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Yield and Trait Associations with Long-Duration Boro Rice Varieties in Northern Bangladesh using Correlation and PCA Approach

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Abstract

For modern breeding program, the role of genetic variation is most important in the desirable genotype selection. This study was conducted to assess the adaptability and selection potential of newly released rice varieties in terms of their yield and analyze the relationships among yield and yield component traits by partitioning correlation coefficients and principal component analysis (PCA). Four long-duration boro rice varieties were assessed in a Randomized Complete Block Design. Yield-boosting factors included panicle number (PN), panicle length (PL), filled grains (FG), and 1000-grain weight (TGW), while spikelet sterility (%) hindered yield. Positive correlations with grain yield were observed for biological yield (BY), harvest index (HI), straw yield (SY), PN, plant height (PH), and PL. Traits like PN, PL, FG, TGW, HI, total tiller numbers (TN), BY, SY, PH, days to 50% maturity (DF), and days to 80% maturity (DM) positively impacted yield. Conversely, spikelet sterility and unfilled grains had negative correlations. PCA demonstrated that the initial three PCs explained 100% of the variance. PC1 highlighted the significance of DF, DM, PH, TN, PN, FG, TGW, SY, BY, and HI. PC2 emphasized the importance of unfilled grains, while PC3 underscored spikelet sterility. These findings imply that grain yield is predominantly influenced by FG, PH, DM, DF, PN, TN, PL, SY, BY, and HI.

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These insights can guide future breeding for enhanced yield potential as well. BRRI dhan89 and BRRI dhan92 might be recommended as superior yield producing rice varieties for northern Bangladesh considering productivity.

Keywords: Biplot, Heatmap, High yielding variety, Principal component analysis, Rice

Introduction

Rice (*Oryza sativa* L.) stands as one of the most crucial cultivated cereal crops in the world and rice is serving as the primary staple food for over half of the world's population (USDA, 2020). Rice is grown in 165.25 million hectares worldwide (Statista., 2021). The people of Asia hold a dominant position regarding rice production as well as its consumption, amounting for nearly 90% of the world's rice production (Bandumula, 2018). World population as well as the population of Bangladesh increasing day by day and the land decreasing due to factors such as urbanization, industrialization, and housing for increased population. Therefore, ensuring food security and for promoting sustainable development of the global economy and society, rice production is a very important issue. Even as any disruption in its production could potentially lead to a standstill in various sectors worldwide. As a staple food, rice cultivation is widespread in Bangladesh across three distinct seasons: Aus (pre-monsoon rice), T. Aman (wet season rice as rain-fed with supplemental irrigation) and Boro (winter season irrigated rice). The total rice production in 2021-22 was 38.15 million tons, cultivated in 11.69 million hectares (BBS, 2022) and the share of Boro rice was 4.82 million hectares, yielding a production of 20.19 million tons and thus accounted for 58.37% of the total rice production (BBS, 2022). So, Boro rice varieties significantly influenced total rice production and hold considerable importance due to its contribution to overall rice production. The overall rice production trend is at increasing in Bangladesh and farmers tend to cultivate new and high yielding rice varieties. The choice of variety itself plays a crucial role in achieving higher yields in rice production. Variety, insect pest and other crop management practices affects yield (Rana et al., 2023; Roy et al., 2025; Roy et al., 2024a). Understanding the yield potential of specific high yielding varieties (HYVs) aids in the selection of the most suitable variety, thereby boosting yield productivity. High-yielding rice varieties can significantly contribute to increasing sustainable rice production. However, an extensive assessment of their yield performance, along with an understanding of the correlation coefficient among different traits influencing yield, is crucial for informed varietal selection and improved crop management practices. Considering various yield contributing parameter of rice notable disparities in yield were observed among genotypes, as well as between different environmental conditions and the interaction of genotypes with the environment (Moosavi et al., 2015). Traditional variety assessment relies mainly on univariate analyses of individual traits, which ignore interrelationships among traits and fail to capture the multidimensional nature of the cultivar's performance.

Principal component analysis (PCA) and cluster analysis are multivariate statistical techniques used to analyze data consisting of multiple inter-correlated quantitative variables, treating them as observations (Mahendran et al., 2015). PCA is utilized to identify similarities among variables and categorize genotypes, whereas cluster analysis is focused on categorizing unclassified materials. PCA further strengthens assessment by reducing complex, correlated datasets into a few independent components that explain most of the variability. PCA eliminates multi-collinearity, highlights dominant traits driving variation, and enables effective grouping of varieties based on overall performance. Together, correlation and PCA provide a holistic, robust framework for multi-trait varietal evaluation compared with traditional methods. The major strength of PCA lies in its capacity to quantitatively evaluate each dimension's significance in elucidating variations within a dataset (Shoba et al., 2019). Together, correlation and PCA provide a holistic, robust framework for multi-trait varietal evaluation compared with traditional methods. The present study was, therefore, carried out to assess the adaptability and potential of newly released long-duration boro rice varieties in terms of their yield and to analyze the relationships among yield and yield component traits by partitioning correlation coefficients and PCA analysis and guide the future breeding programs strategies.

