast, Tulshimala had the lowest 1000-grain weight (11.06 g), while other relatively low values were observed in Kasturi-68 (15.60 g) and Naizershail (17.63 g). The maximum grain yield was produced by BRRI dhan87 (2.40 t ha^{-1}), followed by Bashiraj (2.18 t ha^{-1}), Porajita (2.06 t ha^{-1}), and Champani (2.06 t ha^{-1}), although Sishumoti (2.02 t ha^{-1}), Malshira (2.03 t ha^{-1}) and Ganjia (1.98 t ha^{-1}). Conversely, grain yield was observed lowest in Kachamota (0.32 t ha^{-1}) followed by Ashini (0.75 t ha^{-1}), Isnishona (0.85 t ha^{-1}) and Naizershail (0.99 t ha^{-1}).

BRRI dhan87 (8.08 t ha^{-1}) produced the highest straw yield, followed by Haloi (7.49 t ha^{-1}), Red rice (7.38 t ha^{-1}) and Kachamota (7.37 t ha^{-1}). The lowest straw yield was observed in Isnishona (3.10 t ha^{-1}), followed by Moirul (3.40 t ha^{-1}) and Sishumoti (3.86t ha^{-1}). The harvest index varied widely among the germplasms, with the highest in Sishumoti (34.47%) followed by Bashiraj (31.13%), and Moirul (30.24%). Conversely, the harvest index was recorded lowest in Kachamota (4.16%), Ashini (15.38%), and Pakistani Bashmoti (17.16%).

Variation of amylose and amylopectin content of studied rice germplasm: Amylose content showed highly significant variation among the germplasms. The highest amylose content was recorded in BRRI dhan87. This was followed by Bashful, while a group of germplasms such as Moirul, Nazirshail, and Kachamota also exhibited comparatively higher amylose percentages (Table 3). On the lower side, Tulshimala, Binni, and Ashini exhibited the minimum amylose content. Amylopectin content varied inversely with amylose. The highest amylopectin content was recorded in Ashini, followed by Binni and Tulshimala (Table 3). These germplasms are characterized by high amylopectin levels, which contribute to waxy texture, cohesive grains, and suitability for preparing traditional sticky rice products. The lowest amylopectin content was observed in BRRI dhan87, which also showed the highest amylose level. Germplasms such as Bashful, Moirul, Nazirshail, and Kachamota were also grouped among the lower amylopectin categories, indicating a firmer and fluffier cooked rice texture.

Color variation of the studied germplasm: The color parameters of both husked and unhusked rice grains were measured using the CIE Lab colorimeter, where L^* denotes lightness (0 = black, 100 = white), a^* indicates color along the green–red axis (negative = green, positive = red), and b^* represents color along the blue–yellow axis (negative = blue, positive = yellow). Moreover, C^* (chroma) represents color intensity or saturation, and H (hue angle) determines the overall tone or shade (Table 4). Substantial variation was observed among the studied germplasm for all color parameters. In unhusked grains, Kasturi-68 showed the darkest husk, while Kachamota had a lighter brownish-yellow husks. The a^* values for unhusked grains ranged from –2.01 (Moirul) to 7.46 (Malshira). Bashful (2.91) and BRRI dhan87 (3.18), showed positive a^* values, indicating a reddish-brown hue typical of traditional *aman* rice. A few genotypes such as Moirul and Kachamota had slightly negative a^* values, showing faint greenish tones, while Malshira and Biroi (4.38) exhibited a stronger reddish tint.

The b^* values ranged from 7.61 (Kasturi-68) to 31.89 (Porajita), with higher b^* values signifying stronger yellowish tones. Germplasms such as Porajita (31.89), and red rice (27.87) were highly yellowish, while Binni (20.51) and Moirul (22.23) appeared more subdued in hue. The chroma (C^*) values followed a similar pattern, being highest in Porajita (32.09) and Kachamota(29.03), BRRI Dhan87 (28.45) indicating vibrant pigmentation intensity, and lowest in Kasturi-68 (8.39). The hue angle (H) was highest in Kachamota (88.89) and Zirashail (85.36), indicating lighter yellow tones, while lower hue values such as in Malshira (71.87) corresponded to reddish-brown coloration. After husking, the L^*, a^*, and b^* values changed noticeably, showing that husk removal altered the color characteristics of the grain surface. The L^* values ranged from 22.90 (Indonesian black rice) to 64.49 (Zirashail), confirming that dehusked grains of Indonesian black rice appeared darkest, while Kachamota (61.67), and Tulshimala (63.86) were among the brightest (Table 4).

In husked grains, a^* values varied widely from –1.10 (Kachamota) to 14.39 (Lalbalam). Strongly positive a^* values were recorded in Lalbalam (14.39), Bashful (11.91), Champani (10.15), Ashini (10.18), and Ganjia (12.58), indicating that these genotypes developed reddish or reddish-brown hues after husking. In contrast, negative a^* values, such as in Kachamota (-1.10), Malshira (-0.88), and Pakistani Bashmoti (-0.54), reflected a tendency toward pale or slightly greenish shades (Table 4). The b^* values of husked grains ranged from 8.39 (Binni) to 29.49 (Shishumoti). Germplasms such as Shishumoti (29.49), Bashful (26.24), and Lalbalam (27.70) showed intense yellowish tones, whereas Binni (8.39) and Indonesian black rice (8.72) displayed dull or grayish grains, characteristic of pigmented or black rice types. The C^* values (colour intensity) followed a similar pattern, ranging from 10.65 (Binni) to 31.71 (Shishumoti), indicating the strong colour saturation of some aromatic and local landraces. The hue angle (H) varied from 44.75 (Indonesian black rice) to 89.40 (Nazirshail), showing that most germplasms shifted toward yellowish-white hues, while darker or pigmented ones exhibited lower hue angles.The CIE lab colour analysis revealed a wide range of variation in brightness, redness, and yellowness among the *aman* rice landraces. Light-coloured grains were common in Kachamota, Tulshimala, and Zirashail, while darker or strongly pigmented grains were found in Lalbalam, Binni, Bashful, and Indonesian black rice.

Table 2. Mean performance of different morphological yield related traits of *aman* rice

Germplasm	Plant height (cm)	Number of productive tillers hill^{-1}	Panicle length (cm)	Number of sterile spikelets panicle^{-1}	Number of grains panicle^{-1}	1000 grain weight (g)	Grain yield (t ha^{-1})	Straw yield (t ha^{-1})	Harvest index (%)
Biroi	130.33 c-f	8.13 a-e	23.79 a	15.47 i-k	80.24 b-g	23.70 d-f	1.47 d-g	5.49 b-h	21.16 e-h
Sishumoti	125.87d-f	5.93 e	21.04 a-c	12.93 k	81.20 b-g	33.03 a	2.02 a-c	3.86 g-i	34.47 a
Isnishona	133.13 c-f	8.33 a-e	19.87 bc	13.47 k	58.80 g	22.66 e-g	0.85 i	3.10 i	21.56 d-h
Bashful	151.33 a	7.73 a-e	22.82 ab	16.52 h-k	109.2 ab	24.06 d-f	1.95 a-c	6.83 a-d	22.26 c-h
Champani	134.73 b-f	10.33 ab	21.92 ab	20.01 e-i	86.94 b-g	23.66 d-f	2.06 a-c	5.75 b-g	26.44 a-f
Tulshimala	151.87 a	10.80 a	21.89 ab	18.27 f-j	106.14 a-c	11.06 j	1.63 c-g	4.62 e-i	26.26 a-f
Kachamota	139.07 a-d	6.07 de	21.90 ab	46.10 a	26.20 h	29.53 a-c	0.32 j	7.37 a-c	4.167 i
Malshira	119.27 f-h	10.60 ab	21.01 a-c	16.07 h-k	85.52 b-g	18.10 g-i	2.03 a-c	6.25 a-f	24.65 b-g
Moirul	144.13 a-c	6.13 de	21.78 ab	18.71 f-j	93.92 b-f	25.76 c-e	1.45 e-h	3.40 hi	30.24 a-c
Zirashail	100.67 i	9.53 a-d	20.77 a-c	15.16 jk	72.06 d-g	17.96 g-i	1.64 c-f	5.29 c-h	24.00 b-g
Sada pan kaich	140.60 a-d	7.20 b-e	19.68 bc	17.13 g-k	81.37 b-g	29.43 a-c	1.17 g-i	3.90 g-i	23.23 b-h
Ganjia	134.60 b-f	9.66 a-c	20.90 a-c	17.07 g-k	98.25 b-e	20.03 f-i	1.98 a-c	5.04 d-i	28.26 a-e
Binni	107.67 g-i	10.47 ab	21.57 a-c	20.42 d-h	73.07 d-g	27.73 b-d	1.93 b-d	5.32 c-h	27.07 a-f
Ashini	121.53 e-g	6.60 c-e	18.54 c	15.70 i-k	61.79 g	21.70 e-h	0.75 ij	4.19 f-i	15.38 h
Lalbalam	131.20 c-f	9.73 a-c	20.53 bc	17.45 g-k	68.58 e-g	27.43 b-d	1.68 c-f	5.94 a-g	22.10 c-h
Naizershail	135.67 a-e	8.80 a-e	22.11 ab	31.52 b	71.53 d-g	17.63 hi	0.99 hi	4.32 f-i	18.75 f-h
Porajita	100.60 i	8.53 a-e	20.34 bc	22.83 d-f	131.12 a	22.30 e-h	2.06 a-c	5.36 b-h	27.82 a-e
Haloi	150.20 ab	8.66 a-e	22.52 ab	24.89 cd	97.81 b-e	30.93 ab	1.85 b-e	7.49 ab	20.04 e-h
Pakistani bashmoti	79.00 j	9.46 a-d	20.75 a-c	14.50 jk	80.83 b-g	18.36 g-i	1.36 f-h	6.57 a-e	17.16 gh
Red rice	103.80 hi	8.86 a-e	21.27 a-c	21.24 d-g	76.26 c-g	26.06 c-e	1.91 b-e	7.38 a-c	20.75 e-h
Indonesian black rice	98.93 i	9.93 a-c	20.82 a-c	27.94 bc	64.11 fg	27.93 b-d	1.86 b-e	4.63 e-i	29.80 a-d
Kasturi-68	143.00 a-c	8.73 a-e	22.26 ab	30.27 b	76.40 c-g	15.60 ij	1.46 e-g	4.05 g-i	26.51 a-f
Bashiraj	129.00 c-f	10.20 ab	20.72 a-c	17.27 g-k	83.30 b-g	18.03 g-i	2.18 ab	4.84 d-i	31.13 ab
BRRI dhan 87	102.00 i	9.40 a-e	22.05 ab	23.56 c-e	100.63 a-d	28.13 b-d	2.40 a	8.08 a	22.95 b-g
LSD $_{(0.05)}$	16.38	3.50	3.21	4.65	31.67	4.71	0.47	2.15	8.36
Level of significance	**	**	**	**	**	**	**	**	**
*CV (%)	4.15	12.71	4.79	7.16	12.27	6.40	9.11	12.65	11.24

