Analysis of Genetic Diversity in Some Rice Varieties and Their Performance in Bangladesh

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ABSTRACT: This study was conducted to evaluate the genetic diversity for several rice features and their association with yields, as well as to identify genotypes of short-duration rice. The experiment was conducted in the field in a natural environment, and data were collected on several plant parameters for each genotype at various phases of plant development. Twenty genotypes of rice were examined based on their morphological and physiological characteristics. From July through December of 2020, the experiment was conducted at the Bangladesh Rice Research Institute's regional station in Shyampur, Rajshahi. There was significant diversity among the twenty rice genotypes for all characteristics tested. The genotype BRRI dhan57 displayed the shortest days to flowering. In terms of days to maturity, the genotype BRRI dhan57 was the earliest, with a maturity time of 107.33 days, followed by BRRI dhan56 and BRRI dhan39. The days to blooming had the highest heritability (99.75%), followed by the days to maturity (99.58%), grain yield (85.30%), thousand grain weight (85.22%), grains per panicle (84.91%), plant height (82.21%), and tillers per hill (21.61%). High heritability scores indicated that the researched qualities were less influenced by the surrounding environment. As a percentage of the mean, the genetic gain was greatest for grain yield (36.33%) and lowest for tillers per hill (6.60%) among the yield-contributing factors. In days to flowering, days to maturity, grains per panicle, and plant height, high heritability and genetic progress were seen. According to the principal component analysis (PCA), the Eigen values of the first four components of the total variance accounted for 89.46% of the total variance, indicating that these components were mostly responsible for the genetic diversity of the current materials. It was the largest cluster, containing seven rice genotypes. Clusters II and V contained five and four genotypes of rice, respectively. Clusters III and IV were the smallest, with only two genotypes apiece. The pattern of distribution of genotypes among various clusters demonstrated the significant genetic variety present in the genotypes, which may be the result of adaptation of these genotypes to certain environmental conditions. The largest value of intercluster distance indicated that cluster III genotypes were extremely distinct from cluster IV genotypes. Negative values in both vectors for tillers per hill suggested that this feature contributed the least to the total diversity. The number of panicles per hill, panicle length, weight per thousand grains, and grain yield were all positive in both directions. According to these statistics, these four characteristics contributed the most to the variety.
Keywords: Genotype, Genetic advance, Short duration rice, Genetic divergence, Heritability

1. INTRODUCTION

Rice (Oryza sativa L.) is the most widely cultivated cereal grain in the world. This crop is the principal source of nutrition for more than sixty percent of the world's population. Rice is the second-most important crop in the world after wheat, and it provides more than 70% of the human caloric intake in numerous Asian countries where more than 90% of rice is being cultivated. On around 75% of Bangladesh's total agricultural land and on over 80% of the country's total irrigated land, rice is planted. As the population continues to increase, rice consumption and demand continue to rise. New genes and improved genetic recombination that are not present in cultivated rice varieties or their relatives are necessary to address the world's ever-increasing population and achieve self-sufficiency in rice production.Utilization of the genetic diversity present in indigenous landraces, for instance, has led to the discovery of new, more advantageous genes, which rice breeders have subsequently put to use in the process of germplasm improvement (Oliveira *et al*., 2007 and Thomson *et al*., 2007).

The creation of new varieties is an ongoing process, and the success of a plant breeding program aimed at developing high-yielding, high-quality, fertilizer-responsive, disease- and insect resistant varieties depends on the selection of suitable plants to be employed in the breeding program.The efficiency of the selection is mostly determined by the genetic diversity of the breeding materials. The puspose of the present study is to observe variability and choose rice genotypes based on quantitative features and performance. So, in parent selection, one of the important factors is the genetic diversity. In any breeding effort, the diversity of the parents involved determines the availability of transgressive segregants. Genetic diversity has been used to successfully choose parents in many crop species (Das *et al.,* 1993).

When selecting the appropriate plant genotypes for hybridization in order to develop varieties with high yielding potential, genetic variation among genotypes is an effective tool for determination and genetic discrimination (Bhatt, 1970). For any breeding scheme, parents chosen based on divergence would be more advantageous (Arunachalam, 1981). Different morphological qualities are crucial for increasing rice output and novel plant type attributes are connected to plant yield (Yang *et al.,* 2007). Because it is quick, cheap and easy to score, morphological features are frequently used by plant breeders to evaluate genetic diversity. The rice plants exhibit significant morphological variety in their vegetative characteristics, with plant height and the number of tillers being two examples. Geneticists or rice breeders can categorize rice genotypes according to morphological features (Sohrabi *et al.,* 2012). It has been shown that the yield component qualities work best to increase grain production when they are highly heritable and positively associated with one another (Surek & Beser, 2003).

