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Genetic variation for agronomic and floral traits in prospective maintainer and restorer lines selected from coastal rice collections in Bangladesh

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ABSTRACT

The identification of stable maintainer and restorer lines strengthens sustainable hybrid rice technology to increase its production and support the self-sufficiency of food in Bangladesh. Experiments were conducted to assess the genetic variation among 47 prospective maintainer and restorer lines selected from coastal rice collections in the Genetics and Plant Breeding experimental field and laboratory of Gazipur Agricultural University, Gazipur during 2021-2023. Most of the Agronomic and floral traits were significantly ($P<0.001$) varied. The phenotypic coefficient of variation - was very close to the genotypic coefficient of variation - for almost half of the studied traits, indicating a moderate influence of the environment. High heritability (h^2b) combined with high genetic advance as percent of mean (GAM %) suggests the presence of additive gene effects that influence the traits observed. Principal Component Analysis - and a scree plot showed that the first six components of the traits accounted for 83.29% of the total variation. Grain yield/hill (g) was significantly positively correlated with flowering, maturity, and panicle-related traits, including 1000-grain weight, gain length, and grain breadth, as observed through correlation and biplot analyses, but a negative relationship was also exhibited with some traits. The UPGMA dendrogram grouped the genotypes into six clusters, where L003 and L083 each occupied a single cluster. Based on agronomic and floral traits, the prospective maintainers viz.L006, L013, L019, L025, L038, - and restorers viz. L001, L004, L015, L033, L037, L038, L058, L062, L065, L067, L099 seemed to hold significant potential for future breeding programs for the development of hybrid rice adaptive to coastal regions of Bangladesh.

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Introduction

Rice (*Oryza sativa* L.), the nutrition enriched cereal crop is the pre-eminent staple food consumed by half the world's population. This self-pollinated cereal crop belongs to the Poaceae family, with a chromosome number of 2n=24 (Sarma et al, 2021). Domesticated rice encircles two species of food crops, *Oryza sativa* and *Oryza glaberrima* of food crops. This cereal has impersonated the culture, diet, and economies of millions of people worldwide. Almost 60% of the world's population lives in Asia, and over 90% of the total rice produced and ingested in Asia (Pallavi, 2018). Rice is the premier cereal crop in Bangladesh and has plentiful diversified landraces since it plays a valuable role in the culture, livelihood, and socioeconomic status of the people (Ahmed *et al.*, 2016). The world population is increasing daily and is anticipated to continue growing; in 2050, it will reach 9 billion. Globally, rice is cultivated globally across 163.24 million hectares, resulting in a total production of 740.95 million tons (FAO, 2016). By the end of this century, Bangladesh's population is foretold to reach 249.3 million and thus need to feed 215.4 million people by 2050. Meeting the food requirements of this ever-growing population necessitates substantial progress in the total rice production (Kabir et al., 2015).

Soil salinity, a major constraint in Bangladesh, increases during the dry season and decreases during the monsoon season. Land use changes throughout the year, depending on the season and location. Due to its high salt content, the coastal region is ineffective in winter. During the rainy season, farmers primarily cultivate 'Aman' rice using traditional varieties that can endure salinity, but produce low yields. Furthermore, salinity imposes significant nutrient deficiencies, particularly in nitrogen (N) and phosphorus (P). Micronutrients such as copper (Cu) and zinc (Zn) are also limited in saline soils, resulting in a considerable decrease in crop yields (Shelley et al., 2016). Salinity stress reduces crop yield, restricts plant growth, and limits land use. As the world's population grows rapidly, agricultural land is decreasing owing to industrialization and habitat loss (Safdar *et al.*, 2019). Therefore, the development of salt-tolerant varieties or hybrid varieties is a key strategy to utilize salt-affected land and meet food demands. Tolerance to salt is a polygenic trait influenced by both genetic and environmental factors, which leads to a spectrum of variations in plant responses to salinity stress (Al-Ashkar *et al.*, 2020).

Coastal areas of Bangladesh are renowned for a remarkable array of rice genotypes that thrive there, each uniquely adapted to the region's challenging environment. The development of hybrid varieties through the line method (A, B, and R line) using these coastal landraces would certainly sustain the technology there. These diverse rice genotypes were collected and meticulously analyzed through a series of experiments year after year to identify maintainers (B line) and restorer lines (R line) after crossing with cytoplasmic male sterile lines (A line) for superior hybrids aimed at enhancing agricultural productivity and resilience. In this study, 47 rice genotypes that were previously tested with sterile lines were selected and are now referred to as prospective maintainers and restorer lines.

This study aimed to estimate the agronomic and floral trait variation and diversity among these 47 rice genotypes to select the most suitable diverged parents for future breeding programs aimed at developing suitable hybrid rice varieties in the saline prone areas of Bangladesh.

Materials and methods

Climate and Soil Condition

This experiment was conducted in the research field of the Department of Genetics and Plant Breeding, Gazipur Agricultural University, during the Aman season of 2021. The research field was situated in the middle of the Madhupur Tract (24° 05′ N, 90° 25′ E) within the tropical climatic zone. Heavy rainfall occurs from May to September, with minimal rainfall for the remainder of the year. The region experiences an average annual rainfall of approximately 210 cm, with most falling between July and October. Summer is characterized by high temperatures, humidity, and occasional strong winds. The soil type falls under the Shallow Red Brown Terrace category of the Salna Series in Madhupur Tract (Alam et al., 1993) of Agro Ecological Zone (AEZ) 28 in which silty clay soil with pH value of 3.96 to 5.11 is defined by Ratul et al. (2021).

Experimental Materials

Approximately 100 rice genotypes were previously collected (in 2010) and tested (in 2019 and 2020) against four (IR58A, IR62A, IR68A, and GAN46A) male sterile lines and then 47 lines were selected (Table 1) according to Virmani et al. (1997) which are now called prospective maintainers (B) (17 in numbers) and restorer lines (R) (30 in numbers). The genotypes, that is, germplasm seeds, were stored at the Department of Genetics and Plant Breeding, BSMRAU, and were used as treatments for the experiment. Details of the germplasm are presented in **Table 1**. They were grown in the GPB field during the 2022 T Aman season using standard procedures and protocols to record their agronomic and floral traits.

Table 1. List of the local rice germplasms collected from coastal regions of Bangladesh

Sl. No.	Genotypes	Local Name	Collection Site	Sl. No.	Genotypes	Local Name	Collection Site
1	L1.1	Black tip grain	Cox’s Bazar	25	L038	Gopal bogh**	Bagerhat
2	L001	Alem boro	Cox’s Bazar	26	L041	Hobori maloti	Bagerhat
3	L003	Swarna lata	Cox’s Bazar	27	L046	Kalo mota	Bagerhat
4	L004*	Kalan pajam	Cox’s Bazar	28	L051	Mukta	Bagerhat
5	L006	Nona Khorchi	Khulna	29	L058	Motha mota	Patuakhali

Sl. No.	Genotypes	Local Name	Collection Site	Sl. No.	Genotypes	Local Name	Collection Site
6	L007	2 3 Dhan	Khulna	30	L059	Dinga moni	Patuakhali
7	L008	Khejur chori	Khulna	31	L062	Girmi	Patuakhali
8	L009	Hogla fata	Khulna	32	L063	Chengai	Patuakhali
9	L010	Chini kanai	Khulna	33	L064	Kajol sail	Patuakhali
10	L011	Benapol (brown)	Khulna	34	L065	Kala kora	Patuakhali
11	L013*	Jota balam	Khulna	35	L067	Moulata	Patuakhali
12	L014	Moris shail	Khulna	36	L069	Ghecoach mota	Patuakhali
13	L015	Badsha bogh	Khulna	37	L070**	Kala khora	Patuakhali
14	L017	Chikon Mota	Khulna	38	L071	Kuti aughu rini	Patuakhali
15	L018	Chikondhan(long)	Bagerhat	39	L074	Hailtakala mota	Patuakhali
16	L019	Chikon dhan	Cox's Bazar	40	L076	Tepu dhan	Patuakhali
17	L021	Baish bota	Khulna	41	L081	Gobindo bogh	Cox's Bazar
18	L024	Kalo jira	Khulna	42	L082	Kalam pajam	Cox's Bazar
19	L025	Birani	Khulna	43	L091	Gheecoach aman	Feni
20	L033	Sada mota (brown furrows)	Bagerhat	44	L093	Agon hail	Feni
21	L034	Lal mota (red)	Bagerhat	45	L094	Bajal	Feni
22	L035	Lal mota (reddish light purple)	Bagerhat	46	L096	Kali biraji	Feni
23	L036	Lokma	Bagerhat	47	L099	Reddishpanicle (long plant)	-
24	L037	Paspair	Bagerhat				

Red and green color = Maintainer lines, Black color = Restorer lines.