Notes: Within the same column, the same letters or without letters means do not differ significantly; LSD: least significance differences; CV: coefficient of variation; ** indicates 0.01 significance level of probability.

Table 3. Amylose (%) and amylopectin (%) content of tested T. *aman* rice germplasm

Germplasm	**Amylose** (%)	**Amylopectin** (%)
Biroi	13.25 lm	86.78 cd
Sishumoti	16.96 hi	83.00 gh
Isnishona	18.95 de	81.05 kl
Bashful	22.33 b	77.73 n
Champani	15.99 j	84.04 f
Tulshimala	10.91 n	89.11b
Kachamota	20.79 c	79.16 m
Malshira	14.87 k	85.15 e
Moirul	21.02 c	78.98 m
Zirashail	19.71 d	80.31 l
Sada pan kaich	12.94 m	87.10 c
Ganjia	17.77 gh	82.23 hi
Binni	10.01 o	89.96 ab
Ashini	9.72 o	90.26 a
Lalbalam	15.49 jk	84.54 ef
Naizershail	20.87 c	79.14 m
Porajita	19.57 de	80.43 kl
Haloi	18.79 ef	81.21 jk
Pakistani bashmoti	16.89 i	83.11 g
Red rice	13.92 l	86.10 d
Indonesian black rice	17.95 fg	82.05 ij
Kasturi-68	17.04 hi	82.96 gh
Bashiraj	13.681 m	86.31cd
BRRI dhan 87	24.09 a	75.91 o
LSD $_{(0.05)}$	0.85	0.86
Level of significance	***	***
CV (%)	3.10	0.62

Notes: Within the same column, the same letters or without letters means do not differ significantly; LSD: least significance differences; CV: coefficient of variation; *** indicates 0.001 significance level of probability.

Table 4. Husked and unhusked grain color variation of 24 *aman* landraces rice germplasm

Germplasm	**Unhusked**					**Husked**				
	L^*	**a^***	**b^***	**C^***	**H**	**L^***	**a^***	**b^***	**C^***	**H**
Bashiraj	62.56a-d	1.33k-m	23.24b-f	22.28d-f	86.72a-c	43.57f-i	8.26 c	25.10a-e	26.42b-f	71.78cd
BRRI Dhan87	60.93a-e	3.18c-e	28.28a-c	28.45a-c	83.58a-d	54.50 cd	3.42 j	20.21e	20.49e-g	80.39b
Kachamota	66.08 a	0.56 n	29.03 ab	29.03 ab	88.89 a	61.67 ab	-1.10 m	22.91b-e	22.94d-f	-87.25f
Moirul	63.01a-c	-2.01 0	22.23c-f	22.32d-g	-84.83 h	61.14 ab	-0.87 lm	23.79b-e	23.81d-f	-87.91f
Kasturi68	32.48 h	3.55 c	7.61 g	8.39 h	64.99 g	54.05 cd	-0.34k-m	23.18b-e	23.18d-f	-89.16f
Zirashail	64.39 ab	2.11h-j	26.02a-d	26.11b-e	85.36a-d	64.49 a	-0.32 kl	22.71c-e	22.71d-f	-89.19f
Tulshimala	56.93 de	3.16c-e	22.63c-f	22.45d-g	82.05b-e	63.86 ab	0.29 jk	24.10b-e	24.10d-f	89.31a
Red rice	63.78a-c	1.43 kl	27.87a-c	27.61a-d	87.03a-c	40.41g-i	7.21 gh	21.46de	22.64d-f	71.43cd
Ashini	59.62b-e	1.42 kl	22.77c-f	22.81c-g	86.43a-c	39.82 j	10.18de	22.63c-e	24.81c-f	65.78d
Biroi	44.38 fg	4.38 b	18.36 f	18.87 g	76.58 ef	46.23e-i	4.08 j	25.08a-e	25.41c-f	80.76b
Binni	56.43 e	3.04c-f	20.51d-f	20.73e-g	81.57c-e	26.08 j	6.56 h	8.39 f	10.65h	51.98e
Sada Pan Kaich	63.85a-c	1.07l-n	22.93b-f	22.95c-g	87.32a-c	49.67d-f	3.55 j	20.65 de	20.95f-g	80.25b
Bashful	58.48c-e	2.91d-g	26.53a-d	26.69a-e	83.74a-c	41.40g-i	11.91 c	26.24a-e	28.82a-d	65.59d
Pakistani Bashmoti	63.81a-c	1.09k-n	23.96b-f	23.98b-g	87.39a-c	57.43bc	-0.54 lm	19.69e	19.70fg	-88.43f
Shishumoti	62.24a-e	2.52f-h	24.06b-f	24.19b-g	84.02a-d	46.48e-g	11.65 c	29.49 a	31.71a	68.44cd
Nazirshail	62.01a-e	1.63j-l	22.83c-f	22.29c-g	85.92a-c	52.15c-e	0.19 j	18.15de	18.15e-g	89.40a
Malshira	42.28 g	7.46 a	22.79c-f	23.98b-g	71.87 f	57.98a-c	-0.88 lm	23.53a-e	23.55c-f	-87.86f
Isnishona	64.12a-c	0.71 mn	21.70d-f	21.71d-g	88.13 ab	41.65g-i	9.16 c	23.08a-e	24.83a-e	68.35cd
Indonasian black rice	49.20 f	3.40 cd	18.55 ef	18.86 fg	79.61 de	22.90 j	7.92 f	8.72 f	11.78gh	44.75e
Lalbalam	61.60a-e	2.62e-h	24.58b-e	24.72b-f	83.92a-d	42.26g-i	14.39 a	27.70 ab	31.21ab	62.55d
Champani	64.24a-c	1.70i-k	24.31b-f	24.37b-g	85.99a-c	46.35e-h	10.15 d	25.48a-d	27.43a-d	68.28cd
Porajita	60.68a-e	3.55 c	31.89 a	32.09 a	83.65a-d	63.99 a	-0.82 lm	22.00a-e	22.02c-f	-87.87f
Ganjia	62.12a-e	2.30g-i	24.34b-f	24.45b-g	84.60a-d	39.83 hi	12.58 b	26.71a-c	29.52a-c	64.78cd
Haloi	62.46a-e	1.51j-l	25.14b-d	25.18b-e	87.38a-c	45.79e-i	7.32 fg	20.98b-e	22.22c-f	70.77bc
LSD$_{0.05}$	5.87	0.63	6.16	5.98	6.16	6.64	0.76	7.65	7.65	7.65
Levels of significance	***	***	***	***	***	***	***	***	***	***
CV (%)	6.10	16.77	15.99	15.59	4.91	8.31	9.19	22.21	21.07	20.39

Note: Within the same column, the means with same letters means do not differ significantly at $p \leq 0.05$
L^* (Lightness); a^* (redness/greenness); b^* (yellowness/bluer); C^* (chroma); h^* (hue).