When choosing the best rice varieties to continue with the rice breeding program, phonological characteristics of rice are also linked to the yield potential of the various rice types (Shahidullah *et al.,* 2009). To increase the diversity of promising breeding lines, the different parents may be crossed. For crop variety improvements that are quantifiable, choosing parents from different backgrounds could produce a large gene mixture (Jain, 1981). Diverse objectives, such as generating cultivars with higher yields, more adaptability and pest and disease resistance, require genetic diversity. Participation of a more varied range of parents (within a certain limit), it is believed that increasing the likelihood of attaining maximum heterosis in hybridization will give segregating generations with a wider range of diversity. So, in order to assess the contribution of the different traits towards divergence, this research work was undertaken to choose efficient diverse parents for the utilization in hybrid program to generate high variability for the desired traits, to identify selection criteria for high yielding and short duration genotypes amongst twenty rice genotypes. To achieve this goal, this research was carried out with the goals of obtaining the following results:

i)   To determine the performance of rice genotypes.

ii)   To determine genetic diversity present among the various rice genotypes.

iii)   To identify rice genotype for short duration and high yield.

2. MATERIALS AND METHODS

2.1 Information about the Location, duration and experimental design:

The experimental field was situated at the Bangladesh Rice Research Institute (BRRI), Regional Station, Shyampur, Rajshahi. Geographically, the experimental field was located at 24° 22' 102' N latitude and 88° 39' 36' E longitude at an elevation of 20 m above sea level in the High Ganges River Flood Plain AEZ-11. The experiment was conducted during the period from July to December, 2020, in the autumn season. A randomized complete block design (RCBD) with three replications was used to carry out the experiment. The individual plot size was 2.5 m 2 m (5 m^2). There was a total of $20 \times 3 = 60$ plots.

2.2 Data Collection (Phenological and Physiological Parameters and Yield):

Ten random plants in each of the ten rows of each plot in each block were chosen to give information about each plant. Days to flowering and days to physiological maturity were two of the traits observed in the field that were studied. After harvesting, the characters that were left over were written down. The number of days from planting to when all of the plants in each plot had bloomed was written down. The number of days between planting and the time when about 100 percent of the plants are ready to be picked was written down for each plot. Average length of the five major culms of five randomly selected plants from the ground to the tip of the panicle was measured. Number of tillers per meter square:. The number of panicle-bearing tillers on each randomly selected sample plants was tallied, and the mean was calculated. The number of panicles on each of the five randomly selected sample plants was tallied, and the mean was calculated. The average length of each panicle (cm) of plants from the last node of the rachis to the tip of the main panicle. The number of grains per panicle was counted from one randomly selected panicle of each plant and the average was calculated from the results. Each plot's weight in thousands of grains was determined after adequate cleaning and sun drying. The total increase weight of each plot is determined after at least two days of adequate cleaning, and must be dry enough to handle the sun and water before it is dried out.

2.3 Statistical Analysis

Analysis of variance was performed using the plant breeding statistical program (PLABSTAT, Version 2N, Utz, 2007) with the following model:

$Y_{ij} = g_i + r_j + \varepsilon_{ij}$

Where,

Y_{ij} = observation of genotype I in replication j,

g_i = effects of genotype i

r_j = effects of replication j,

ε_{ij} = the residual error of genotype I in replicate j.

The replicates were considered as random variable. Multiple mean comparisons were made with Fisher's least significant difference (LSD) procedure using Stat Graphics Plus for Windows 3.0 (Statistical Graphics Crop. Rockville, USA).

2.4.1   Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al*., 1955.

Genotypic co-efficient of variations $= \dfrac{\sigma 2g}{\overline{X}} \times 100$

Genotypic variance, $\sigma^2 g =$

$$\frac{GMS- \ EMS}{r}$$

Where,

GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

Phenotypic variance, $\sigma^2 p = \sigma^2 g + EMS$

Where,

$\sigma^2 g$ = Genotypic variance

EMS = Error mean square

2.4.2   Estimation of genotypic and phenotypic co-efficient of variations

Genotypic co-efficient of variations (GCV) and phenotypic co-efficient of variations (PCV) were estimated according to Burton (1952), and Singh and Chaudhary (1985).

Phenotypic co-efficient of variations $= \dfrac{\sigma 2p}{\overline{X}} \times 100$

Where,

$\sigma^2 p$ = Phenotypic variance; and

$\overline{X}$ = Population mean

Genotypic co-efficient of variation $= \dfrac{\sigma 2g}{\overline{X}} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance; and

$\overline{X}$ = Population mean

2.4.3   Estimation of heritability

Heritability in broad sense (h²b) was estimated according to the formula suggested by Johnson *et al*., (1955) and Hanson *et al*., (1956).

Heritability $= \frac{\sigma 2g}{\sigma 2p} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance; and

$\sigma^2 p$ = Phenotypic variance.

2.4.4   Estimation of genetic advance

Estimation of genetic advance was done by the following formula given by Johnson *et al*., (1955) and Allard (1960).