Data Collection

Data were recorded on days to first flowering, days to 50% flowering (when 50% of the plants in the plot reached heading), days to maturity, plant height (cm), number of tillers/plants, number of effective tillers/plants, flag leaf length (cm), flag leaf breadth (cm), flag leaf angle (^{o}), total panicle length (cm), panicle length (cm), panicle exertion rate (%), filled spikelet/plant, unfilled spikelet/plant, total spikelet/plant, outcrossing rate (%), grain length (mm), grain breadth (mm), thousand-grain weight (g), and grain yield/hill (g).

Statistical Analysis of Data

Preliminary statistical analysis of the data was conducted following standard texts and procedures (Snedecor and Cochran, 1967; Clark, 1973). Analysis of variance (ANOVA) and biplot analysis were performed using IRRI PB tools software. Descriptive statistics were analyzed using the Statistical Tool for Agricultural Research (STAR). Error variances (σ^2e), genotypic variance (σ^2g), and phenotypic variance (σ^2p) were enumerated from the expected mean squares of the analysis of variance using the formula suggested by Carena et al. (2010). PCV and GCV values were categorized as low, moderate, and high, as indicated by Sivasubramanian and Menon (1973) as follows: 0-10% = low, 10-20% = moderate, and >20% = high. Heritability in Broad Sense was categorized as low (0-30%), moderate (30-60%), and high (>60), as indicated by Robinson et al. (1949). Genetic advance (GA) and genetic advance as a percentage of mean (GAM) were calculated as described by Johnson et al. (1955). The simple correlation between grain yield per hill and other yield components and floral traits was estimated following the procedure outlined by Khan et al. (2018). Principal component, cluster, and dendrogram analyses were performed using MINITAB® 17 with all observed data.

Results and discussion

ANOVA for Agronomic and floral Traits

The results of the analysis of variance (ANOVA) of the quantitative traits of the tested genotypes are presented in **Table 2**. The mean sum of squares of genotypes was highly significant at P<0.001 for all traits except the number of total tillers/plant. These significant differences revealed that there was considerable variation among the genotypes for the studied traits.

The results were corroborated by the findings of Anis et al. (2016), who found highly significant variation in their experiment for several traits such as duration (day), plant height (cm), number of panicles per plant, panicle length (cm), number of filled grains/panicles, and grain yield (kg/m2). Similarly, Rashmi et al. (2017) and Sravan et al. (2016) claimed that days to 50% flowering, number of productive tillers/plant, number of chaffy grains/panicles, and thousand grain weight (g) also showed significant variation.

General Variability Parameters of Phenotypic Traits

The coefficient of variation ranged from 1.86 to 82.65% for all traits among the populations. A high CV (%) was observed for the unfilled spikelet/plant (82.65%), followed by the total spikelet/plant (39.53%), filled spikelet/plant (38.69%), number of effective tillers/plants (28.93%), grain yield/plants (28.67%), and number of tillers/plants (28.65%). A low CV (%) was observed for days to 50% flowering (1.86%), followed by days to maturity (2.09%), days to first flowering (2.26%), panicle exertion rate (%) (3.22%), and grain length (3.91%).

Devi et al. (2016) reported that the highest range of mean variation was observed in the number of filled grains/panicles and effective tillers. Afsana et al. (2020) also reported a wide range of traits such as effective tillers/hill, panicle length, filled grain/panicle, and 1000-grain weight. Similar results were reported by Iqbal et al. (2018).

Table 2. Descriptive statistics, ANOVA and general variability of twenty agronomic and floral traits in forty-seven coastal rice genotypes

Characters	Range	Mean ± SE	SD	CV (%)	Significant level
DFF	44 - 101	74.44±1.37	12.24	2.26	***
DPF	46 - 109.33	86.11±1.31	14.32	1.86	***
DTM	88 - 137.67	123.64±2.11	12	2.09	***
PHT	116.5 - 217	176.16±7.58	19.66	5.27	***
NTP	6.33 - 22	12.65±2.96	2.85	28.65	**
NEP	5.33 - 18	10.02±2.37	2.52	28.93	***
FLL	56.93 - 91	75.45±4.69	7.65	7.62	***
FLB	0.8 - 1.77	1.25±0.1016	0.22	9.94	***
FLA	11 - 26.33	18.02±3.24	4.07	22.05	***
EPL	17.67 - 29.67	25.44±1.36	2.4	6.53	***
TPL	21.37 - 29.67	25.98±1.32	1.93	6.24	***
PER	74.63 - 100	97.88±2.57	4.63	3.22	***
FSP	550.33 - 4377.6	1315.54±415.61	622.68	38.69	***
USP	72.33 - 939.33	260.19±175.58	186.85	82.65	***
TSP	646.33 - 5144.4	1575.73±508.61	725.88	39.53	***
OCR	60.65 - 94.15	84.21±6.78	7.69	9.86	***
GLT	5.82 - 9.96	8.13±0.2595	0.97	3.91	***
GBT	1.67 - 3.6	2.89±0.1534	0.52	6.51	***
TGW	8.71 - 37.34	26.98±1.00	7.38	4.55	***
GYH	10.64 - 58.69	34±7.96	12.3	28.67	***

** and *** are significant at 1% and 0.1% level of probability.

Genotypic and Phenotypic Coefficients of Variation

A high GCV was observed (**Table 3**) for the number of unfilled spikelets/plants (65.73), number of filled spikelets/plants (51.11), total spikelet/plant (49.01), grain yield/hill (g) (39.38), thousand-grain weight (g) (33.34), number of effective tillers/plants (23.04), flag leaf angles (°) (22.83), grain breadth (mm) (21.77), days to 50% flowering (20.32), flag leaf breadth (cm) (20.11), and days to first flowering (20.07). Moderate values were recorded for the number of tillers per plant (18.66), grain length (mm) (14.35), plant height (cm) (13.15), days to maturity (11.80), flag leaf length (cm) (11.18), and panicle length (cm) (10.59). The remaining traits, such as outcrossing rate (%) (8.75), total panicle length (cm) (7.98), and panicle exertion rate (%) (5.33), showed a low genotypic coefficient of variation.

A high PCV was observed (**Table 3**) for unfilled spikelets/plants (105.60), filled spikelet/plant (64.10), total spikelet/plant (62.96), grain yield/hill (g) (48.71), number of effective tillers/plants (36.99), number of tillers/plants (34.20), thousand-grain weight (g) (33.65), flag leaf angle (°) (31.74), grain breadth (mm) (22.72), flag leaf breadth (cm) (22.44), days to 50% flowering (20.41), and days to first flowering (20.20). In contrast, moderate values were observed for grain length (mm) (14.88), plant height (cm) (14.17), flag leaf length (cm) (13.53), outcrossing rate (%) (13.18), panicle length (cm) (12.44), days to maturity (11.98), and total panicle length (cm); (10.13). The remaining trait, the panicle exertion rate (6.23%) () showed a lower phenotypic coefficient of variation.