Cooking quality characteristics of high-yielding *aman* rice germplasms

The results of the cooking quality assessment for 24 *aman* rice germplasms are presented in Table 5.

Rice length and elongation ratio: The raw grain length ranged from 4.41 mm in Tulshimala to 7.63 mm in Red rice, while the cooked length ranged between 7.23 mm in Ganjia and 9.92 mm in Red rice. The elongation ratio varied from 1.16 (Indonesian black rice) to 1.69 (Porajita), indicating substantial differences in kernel expansion upon cooking. Porajita, Tulshimala, and Bashiraj showed the highest elongation ability, while Indonesian black rice and Binni exhibited the lowest elongation, typical of short-grained types (Table 5).

Time for cooking and ratio of water absorption: Cooking time ranged from 27 minutes in Malshira to 43 minutes in Red rice, indicating significant variability in cooking duration. Germplasms such as Bashful (42 min), Tulshimala (35 min), and Bashiraj (33 min) required longer cooking times, while Malshira and Haloi cooked relatively faster. The water absorption ratio ranged from 2.07 (Red rice) to 3.51 (Zirashail), followed by Tulshimala (3.47) and BRRI dhan87 (3.37). In contrast, Red rice and Indonesian black rice showed lower absorption, likely due to their compact grain structure and higher pigment content (Table 5).

Alkali spreading value: The alkali spreading value (ASV), which reflects gelatinization temperature (GT), ranged from 2.50 to 4.00. Higher ASV values in BRRI dhan87 (4.00), Bashiraj (3.83), and Red rice (3.83) indicated low to intermediate gelatinization temperature, which corresponds to softer cooked rice. Lower ASV values showed in Lalbalam (2.50) and Champani (2.83) (Table 5).

Table 5. Cooking and eating quality of *aman* landraces rice

Germplasm	Rice length (mm)		Elongation ratio	Cooking time (minute)	Water absorption ratio	Alkali spreading value
	Raw	Cooked				
BRRI-dhan 87	6.63b-f	7.87e-g	1.19 hi	29.00 de	3.37	4.00 a
Porajita	5.30 i	8.98 b	1.69 a	29.00 de	3.35	3.50 b
Bashiraj	6.11	9.03 b	1.48 b	33.00 c	3.22 d-f	3.83 a
Champani	5.87f-i	7.96ef	1.36d-f	28.00 ef	2.79 jk	2.83 f
Malshira	5.61hi	7.91ef	1.41b-d	27.00 fg	3.13 f-h	3.50 b
Shishumoti	6.60c-g	8.76 b	1.33 ef	33.00 c	3.02 i	3.30 b-d
Bashful	6.01e-i	8.83 b	1.39 bc	42.00 a	2.74 jk	3.00 ef
Binni	6.98a-c	8.65bc	1.24 gh	32.00 c	2.62 l	3.00 ef
Red rice	7.63 a	9.92 a	1.30 gh	43.00 a	2.07 n	3.83 a
Ganjia	5.86g-i	7.23hi	1.23g-i	32.00 c	2.80 j	3.17 c-e
Indonesian black rice	7.37 ab	8.55b-d	1.16 i	30.00 d	2.37 m	3.00 ef
Haloi	5.80 hi	8.09c-e	1.39c-e	28.00 ef	2.70 jk	3.33 bc
Lal balam	6.85b-d	8.56 bc	1.25gh	29.00 de	2.74	2.50 g
Zirashail	6.75b-e	9.85 a	1.46 bc	29.00 de	3.51 a	3.17 bc
Tulshimala	4.41 i	7.29 hi	1.65 a	35.00 b	3.47 ab	3.33 bc
Kachamota	6.10d-h	7.30g-i	1.20 hi	27.00 fg	3.10 g-i	3.04 d-f
Moirul	5.90f-i	7.12 hi	1.21 hi	29.00 de	3.11 g-i	3.14 c-e
Kasturi68	5.45f-h	6.76 i	1.21 hi	29.00 de	3.09 hi	3.07 c-f
Pakistani basmati	7.10a-c	9.96 a	1.40 b-e	26.00 g	3.22 d-f	3.09 c-f
Sada pan kaich	5.98f-i	7.30g-i	1.22 hi	29.00 de	3.24 de	3.02 ef
Ishishona	6.11d-h	7.40f-h	1.21 hi	27.00 fg	3.19 e-g	3.11 c-e
Biroi	5.30 gh	7.98de	1.47 bc	26.00 g	3.38 bc	3.32 bc
Ashini	6.10d-h	7.40f-h	1.21 hi	29.00 de	3.29 cd	3.12 c-e
Nazirshail	6.60c-g	7.90 ef	1.20 hi	27.00 fg	3.09 hi	3.33 bc
Least significance difference	0.76	0.58	0.08	1.59	0.10	0.26
Levels of significance	***	***	***	***	***	***
Coefficient of variation	7.47	4.30	3.54	3.19	1.99	4.99

Note: Within the same column, the means with same letters means do not differ significantly at p≤0.05

Determination of genetic diversity, heritability and genetic advancement for yield contributing traits

Variability parameters: For studied all traits, indicating that environmental factors contributed to trait expression. However, the differences between PCV and GCV were generally small. High variability was recorded in amylose content (PCV 79.64%, GCV 79.50%) and grain yield (PCV 32.18%, GCV 30.87%). Sterile spikelets per panicle also showed very high variability (PCV 36.51%, GCV 35.80%). In contrast, traits such as panicle length (PCV 6.55%, GCV 4.47%) and amylopectin content (PCV 5.52%, GCV 5.33%) exhibited very low variability (Table 6).

Heritability: The estimation of broad sense heritability ranged from moderate (30-60%) to very high (>60%). In this study, heritability was appropriately estimated across the entire set of 24 germplasms, reflecting the collective variability present in the population rather than within individual varieties. Heritability was found highest for amylose content (99.64%), sterile spikelets panicle^{-1} (96.16%), plant height (93.36%), amylopectin content (93.13%), and 1000-grain weight (92.89%). Grain yield (92.02%) also recorded high heritability, confirming the possibility of successful selection. Conversely, relatively lower heritability was found for total tillers hill^{-1} (41.54%) and panicle length (46.54%), indicating that these characters are more influenced by the environment and therefore, less reliable for direct selection. Effective tillers hill^{-1} (59.15%) and biological yield (82.05%) exhibited moderate to high heritability (Table 6).

Genetic advance: Genetic advancement as mean percentage (GA%) provides a clearer picture of expected improvement through selection. The highest GA% was recorded in amylose content (163.47%). Grain yield also exhibited high GA% (61.01%), followed by harvest index (47.84%), non-effective tillers hill^{-1} (46.53%), 1000-grain weight (45.91%), and number of grains panicle^{-1} (44.13%). On the contrary, traits such as panicle length (6.28%) and amylopectin content (10.59%) showed low GA%, which indicated limited improvement potential (Table 6).

Table 6. Genetic parameters estimation for morphological characters of 24 *aman* germplasms

Sl No	Characters	PCV (%)	GCV (%)	Heritability (%)	GA	GA%
1	Plant height (cm)	16.09	15.54	93.36	38.78	30.94
2	Number of total tillers hill^{-1}	19.04	12.27	41.54	1.81	16.30
3	Number of effective tillers hill^{-1}	19.88	15.29	59.15	2.12	24.23
4	Numbers of non-effective tillers hill^{-1}	25.87	24.17	87.31	1.13	46.53
5	Panicle length (cm)	6.55	4.47	46.54	1.34	6.28
6	Number of sterile spikelets panicle^{-1}	36.51	35.80	96.16	14.90	72.31
7	Number of grains panicle^{-1}	27.00	24.05	79.34	36.14	44.13
8	1000 grain weight (g)	23.99	23.12	92.89	10.73	45.91
9	Amylose (%)	79.64	79.50	99.64	10.38	163.47
10	Amylopectin (%)	5.52	5.33	93.13	9.92	10.59
11	Grain yield (t ha^{-1})	32.18	30.87	92.02	0.99	61.01
12	Straw yield (t ha^{-1})	27.70	24.64	79.14	2.43	45.16
13	Biological yield (t ha^{-1})	24.44	22.14	82.05	2.90	41.31
14	Harvest index (%)	27.77	25.40	83.62	11.29	47.84

Note: Low heritability (<30%); moderate heritability (30-60%); high heritability (>60%)

Traits associated Growth and Yield Contribution: The correlation coefficients (genotypic and phenotypic) among different yield and yield-contributing traits revealed a close resemblance in the direction of association for most character pairs. Both genotypic and phenotypic analyses demonstrated that grain yield (t ha^{-1}) was significantly and positively associated with the total tillers number hill^{-1} ($r_g = 0.506$, $r_p = 0.435$), effective tillers number hill^{-1} ($r_g = 0.533$, $r_p = 0.493$), and number of grains panicle^{-1} ($r_g = 0.681$, $r_p = 0.656$). Panicle length (cm) showed a positive but non-significant association with grain yield at both genotypic (0.224) and phenotypic (0.202) levels (Table 7).