Genetic advance (GA),

$$GA = \frac{K \times \sqrt{\sigma^2 p} \times \sigma^2 g}{\sigma^2 p}$$

Where,

K= Standardized selection differential at 5% selection intensity, the value of k is 2.063

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance.

Genetic advance as percent of mean,

$$GAM(\%) = \frac{GA}{x} \times 100$$

Where,

GAM= Genetic advance as percent of mean

X= Population mean

2.4.5   Multivariate analysis (D^2 statistics)

Multivariate analysis was done by using SPSS 26.0 and Microsoft Excel 2007 software through four techniques viz. principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis.

2.4.5.1   Principal component analysis (PCA)

The correlations between 11 quantitative traits were examined using the PCA method. The correlation matrix was used to compute the principal component (obtained from sum of squares and products matrix of the traits) and genotype scores (obtained from the first component and the succeeding component with latent roots greater than unity). The latent roots are known as 'Eigen values'. The ability to account for the most variability is a feature of the first component. As a result of finding a linear combination of a collection of variables that maximizes the variation contained within them, the PCA shows the majority of the original variability in a smaller number of dimensions. The latent vectors of the first two principal components are used to discuss how various traits contributed to divergence.

2.4.5.2   Principal coordinate analysis (PCO)

Principal Coordinate Analysis was used to calculate the inter genotype distance and give the minimum distance between each pair of the N points using similarity matrix through the use of all dimensions of P (Digby *et al.,* 1989).

2.4.5.3   Cluster analysis (CA)

Cluster analysis was done by D^2 statistics (originally outlined by Mahalanobis, 1928 and 1936), which divides the genotypes based on the data set into more or less homogenous groups. D^2 is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming correlated variables through Pivotal condensation method). Clustering was done by using non-hierarchical and hierarchical classification.

D^2 statistic is defined by –

$$D^2{}_x = \sum_{k=1}^{P} (\lambda^{ij}) d_i d_j$$

Where,   X = Number of metric in point

   P = Number of populations or genotypes

   λ^{ij} = The matrix reciprocal to the common dispersion matrix

   $d_i d_j$ = The differences between the mean values of the two genotypes

   for the ith and j^{th} traits respectively

In simpler form, D^2 statistic is defined by the following formula-

$$D^2 = \sum_{i=1\ to\ x}^{p} d_i^2 = \sum_{i=1\ to\ x}^{p} (y_i^j - y_j^k) \qquad (j \neq k)$$

Where,　y = Uncorrelated variable which varies from i=1 to X

　　　　　X = Number of traits.

　　Superscripts j and k to y = a pair of any two genotypes

Cluster analysis was performed by computer software SPSS 26.0, which used to search for optimal values of the chosen criterion. The algorithm did some initial classification of the genotypes into required number of groups and then repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer could be found to improve the criterion, the algorithm switched to a second stage, which examined the effect of swooping of two genotypes of different groups, and so on.

2.4.5.4　　　Canonical variate analysis (CVA)

CVA complementary to D^2 statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and amount of variation accounted for by each of such axes are respectively derived. Canonical vector analysis finds linear combination of original variability that maximize the ratio between groups to within groups variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximize the ratio among groups to within group variation.

2.4.5.5　　　Computation of average intra-cluster distance

The average intra-cluster distance for each cluster was calculated by taking all possible D^2 values within the members of a cluster obtained from PCO. The formula used to measure the average intra-cluster distance was-

Intra-cluster distance $= \dfrac{\sum D^2}{n}$

Where,

　　$\sum D^2$ = The sum of distances between all possible combinations (n) of the genotypes included in a cluster.

　　n = Number of all possible combination

3. RESULTS AND DISCUSSION

3.1 Assessment of rice genotypes' performance

3.1.1 Analysis of variance

The analyses of variance of various advanced lines for morphological features displayed in table 1. The analysis of variance revealed that the differences between twenty rice genotypes for eleven traits examined, namely plant height, days to flowering, days to maturity, number of tillers per m^2, number of panicles per m^2, number of grains per panicle, number of tillers per hill, number of panicles per hill, panicle length, 1000 grain weight, yield of grain per hectare were highly significant. This showed that genotypic variance exists for all this qualities. Significant variation for these parameters was also discovered in previous rice research (Yaqoob *et al.,* 2012 and Tiwari *et al.,* 2011). Although other studies also revealed non-significant variation for these parameters in rice, genotypes proved that all are significant (Seyoum *et al.,* 2012 Md. Abdus Sattar Karikor *et al* 2022) discovered a similar outcome. This demonstrates the contribution of each grain to yield enhancement. In the present investigation, the significant differences between genotypes for grain length-width and weight parameters support the hypothesis.

Table 1: Analysis of variance (mean square values) for different traits of twenty rice genotypes.