PCV was found much higher from the GCV of the characters unfilled spikelet/plant (105.60 > 65.73), number of tiller/plant (34.20>18.66), number of effective tiller/plant (36.99>23.04), filled spikelet/plant (64.10>51.11), total spikelet/plant (62.96>49.01), grain yield/hill (g) (48.71>39.38), flag leaf angle (o) (31.74>22.83), outcrossing rate (%) (13.18>8.75). **Table 3** shows the higher influence of the environment and the low genetic contributions. However, Dey *et al.* (2019) found that flag leaf area, effective tillers per plant, filled grains per panicle and 100 grain weight exhibited moderate to high estimates of PCV and GCV, indicating that these traits are primarily governed by genetic factors and are minimally influenced by environment.

The percent genotypic and phenotypic coefficient of variation (GCV and PCV) for days to first flowering (20.07 and 20.20), days to 50% flowering (20.32 and 20.41), days to maturity (11.80 and 11.98), plant height (cm) (13.15 and 14.17), flag leaf length (cm) (11.18 and 13.53), flag leaf breadth (cm) (20.11 and 22.44), panicle length (cm) (10.59 and 12.44), total panicle length (cm) (7.98 and 10.13), grain length (mm) (14.35 and 14.88), grain breadth (mm) (21.77 and 22.72), thousand grain weight (g) (33.34 and 33.65), and panicle exertion rate (%) (5.33 and 6.23) were very close to each other.

The difference between PCV and GCV was found to be smaller for the traits like day to 50% flowering plant height, yield per plant, kernel length, kernel width, 1000-grain weight, and grain yield per plant (Dhurai et al., 2014). Devi et al. (2016) reported that higher estimates of PCV and GCV were observed for yield per plant and filled seeds per panicle, and the lowest estimates were recorded for kernel width and flag leaf width.

Table 3 indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these

Table 3. Genetic parameters of twenty agronomic and floral traits in forty-seven coastal rice genotypes

Parameters Characters	GV (ʒ^{2}g)	PV(ʒ^{2}p)	GCV (%)	PCV (%)	h^{2}b	GA	GAM (%)
DFF	223.23	226.06	20.07	20.20	98.75	30.63	41.15
DPF	306.25	308.80	20.32	20.41	99.17	35.95	41.75
DTM	212.76	219.44	11.80	11.98	96.95	29.63	23.96
PHT	536.43	622.72	13.15	14.17	86.14	44.35	25.17
NTP	5.57	18.71	18.66	34.20	29.79	2.66	21.01
NEP	5.33	13.74	23.04	36.99	38.81	2.97	29.62
FLL	71.22	104.26	11.18	13.53	68.30	14.39	19.07
FLB	0.06	0.08	20.11	22.44	80.30	0.46	37.18
FLA	16.93	32.70	22.83	31.74	51.76	6.11	33.89
EPL	7.26	10.02	10.59	12.44	72.44	4.73	18.60
TPL	4.29	6.92	7.98	10.13	62.04	3.37	12.96
PER	27.25	37.18	5.33	6.23	73.30	9.22	9.42
FSP	452047.61	711140.79	51.11	64.10	63.57	1105.87	84.06
USP	29250.38	75493.92	65.73	105.60	38.75	219.62	84.41
TSP	596338.91	984370.54	49.01	62.96	60.58	1239.98	78.69
OCR	54.32	123.24	8.75	13.18	44.08	10.09	11.99
GLT	1.36	1.46	14.35	14.88	93.10	2.32	28.57
GBT	0.40	0.43	21.77	22.72	91.81	1.24	43.03
TGW	80.93	82.44	33.34	33.65	98.17	18.39	68.16
GYH	179.28	274.31	39.38	48.71	65.36	22.33	65.68

GV (ʒ^{2}g) = Genotypic variance, PV (ʒ^{2}p) = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance, GAM (%) = Genetic advance as percent of mean, h^{2}b = Heritability in broad sense.

DFF = Days to first flowering; DPF = Days to 50% flowering; DTM = Days to maturity; PHT = Plant height (cm); NTP = Number of tiller/plant; NEP = Number of effective tiller/plant; FLL = Flag leaf length (cm); FLB = Flag leaf breadth (cm); FLA = Flag leaf angle (^{o}); EPL = Exerted panicle length (cm); TPL = Total panicle length (cm); PER = Panicle exertion rate (%); FSP = Filled spikelet/plant; USP = Unfilled spikelet/plant; TSP = Total spikelet/plant; OCR = Outcrossing rate (%); GLT = Grain length (mm); GBT = Grain breadth (mm); TGW = Thousand grain weight (g); GYH = Grain yield/hill (g).

traits. Singh et al. (2018) found similar results in wheat inbreed lines.

Heritability, Genetic Advance and Genetic Advance as Percent of Mean

Traits such as days to first flowering (98.75), days to 50% flowering (99.17), days to maturity (96.95), plant height (cm) (86.14), flag leaf length (cm) (68.30), flag leaf breadth (cm) (80.30), exerted panicle length (cm) (72.44), total panicle length (cm), (62.04), panicle exertion rate (%) (73.30), filled spikelet/plant (63.57), total spikelet/plant (60.58), grain length (mm) (93.10), grain breadth (mm) (91.81), thousand grain weight (g) (98.17), grain yield/hill (g) (65.36) exhibited high heritability (>60%) accompanied with high to moderate genotypic and phenotypic coefficient of variation and genetic advance which indicated that most likely the heritability was due to additive gene effects and for these traits, selection may be effective. Similar results have been reported by Adhikari et al. (2018) and Rafii et al. (2014).

The estimates of high heritability (>60%) coupled with high genetic advance as percent of mean (>20%) were recorded (Table 4) for days to first flowering (h^2b = 98.75, GAM = 41.15%), days to 50% flowering (h^2b = 99.17, GAM = 41.75%), days to maturity (h^2b = 96.95, GAM = 23.96%), plant height (cm) (h^2b = 86.14, GAM = 25.17%), flag leaf breadth (cm) (h^2b = 80.30, GAM = 37.18%), filled spikelet/plant (h^2b = 63.57, GAM = 84.06%), total spikelet/plant (h^2b = 60.58, GAM = 78.69%), grain length (mm) (h^2b = 93.10, GAM = 28.57%), grain breadth (mm) (h^2b = 91.81, GAM = 43.03%), thousand grain weight (g) (h^2b = 98.17, GAM = 68.16%), grain yield/hill (g) (h^2b = 65.36, GAM = 65.68%) which exhibited good scope for improving these traits through phenotypic selection due to the additive gene action. However, flag leaf length (cm) (h^2b = 68.30%, GAM = 19.07%), exerted panicle length (cm) (h^2b = 72.44, GAM = 18.60%), total panicle length (cm) (h^2b = 62.04, GAM = 12.96%), panicle exertion rate (%) (h^2b = 73.30, GAM = 9.42%) with high heritability and moderate to low genetic advance; number of tiller/plant (h^2b = 29.79, GAM = 21.01%), number of effective tiller/plant (h^2b = 38.81, GAM = 29.62%), flag leaf angle (o) (h^2b = 51.76, GAM = 33.89%), unfilled spikelet/plant (h^2b = 38.75, GAM = 84.41%) with moderate to low heritability and high genetic advance and outcrossing rate (%) (h^2b = 44.08, GAM = 11.99%) with moderate heritability and moderate genetic advance had non-additive gene action, thus, simple selection may not be rewarding. Hybridization followed by selection is desirable for improving these traits. Similar findings have been reported by Ogunbayo et al. (2014) in rice and Pour (2015) in wheat.

Principal Component Analysis

The computed eigenvalues of 20 variables of 47 local rice genotypes were subjected to principal component analysis; eigenvalues, variability percentage, and cumulative explained variance are presented in **Table 4**. The eigenvalues of the first 10 principal components are shown in the scree plot (**Figure 1**), which revealed that the first principal component explained the majority of the variation expressed by the population.