Materials and Methods

Experimental site, design and materials

Field experiment was conducted at four locations (Figure 1) in Rangpur Division, Bangladesh during boro season of 2021-22 (from November 2021 to May 2022). The locations of the experiments viz.; BRRI regional station, Rangpur (25.695757, 89.268145); Mithapukur, Rangpur (25.530300, 89.187044); Kaunia, Rangpur (25.77997, 89.42874) and Sadar, Nilphamari (25.9199202, 88.8244434). The experimental site experienced a cold season (Maximum: 22-27 °C; minimum:11-16 °C and mean temperature:16-24°C) from the seedling to the maximum tillering stage, followed by alternating hot (Maximum: 29-31°C; minimum:18-23°C and mean temperature:24-27°C) and rainy season from booting to maturity stage (Table 1). The experiment was carried out using a Randomized Complete Block Design (RCBD) with two factors, comprising i) four rice varieties (i.e., BRRI dhan29, BRRI dhan58, BRRI dhan89 and BRRI dhan92) and ii) four locations with three replications. The field of each experimental plot was medium high land with loamy soil.

Table 1: Weather information of study area (collected from BRRI regional station Rangpur weather station)

Year	Month	Growth stage	Maximum temperature (°C)	Minimum temperature (°C)	Mean temperature (°C)	Rain fall (mm)	Relative Humidity %
2021	November	Seedling	27.54	16.04	21.79	0.00	68.72
2021	December	Seedling	24.61	13.39	19.00	0.13	69.53
2022	January	Active Tillering	22.28	11.44	16.86	0.24	78.84
2022	February	Active Tillering-Maximum Tillering	23.38	11.60	17.49	2.54	72.59
2022	March	Maximum tillering-Booting	30.95	18.39	24.67	0.00	66.24
2022	April	Heading to flowering	29.23	22.07	25.65	6.37	83.42
2022	May	Maturity	30.79	23.11	26.95	8.85	79.82

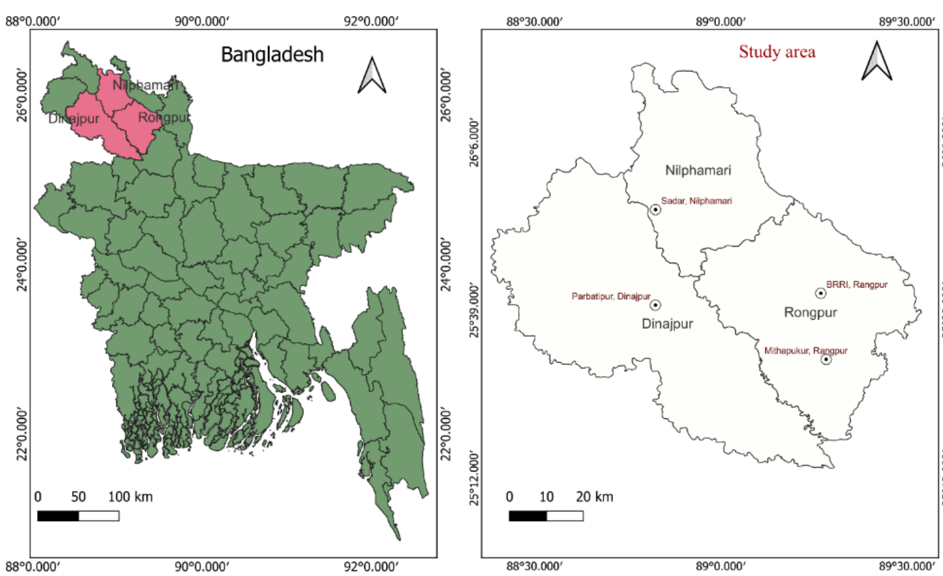

Fig. 1. Geographical position of studied locations

Agronomic management practices

The seeds were treated with 2.00 g of carbendazim 50WP (Bavistin 50 WP) per liter of water for a kg seeds to prevent seed and soil-borne diseases. Pre-germinated seeds were then sown in a wet seedbed at BRRI, Rangpur research field on 25 November 2021. Thirty-five-day-old seedlings were subsequently transplanted, with a single seedling hill^{-1}, in four different locations of Rangpur region as per recommendation (Badshah et al., 2023). The size of the single plot was (5m x 8 m) 40 m^2 and spacing was 20 cm x 20 cm. The experimental plot was fertilized uniformly with Nitrogen, Phosphorus, K_2O, Gypsum and Zinc sulfate @130, 50, 80, 45 and 2.0 kg ha^{-1} respectively. The entire amount of TSP, Gypsum, Zinc sulfate and two-third of potash were applied during the final land preparation. One third of urea fertilizer was applied as a basal dose at 10 days after transplanting (DAT). The remaining urea fertilizer was top dressed in two equal split doses at 25 DAT and 45 DAT respectively. On the other-hand the rest one third of muriate of potash fertilizer was applied during 3rd top dressing of urea at 45 DAT. Herbicide was used for the management of weeds (Pretilachlor i.e. Rifit 500 EC at the rate of 988 mL ha^{-1} as pre-emergence weedicide was used within 5 DAT). Besides this, hand weeding was performed using a "Khurpi" at 25 DAT for weed management. Irrigation was applied as per requirement (alternate wetting and drying: AWD method) until the rice reached soft dough stage. To prevent insect infestation, the Cartap+Fipronil (Suntap Plus 50WP) was applied at the rate of 750 g ha^{-1} at the heading stage of crops. Throughout the experiment, the fungal diseases were managed by applying Azoxystrobin+Difenoconazole (Amistar Top 325SC) at the rate of 500 mL ha^{-1}.