Traits	Source of variations		
	Replication (df=2)	**Genotype (df=19)**	**Error (df=38)**
PH	149.261	430.965**	29.001
DF	0.217	616.491**	0.515
DM	0.867	523.295**	0.726
TM^{-2}	404.717	1603.611**	294.629
PM^{-2}	404.717	1603.611**	294.629
GP^{-1}	9.267	773.168**	43.249
TH^{-1}	0.755	3.762*	2.059
PH^{-1}	1.839	6.179**	1.644
PL	1.839	7.346**	1.644
TGW	3.930	30.556**	1.670
GY	0.121	2.301**	0.125

Note: PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tillers per m^2, PM^{-2}= panicles per m^2, GP^{-1}= grains per panicle, TH^{-1}= tillers per hill, PH^{-1}= panicles per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield

3.1.2 Performance of the genotypes for phenological, physiological and yield contributing traits

The univariate statistical analysis offered a useful opportunity to investigate and classify the genotypes in accordance with the characteristics that are unique to each of them. Table 2 presented the results of the 20 rice genotypes in terms of their average performance of the relevant traits.

The average height of plant of all genotypes was 123.17 cm, although it varied from 98.33 cm to 149.67 cm. Maximum plant height (149.67 cm) was observed in genotype BRRI dhan34 which was followed by BR5, BRRI dhan40 and BRRI dhan37, while minimum (98.33 cm) in genotype BRRI dhan51. Rice plant height is a complex trait that results from a number of genetically regulated elements (Cheema *et al.,* 1987). Plants resistance to lodging may be increased and the substantial yield losses caused by this trait could be reduced if their height were reduced (Abbasi *et al*., 1995). Considering the flowering days among the genotypes varied from 83.00 to 130.00 days with an average value of 108.33 days. Maximum flowering days was found in genotype BR23 followed by BRRI dhan38, BRRI dhan37 and BR5. The minimum days to flowering was found in genotype BRRI dhan57 which was followed by BRRI dhan33, BRRI dhan56 and BRRI dhan53. In case of maturity days, genotypes exhibited range (107.33 to 148.33 days) with an average of 131.37 days. The genotype BRRI dhan57 had the smallest maturity period i.e. 107.33 days representing earliness which was followed by BRRI dhan56 and BRRI dhan39 i.e. 112.33 days. BR23 had the highest maturity period i.e. 148.33 days which was followed by BR5 and BRRI dhan37. Differences in the period of crop could be employed directly under diverse agro-ecological environment as well as breeding program. In case of number of tillers per m^2, maximum value (275.00) was obtained in genotype BRRI dhan52 followed by BR10 and BRRI dhan30.

The minimum value was 193.67 which was obtained in BRRI dhan37 followed by BRRI dhan32 and BRRI dhan54. The mean value was 247.63. In case of number of panicles per m^2, maximum value (261.33) was obtained in genotype BR5 followed by BRRI dhan52 and BRRI dhan31. The minimum value was 172.67 which was obtained in BRRI dhan37 followed by BRRI dhan32 and BRRI dhan38. The mean value was 229.85. The number of grains per panicle varied from 145.00 to 220.33 among the genotypes with an average of 167.72. The maximum value of grains per panicle (220.33) was found in genotype BRRI dhan51 which was followed by BRRI dhan38 and BRRI dhan41, while minimum value of grains panicle^{-1} (145.00) was observed in genotype BR22 which was followed by BR10 and BRRI dhan39. The number of tillers per hill ranged from 8.60 to 12.87 among the genotypes, with an average of 10.94. The maximum value of tillers per hill (12.87) was observed in genotype BRRI dhan38 which was followed by BRRI dhan57 and BRRI dhan53, while minimum value of tillers per hill (8.60) was observed in genotype BRRI dhan31 which was followed by BRRI dhan41 and BRRI dhan54.

The number of panicles per hill ranged from 8.13 to 12.87 among the genotypes, with an average of 11.35. The maximum value of panicles per hill (12.87) was observed in genotype BRRI dhan52 which was followed by BRRI dhan40 and BRRI dhan30, while minimum value of panicles per hill (8.13) was observed in genotype BR5 which was followed by BRRI dhan34 and BRRI dhan57. Regarding the panicle length, maximum value (25.87 cm) was obtained in genotype BRRI dhan52 followed by BRRI dhan40 and BRRI dhan30. The lowest panicle length was obtained in genotype BR5 (20.13 cm) followed by BRRI dhan34 and BRRI dhan57. The mean value was 24.31.

The thousand grain weight was ranged from 13.93 gm to 23.63 gm with an average of 21.31 gm. The maximum value of thousand grains weight (23.63 gm) was observed in genotype BRRI dhan40 which was followed by BRRI dhan30 and BRRI dhan52, while minimum value of thousand grains weight (13.93 gm) was observed in genotype BRRI dhan34 which was followed by BRRI dhan37 and BR5. Maximum value for the grain yield (tha^{-1}), (5.43) was obtained in genotype BRRI dhan51 followed by BRRI dhan52 and BRRI dhan40. The lowest value for the grain yield (tha^{-1}), (2.58) was obtained in genotype BR5 followed by BRRI dhan38 and BRRI dhan37. The mean value was 4.47 ton per hectare.