PC1, PC2, PC3, PC4, PC5, and PC6 explained 28.69%, 46.9%, 59.75%, 70.01%, 77.76%, and 83.29% of the total morphological variation, respectively (**Table 4**). Our findings are consistent with those of Sameera et al. (2016), who reported that six principal components accounted for 83% of the variation in a wide range of quantitative traits. Afsana et al. (2020) also observed that seven principal components (PCs) explained 79.5% of the variation.

Table 4. Eigen value and total variance of principal components for 47 local rice genotypes

Statistics	Standard Deviation	Proportion of variance (%)	Cumulative proportion (%)	Eigen Values
PC1	2.40	28.69	28.69	5.74
PC2	1.91	18.22	46.90	3.64
PC3	1.60	12.85	59.75	2.57
PC4	1.43	10.26	70.01	2.05
PC5	1.25	7.75	77.76	1.55
PC6	1.05	5.53	83.29	1.11
PC 7	0.91	4.18	87.48	0.84
PC 8	0.84	3.57	91.05	0.71
PC 9	0.72	2.57	93.61	0.51
PC10	0.59	1.76	95.38	0.35
PC11	0.50	1.27	96.64	0.25
PC12	0.47	1.1	97.75	0.22
PC13	0.38	0.72	98.47	0.15
PC14	0.34	0.57	99.04	0.11
PC15	0.29	0.42	99.46	0.08
PC16	0.24	0.28	99.74	0.06
PC17	0.18	0.16	99.9	0.03
PC18	0.14	0.10	100	0.02
PC19	0.02	0	100	0.00
PC20	0.0	0	100	0

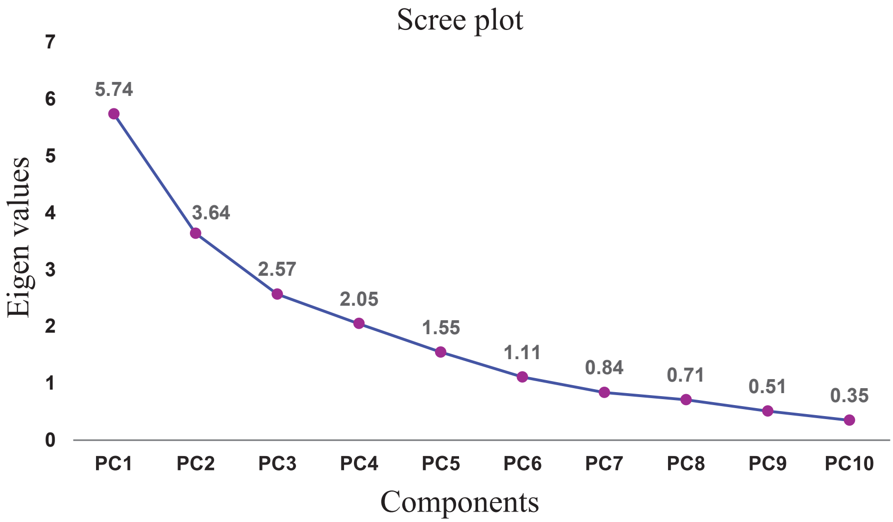


Fig. 1. Scree plot explaining how much variation each principal component capture from the data along with the breakdown point of principal components

The contributions of the different characteristics of the principal components are presented in **Table 5**. In PC1, the important characteristics that showed the most variation were grain breadth (mm) (0.31), days to maturity (0.30), days to first flowering (0.28), plant height (cm) (0.27), thousand grain weight (g) (0.27), flag leaf length (cm) (0.25), days to 50% flowering (0.24), panicle length (cm) (0.22), total panicle length (cm) (0.22), grain length (mm) (0.22), and panicle exertion rate (%) (0.11), and these parameters showed positive loadings. Flag leaf breadth (cm) (0.00) showed no loading, and the other remaining parameters showed negative loadings in PC1. PC2 accounted for 46.9% of the variation due to the number of effective tillers/plant (0.38), number of tillers/plant (0.35), grain yield/hill (g) (0.35), unfilled spikelets/plant (0.32), total spikelets/plant (0.32), filled spikelets/plant (0.27), days to maturity(0.22), grain breadth (mm) (0.21), days to first flowering (0.20), plant height (cm) (0.19), total panicle length (cm) (0.19), panicle length (cm) (0.15), flag leaf length (cm) (0.13), thousand grain weight (g) (0.13), days to 50% flowering (0.10), and grain length (mm) (0.01). Flag leaf breadth (cm), flag leaf angle (°), and outcrossing rate (%) contributed negatively to the second principal component. The first component signifies the importance of this PC for traits related mostly to plant growth, and the second to yield. These results corroborate with the findings of Afsana et al. (2020).

Table 5. Principal component analysis (PCA) of twenty yield contributing traits in forty-seven coastal rice genotypes

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15	PC16	PC17	PC18	PC19	PC20
DFF	0.28	0.20	0.15	0.22	0.24	-0.05	0.15	-0.08	0.25	-0.05	-0.40	0.33	-0.41	0.42	0.00	-0.16	-0.10	-0.10	0.01	0.00
DPF	0.24	0.10	0.00	0.34	0.27	-0.13	0.26	0.06	0.55	-0.08	0.16	-0.08	0.40	-0.31	0.14	0.02	0.15	0.13	0.00	0.00
DTM	0.30	0.22	0.02	0.08	0.02	-0.18	0.24	-0.35	-0.32	-0.09	0.19	-0.20	-0.43	-0.41	-0.25	-0.01	0.17	-0.06	0.01	0.00
PHT	0.27	0.19	-0.11	0.02	-0.09	0.13	0.21	0.62	-0.10	0.04	0.31	-0.40	-0.14	0.36	0.04	-0.09	-0.01	-0.01	0.00	0.00
NTP	-0.19	0.35	-0.13	-0.03	0.24	-0.05	-0.04	0.05	-0.24	-0.68	-0.02	0.03	0.05	0.04	0.36	0.29	-0.05	-0.17	-0.01	0.00
NEP	-0.23	0.38	0.06	-0.12	0.13	0.00	-0.11	0.11	0.01	-0.21	0.21	0.23	0.18	-0.01	-0.52	-0.53	-0.03	0.14	-0.01	0.00
FLL	0.25	0.13	-0.21	0.01	-0.33	-0.11	-0.07	0.49	-0.12	0.01	-0.35	0.42	-0.02	-0.44	0.01	0.02	0.05	0.02	0.01	0.00
FLB	0.00	-0.21	0.30	-0.02	-0.53	-0.08	0.09	-0.03	0.23	-0.38	0.44	0.30	-0.21	0.03	0.20	-0.08	-0.02	0.02	-0.01	0.00
FLA	-0.06	-0.03	-0.20	-0.22	-0.15	0.49	0.71	-0.15	-0.03	-0.14	-0.21	0.09	0.15	-0.03	-0.05	-0.05	-0.03	0.09	0.00	0.00
EPL	0.22	0.15	-0.42	-0.14	-0.18	-0.03	-0.19	-0.25	0.19	-0.03	0.09	-0.01	0.07	0.14	-0.02	0.00	-0.05	-0.04	0.73	0.00
TPL	0.22	0.19	-0.29	-0.07	-0.35	-0.31	-0.05	-0.27	0.07	-0.04	-0.05	-0.07	0.28	0.29	-0.13	0.07	-0.04	-0.02	-0.58	0.00
PER	0.11	0.00	-0.40	-0.17	0.20	0.46	-0.31	-0.06	0.29	0.00	0.21	0.08	-0.35	-0.20	0.13	-0.06	-0.02	-0.01	-0.35	0.00
FSP	-0.32	0.27	-0.04	-0.12	-0.13	-0.17	0.11	-0.03	0.15	0.23	-0.07	-0.14	-0.11	-0.11	0.31	-0.27	0.04	-0.21	-0.01	-0.64
USP	-0.14	0.32	0.07	0.39	-0.24	0.25	-0.16	-0.10	-0.02	0.01	-0.07	-0.08	-0.12	0.04	0.01	0.22	-0.03	0.68	0.01	-0.19
TSP	-0.31	0.32	-0.02	-0.01	-0.17	-0.08	0.06	-0.05	0.13	0.20	-0.08	-0.14	-0.12	-0.08	0.27	-0.18	0.03	0.00	-0.01	0.74
OCR	-0.06	-0.16	-0.17	-0.46	0.25	-0.46	0.17	0.09	0.06	-0.01	0.00	0.03	-0.22	0.05	0.06	0.07	-0.04	0.59	0.01	0.00
GLT	0.22	0.01	0.36	-0.31	-0.09	0.09	-0.18	0.04	0.23	-0.30	-0.35	-0.49	-0.01	-0.21	-0.06	-0.10	-0.35	0.03	0.01	0.00
GBT	0.31	0.21	0.21	-0.12	0.11	0.05	0.03	-0.15	-0.29	0.30	0.24	0.23	0.22	-0.07	0.35	-0.08	-0.54	0.10	-0.02	0.00
TGW	0.27	0.13	0.28	-0.33	0.03	0.15	-0.15	-0.09	-0.11	0.00	-0.08	0.05	0.14	0.13	0.24	-0.11	0.72	0.14	0.00	0.00
GYH	-0.08	0.35	0.26	-0.33	-0.01	0.06	0.09	0.10	0.28	0.23	0.14	0.14	-0.05	-0.01	-0.28	0.63	0.01	-0.18	0.01	0.00