On the contrary, plant height ($r_g = –0.238$; $r_p = –0.231$), number of sterile spikelets panicle^{-1} ($r_g = –0.362$; $r_p = –0.357$), and average amylose content ($r_g = –0.237$; $r_p = –0.232$) were negatively associated with grain yield at both levels. The correlation between 1000-grain weight and grain yield was positive but negligible ($r_g = 0.050$; $r_p = 0.048$). The number of total tillers hill^{-1} exhibited a strong and positive correlation with effective tillers hill^{-1} both genotypically (0.823) and phenotypically (0.811). Conversely, non-effective tillers hill^{-1} showed weak or negative correlations with most yield-related traits. Panicle length maintained a positive correlation with the number of grains panicle^{-1} but a negative association with sterile spikelets panicle^{-1} (Table 7).

Path Coefficient Analysis at Genotypic and Phenotypic Levels: The path analysis indicates the complex interrelationships among morphological traits and their relative contribution to yield. The residual effects were 0.127 and 0.237 for genotypic and phenotypic levels, respectively, highlighting that the traits studied explained about 87.3% and 76.3% of the total variation in grain yield at the respective levels (Table 8a, Table 8b). At the genotypic level, the number of grains panicle^{-1} demonstrated the positive, highest and direct effect (0.441) on grain yield, followed by thousand grain weight (0.503), effective tillers number hill^{-1} (0.238), total tillers number hill^{-1} (0.391), and length of panicle (0.286). Among these, grains number panicle^{-1} also had strong positive and indirect effects through total tillers (0.073) and effective tillers (0.063), reinforcing its role as the most crucial yield component. Conversely, number of sterile spikelets panicle^{-1} (–0.254), non-effective tillers hill^{-1} (–0.328), amylose content (–0.211), and plant height (–0.073) exhibited direct negative effects. The grains number panicle^{-1} (0.485) again demonstrated the highest positive and direct effect on yield, followed by effective tillers hill^{-1} (0.330), total tillers hill^{-1} (0.182), and panicle length (0.202). Positive indirect effects of grains panicle^{-1} through total and effective tillers further emphasized their interrelated contribution to yield. Traits such as sterile spikelets number panicle^{-1} (–0.215), non-effective tillers number hill^{-1} (–0.176), amylose content (–0.181), and plant height (–0.101) exerted negative and direct effects (Table 8a, Table 8b).

Principal Component Analysis (PCA): Principal component analysis (PCA) was conducted to assess the contribution of different morphological characters toward total variation among the 24 *aman* rice genotypes. The first four principal components (PCA1–PCA4) exhibited eigenvalues greater than 1, together explaining a maximum proportion (77.29%) of the total phenotypic variability (Fig. 1; Fig. 2).

The first PCA1 alone responsible for the maximum variance (30.25%) with an eigenvalue of 3.025, suggesting that it played the most dominant role in explaining genetic diversity among the landraces. Traits with high loading on PCA1 likely include plant height and yield-contributing characters, implying their major influence on genotype differentiation. The PCA2 accounted 18.80% of the total variation with an eigenvalue of 1.880, mainly reflecting differences associated with tiller-related attributes. The PCA3 contributed for 15.08% of the total variance (eigenvalue 1.508), indicating the contribution of effective tillers and panicle traits in explaining genetic divergence. Similarly, PCA4 contributed 13.156% of the total variance (eigenvalue 1.316), largely governed by non-effective tillers and panicle length.

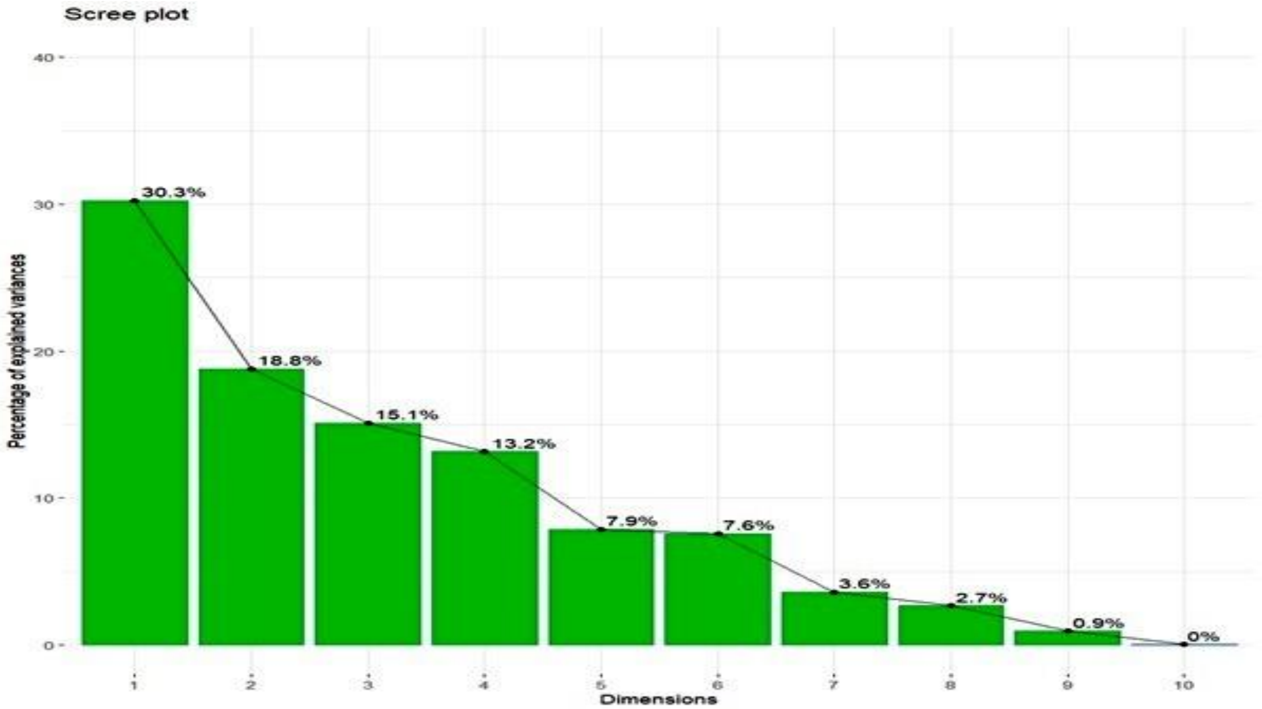

Fig. 1: Scree plot for studied traits

Table 7. Genotypic correlation and phenotypic correlation among diverse yield and yield contributing traits for different *aman* rice germplasms

Parameters	Plant height (cm)	Number of total tillers hill^{-1}	Number of effective tillers hill^{-1}	Numbers of non-effective tillers hill^{-1}	Panicle length (cm)	Number of sterile spikelets panicle^{-1}	Number of grains panicle^{-1}	1000 grain weight (g)	Amylose (%)	Grain yield (t ha^{-1})
Plant height (cm)	-	-0.305	-0.298	-0.029	0.337	0.138	0.041	-0.018	0.259	-0.238
Number of total tillers hill^{-1}	-0.242	-	0.823**	0.425*	0.068	-0.090	0.188	-0.331	-0.369	0.506*
Number of effective tillers hill^{-1}	-0.259	0.811**	-	0.126	0.063	-0.173	0.266	-0.475*	-0.249	0.533**
Numbers of non-effective tillers hill^{-1}	-0.025	0.364	0.101	-	0.047	0.157	-0.174	0.306	-0.381	0.001
Panicle length (cm)	0.297	0.089	0.072	0.019	-	0.331	0.137	0.020	0.238	0.224
Number of sterile spikelets panicle^{-1}	0.136	-0.065	-0.147	0.155	0.278	-	-0.387	0.146	-0.154	-0.362
Number of grains panicle^{-1}	0.039	0.13	0.222	-0.176	0.175	-0.381	-	-0.196	-0.049	0.681**
1000 grain weight (g)	-0.021	-0.304	-0.450*	0.292	0.013	0.144	-0.189	-	-0.029	0.050
Amylose (%)	0.257	-0.316	-0.227	-0.373	0.207	-0.153	-0.046	-0.027	-	-0.237
Grain yield (t ha^{-1})	-0.231	0.435*	0.493*	-0.0002	0.202	-0.357	0.656**	0.048	-0.232	-

Note: Above diagonal: genotypic correlation; below diagonal: phenotypic correlation; ** = Significant at 0.01; * = Significant at 0.05

Table 8a. Direct and indirect effects of partitioning on different morphological traits of 24 rice genotypes (Genotypic level)