Data collection

After reaching physiological maturity, 20 m^2 of the area was harvested for the determination of yield and yield contributing parameters rom every plot of each location. Five hills were selected randomly in the middle portion of each experimental plot to record panicle length and the number of spikelets per panicle. Plant height, number of tillers and number of effective tillers were recorded from the 1.00 m^2 middle area (but outside of 20 m^2 area previously mentioned) of each experimental plot. The 1000 grain weight (collected from outside of 20 m^2 area), grain yield and straw yield (rice plant of one-meter square was collected by cutting around the baseline of plant and after fully sundried weight was taken) after harvesting. The biological yield and harvest index (%) were calculated by using the following formula:

Biological yield (t ha^{-1}) = Grain yield (t ha^{-1}) + Straw yield (t ha^{-1})

Harvest Index % = $\frac{Grain\ Yield}{Biological\ Yield}$x100

Statistical analysis

All data were subjected to statistical analysis separately by using analysis of variance technique using R software (versions 4.2.1, 2022). Analysis of variance (ANOVA) was performed by using “doebioresearch” package. The difference among treatment means was compared by using the Least Significant Difference (LSD) test at 5% probability levels. We used “ggplot2” and “metan” package to perform heatmap. Map was created by using “QGIS" software version 3.22.9. Correlation coefficient was analyzed by using “metan” package. The PCA was analyzed by “FactoMineR” and “factoextra” package and cluster analysis was by “FactoMineR”, “factoextra” and “cluster”.

Results and Discussion

Analysis of variance

The combine analysis of variance demonstrated on different yield and yield contributing traits were presented in Table 2. The results indicated that numerous characteristics, grain yield (GY), days to flowering (DF), days to maturity (DM), plant height (PH), tiller number (TN), panicle number (PN), filled grain (FG), unfilled grain (UFG), spikelet sterility percentage (SSp), panicle length (PL), thousand grain weight (TGW), straw yield (SY), biological yield (BY) and harvest index (HI) was played significant statistical differences among various rice genotypes. Conversely, when considering for different locations, all these parameters related to yield, exhibited significant disparities. These results underscore the unique influence of environmental factors on the expression of rice traits and the different genotypes responses to parameters affecting yield. Several studies have emphasized the substantial impact of genotype-environment interactions on rice yield and its associated attributes (Hairmansis et al., 2022; Ranjkesh and Talubaghi, 2022). Diverse genotypes exhibit distinct performances in different environments, displaying variations in agronomic traits and grain yield. The specific genotypes identified as excelling in particular environments (Shrestha et al., 2020). The present investigation aligns with the findings of (Islam et al., 2020), who observed significant influences of genotype-environment interactions on yield-related attributes such as panicle count, grain density per square meter, and 1000-grain weight. Recognizing and accounting for genotype-environment interactions it is pivotal in the selection and breeding of rice genotypes geared towards enhanced yield.

Table 2. Combined analysis of variance (ANOVA) of different yield and agronomic traits of four long duration rice varieties in four locations

Source of variation	df	Mean sum of squares													
		GY	DF	DM	PH	TN	PN	FG	UFG	SSp	PL	TGW	SY	BY	HI
Location	3	0.35***	36.25***	8.19***	7.77***	8.19***	8.19***	440.19***	108.5***	180.74***	2.235***	3.27***	0.13***	0.70***	1.15***
Genotypes	3	2.43***	172.25***	107.19***	94.56***	3.50**	6.69***	117.69***	276.50***	296.23***	13.45***	0.22***	0.73***	5.44***	6.04***
Genotypes × Location	9	0.26***	13.75***	8.52***	8.53***	1.83*	1.69*	208.02***	165.67***	177.72***	2.07***	0.43***	0.04***	0.43***	2.28***
Error	30	0.00558	0.1167	0.1167	0.2384	0.6875	0.6875	5.6167	5.6460	5.9381	0.0195	0.00629	0.0051	0.00911	0.1325
Total	47														

(Where, df-degree of freedom, GY-grain yield, DF-days to flowering (50%), DM- days to maturity (80%), PH-plant height, TN- total tiller numbers hill^{-1}, PN-panicle number hill^{-1}, FG-filled grains panicle^{-1}, UFG-unfilled grains panicle^{-1}, SSp-spikelet sterility percentage, PL-panicle length, TGW-1000 grain weight, SY-straw yield, BY-biological yield, and HI-harvest index)

Plant height (cm): The study revealed significant variations in plant height among the tested rice varieties (Table 2A). BRRI dhan92 exhibited the tallest plants, distinct from other varieties. Conversely, BRRI dhan29 displayed the shortest height. Plant height differs from variety to variety due to varietal character and environmental conditions (Roy et al., 2024).

Days to flowering (50%) and days to maturity (80%): Regarding flowering and maturity, BRRI dhan92 took the longest duration to reach 80% maturity, while BRRI dhan29 had the lengthiest flowering period (Table 2A). In contrast, BRRI dhan58 demonstrated the shortest durations for both flowering (50%) and maturity (80%). Days to flowering is influenced by varietal characteristics, and environmental conditions.