DFF = Days to first flowering; DPF = Days to 50% flowering; DTM = Days to maturity; PHT = Plant height (cm); NTP = Number of tiller/plant; NEP = Number of effective tiller/plant; FLL = Flag leaf length (cm); FLB = Flag leaf breadth (cm); FLA = Flag leaf angle (°); EPL = Exerted panicle length (cm); TPL = Total panicle length (cm); PER = Panicle exertion rate (%); FSP = Filled spikelet/plant; USP = Unfilled spikelet/plant; TSP = Total spikelet/plant; OCR = Outcrossing rate (%); GLT = Grain length (mm); GBT = Grain breadth (mm); TGW = Thousand grain weight (g); GYH = Grain yield/hill (g)

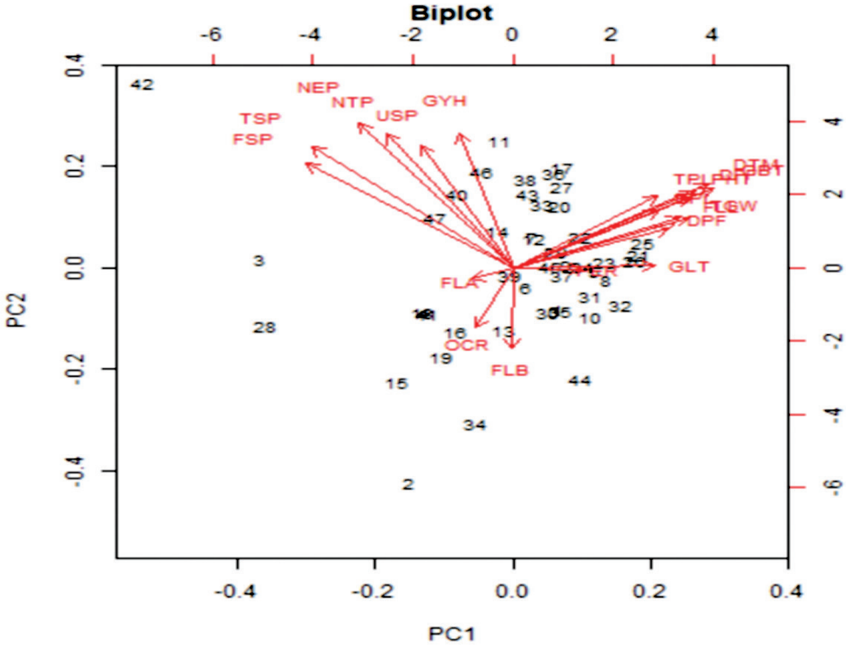


Fig. 2. Principal Components Analysis (PCA) ordination graph; PC1 vs PC2 biplot

Biplot Analysis Based on Principal Component Analysis

A biplot considering PC1 and PC2 together showed that the differences among the parameters were well represented, as illustrated in **Figure 2**.

From the Biplot (**Figure 2**), the acute angle between thousand grain weight (g) and days to 50% flowering, days to maturity, plant height (cm), flag leaf length (cm), total panicle length (cm), panicle length (cm), grain length (mm), grain breadth (mm), and panicle exertion rate (%) provided clear evidence that they had strong positive correlations.

Moreover, grain yield/hill (g) was positively correlated with the number of tillers per plant, effective tillers/plants, filled spikelets/plants, unfilled spikelets/plants, and total spikelets/plants. It also had a slightly positive correlation with total panicle length (cm), panicle length (cm), plant height (cm), days to maturity, days to first flowering, grain breadth, and flag leaf angle (^{o}).

Therefore, grain yield per hill (g) had a slightly negative correlation with grain length (mm) and panicle exertion rate (%). Again, thousand-grain weight was negatively correlated with the number of tillers/plants, number of effective tillers/plants, number of filled spikelets/plants, number of unfilled spikelets/plants, number of total spikelets/plants, and flag leaf angle (^{o}). The outcrossing rate (%) and flag leaf breadth (cm) were

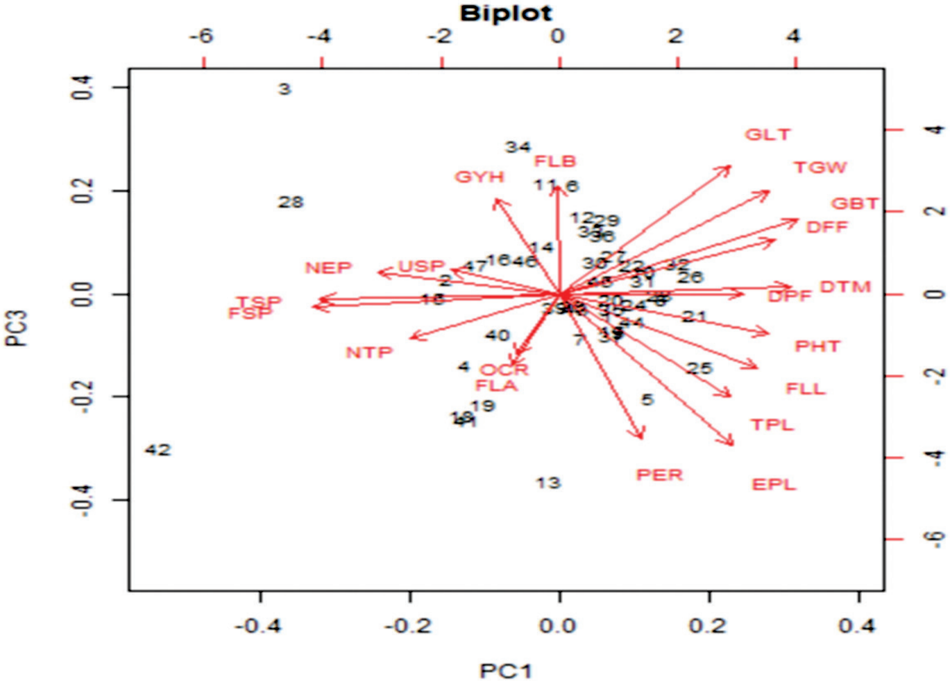


Fig. 3. Principal Components Analysis (PCA) ordination graph; PC1 vs PC3 biplot

positively correlated with each other but negatively correlated with both thousand grain weight (g) and grain yield/hill (g). Biplot analysis showed the trait profiles of the genotypes, especially those positioned far away from the origin, and the results indicated a correlation between traits and genotypes.