Parameters	Plant height (cm)	Number of total tillers hill^{-1}	Number of effective tillers hill^{-1}	Numbers of non-effective tillers hill^{-1}	Panicle length (cm)	Number of sterile spikelets panicle^{-1}	Number of grains panicle^{-1}	1000 grain weight (g)	Amylose (%)	Grain yield (t ha^{-1})
Plant height (cm)	-0.073	-0.119	-0.071	0.010	0.096	-0.035	0.018	-0.009	-0.055	-0.238
Number of total tillers hill^{-1}	0.022	0.391	0.196	-0.140	0.019	0.023	0.083	-0.167	0.078	0.506*
Number of effective tillers hill^{-1}	0.022	0.322	0.238	-0.041	0.018	0.044	0.117	-0.239	0.052	0.533**
Numbers of non-effective tillers hill^{-1}	0.002	0.166	0.030	-0.328	0.013	-0.040	-0.077	0.154	0.080	0.001
Panicle length (cm)	-0.025	0.027	0.015	-0.015	0.286	-0.084	0.060	0.010	-0.050	0.224
Number of sterile spikelets panicle^{-1}	-0.010	-0.035	-0.041	-0.052	0.095	-0.254	-0.171	0.073	0.032	-0.362
Number of grains panicle^{-1}	-0.003	0.073	0.063	0.057	0.039	0.098	0.441	-0.099	0.010	0.681**
1000 grain weight (g)	0.001	-0.129	-0.113	-0.100	0.006	-0.037	-0.086	0.503	0.006	0.050
Amylose (%)	-0.019	-0.144	-0.059	0.125	0.068	0.039	-0.022	-0.015	-0.211	-0.237

Residual effect: 0.127; Bold numeric value indicates direct effect; * and ** indicate significant at 0.05 and 0.01 levels of probability, respectively.

Table 8b. Direct and indirect effects of partitioning on different morphological traits of 24 rice genotypes (Phenotypic level)

Parameters	**Plant height (cm)**	**Number of total tillers hill^{-1}**	**Number of effective tillers hill^{-1}**	**Numbers of non-effective tillers hill^{-1}**	**Panicle length (cm)**	**Number of sterile spikelets panicle^{-1}**	**Number of grains panicle^{-1}**	**1000 grain weight (g)**	**Amylose** (%)	**Grain yield (t ha^{-1})**
Plant height (cm)	**-0.101**	-0.044	-0.085	0.004	0.060	-0.029	0.019	-0.009	-0.046	-0.231
Number of total tillers hill^{-1}	0.024	**0.182**	0.267	-0.064	0.018	0.014	0.063	-0.126	0.057	0.435*
Number of effective tillers hill^{-1}	0.026	0.147	**0.330**	-0.018	0.015	0.032	0.108	-0.187	0.041	0.493*
Numbers of non-effective tillers hill^{-1}	0.003	0.066	0.033	**-0.176**	0.004	-0.033	-0.085	0.122	0.067	-0.0002
Panicle length (cm)	-0.030	0.016	0.024	-0.003	**0.202**	-0.060	0.085	0.005	-0.037	0.202
Number of sterile spikelets panicle^{-1}	-0.014	-0.012	-0.048	-0.027	0.056	**-0.215**	-0.185	0.060	0.028	-0.357
Number of grains panicle^{-1}	-0.004	0.024	0.073	0.031	0.035	0.082	**0.485**	-0.079	0.008	0.656**
1000 grain weight (g)	0.002	-0.055	-0.148	-0.051	0.003	-0.031	-0.092	**0.416**	0.005	0.048
Amylose (%)	-0.026	-0.057	-0.075	0.066	0.042	0.033	-0.022	-0.011	**-0.181**	-0.232

Residual effect: 0.237; Bold numeric value indicates direct effect; * and ** indicate significant at 0.05 and 0.01 levels of probability, respectively.

Fig. 1: Scree plot for studied traits

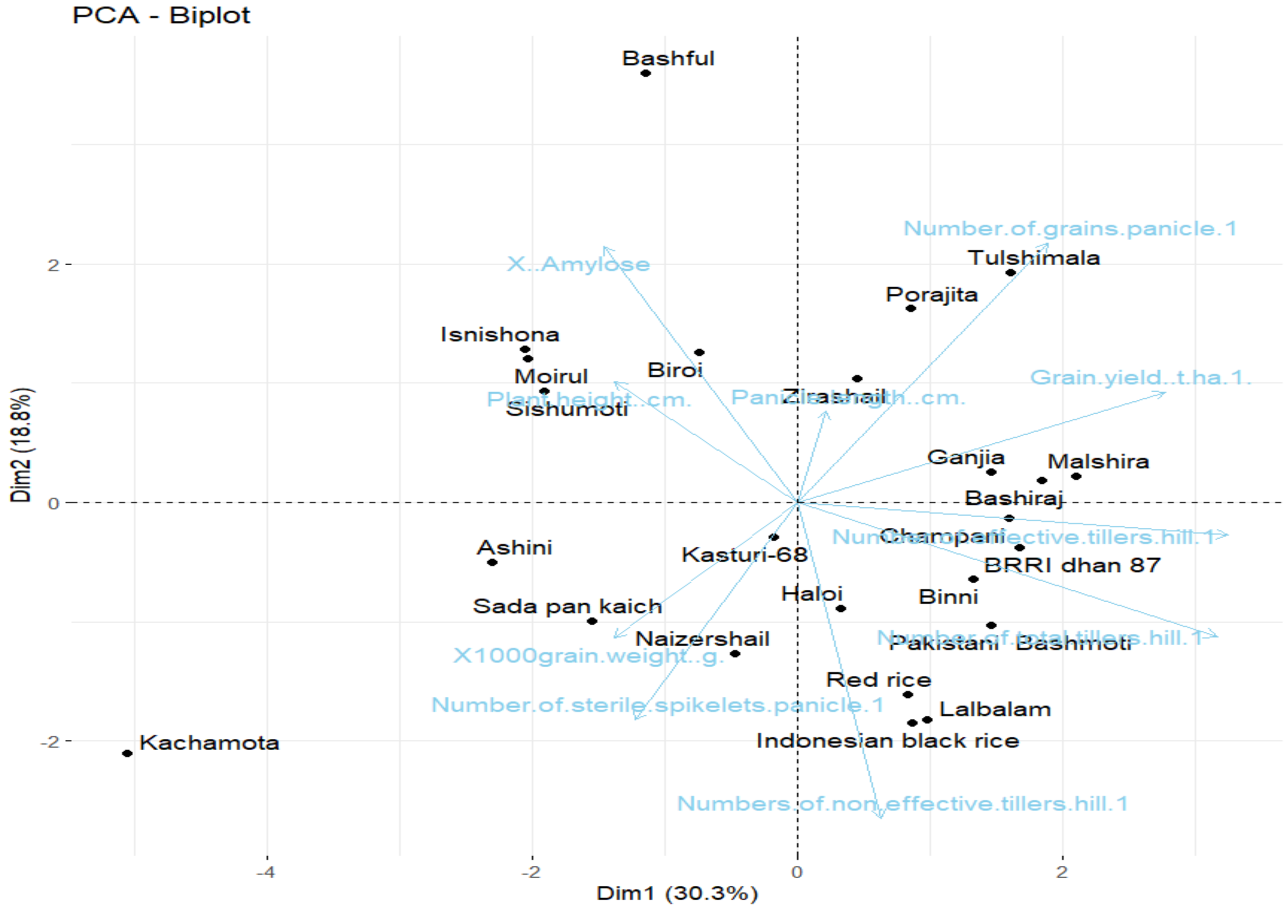

Fig. 2: PCA biplot for corresponding 10 characters in rice germplasms

PCA (character wise): The character-wise principal component analysis (PCA) revealed the relative contribution of individual traits to the principal components that explain the variability among 24 *aman* rice genotypes (Fig. 2). The PCA1 was strongly and positively associated with total tillers number hill^{-1} (0.502), effective tillers number hill^{-1} (0.516), number of grains panicle^{-1} (0.300) and grain yield (0.440). The PCA2 showed high positive loadings for the non-effective tillers number hill^{-1} (0.532) and sterile spikelets number panicle^{-1} (0.367), whereas negative loadings were observed for amylose content (-0.431) and number of grains panicle^{-1} (-0.436). The PCA3 was dominantly influenced by panicle length (0.716), plant height (0.467), and number of sterile spikelets panicle^{-1} (0.429). The PCA4 was mainly associated with number of grains panicle^{-1} (0.332), 1000-grain weight (0.679) and grain yield (0.434).

Cluster Analysis: The rice germplasms in this study were categorized according to the D2 value and Euclidean distance, which follows Ward's method. Germplasms from the same cluster often performed similarly, but highly divergent from other clusters. Cluster analysis grouped the 24 *aman* rice genotypes into five clusters (Table 9). Cluster III was the largest, containing 8 genotypes (33.33%), followed by Cluster V with 6 genotypes (25.00%), Cluster I with 5 genotypes (20.83%), Cluster II with 4 genotypes (16.67%), and Cluster IV, which included only 1 genotype (4.17%). Cluster I included Biroi, Isnishona, Bashful, Zirashail, and Porajita. Cluster II consisted of Sishumoti, Moirul, Sada pan kaich, and Ashini. Cluster III contained Champani, Tulshimala, Malshira, Ganjia, Naizershail, Haloi, Kasturi-68, and Bashiraj. Cluster IV was represented solely by Kachamota. Cluster V included Binni, Lalbalam, Pakistani bashmoti, Red rice, Indonesian black rice, and BRRI dhan87 (Fig. 2; Fig. 3).