Number of tillers hill^{-1}**:** Total tiller number hill^{-1} and panicle number hill^{-1} especially, panicle number influenced yield potential. The trait, having a high number of panicle-bearing tillers is strongly linked to achieving a higher grain yield per plant. There was significant difference of total tiller number and panicle number among tested rice varieties (Table 2A). BRRI dhan89 stood out with the highest total tiller and panicle numbers, while the remaining varieties showed statistically similar total tiller numbers per hill. Varieties with higher effective tiller counts correspondingly yielded more. This variability in tiller numbers per hill can be attributed to specific varietal characteristics as reported by (Roy et al., 2022). Generally, rice plants having more tillers, can exhibit a higher inconsistency in mobilizing assimilates and nutrients among tillers resulting in variations in grain development and yield (Wang et al., 2016).

Panicle length: Panicle length emerged as another crucial trait influencing yield potential. BRRI dhan92 exhibited the longest panicle length, while BRRI dhan58 had the shortest. Table 2A indicates that panicle length is influenced by both variety and environmental factors. Though somewhat influential, panicle length should be considered in conjunction with panicle numbers, as both are pivotal yield components contributing to the final grain yield (Roy et al., 2024).

***Number of grains per panicle**:* There were statistically significant differences in number of grains (both filled and unfilled) panicle among tested rice varieties (Table 2A). BRRI dhan29 exhibited the highest filled spikelet count, while BRRI dhan58 had the lowest. Variations in grain filling may have occurred due to genetic, environmental or cultural management practices adopted (Roy et al., 2022). The highest number of unfilled spikelets found at BRRI dhan58 and lowest was observed at BRRI dhan89. The highest percent of sterile spikelet was observed at BRRI dhan58 which was statistically different from others. BRRI dhan92, BRRI dhan29 and BRRI dhan89 showed statistically similar spikelet sterility. Our present findings demonstrated 21-32% sterile grains which a varietal character and varied on management practice and environment (Rana et al., 2023). Rice produces 15-20% sterile grains (BRKB, 2016). Number of filled grains per panicles influenced significantly grain yield

1000-grain weight (g): The 1000-grain weight was found statistically significant among tested rice varieties (Table 2A). The highest 1000-grain weight was observed at BRRI dhan89 and lowest was at BRRI dhan58 and BRRI dhan92. So, the 1000-grain weight varied due to variety. Previous study of different rice varieties and found differences in weight of thousand grains due to morphological, environmental factor and varietal variation (Roy et al., 2022; Rana et al., 2023).

Yield: The highest yield was recorded at BRRI dhan89 which was statically differed from others but followed by BRRI dhan92. The result showed (Table 2A) that the lowest grain yield was found at BRRI dhan29. Therefore, variety which have higher effective tiller number per hill, higher panicle length, higher filled grains per panicle and 1000-grain weight also produced higher yields. Our findings also supported by the findings of (Roy et al., 2022) and (Dutta et al., 2002) who stated that grain yield differs from variety to variety due to genetic traits such as the number of effective tillers per hill, panicle length, filled grains per panicle and 1000 grain weight etc. Yield differences due to varieties were recorded by Islam et al., 2014 who reported variable grain yield among different varieties.

Straw Yield: Results from Table 2A it is noticed that straw yield showed significant variation among tested rice varieties. The highest straw yield was observed at BRRI dhan92, which was statistically significant to BRRI dhan89which might be due to their longest plant height and maximum tiller numbers. Roy et al., 2022 reported that rice variety which have long plant height, can produce more straw yield that can be used for fodder purposes. The lowest straw yield was found at BRRI dhan58 which was statistically significant to BRRI dhan29. So, it might be concluded that straw yield was affected by plant height and tiller number per hill of respective rice varieties.

Biological yield: Biological yield showed significant variation among tested rice varieties (Table 2A). Maximum biological yield was observed at BRRI dhan89 which was similar to BRRI dhan92. The lowest biological yield was observed at BRRI dhan29.

Harvest Index (HI): The harvest index (%) did not vary significantly among tested rice varieties and did not follow any regular trend (Table 2A). Numerically the highest HI was found at BRRI dhan89 (52.64%) and lowest was at BRRI dhan29 (51.06%) among the tested rice varieties. The trend of results was supported by Roy et al., 2022. So, the variety which has the highest yield, has the higher HI. The previous report stated that the highest grain yield of rice has contributed to the higher harvest index (Sarkar et al., 2021).

Table 2 A. Morpho-physiological characteristics of tested boro rice varieties

Genotype	PH (cm)	TN	PN	DF	DM	FG	UFG	SSp	TGW (g)	PL (cm)	GY (t $ha^{-1)}$	SY (t ha^{-1})	BY (t ha^{-1})	HI
BRRI dhan29	101.88 d	12.50 b	11.75 c	137.75 a	162.50 b	124.75 a	27.75 bc	22.56 b	24.10 b	24.125 b	6.97 d	6.678 b	13.64 c	51.06 d
BRRI dhan58	104.08 c	12.75 b	11.27 bc	129.50 c	156.75 d	117.25 a	37.00 a	32.55 a	24.00 c	22.575 d	7.13 c	6.633 b	13.83 b	51.57 c
BRRI dhan89	106.18 b	13.75 a	13.50 a	136.75 b	161.50 c	122.00 b	26.25 c	21.85 b	24.30 a	23.95 c	7.86 a	7.06 a	14.92 a	52.65 a
BRRI dhan92	108.42 a	13.00 b	12.75 b	136.50 b	163.50 b	122.25 b	29.00 b	23.84 b	24.03 c	25.15 a	7.78 b	7.098 a	14.88 a	52.27 b
Levels of significance	**	***	***	***	***	***	***	***	***	***	***	***	***	***
$LSD_{0.05}$	0.41	0.69	0.69	0.28	0.28	3.95	1.98	2.03	0.07	0.12	0.12	0.06	0.08	0.30
CV	0.46	6.38	6.60	0.25	0.21	1.95	7.92	9.67	0.33	0.58	1.01	1.04	0.67	0.70