When PC1 and PC3 were included in the biplot (Figure 3), the differences among all traits were well represented. In Figure 3, an acute angle was observed between grain yield/hill and grain length (mm), flag leaf breadth (cm), unfilled spikelet/plant, number of effective panicles/plants, number of total spikelets/plants, and number of filled spikelets/plants, indicating positive correlations. However, interestingly, the number of tillers/plant and thousand grain weight (g) had almost no correlation with grain yield per hill (g).

Again, grain yield/hill (g) had a strong negative correlation with outcrossing rate (%), flag leaf angle (°), panicle exertion rate (%), panicle length (cm), total panicle length (cm), flag leaf length (cm), plant height (cm), days to 50% flowering, and days to maturity.

Furthermore, PC2 and PC3 associated Biplot (Figure 4) showed well-defined differences in all traits. The relevant biplot also showed a negative correlation between grain yield/hill (g) and flag leaf breadth (cm), outcrossing rate (%), flag leaf angle (°), panicle exertion rate

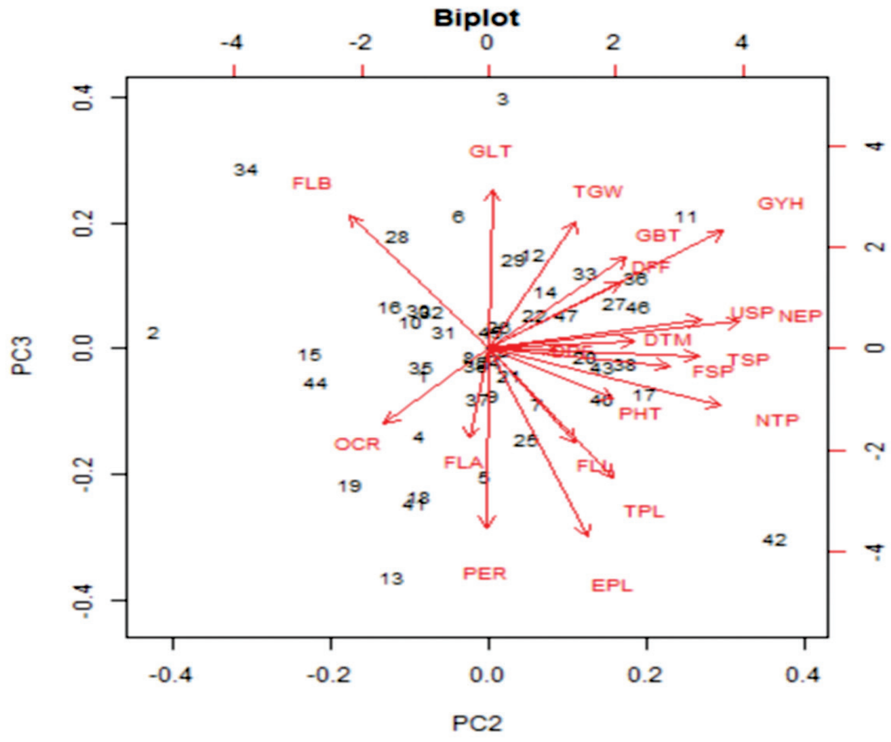


Fig. 4. Principal Components Analysis (PCA) ordination graph; PC2 vs PC3 biplot

(%), and panicle length (cm). Other traits were positively correlated with the grain yield per hill.

Correlation Co-efficient Studies of Twenty Yield Contributing Traits

The interrelationships among the 20 morphological traits of the 47 rice genotypes are presented in Table 6. The current study showed that grain yield/hill was significantly and positively correlated with the number of effective tillers/plants (0.70***), filled spikelet/plant (0.57***), total spikelet/plant (0.55***), thousand grain weight (g) (0.43**), number of tillers/plant (0.38**), grain length (mm) (0.33*), and grain breadth (mm) (0.32*). These results are similar to those reported by Kumar et al. (2018) and Barhate et al. (2021).

Days to first flowering had strong positive correlations with days to 50% flowering (0.76***), days to maturity (0.67***), plant height (cm) (0.43**), flag leaf length (cm) (0.30*), grain length (mm) (0.31*), grain breadth (mm) (0.65***), and thousand grain weight (g) (0.46**), indicating that if days to first flowering were delayed, then days to 50% flowering, days to maturity would be delayed and plant height (cm), flag leaf length (cm), grain length (mm), grain breadth (mm), and thousand grain weight (g) would also decrease.

In contrast, days to first flowering showed a negative correlation with filled spikelet/plant (-0.38**), total spikelet/plant (-0.30*), and outcrossing rate (%) (-0.32*).

Days to 50% flowering were positively correlated with days to maturity (0.53***), plant height (cm) (0.44**), and grain breadth (mm) (0.38**). This result indicates that an increase in days to 50% flowering can increase days to maturity, plant height (cm), and grain breadth (mm). In contrast, it was negatively correlated with filled spikelet/plant (-0.38**), total spikelet/plant (-0.33*), etc. Barhate et al. (2021) reported a significant positive correlation between days to 50% flowering, and days to maturity.

Days to maturity displayed strong positive correlations with plant height (cm) (0.50***), total panicle length (cm) (0.57***), grain breadth (mm) (0.73***), thousand grain weight (g) (0.48***), flag leaf length (cm) (0.41**), and panicle length (cm) (0.44**). Filled spikelet/plant (-0.31*), number of effective tillers/plants (-0.16), flag leaf breadth (cm) (-0.14), flag leaf angle (°) (-0.11), total spikelet/plant (-0.26), and outcrossing rate (%) (-0.19) were negatively correlated. Barhate et al. (2021) reported a significant positive correlation between the number of days to maturity and plant height (cm). According to Adhikari et al. (2018), flowering days showed strong positive correlation with days to maturity.

Plant height (cm) was positively correlated with flag leaf length (cm) (0.70***), panicle length (cm) (0.44**), grain breadth (mm) (0.49***), total panicle length (cm) (0.43**), and thousand grain weight (g) (0.36*). Filled spikelet/plant (-0.29*) expressed a significant but negative correlation and other traits, *viz.* number of tillers/plant, number of effective tillers/plant, flag leaf breadth, total spikelet/plant, outcrossing rate (%), and grain yield/hill were negatively or non-significantly correlated with plant height.

Number of tiller/plant showed significant positive correlation with number of effective tiller/plant (0.81***), filled spikelet/plant (0.60***), unfilled spikelet/plant (0.42**), total spikelet/plant (0.63***), grain yield/hill (g) (0.38**) and significant negative correlation with flag leaf breadth (cm) (-0.49***), grain length (mm) (-0.33*). The thousand grain weight (g) (-0.18), flag leaf length (cm) (-0.13), and grain breadth (mm) (-0.13) were also negatively correlated with the number of tillers/plants.

Number of effective tiller/plant displayed significant positive correlation with filled spikelet/plant (0.75***), unfilled spikelet/plant (0.49***), total spikelet/plant (0.77***) and grain yield/hill (g) (0.70***). In addition, it was negatively correlated with flag leaf breadth (cm) (-0.30*), flag leaf length (cm) (-0.22), panicle length (cm) (-0.15), and total panicle length (cm) (-0.14).

Flag leaf length (cm) was significantly positively correlated with the total panicle length (cm) (0.66***), panicle length (cm)

(0.61***), and grain breadth (mm) (0.34*). The other parameters showed nonsignificant and negative correlations. Flag leaf breadth (cm) showed a significant positive correlation with grain length (mm) (0.33*) and a significant negative correlation with panicle exertion rate (%) (-0.45**). The other parameters showed no significant correlation.