Table 9. Cluster of different rice germplasms

Cluster name	No. of germplasms	Percent (%)	Name of germplasms
I	5	20.83	Biroi, Isnishona, Bashful, Zirashail, and Porajita
II	4	16.67	Sishumoti, Moirul, Sada pan kaich, and Ashini
III	8	33.33	Champani, Tulshimala, Malshira, Ganjia, Naizershail, Haloi, Kasturi-68 and Bashiraj
IV	1	4.17	Kachamota
V	6	25.00	Binni, Lalbalam, Pakistani bashmoti, Red rice, Indonesian black rice and BRRI dhan 87

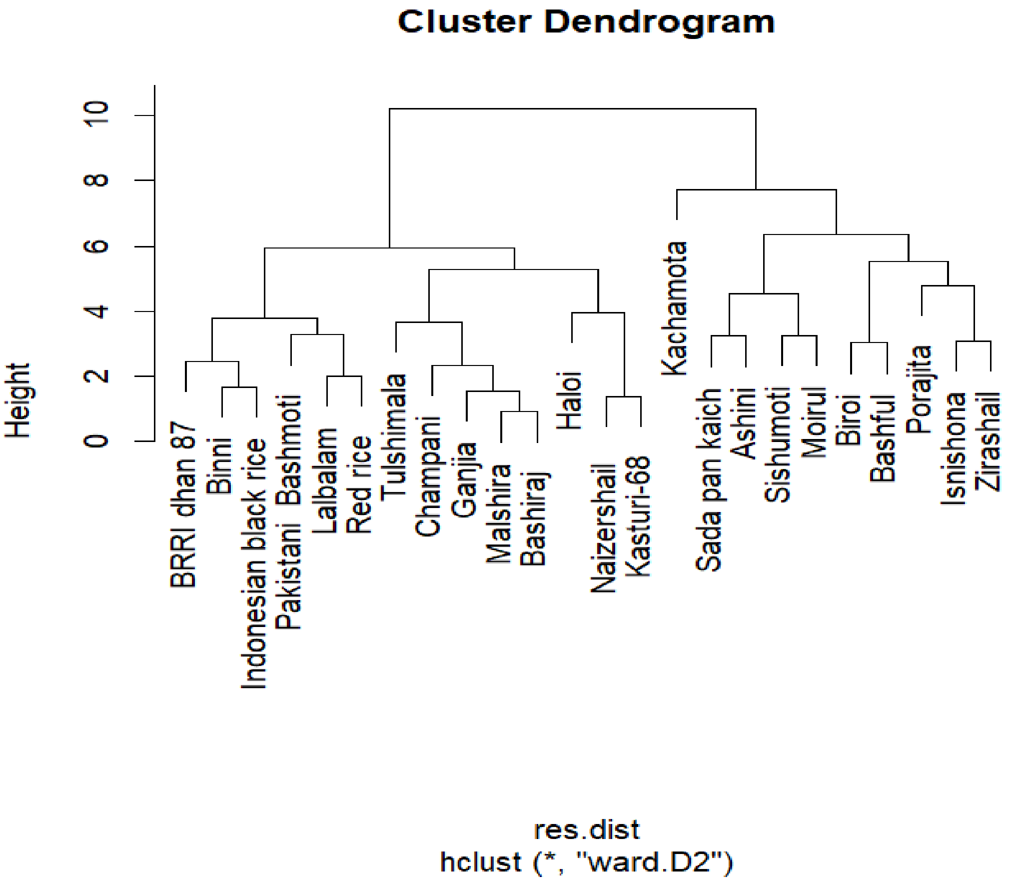

Fig. 3. Cluster dendrogram.

Distances of Inter and Intra Cluster: The study revealed that distances of inter-cluster were generally higher than distances of intra-cluster, indicating considerable genetic diversity among the studied rice genotypes (Supplementary Table 3). The distance of intra-cluster was observed maximum in Cluster I (1090.47), while the minimum intra-cluster distance was documented in Cluster V (151.35). The highest inter-cluster distance (1691.05) was observed between Cluster I and Cluster V, followed by Cluster IV and Cluster V (1620.12) and Cluster III and Cluster IV (1469.58). The distance of inter-cluster (329.94) was observed lowest between Cluster III and Cluster V.

DISCUSSION

The significant variation observed among the 24 genotypes of *aman* rice for all morphological, yield and grain contributing traits reflected the presence of broad genetic base within landraces and modern cultivars of Bangladesh. Such variability reflects the broad genetic base of the germplasm and provides opportunities for selection and improvement. Variation in plant height ranged from semi-dwarf genotypes such as Pakistani Bashmoti to tall traditional landraces like Tulsimala and Bashful. Whereas tall statured landraces are often associated with lodging susceptibility as well as inefficient assimilate partitioning, which may explain comparatively lower grain yield despite produced higher biomass (Zhu *et al.,* 2023). Conversely, BRRI dhan87 exhibited moderate plant height combined with superior grain yield, confirming that balanced architecture can enhance assimilate translocation and enhance yield stability (Roy *et al.,* 2024b). Grain yield was strongly influenced by tillering capacity, particularly the effective tillers number hill^{-1}. Genotypes such as tillering capacity, Tulshimala, Malshira, Champani and Binni produced higher effective tillers, translating into greater sink. However, total tiller numbers did not always ensure higher yield, as seen in Lalbalam and Pakistani Bashmoti, where a considerable proportion of tillers were non-productive. So, effective tiller efficiency rather than tiller number is very critical for rice yield formation (Roy *et al*., 2024a, b). Similarly, panicle length and grain number panicle^{-1} (Porajita and Bashful) exhibited substantial variation and contributed positively to yield performance, as higher grain numbers reflect improved spikelet differentiation and fertilization efficiency (Faysal *et al.,* 2022; Kulsum *et al.,* 2022; Ullaha *et al.,* 2023). Spikelet sterility has been linked with poor assimilate availability, genetic constraints and sensitivity to environment stresses during anthesis period (Jagadish *et al*., 2010; Roy *et al*., 2024b). The BRRI dhan87 outperforming all landraces due to balance plant architecture, number of high effective tiller and grain number, and optimized harvest index. Despite their lower productivity, many traditional landraces possess valuable adaptive traits and quality attributes because they were historically selected for biotic and abiotic resilience, grain quality and adaptation rather than yield maximization (Khanal *et al.,* 2025). This explains the comparable yield performance of some landraces such as Bashiraj, Porajita and Champanj with modern cultivars and landraces (Begum *et al.,* 2015; Alam *et al.,* 2025), which emphasizing the importance of conserving landrace diversity for future genetic improvement for breeding program.

The wide variation in amylose content (9.72-24.09%) further confirmed the presence of diverse grain quality types within the germplasm, including waxy, intermediate and high amylose ricc. This diversity is genetically controlled by allelic variation at the W_x locus and modifier genes influencing starch biosynthesis (Wang *et al.,* 2017). High amylose content germplasm such as BRRI dhan87 and Bashful are associated with firm, fluffy cooked rice, lower glycemic index and wider consumer acceptance in non-sticky rice preferring regions (Emi *et al.,* 2021; Bao *et al.,* 2023). Conversely, low amylose and high amylopectin germplasms like Ashini, Binni, Tulshimala exhibited waxy characteristics, which make them suitable for preparation of traditional rice. These germplasms are culturally significant and having high value in premium rice market despite lower grain yield.

The variation in CIE lab color parameters among both husked and unhusked grains reflects differences in husk pigmentation, bran composition as well as bioactive compound accumulation. Pigmented and darker grains like Indonesian black rice and Lalbalam demonstrated lower L^* values and higher redness (a^*) or chroma, indicative of anthocyanin and phenolic accumulation (Colombo *et al.,* 2023). Differences in a^* and b^* values indicated genetic and biochemical variation in pigment compounds such as anthocyanins, carotenoids, and phenolics among germplasms (Xia *et al*., 2023; Zhao *et al*., 2025). These pigments are associated with antioxidant activity and health benefits, contributing to rising consumer demand for nutritionally enriched colored rice despite lower yields. The observed shifts in color parameters after husking highlight the important contribution of bran layers to grain appearance and nutritional quality. The quality of cooking is a vital aspect for consumer preference of rice and market value. Grain elongation ratio a key quality trait for premium quality rice was highest in Porajita, Tulshimala and Bashiraj suggesting superior cooking quality and consumer preference. Differences in water absorption and alkali spreading values observed in BRRI dhan87 and Bashiraj indicate lower gelatinization temperature and softer cooked rice, while genotypes like Lalbalam require longer cooking time due to lower alkali spreading values (Bao *et al.,* 2023; Mapoung *et al.,* 2023; Karim *et al.,* 2024).