Table 2: Mean performance of the rice genotypes for phenological, physiological and yield contributing traits

Variety	PH (cm)	DF	DM	TM^{-2}	PM^{-2}	GP^{-1}	TH^{-1}	PH^{-1}	PL (cm)	TGW (gm)	GY (t/ha)
BR5	135.67 b	125.00 bc	148.00 a	265.00 ab	261.33 a	165.33 cdef	11.80 abc	8.13 e	20.13 e	16.13 bc	2.58 h
BR10	130.67 bcd	110.00 f	130.00 g	274.67 a	248.00 ab	147.33 g	11.20 abc	11.90 ab	24.90 ab	22.90 a	5.22 abc
BR22	128.00 bcde	124.00 c	145.67 b	252.67 abcd	236.33 abcd	145.00 g	11.27 abc	11.33 abcd	24.33 abcd	22.33 a	4.48 cde
BR23	127.00 bcde	130.00 a	148.33 a	237.33 bcd	221.67 bcde	172.00 bcd	10.93 abcd	12.47 a	25.47 a	23.47 a	3.68 fg
BRRI dhan30	122.00 cdef	113.00 e	136.00 d	250.33 abcd	236.00 abcd	176.00 bcd	10.60 abcd	12.57 a	25.57 a	23.57 a	5.16 abcd
BRRI dhan31	120.00 defg	108.67 f	130.67 fg	265.67 ab	250.00 ab	170.33 bcd	8.60 d	12.00 ab	25.00 ab	23.00 a	4.99 abcde
BRRI dhan32	117.33 efg	99.00 h	119.00 h	200.00 ef	187.67 ef	154.67 fg	10.13 cd	12.27 a	25.27 a	23.27 a	5.01 abcd
BRRI dhan33	108.33 gh	85.33 l	114.33 i	253.00 abcd	235.00 abcd	162.33 def	11.00 abc	12.07 a	25.07 a	23.07 a	4.23 ef
BRRI dhan34	149.67 a	116.00 d	138.00 c	236.67 bcde	220.67 bcde	163.33 ef	10.20 bcd	8.93 de	21.93 de	13.93 c	3.29 gh
BRRI dhan37	132.67 bc	126.00 b	147.33 ab	193.67 f	172.67 f	176.33 bcd	11.00 abc	9.27 bcde	22.27 bcde	15.27 bc	3.19 gh
BRRI dhan38	132.00 bc	126.00 b	147.00 ab	224.33 cdef	198.67 def	180.00 b	12.87 a	10.87 abcde	23.87 abcd	17.87 b	2.85 h
BRRI dhan39	109.00 gh	93.67 i	112.67 ij	253.33 abc	230.67 abcd	148.00 g	10.93 abcd	12.30 a	25.30 a	23.30 a	4.85 abcde
BRRI dhan40	135.33 b	109.67 f	131.67 fg	261.67 ab	240.67 abc	166.67 bcdef	10.20 bcd	12.63 a	25.63 a	23.63 a	5.30 ab
BRRI	132.00	112.00	135.00	261.00	245.33	178.33	9.47	12.47 a	25.47	23.47	4.60

dhan41	bc	e	de	abc	abc	bc	cd		a	a	bcde
BRRI dhan51	98.33 h	110.00 f	139.33 c	265.33 ab	247.67 ab	220.33 a	11.80 abc	11.37 abcd	24.37 abcd	22.37 a	5.43 a
BRRI dhan52	116.33 efg	106.00 g	134.00 e	275.00 a	252.33 ab	168.33 bcdef	9.93 cd	12.87 a	25.87 a	23.53 a	5.34 ab
BRRI dhan53	113.00 fg	91.67 j	118.67 h	264.67 ab	250.00 ab	168.67 bcdef	12.53 ab	12.43 a	25.43 a	23.00 a	4.83 abcde
BRRI dhan54	126.00 bcde	110.00 f	132.00 f	216.00 def	208.00 cdef	166.33 bcdef	9.87 cd	11.73 abc	24.73 abc	22.67 a	4.91 abcde
BRRI dhan56	117.00 efg	87.67 k	112.33 j	251.67 abcd	228.33 abcd	155.67 efg	11.67 abc	10.47 abcde	23.47 abcd	22.03 a	4.98 abcde
BRRI dhan57	113.00 fg	83.00 m	107.33 k	250.67 abcd	226.00 abcde	169.33 bcde	12.87 a	9.03 cde	22.03 cde	17.37 b	4.41 def
Mean	123.17	108.33	131.37	247.63	229.85	167.72	10.94	11.36	24.31	21.31	4.47
CV (%)	4.37	0.66	4.65	6.93	8.17	3.92	13.11	11.29	5.28	6.06	7.93

Note: PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tillers per m^2, PM^{-2}= panicles per m^2, GP^{-1}= grains per panicle, TH^{-1}= tillers per hill, PH^{-1}= panicles per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield, CV= Coefficient of variation

3.2 Estimation of genetic parameters of rice genotypes

Table 3 displayed the genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance (GA), and genetic advance as a percentage of the mean GAM (%), for all yield contributing characteristics.