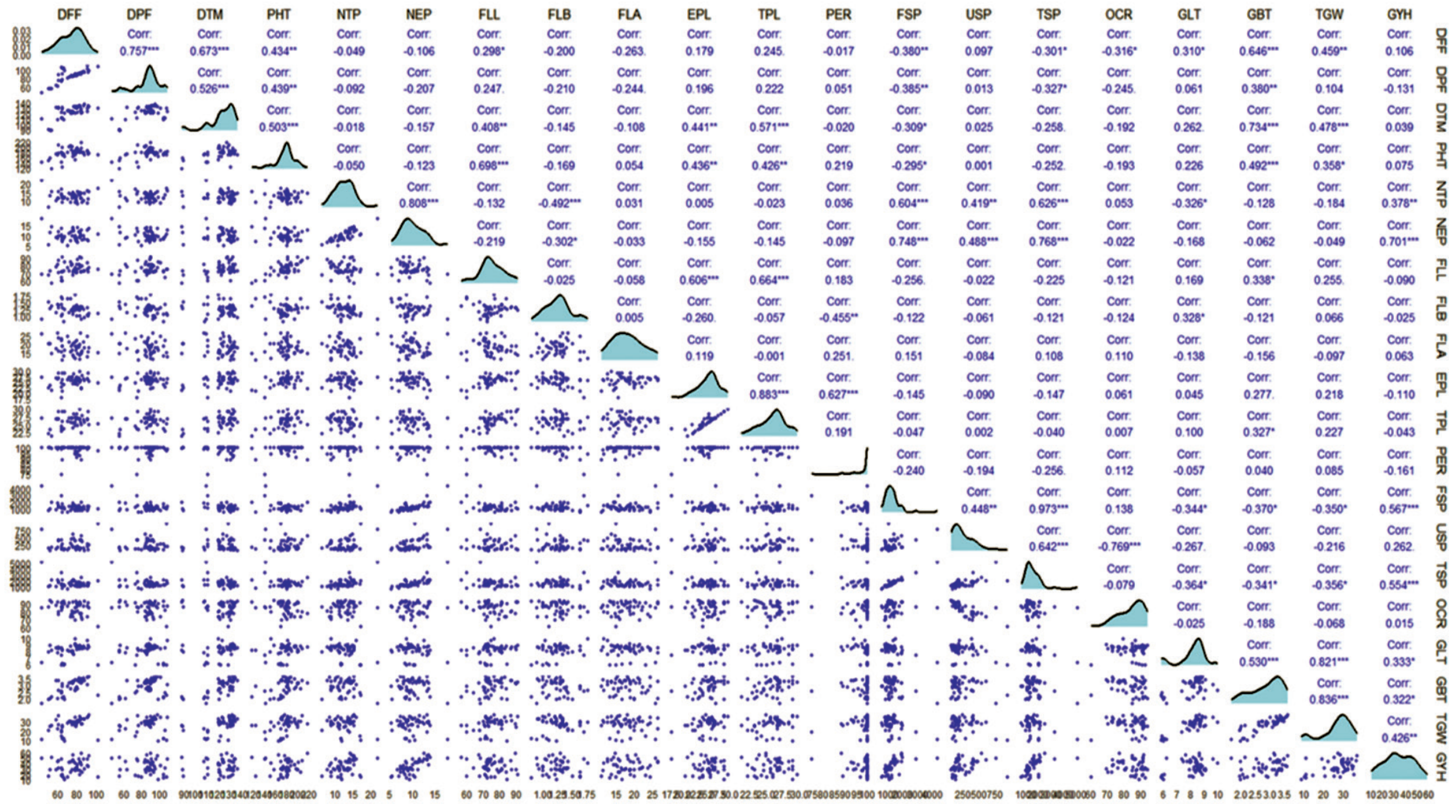
Exerted panicle length (cm) was significantly positively correlated with the total panicle length (cm) (0.88***) and panicle exertion rate (%) (0.63***). This trait was negatively correlated with filled spikelets/plants (-0.14), unfilled spikelets/plants (-0.09), total spikelets/plants (-0.15), and grain yield/hill (g) (-0.11). Ghosal et al. (2010) reported that panicle length showed a negative correlation with spikelet sterility (%) and a positive correlation with yield. Mirza et al. (1992) reported a positive correlation between panicle length and the number of grains per panicle, 1000-grain weight, and grain yield/plant.

The total panicle length (cm) displayed a significant positive correlation with the grain breadth (mm) (0.33*). Filled spikelets/plants showed significant positive correlations with unfilled spikelets/plant (0.45**), total spikelets/plant (0.97***), and grain yield/hill (g) (0.57***), and a significant negative correlation with grain length (mm) (-0.34*), grain breadth (mm) (-0.37*), and thousand grain weight (g) (-0.35*). Unfilled spikelets/plants showed a significant positive correlation with total spikelets/plants (0.64***) and a significant negative correlation with outcrossing rate (%) (-0.77***).

Total spikelet/plant was significantly positively correlated with grain yield (g) (0.55***) and significantly negatively correlated with grain length (mm) (-0.36*), grain breadth (mm) (-0.34*), and thousand grain weight (g) (-0.36*). On the other hand, grain length (mm) showed a significant positive correlation with grain breadth (mm) (0.53***), thousand-grain weight (g) (0.82***), and grain yield/hill (g) (0.33*). Grain breadth (mm) was significantly positively correlated with thousand-grain weight (g) (0.84***) and grain yield/hill (g) (0.32*).

The thousand grain weight (g) showed a significant positive correlation with grain yield/hill (g) (0.43**). Barhate et al. (2021) reported that the grain yield per plant showed a highly significant positive correlation with the number of grains/panicles and productive tillers/plants. Kumar et al. (2018) also reported similar results.

Table 6. Simple correlation matrix among the twenty yield contributing traits in forty-seven local rice genotype