The close proximity between phenotypic and genotypic coefficients of variation for most traits indicates that genetic factors predominantly influenced trait expression with limited environmental interference (Maruti *et al*., 2025). Exceptionally, high heritability combined with high genetic advance for amylose content, grain yield and sterile spikelet panicle^{-1} highlights the action of dominance additive gene, which making these traits for ideal selection of breeding (Shrivastav *et al.,* 2023). Conversely, traits such as panicle length and amylopectin content exhibited low genetic advance despite high heritability, highlighting non-additive gene effect and limited response to simple selection. This indicating limited genetic variability, highlighting limited potential for improvement through direct selection and require hybridization and progeny testing for improvement, similar for panicle length and tillers Lingaiah *et al.* (2020).

Correlation and path analysis consistently identified effective tillers number hill^{-1}, total tillers number hill^{-1}, panicle length and number of grains panicle^{-1} as the most influential traits governing grain yield (Roy *et al*., 2024a; Islam *et al*., 2025; Roy *et al*., 2026). These positive and significant correlations indicated that increases in these traits would result in corresponding increases in grain yield, suggesting their importance as reliable selection indices in breeding programs aimed at yield improvement. Conversely, non-effective tillers hill^{-1} showed weak or negative correlations with most yield-related traits, confirming their minimal role in yield determination. Direct negative effects of sterile spikelets, excessive plant height and amylose content emphasize the direct need to reduce sterility and to optimize plant architecture while balancing grain quality. These negative relationships suggested that taller plants, higher spikelet sterility, and greater amylose percentage adversely affect yield, possibly due to poor partitioning efficiency and lower fertility. The higher magnitude of genotypic correlations compared to phenotypic ones further indicated that environmental factors compounded trait associations at the field level. Analysis of path coefficient at both genotypic and phenotypic levels was performed to assess the direct and indirect effects of yield-contributing traits on grain yield of *aman* rice landraces. The higher residual value at the phenotypic level implied a greater environmental influence on yield expression compared to the genetic level (Ikbal *et al.*, 2023; Par*aman*ik *et al.,* 2023; Sahithi *et al.,* 2023). These were showing very high additive gene effects and suggesting that direct selection would be highly effective in breeding program.

Multivariate analyses further supported the existence of substantial genetic divergence among the studied genotypes. The PCA exhibited that the first four components were explained more than 77% of total variation, with traits related to tillering ability, grain yield, panicle length, grains panicle^{-1} and amylose content contributing most strongly to genotype discrimination (Rani *et al.*, 2022; Roy *et al.*, 2024b; Srinivas *et al.*, 2025; Roy *et al.*, 2026). Cluster analysis grouped the genotypes into distinct clusters with considerable inter-cluster distances, indicating the presence of diverse genetic backgrounds. The maximum inter-cluster distance observed between Cluster I and Cluster V, suggests that crosses between genotypes from these clusters could generate greater heterosis and transgressive segregants (Shanmugam *et al.*, 2023). Such types of multivariate grouping are crucial for identifying diverse parents for breeding strategies aimed at yield and quality balance.

Conclusion: The study demonstrated substantial variability in plant height, tillering capacity, panicle characteristics, grain weight, and grain quality parameters such as amylose and amylopectin content, which are critical for both yield performance and end-use quality. High heritability estimates and genetic gains suggested that traits like amylose content, sterile spikelets, plant height, and grain yield can be effectively selected for crop improvement. Correlation and path analysis identified key traits—particularly the number of grains panicle^{-1}, effective tillers, and grain weight—as major contributors to yield, with some traits such as plant height and sterile spikelets showing negative associations. The observed wide range of variation and genetic distances among the clusters provide valuable insights for targeted breeding programs aimed at developing high-yielding, quality-assured *T. aman* rice cultivars suited to local preferences and environmental conditions. Future multi-season and multi-location trials are necessary to validate the consistency and broader applicability of our findings.

Conflict of interest: The authors declare no conflict of interest.

Funding Statement: The research was financially supported by the Bangladesh Agricultural University Research System (BAURES) through the project titled "Characterization and Conservation of Rice Germplasms Collected from Different Ecosystems of Bangladesh" (Project Number: 2022/7/BAU).

Author's contribution: MNS conducted this study as part of her M.S. research work under the supervision of MGA and AKH. MMR did the data collection and write the manuscript. TKR helped in the statistical analysis and formatting of the manuscript. MMR, TKR, and MKH helped in reviewing the manuscript. All authors read and approve the final manuscript.

REFERENCES

Ahmed, M., E. Rashid, N. Akter, and M. Khalequzzaman (2019). Morphological characterization and diversity of T. *aman* rice germplasm of Bangladesh. Bangladesh Rice J. 22(2): 13–22. https://doi.org/10.3329/brj.v22i2.44038

Alam, I., B. Das, K.M.Y. Tanim, R. Zannat, A. D. Hridoy, H. M. Hossain, T. Islam and M.A.R. Bhuiyan (2025). Agro-morphological characterization and diversity studies of local and modern rice genotypes in the coastal region of Bangladesh. Sarhad J. Agric. 41(1):1-11. https://doi.org/10.17582/journal.sja/2025/41.1.1.11

Bangladesh Bureau of Statistics (BBS) (2023). Statistical Year Book of Bangladesh Bureau of Statistics. Statistics and Information Division, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka, Bangladesh.

Bao, J., B. Deng and L. Zhang (2023). Molecular and genetic bases of rice cooking and eating quality: an updated review. Cereal Chem. 100:1220-1233. https://doi.org/10.1002/cche.10715

Begum, M., M. A. Hossain, F. M. M. Hossain and A. K. Hasan (2015). Genetic variability for grain yield and yield associated traits in transplant Aman rice (*Oryza sativa* L.). Res. Agric. Livest. Fish. 2(2): 207–213. https://doi.org/10.3329/ralf.v2i2.25000

Colombo, F., C. Cappa, C. Bani, M. Magni, S. Biella, P. Restani and C. Di Lorenzo (2023). Characterization of color, phenolic profile, and antioxidant activity of Italian pigmented rice varieties after different technological treatments. Food Biosci. 53: 102674. https://doi.org/10.1016/j.fbio.2023.102674

Deb, D. (2021). Rice Cultures of Bengal. Gastronomica. 21(3): 91–101. https://doi.org/10.1525/GFC.2021.21.3.91

Donald, C.M. and J. Hamblin (1976). The Biological Yield and Harvest Index of Cereals as Agronomic and Plant Breeding Criteria. Adv. Agron. 28: 361-405. http://dx.doi.org/10.1016/S0065-2113(08)60559-3

Emi, F.R., H. Khatun, F. Yasmine, A.K. Hasan and M.A. Hossain (2021). Morphological variability and genetic diversity of *Aman* rice germplasm of Bangladesh cultivated in Mymensingh region. Plant Sci. Today. 8(4):972–985. https://doi.org/10.14719/pst.1304

Faysal, A. S. M., L. Ali, M. G. Azam, U. Sarker, S. Ercisli, K. S. Golokhvast and R. A. Marc (2022). Genetic variability, character association, and path coefficient analysis in transplant *Aman* rice genotypes. Plants. 11(21): 2952. https://doi.org/10.3390/plants11212952

Hossain, M. and W. M. H. Jaim (2009). Diversity and diffusion of rice varieties: A database for Bangladesh. IFPRI, Harvest Plus Project, July.

Hossain, M., W. M. H. Jaim, T. R. Paris and B. Hardy (2012). Adoption and diffusion of modern rice varieties in Bangladesh and eastern India. International Rice Research Institute, Los Baños, Philippines.

Ikbal, M.F., M.Y. Rafii, S.I. Ramlee, M.N. Yaapar, M.M. Islam, R. Shultana, M.M. Rana M. Anisuzzaman and M.A. Haque (2024). Growth performance of rice genotypes at the seedling stage under different salinity stresses. Indian J. Agric. Res. 58(3): 415-422. doi: 10.18805/IJARe.AF-832.

Islam, M. Z., T. Chakrabarty, N. Akter, M. Khalequzzaman, M. F. R. K. Prince, B.R. Pittendrigh, M. Tomita and M. P. Ali (2025). Genetic variability, correlation and path coefficient analysis of phenotypic traits and genetic diversity of Aman rice landraces (*Oryza sativa* L.). Sci. Rep. 15(1): 18606. https://doi.org/10.1038/s41598-025-03547-x

Jagadish, S.V.K., R. Muthurajan, R. Oane, T.R. Wheeler, S. Heuer, J. Bennett and P.Q. Craufurd (2010). Physiological and proteomic approaches to address heat tolerance during anthesis in rice (*Oryza sativa* L.). J. Exp. Bot. 61: 143-156. https://doi.org/10.1093/jxb/erp289

Juliano, B.O. (1971). A simplified assay for milled rice amylose. Cereal Sci. Today. 16: 334–340.