3.2.1 Variability parameters

Twenty rice genotypes exhibited a wide range of variance for eleven yield contributing characteristics and yield. According to an analysis of the data, the variance for each attribute was quite significant (Table 3). This indicated that genotypes possessed underlying genetic distinctions. The significant genetic diversity in a large number of component factors that was displayed by the genotypes suggested that these features might be valuable for the further improvement of rice. For all traits, the phenotypic variance was greater than the genotypic variance, highlighting the environmental influences on these traits. Similar findings were previously reported by Devi *et al*., (2006), Hossain *et al*.,2021, Mohamed Ahmed Mohamud *et al*.,2022 and Prajapati *et al*., (2011). Estimates of the phenotypic coefficient of variation (PCV) were greater than estimates of the genotypic coefficient of variation (GCV) for all traits (Table 2.1), indicating that they all interacted with the environment to some extent. Bhadru *et al.*, (2012) demonstrated the identical outcome with rice. Among the all traits, high GCV and PCV were found for panicles per m^{-2} (183.70 and 325.51 %, respectively) followed by for tillers per m^{-2} (176.20 and 295.18 %), days to flowering (189.53 and 190.01 %), grains per panicle (145.07 and 170.86 %), days to maturity (132.60 and 133.15 %) and plant height (108.79 and 132.33 %). The large GCV and PCV values for these traits indicated the prospect of yield enhancement through trait selection. Low genotypic and phenotypic coefficients of variation were observed for

panicle length (7.82 and 14.58%), tillers per hill (5.19 and 24.00%), panicles per hill (13.31 and 27.79%), thousand grain weight (45.19 and 53.02%), and grain yield per hectare (16.24 and 19.04%) (PCV). Shinha *et al*., (2004) and Patil *et al*., (2003), respectively, likewise showed low PCV & GCV estimations for days to maturity.

3.2.2 Heritability

Assessment of heritability, serves as a forecasting tool for determining the dependability of phenotypic value. High heritability hence helps the efficient selection of a particular trait. According to Johnson *et al*., heritability is categorized as low (below 30%), medium (30-60%), and high (above 60%). (1955). The heritability estimates for the traits investigated in this research ranged from 21.61 to 99.75%. Among the traits, highest heritability was recorded by days to flowering (99.75%) followed by days to maturity (99.58%), grain yield (85.30%), thousand grain weight (85.22%), grains per panicle (84.91%), plant height (82.21%) and lowest heritability value was recorded by tillers per hill (21.61%), (Table 4.3). High heritability values showed that the qualities under study were less influenced by the environment. Consequently, plant breeder can make secure selections based on the phenotypic manifestation of these qualities in the individual plant using simplified selection strategies. In addition, Patel *et al*., (2012) reported the highest heritability for days to 50% flowering, unfilled grain panicle^{-1}, total tillers, days to maturity, grain panicle^{-1}, filled grain panicle^{-1}, grain yield, and thousand grains weight.

3.2.3 Genetic advance

Genetic advancement is a good indicator of expected progress, resulting from the application of selection to the relevant population. A more accurate indicator of selection value would be provided by heritability in associated with genetic advancement (Johnson *et al.,* 1955). Genetic advance is categorized as low (<10%), medium (10-20%) and high (>20%). In the present research work, genetic advance was highest for tillers per m^{-2} (33.29) followed by panicles per m^{-2} (31.85), days to flowering (29.52) and lowest for tillers per hill (0.72) among yield contributing attributes (Table 2.1).

The genetic advance as percent of mean was greatest for grain yield (36.33%), while lowest recorded by tillers per hill (6.60%) among yield contributing traits. Babu *et al*., (2012) also discovered the highest genetic advance for the number of filled grains per panicle and the highest genetic advance as a proportion of the mean for grain width.

The information on genetic variability, heritability, and genetic advance helps to forecast the genetic gain that can be achieved in future generations if the trait under investigation is selected for improvement.

In general, additive gene action governs features with high heritability and genetic advancement (Panse and Sukhatme, 1957) and can be augmented by simple or progeny selection strategies.

Selection for traits with high heritability and high genetic advance is likely to lead to the accumulation of additional additive genes, resulting in further performance enhancement. High heritability and genetic advance were seen in present investigation for the traits days to flowering, days to maturity, grains per panicle and plant height. Other qualities with high or moderate heritability and moderate or low genetic advance can be improved by intercrossing superior genotypes of segregating populations obtained by combination breeding, as indicated by Samadia (2005).