Table 2 B. Morpho-physiological characteristic of boro rice varieties at different locations

Location	GY t ha^{-1}	DF	DM	PH cm	TN	PN	FG	UFG	SSp	PL cm	TGW g	SY t ha^{-1}	BY t ha^{-1}	HI
L1	7.47b	135 c	161.25 b	105.05 c	12.25 c	12.0 b	125 a	28.25 b	22.60 b	24.3 a	24.75 a	6.89 b	14.36 b	52.01 a
L2	7.19 c	136.75 a	162 a	105.88 a	12.25 c	11.75 b	112.75 c	34.50 a	30.93 a	23.35 c	23.48 d	6.72 c	13.97 c	51.42 b
L3	7.58 a	136 b	161 b	105.59 a	13.25 b	13.0 a	126 a	28.50 b	22.89 b	24.225 a	24.05 c	6.97 a	14.54 a	52.09 a
L4	7.50 b	132.7 d	160 c	104.05 b	14.25 a	13.5 a	122.5 b	28.75 b	24.30 b	23.93 b	24.15 b	6.90 b	14.40 b	52.02 a
Levels of significance	***	***	***	***	***	***	***	***	***	***	***	***	***	***
$LSD_{0.05}$	0.06	0.29	0.29	0.47	0.69	0.69	1.98	1.98	2.03	0.11	0.00	0.06	0.08	0.30
CV	1.01	0.25	0.21	0.46	6.38	6.60	1.96	7.92	9.67	0.58	0.33	1.04	0.67	0.70

(Where, df-degree of freedom, GY-grain yield, DF-days to flowering (50%), DM-days to maturity (80%), PH-plant height, TN- total tiller numbers hill^{-1}, PN-panicle number hill^{-1}, FG-filled grains panicle^{-1}, UFG-unfilled grains panicle^{-1}, SSp-spikelet sterility percentage, PL-panicle length, TGW-1000 grain weight, SY-straw yield, BY-biological yield, and HI-harvest index; L_1=Kaunia, Rangpur; L_2= Mithapukur, Rangpur; L_3=Sadar, Nilphamari; L_4=BRRI, Rangpur)

Multi-locational yield and yield contributing characters: The longest plant height was found at Mithapukur, Rangpur in case of BRRI dhan92. BRRI dhan89 and BRRI dhan58 showed the longest plant height at Nilphamri (Sadar) and BRRI dhan29 at Kaunia, Rangpur. The maximum number of tillers was found at BRRI, Rangpur for BRRI dhan29, BRRI dhan58, and BRRI dhan89, and Nilphamari (Sadar) for BRRI dhan92. Maximum number of panicles was found at BRRI Rangpur for BRRI dhan89 and BRRI dhan58 and others two varieties produces more or less same number of tillers for all four locations (Figure 2). The highest number of filled grains was produced by BRRI dhan58 at Kaunia, Rangpur may be due to produced lowest number of tillers. That may be because of lower tiller can assimilate shrank and sink to the grain due to lower competition of nutrient uptake, and that's reduced the unfilled grains. BRRI dhan29 and BRRI dhan92 produced highest number of filled grains at, Sadar, Nilphamari and BRRI dhan89 at BRRI, Rangpur. Highest number of unfilled grains was found at BRRI dhan58 at BRRI, Rangpur also lowest number produced here at BRRI dhan89. BRRI dhan89 and BRRI dhan92 produced highest unfilled grain at Nilphamari (Sadar) and Mithapukur, Rangpur, respectively. The longest panicle length was observed at BRRI dhan92 at Sadar, Nilphamari and in case of BRRI dhan89 at Kaunia, Rangpur. TGW was found highest in Kaunia, Rangpur for all tested rice varieties. The highest percent of HI was found at BRRI, Rangpur location for all tested rice varieties except BRRI dhan58. The highest HI was found at Kaunia, Rangpur for BRRI dhan58. Among four locations, the highest yield (t ha^{-1}) was found at BRRI, Rangpur for BRRI dhan89. For BRRI dhan92 at Sadar, Nilphamari and BRRI dhan58 at Kaunia, Rangpur. The highest yield was found at BRRI, Rangpur for BRRI dhan89 and Sadar, Nilphamari for rest rice varieties. Significantly highest yield was demonstrated at Sadar, Nilphamari which is followed by BRRI, Rangpur. It may be due to highest TN, PN, FG and PL produced these locations. Yield and yield contributing characters varied significantly (Table 2) variety to variety and location to location due to varietal characters, soil and environment.