Karim, M.D., M. Abuhen, M. D. Hossain and M.M. Billah (2024). Assessment and comparison of cooking qualities and physico-chemical properties of seven rice varieties in terms of amylose content. Food Phy. 1(100014). https://doi.org/10.1016/j.foodp.2024.100014

Khanal, D., D. Banjade, N.P. Belbase, B.D. Pant, A. Kunwar, D. R. Bist, D.C. Yadav and A. Dhami (2025). Evaluation of rice landraces for yield and related traits under rainfed conditions in Nepal. Agro Environ. Sustain. 3(2): 130-139. https://doi.org/10.59983/s2025030205

Kovach, M.J. and S.R. McCouch (2008). Leveraging natural diversity: back through the bottleneck. Curr. Opin. Plant Biol. 11(2): 193–200. https://doi.org/10.1016/j.pbi.2007.12.006

Kulsum, U., U. Sarker and M.G. Rasul (2022). Genetic variability, heritability and interrelationship in salt-tolerant lines of T. *Aman* rice. Genetika. 54(2): 761–776. https://doi.org/10.2298/GENSR2202761K

Lingaiah, N., B.S. Chandra, V. Venkanna, K.R. Devi and Y. Hari (2020). Genetic variability and correlation studies in yield traits of elite rice (*Oryza sativa* L.) genotypes. Ind. J. Pure Appl. Biosci. 8(6): 359–363. http://dx.doi.org/10.18782/2582-2845.8428

Loughrey, K. (2002). Overview of Color Analysis. Curr. Protoc. Food Anal. Chem. 3: F5.1.1-F5.1.13. https://doi.org/10.1002/0471142913.faf0501s03

Mapoung, S., W. Semmarath and P. Arjsri (2023). Comparative analysis of bioactive-phytochemical characteristics, antioxidants activities, and anti-inflammatory properties of selected black rice germ and bran (*Oryza sativa* L.) varieties. Eur. Food. Res. Technol. 249: 451–464. https://doi.org/10.1007/s00217-022-04129-1

Maruti, K., Y. Prashanth, K. Sruthi and Ch. Anuradha (2025). Assessment of genetic variability, heritability and genetic advance for yield and nutritional traits in rice (*Oryza sativa* L.) Genotypes. J. Exp. Agric. Int. 47(7): 982–993. https://doi.org/10.9734/jeai/2025/v47i73641

Par*aman*ik, S., M.S. Rao, K. Rashmi, K.K. Panda and A. Chakraborty (2023). Studies on genetic variability, heritability and genetic advance for quantitative traits and nutritional traits in rice (*Oryza sativa* L.). Electron. J. Plant Breed. 14(4): 1527–1537. https://doi.org/10.37992/2023.1404.157

Perez, C.M. and B.O. Juliano (1978). Modification of the simplified amylose test for milled rice. Starch/Stärke. 30(12): 424–426. https://doi.org/10.1002/star.19780301206

Ranalli, R.P., T. A. Howell Jr. and T.J. Siebenmorgen, (2003), Effects of Controlled Ambient Aeration on Rice Quality During On-Farm Storage. Cereal Chem. 80: 9-12. https://doi.org/10.1094/CCHEM.2003.80.1.9

Rani, M.H., M. Faruquee, M.S.R. Khanom and S. N. Begum (2022). Genetic variability and multivariate studies on the grain physical properties of rice (*Oryza sativa* L.) landraces. SABRAO J. Breed. Genet. 54(1): 1–10. http://doi.org/10.54910/sabrao2022.54.1.1

Roy, A.R., S.R. Rout, L.H. Hijam, S.S. Sadhu, A.G. Ghosh, M.C. Chakraborty, N.S. Sahana, S.S. Singla and S.D. Das (2024a). Multivariate genetic analyses unveil the complexity of grain yield and attributing traits diversity in *Oryza sativa* L. landraces from north-eastern India. Plant Sci. Today. 11: 1–12. https://doi.org/10.14719/pst.2500

Roy, T. K., A. Sannal, S. S.Tonmoy , S. Akter, B. Roy, M. M. Rana, Z. Alam and M.R. Hasan (2024b). Trait analysis of short duration boro rice (*Oryza sativa* L.) varieties in northern region of Bangladesh: Insights from heatmap, correlation and PCA. Nova Geodesia. 4(2): 175. https://doi.org/10.55779/ng42175

Roy, T.K., A. Sannal, S.M.M.S.Tonmoy, M.A. Biswas, M.N.I. Nahid, A. Nayeem, A. Akter and M.R. Hasan (2026). Yield and trait associations with long-duration Boro rice varieties in northern Bangladesh using correlation and PCA approach. SAARC J. Agric. 23(2): 43–61. https://doi.org/10.3329/sja.v23i2.80865

Sahithi, M., R.A. Fiyaz, S.K. CV and G.S. Laha (2023). Genetic variability and character association studies for yield and yield-related traits in rice (*Oryza sativa* L.). Pharma Innovation. 12(9): 598–602.

Shanmugam, A., R. Suresh, A. R*aman*athan, P. Anandhi and D. Sassikumar (2023). Unravelling genetic diversity of South Indian rice landraces based on yield and its components. Electron. J. Plant Breed. 14(1):160–169. https://doi.org/10.37992/2023.1401.007

Shrivastav, S. P., O.P. Verma, K. Lal and D. Prasad (2023). Estimates of genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under sodic soil. J. Rice Res. 16(1). https://doi.org/10.58297/wqwi6097

Siddique, M. A., M. Khalequzzaman, A. Bhuiya, E. S. M. H. Rashid, M. H. K. Baktiar, M. S. Ahmed, M. Z. Islam and P.S. Biswas (2025a). Genetic diversity analysis in Boro rice (*Oryza sativa* L.) landraces of Bangladesh using SSR markers. Bangladesh Rice J. 27(2): 1–16. https://doi.org/10.3329/brj.v27i2.77686

Srinivas, B., P.G. Nayak, P. Madhukar, B.L. Prasanna, D. Sreelatha and G. Sreenivas (2025). Principal component analysis and correlation studies in rice (*Oryza sativa* L.) genotypes. Plant Arch. 25(2): 3187–3193. https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-2.408

Terfa, G.N. and G.N. Gurmu (2020). Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) genotypes for seed yield and other agronomic traits. Oil Crop Sci. 5(3): 156–160. https://doi.org/10.1016/j.ocsci.2020.08.002

Thuy, N.P., N.N. Trai, B.D. Khoa, N.H.X. Thao, V.T. Phong and Q.V.C. Thi (2023). Correlation and path analysis of association among yield, micronutrients and protein content in rice accessions grown under aerobic condition from Karnataka, India. Plant Breed. Biotech. 11: 117–129. https://doi.org/10.9787/PBB.2023.11.2.117

Ullaha, M.Z., M.S. Alam, M. Samsuzzaman and M.N. Huda (2023). Genetic analysis of local *Aman* rice (*Oryza sativa* L.) genotypes based on morphological traits. Acta sci. Malaysia. 7(1): 50-59.

Wang, K., Z. Qunfeng, J. Liu, F. Qiu, F. Qiu, M.A. dela Paz, W. Larazo, Y. Yang and F. Xie (2017). Genetic effects of wx allele combinations on apparent amylose content in tropical hybrid rice. Cereal Chem. 94(5): 887–891. https://doi.org/10.1094/CCHEM-03-17-0065-R

Xia, H., X. Pu, X. Zhu, X. Yang, H. Guo, H. Diao, Q. Zhang, Y. Wang, X. Sun, H. Zhang and Z. Zhang (2023). Genome-wide association study reveals the genetic basis of total flavonoid content in brown rice. Genes*.* 14(9): 1684. https://doi.org/10.3390/genes14091684

Yunus, M., S. Rashid and S. Chowdhury (2019). Per capita rice consumption in Bangladesh: available estimates and IFPRI's validation survey results. International Food Policy Research Institute, Report No. 15738, Dhaka, Bangladesh.

Zhang, D., H. Zhang, M. Wang, J. Sun, Y. Qi, F. Wang, X. Wei, L. Han, X.Wang and Z. Li (2009). Genetic structure and differentiation of *Oryza sativa* L. in China revealed by microsatellites. Theor. Appl. Genet. 119(6): 1105–1117. https://doi.org/10.1007/s00122-009-1112-4

Zhao, M., X. Xiao, D. Jin, L. Zhai, Y. Li, Q. Yang, F. Xing, W. Qiao, X. Yan and Q. Tang (2025). Composition and biological activity of colored rice—A comprehensive review. Foods. 14(8): 1394. https://doi.org/10.3390/foods14081394

Zhu, G., H. Wu, Y. Chen, S. Mondal and A. M. Ismail (2023). Growth characteristics and yield of contrasting rice genotypes under long-term stagnant flooding. Field Crops Res. 301: 109020. https://doi.org/10.1016/j.fcr.2023.109020