Table 3: Estimation of genetic parameters of twenty rice genotypes

Traits	$(\delta^2 p)$	$(\delta^2 g)$	PCV	GCV	$H^2 b$ (%)	GA	GAM (%)
PH	162.99	133.99	132.33	108.79	82.21	21.65	17.58
DF	205.84	205.33	190.01	189.53	99.75	29.52	27.25
DM	174.92	174.19	133.15	132.60	99.58	27.17	20.68
TM^{-2}	730.96	436.33	295.18	176.20	59.69	33.29	13.44
PM^{-2}	748.19	422.25	325.51	183.70	56.44	31.85	13.86
GP^{-1}	286.56	243.31	170.86	145.07	84.91	29.65	17.68
TH^{-1}	2.63	0.57	24.00	5.19	21.61	0.72	6.60
PH^{-1}	3.16	1.51	27.79	13.31	47.90	1.76	15.46
PL	3.54	1.90	14.58	7.82	53.62	2.08	8.57
TGW	11.30	9.63	53.02	45.19	85.22	5.91	27.73
GY	0.85	0.73	19.04	16.24	85.30	1.62	36.33

Note: $(\delta^2 p)$ = Phenotypic variance, $(\delta^2 g)$ = Genotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, $H^2 b$= Heritability, GA= Genetic advance, GAM(%)= Genetic advance as percent of mean.
PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tillers per m^2, PM^{-2}= panicles per m^2, GP^{-1}= grains per panicle, TH^{-1}= tillers per hill, PH^{-1}= panicles per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield.

3.3 Multivariate analysis (D^2 statistics)
3.3.1 Principle component analysis
Eigen values from principal component analysis are typically employed to determine the number of retained factors. In the principal component analysis (PCA), Eigen values for the first four components of the total variance were found 89.46% (Table 6), indicating that these components were mostly responsible for the genetic diversity in the present materials. Principal component analysis reveals the significance of the factor that contributes the most to the total variance (Sharma, 1998).

Table 4: Eigen values (latent roots) and percent contribution for corresponding 11 traits towards diversity of twenty rice genotypes

Principal component axes	Eigen values	Percent of variance	Cumulative percent of variance
PH	4.657	42.33	42.33
DF	2.168	19.71	62.05
DM	1.738	15.80	77.85
TM^{-2}	1.278	11.61	89.46
PM^{-2}	0.635	5.77	95.24
GP^{-1}	0.222	2.02	97.26
TH^{-1}	0.214	1.94	99.20
PH^{-1}	0.060	0.55	99.75
PL	0.017	0.16	99.90
TGW	0.009	0.08	99.98
GY	0.002	0.02	100.00

Note: PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tillers per m^2, PM^{-2}= panicles per m^2, GP^{-1}= grains per panicle, TH^{-1}= tillers per hill, PH^{-1}= panicles per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield

3.3.2 Non-hierarchical clustering

In terms of grain yield and many morpho-physiological parameters, the genotypes differed significantly from one another. The twenty genotypes of rice were classified into five different clusters using Mahalonobis' D^2 statistics and Tocher's technique (Table 5).

Cluster I was the largest cluster, containing seven rice genotypes. Clusters II and V contained five and four genotypes of rice, respectively. Clusters III and IV were the smallest, with only two genotypes each. The genotypes in the same cluster were more closely related than those in a different cluster. The pattern of distribution of genotypes among different clusters demonstrated the genotypes high genetic diversity, which might be the result of adaptation to certain environmental factors. Ferdous *et al*., (2011) conducted an experiment using 24 different genotypes of bread wheat and found that the results were consistent across five different clusters. Arega *et al*., (2007) studied on exotic and indigenous durum wheat genotypes in the northeast of Ethiopia and got results that were comparable to those found in this study.

Table 5: Distribution of 20 rice genotypes among the five clusters based on Mahalonobis' D^2 value

Cluster	Number of genotypes	% of total entries	Genotypes
I.	7	35	BR5, BR10, BR22, BRRI dhan30, BRRI dhan31, BRRI dhan40, BRRI dhan41
II.	5	25	BRRI dhan33, BRRI dhan39, BRRI dhan53, BRRI dhan56, BRRI dhan57
III.	2	10	BRRI dhan32, BRRI dhan37
IV.	2	10	BRRI dhan51, BRRI dhan52
V.	4	20	BR23, BRRI dhan34, BRRI dhan38, BRRI dhan54

3.3.3 Canonical variate analysis

An examination of the canonical variate was carried out in order to obtain the inter cluster and intra cluster distances, which was presented in Table 6. It could be deduced from the fact that the average inter-cluster distances were greater than the intra-cluster distances, indicated that there was a greater degree of genetic variation among the genotypes of various clusters in comparison to those of the same cluster. Rice yielded comparable findings, according to Choudhury *et al*., (2006) Mohamed Ahmed Mohamud *et al*. (2022)

The inter cluster distance was greatest between clusters Ⅲ and Ⅳ (10.683) followed by the distance between clusters Ⅰ and Ⅲ (9.688), while the distance was smallest between clusters Ⅰ and Ⅱ (6.385) followed by the distance between clusters Ⅲ and Ⅴ (6.901). The distance between two clusters was the measure of the degree of diversification. The largest value of inter cluster distance indicated that cluster III genotypes were far diversed from cluster IV genotypes. Similarly, the greater inter cluster values between clusters Ⅰ and Ⅲ, clusters Ⅱ and Ⅲ, clusters Ⅳ and Ⅴ and clusters Ⅱ and Ⅳ indicated that the genotypes belonging to each pair of clusters were far diversed.