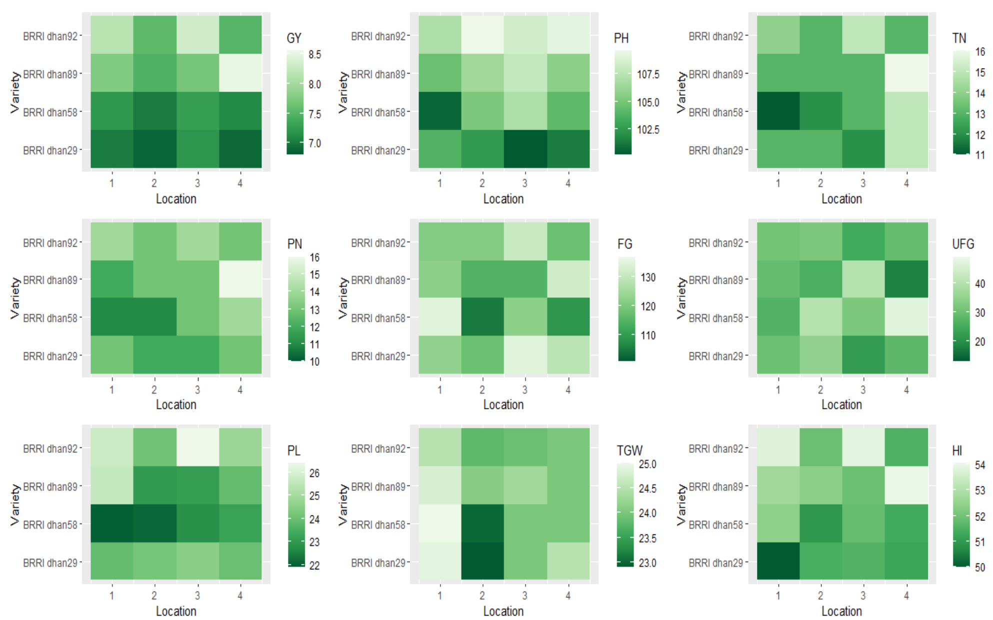

Fig. 2. Heatmap of multi-locational yield and yield contributing parameters

(Where, L_1=Kaunia, Rangpur; L_2= Mithapukur, Rangpur; L_3=Sadar, Nilphamari; L_4=BRRI, Rangpur; PH-plant height, TN- total tiller numbers $hill^{-1}$, PN-panicle number $hill^{-1}$, FG-filled grains $panicle^{-1}$, UFG-unfilled grains $panicle^{-1}$, PL-panicle length, TGW-1000 grain weight, and HI-harvest index)

Correlation between yield and yield components:

Biological yield showed very high positive and significant association with yield followed by HI, SY. The yield exhibited a moderately significant positive correlation with PN, PH, and PL. Conversely, it showed a non-significant positive correlation with FG, TN, DM, DF, and TGW. But, sterile spikelet and number of unfilled grains per hill exhibited a negative significant association with yield (Figure 3). So, for developing a yield improvement breeding protocol these yield influencing traits should be taken under consideration. Selecting for enhancement of certain traits linked to yield can lead to simultaneous changes in correlated characters. Our research findings were also supported by several researchers on different characters viz., the association of grain yield with number of FG (Moosavi et al., 2015; Yesmin et al., 2022) TGW, DF, TN, BY and HI (Mandal et al., 2023; Rahman et al., 2012).

Correlation between characters:

The study examined correlation coefficients among thirteen yield-related traits across four locations and four long-duration rice varieties. Days to maturity (DM) was highly correlated with DF (0.92) and PL (0.72) and non-significant positive association with other traits except percent HI, TGW, TN, PN, percent spikelet sterility and UFG where, they were showed negative correlation with DM. Our finding supported by (Rahman et al., 2012; Roy et al., 2024). DF showed significant positive correlation with PL (0.61) and non-significant positive correlations with SY, PH and FG, whereas BY, HI, TGW, TN, PN, SSP, and UFG exhibited negative, non-significant associations with DF. This contrasts with (Kayastha et al., 2022) findings, which showed positive correlations between TN and PN with DF. Plant height (PH) was found significantly positive association with SY (0.69) and BY (0.60) while non-significant positive association with other traits except TGW and FG were found non-significant negative correlation.