	DFF	DPF	DTM	PHT	NTP	NEP	FLL	FLB	FLA	EPL	TPL	PER	FSP	USP	TSP	OCR	GLT	GBT	TGW	GYH
DFF		Corr: 0.757***	Corr: 0.673***	Corr: 0.434**	Corr: -0.049	Corr: -0.106	Corr: 0.298*	Corr: -0.200	Corr: -0.263.	Corr: 0.179	Corr: 0.245.	Corr: -0.017	Corr: -0.380**	Corr: 0.097	Corr: -0.301*	Corr: -0.316*	Corr: 0.310*	Corr: 0.646***	Corr: 0.459**	Corr: 0.106
DPF			Corr: 0.526***	Corr: 0.439**	Corr: -0.092	Corr: -0.207	Corr: 0.247.	Corr: -0.210	Corr: -0.244.	Corr: 0.196	Corr: 0.222	Corr: 0.051	Corr: -0.385**	Corr: 0.013	Corr: -0.327*	Corr: -0.245.	Corr: 0.061	Corr: 0.380**	Corr: 0.104	Corr: -0.131
DTM				Corr: 0.503***	Corr: -0.018	Corr: -0.157	Corr: 0.408**	Corr: -0.145	Corr: -0.108	Corr: 0.441**	Corr: 0.571***	Corr: -0.020	Corr: -0.309*	Corr: 0.025	Corr: -0.258.	Corr: -0.192	Corr: 0.262.	Corr: 0.734***	Corr: 0.478***	Corr: 0.039
PHT					Corr: -0.050	Corr: -0.123	Corr: 0.698***	Corr: -0.169	Corr: 0.054	Corr: 0.436**	Corr: 0.426**	Corr: 0.219	Corr: -0.295*	Corr: 0.001	Corr: -0.252.	Corr: -0.193	Corr: 0.226	Corr: 0.492***	Corr: 0.358*	Corr: 0.075
NTP						Corr: 0.808***	Corr: -0.132	Corr: -0.492***	Corr: 0.031	Corr: 0.005	Corr: -0.023	Corr: 0.036	Corr: 0.604***	Corr: 0.419**	Corr: 0.626***	Corr: 0.053	Corr: -0.326*	Corr: -0.128	Corr: -0.184	Corr: 0.378**
NEP							Corr: -0.219	Corr: -0.302*	Corr: -0.033	Corr: -0.155	Corr: -0.145	Corr: -0.097	Corr: 0.748***	Corr: 0.488***	Corr: 0.768***	Corr: -0.022	Corr: -0.168	Corr: -0.062	Corr: -0.049	Corr: 0.701***
FLL								Corr: -0.025	Corr: -0.058	Corr: 0.606***	Corr: 0.664***	Corr: 0.183	Corr: -0.256.	Corr: -0.022	Corr: -0.225	Corr: -0.121	Corr: 0.169	Corr: 0.338*	Corr: 0.255.	Corr: -0.090
FLB									Corr: 0.005	Corr: -0.260.	Corr: -0.057	Corr: -0.455**	Corr: -0.122	Corr: -0.061	Corr: -0.121	Corr: -0.124	Corr: 0.328*	Corr: -0.121	Corr: 0.066	Corr: -0.025
FLA										Corr: 0.119	Corr: -0.001	Corr: 0.251.	Corr: 0.151	Corr: -0.084	Corr: 0.108	Corr: 0.110	Corr: -0.138	Corr: -0.156	Corr: -0.097	Corr: 0.063
EPL											Corr: 0.883***	Corr: 0.627***	Corr: -0.145	Corr: -0.090	Corr: -0.147	Corr: 0.061	Corr: 0.045	Corr: 0.277.	Corr: 0.218	Corr: -0.110
TPL												Corr: 0.191	Corr: -0.047	Corr: 0.002	Corr: -0.040	Corr: 0.007	Corr: 0.100	Corr: 0.327*	Corr: 0.227	Corr: -0.043
PER													Corr: -0.240	Corr: -0.194	Corr: -0.256.	Corr: 0.112	Corr: -0.057	Corr: 0.040	Corr: 0.085	Corr: -0.161
FSP														Corr: 0.448**	Corr: 0.973***	Corr: 0.138	Corr: -0.344*	Corr: -0.370*	Corr: -0.350*	Corr: 0.567***
USP															Corr: 0.642***	Corr: -0.769***	Corr: -0.267.	Corr: -0.093	Corr: -0.216	Corr: 0.262.
TSP																Corr: -0.079	Corr: -0.364*	Corr: -0.341*	Corr: -0.356*	Corr: 0.554***
OCR																	Corr: -0.025	Corr: -0.188	Corr: -0.068	Corr: 0.015
GLT																		Corr: 0.530***	Corr: 0.821***	Corr: 0.333*
GBT																			Corr: 0.836***	Corr: 0.322*
TGW																				Corr: 0.426**
GYH																				

*P<0.05; **P<0.01; ***P<0.001and NS: Non-significant

DFF = Days to first flowering; DPF = Days to 50% flowering; DTM = Days to maturity; PHT = Plant height (cm); NTP = Number of tiller/plant; NEP = Number of effective tiller/plant; FLL = Flag leaf length (cm); FLB = Flag leaf breadth (cm); FLA = Flag leaf angle (°); EPL = Exerted panicle length (cm); TPL = Total panicle length (cm); PER = Panicle exertion rate (%); FSP = Filled spikelet/plant; USP = Unfilled spikelet/plant; TSP = Total spikelet/plant; OCR = Outcrossing rate (%); GLT = Grain length (mm); GBT = Grain breadth (mm); TGW = Thousand grain weight (g); GYH = Grain yield/hill (g)

4.6 Cluster Analysis

The distribution pattern in the D^2 analysis indicated that the 47 genotypes fell into six clusters (Table 7 and Figure 5). The maximum number of genotypes (18) were grouped into cluster I followed by cluster IV (15), whereas a single genotype was contained in cluster III and cluster VI, followed by cluster V, which contained five genotypes. Rashid et al. (2014), Behera et al. (2018), and Singh et al. (2020) reported similar results in a divergence study of rice cultivars.

Table 7. Cluster membership of forty-seven local rice genotypes in six different clusters

Cluster	No. of genotypes	Member inbred
I	18	L1.1, L006, L009, L010, L011, L034, L036, L037, L038, L041, L058, L059, L062, L063, L064, L067, L074, L093
II	7	L001, L004, L007, L018, L019, L051, L065
III	1	L003
IV	15	L008, L013, L014, L017, L021, L033, L035, L046, L069, L070, L071, L091, L094, L096, L099
V	5	L015, L024, L025, L076, L081
VI	1	L082

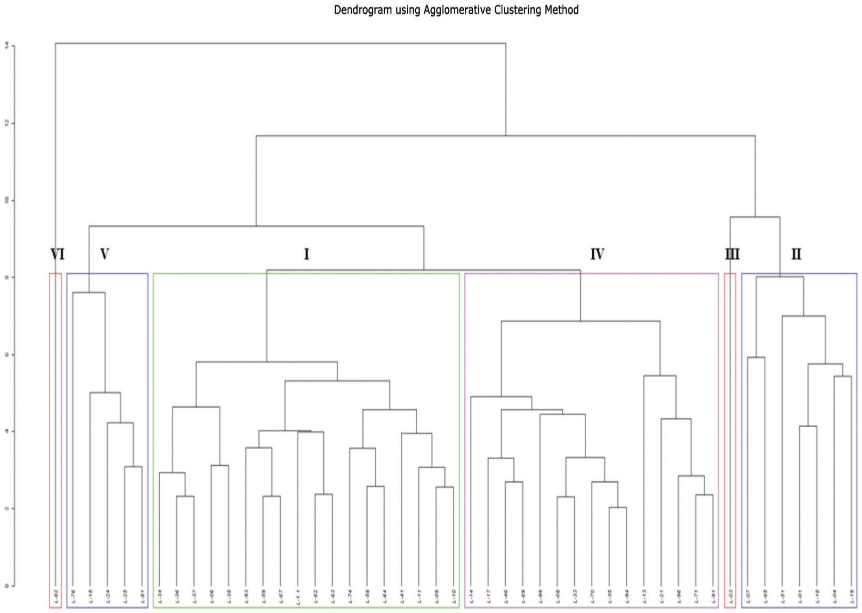


Fig. 5. Dendrogram showing cluster analysis of forty-seven local coastal rice genotypes

Conclusion

A thorough statistical analysis performed on various agro-morphological and floral traits of 47 rice genotypes showed substantial differences among all the characteristics of the rice genotypes. ANOVA demonstrated significant differences ($P < 0.01$) among the genotypes for all considered traits, suggesting ample variability among the genotypes and thus offering ample scope for their potential improvement. The traits showed high heritability estimates (>60%) coupled with substantial genetic advance as a percentage of the mean (>20%), indicating promising opportunities for enhancing these traits through phenotypic selection, primarily influenced by additive gene action. The simple correlation matrix, principal component analysis, and biplot analysis results indicated that grain yield/hill (g) had a positive correlation with the number of tillers/plants, number of effective tillers/plants, number of filled spikelets per plant, and number of unfilled spikelets/ plants. The distribution pattern in the D^2 analysis and UPGMA dendrogram indicated that the 47 genotypes fell into six clusters. Cluster I contained the maximum number of genotypes (18), followed by cluster IV with 15 genotypes, while clusters III and VI each had one genotype. Based on morphological and reproductive traits, prospective maintainers, such as L006, L013, L019, L025, and L038, have been suggested to convert sterility into local genotypes through repeated backcrossing and restorer viz. L001, L004, L015, L033, L037, L038, L058, L062, L065, L067, L099, etc., to test hybrid production with high heterotic effects. This study highlights a robust gene pool comprising coastal rice genotypes that holds significant potential for future hybrid breeding programs suitable for the coastal regions of Bangladesh.

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