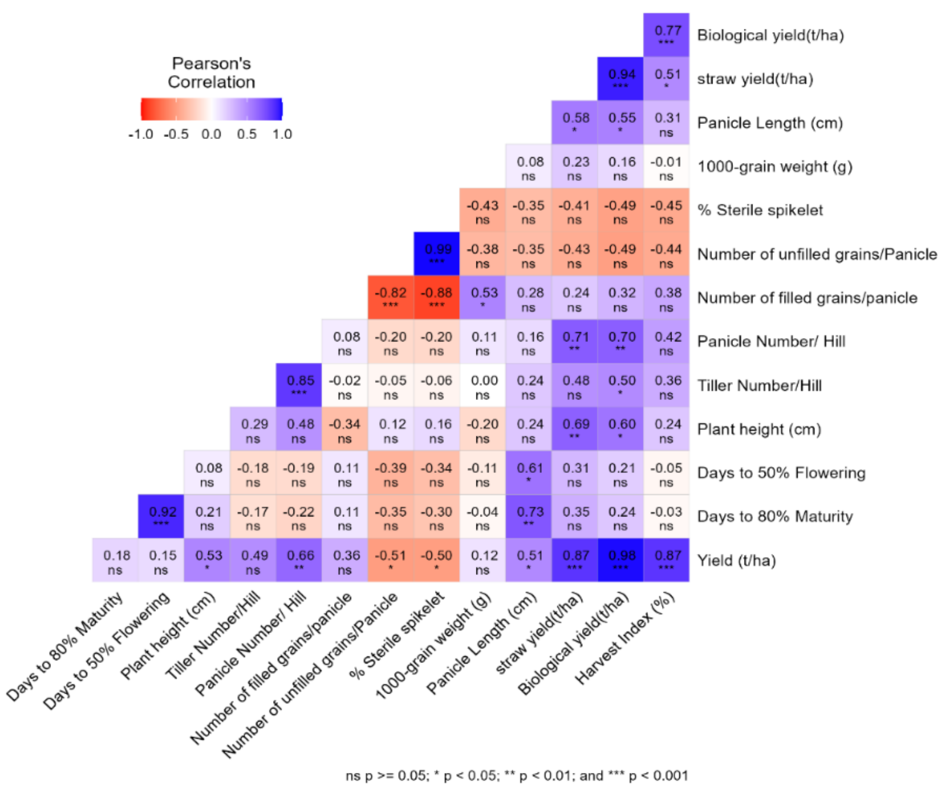

Fig. 3. Correlation between yield and yield components

TN exhibited positive significant correlation with biological yield (0.50) and non-significant positive association with SY, HI, PL and PN. There was no correlation of TN with TGW and negative non-significant correlation was observed in UFG and percent sterile spikelet. PN demonstrated highly positive significant correlation with TN (0.85), SY (0.71) and BY (0.70) while non-significant correlation was observed with others traits except FG, percent spikelet sterility and UFG. Similar findings also observed by (Roy et al., 2024). There was positive significant association between FG and TGW (0.53) and non-significant correlation (Figure 3) with HI, BY, PL and SY. FG was highly negative and significantly correlated with UFG (-0.82) and percent spikelet sterility (-0.88), previously demonstrated by (Roy et al., 2024). It might be concluded that, if FG increase, the number of UFG and percent spikelet sterility decrease and thus increase grain yield. UFG showed very high positive and significant correlation with percent spikelet sterility. So, spikelet sterility increased by increased UFG. UFG and percent sterile spikelet had non-significant and negative correlations with TGW, PL, SY, BY and HI. Other-hands, PL showed significantly positive association with SY and BI. SY and BY exhibited a significant association with PL, while BY also had a high positive significant association with HI.

Scree plot

The scree plot visually represents the distribution of explained variance associated with each principal component generated by plotting the percentage of explained variances and principal components numbers. Notably, PC1 demonstrated a significant variability of 58.8% with an eigenvalue of 8.228 (Table 3). Subsequently, the variability gradually diminished in subsequent components (Figure 4). (Roy et al., 2024; Umadevi et al., 2019) also reported the analysis revealed PC1 to exhibit the highest variability, supported by an eigenvalue surpassing 1. The visual representation distinctly illustrates that PC1 manifests the highest variation compared to other principal components. Thus, opting for selections from PC1 proves to be advantageous. The principal components with multiple eigenvalues signify amplified diversity within the rice genotypes, rendering them excellent contenders for the selection of diverse parental lines. These findings align with those of a previous study conducted by (Roy et al., 2024; Shoba et al., 2019).

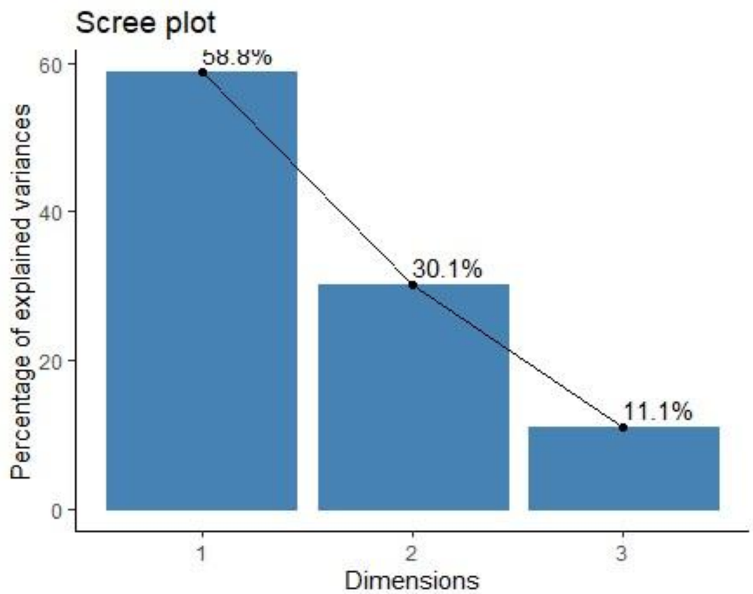

Fig. 4. Scree plot showing percentage of explained variances

Principal component analysis (PCA)

Various morphological traits contribute to the overall variance computed for each component. The first PCA explained over 70% of the total variance, with positive notable contribution observed by grain yield (0.890), DF (0.710), DM (0.731), PH (0.663), TN (0.770), PN (0.788), FG (0.495), TGW (0.651), SY (0.952), BY (0.919) and SSP (-0.793) (Table 3). Furthermore, PC2 the subsequent principal component, exhibited an eigenvalue of 4.22, contributing to the explanation of 30.14% of the overall identified yield component variables i.e., UFG (0.541), SSP (0.576), SY (0.571), HI (0.718) but FG (-0.868) displayed negative contributions. Additionally, the third principal component PC3, had an eigenvalue 1.553 and contributed 11.89% of the total variance related to TGW (-0.759) which was negatively contributed.

Table 3. Contributions of principal component (PC) of 14 traits for 4 long duration rice varieties

Traits	Principal components		
	PC1	PC2	PC3
GY	0.890	0.442	0.116
DF	0.710	-0.703	-0.043
DM	0.731	-0.623	0.279

Traits	Principal components		
	PC1	PC2	PC3
PH	0.663	0.545	0.512
TN	0.770	0.499	-0.397
PN	0.788	0.574	-0.223
FG	0.495	-0.868	-0.037
UFG	-0.813	0.541	0.215
SSP	-0.793	0.576	0.199
PL	0.741	-0.446	0.502
TGW	0.651	-0.018	-0.759
SY	0.952	0.209	0.224
BY	0.919	0.362	0.155
HI	0.696	0.718	-0.024
% Variance	58.77	30.14	11.089
Cumulative % of variance	58.77	88.911	100
Eigenvalues	8.228	4.220	1.553

The first, second, and third principal components are associated with variables related to phenology, yield, yield attributes, and grain characteristics. These findings align with similar patterns observed in previous studies by (Dhakal et al., 2020; Roy et al., 2024; Sanni et al., 2012; Umadevi et al., 2019). In the PCA, the initial three components encapsulate 100% of the variability. Each of these components exhibits eigenvalues surpassing one, encompassing the entire genotypic diversity across all fourteen traits evaluated. The first three principal components often play a crucial role in illustrating the patterns of variation among accessions and the traits linked to these components prove to be particularly valuable in discerning differences between accessions reported by (Guei, 2005; Roy et al., 2024; Sanni et al., 2012). From the factors considered, including PH, TN, PN, FG, PL, and TGW can be inferred that the most significant contribution to the observed variability can be strategically used in selecting parent lines for breeding initiatives. Traits that consistently appear across different principal components, thereby explaining the variance, demonstrate a tendency to co-occur.

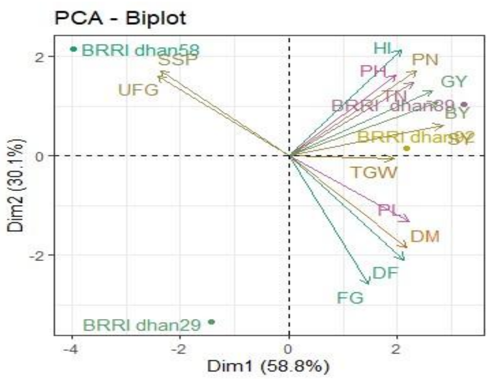

Fig. 5A. PCA-biplot based on principal component analysis of fourteen traits

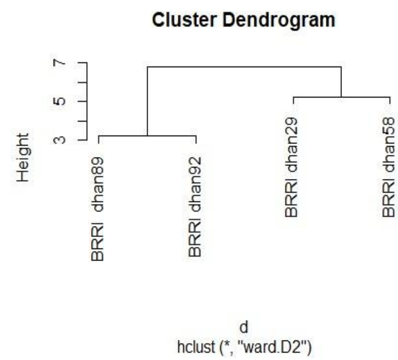

Fig. 5B. cluster plot based on principal component analysis

(Where, GY=grain yield (t ha^{-1}), PH=plant height (cm), TN=tiller number hill^{-1}, PN=panicle number hill^{-1}, FG=filled grain panicle^{-1}, HI=harvest index, PL=panicle length, BY=biological yield, StSp= spikelet sterility percentage)

These aspects should be taken into consideration when incorporating these traits into the breeding program, aligning with similar findings by previous studies (Chakravorty, 2013; Dhakal et al., 2020; Roy et al., 2024). Performing hierarchical clustering analysis, which has played a pivotal role in prediction and discerning three distinct groups, each reflective of specific growing conditions. To facilitate a straightforward interpretation and prediction, genetic traits were additionally grouped into four distinct categories (Figure 5B). To deepen our comprehension of the associations between these genotypes and their interconnected attributes, they were further elucidated through a PCA biplot (Figure 5A). BRRI dhan29 and BRRI dhan58 in cluster1 and established based on traits SSP, UFG. The second cluster (BRRI dhan89 and BRRI dhan92) established based on FG, DF, HI, GY, PN, TN, BY, PH, SY, DM, PL and TGW. Among all tested genotypes BRRI dhan92 demonstrate greater stability due to proximity to PC=0 followed by BRRI dhan89 and BRRI dhan29. Inference from PC1 and PC2 suggests that FG, PH, DM, DF, PN, TN, PL, SY, BY, and HI significantly contribute to grain yield. These traits play a substantial role in the overall variability seen in the genotypes, highlighting their importance in future breeding initiatives.

Conclusion

The analysis of yield contributing characteristics in tested long duration boro rice varieties indicated that yield increased with the number of effective tillers per hill, PL, FG, TGW and lower percent of spikelet sterility (SSP) The correlation studies result indicated that grain yield had a significant positive correlation with BY, HI, SY, TN, PH, and PL. Moreover, BY, HI, SY, TN, PH, PL PN, TGW, FG, DF, and

DM exhibited positive and direct effect on yield. While SSP and UFG had significant and negative correlation with grain yield. Results showed that BRRI dhan89 and BRRI dhan92 had better yield potential. Yield potential of BRRI dhan58 and BRRI dhan29 were moderate. PC analysis underscores the significance of PC1, the role of key traits in explaining genotypic variability, and the potential for strategic genotype selection in rice breeding programs. Further research is needed to explore additional factors including weather variable influencing rice yield and to validate the results in broader geographical contexts.

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