Cluster III had the greatest intra cluster distance, while cluster II had the smallest intra cluster distance. These results demonstrated the grouping pattern of the genotypes as determined by principal component analysis (PCA).

Table 6: Average intra (bold) and inter cluster distances for 20 rice genotypes

Cluster	I.	II.	III.	IV.	V.
I.	**0.865**				
II.	6.385	**0.692**			
III.	9.688	9.285	**0.969**		
IV.	7.943	8.490	10.683	**0.715**	
V.	7.080	7.723	6.901	8.969	**0.873**

3.3.4 Contribution of traits towards divergence

When picking the cluster to be used for subsequent selection and when choosing the parents for hybridization, the feature contributing the most to diversity is given greater importance (Jagadev and Samal, 1991). Table 9 displayed the contributions of characteristics to diversity as determined using Canonical Variable Analysis (CVA). Traits that had negative values in any of the vectors showed that the trait contributed less to diversity, while positive values indicated that the trait contributed more.

Negative values in both vectors for tillers per hill suggested that this attribute contributed the least to the total diversity among twenty rice genotypes. Considering vector I, tillers per m^2, panicles per m^2, panicles per hill, panicle length, thousand grain weight and grain yield had the positive values and responsible for diversity. While in vector II, plant height, days to flowering, days to maturity and grains per panicle were important traits. Panicles per hill, panicle length, 1000 grain weight and grain yield had positive values in both vectors. According to these findings, the most significant contributors to the diversity that existed among the twenty rice genotypes were these four characteristics.

The conclusion revealed that the current materials diversity as a result of these four traits provides enough opportunity for improvement. The study on genetic diversity by Zaman *et al.,* (2010) and Hossain *et al.,*2021 revealed that days to maturity and thousand grains weight contributed to overall diversity.

Table 7: Latent vectors for eleven traits of 20 rice genotypes.

Traits	Vector Ⅰ	Vector Ⅱ
PH	-0.651	0.447
DF	-0.589	0.742
DM	-0.564	0.715
TM^{-2}	0.505	-0.107
PM^{-2}	0.463	-0.046
GP^{-1}	-0.073	0.116
TH^{-1}	-0.282	-0.625
PH^{-1}	0.833	0.459
PL	0.827	0.439
TGW	0.914	0.292
GY	0.894	0.029

Note: PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tiller per m^2, PM^{-2}= panicle per m^2, GP^{-1}= grain per panicle, TH^{-1}= tiller per hill, PH^{-1}= panicle per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield

3.3.5 Intra-cluster mean

Intra cluster mean for eleven traits was demonstrated in table 8. These findings demonstrated that the clusters were surprisingly distinct for the majority of the traits, which was suggestive of proper clustering and indicated the important contribution of the genotypes of these clusters into the total diversity among 20 rice genotypes for these traits. In cluster I, panicles per hill and panicle length had the greatest cluster means, whereas tillers per hill had the lowest cluster mean. Cluster II had the greatest cluster mean for tillers per hill but the least for days to flowering, days to maturity, and grains per panicle. Cluster III had the lowest cluster mean values for tillers per m^2, panicles per m^2, panicles per hill, panicle length, and 1000 grain weight. While in cluster IV, it had the greatest cluster mean for tillers per m^2, panicles per m^2, grains per panicle, 1000 grain weight and grain yield but the lowest cluster mean value for plant height. Cluster V had the highest mean values for plant height, days to flowering and days to maturity, but the lowest mean value for grain yield.

Table 8: Cluster means for the 11 traits of 20 rice genotypes

Traits	Cluster Mean				
	I	II	III	IV	V
PH	127.50	112.07	125.00	98.33	133.67
DF	113.54	88.27	112.50	110.00	120.50
DM	136.38	113.07	133.17	139.33	141.33
TM^{-2}	263.25	254.67	196.83	265.33	228.58
PM^{-2}	246.25	234.00	180.17	247.67	212.25
GP^{-1}	164.67	160.80	165.50	220.33	170.42
TH^{-1}	10.38	11.80	10.57	11.79	10.97
PH^{-1}	11.74	11.26	10.77	11.37	11.00
PL	24.61	24.26	23.77	24.37	24.00
TGW	22.32	21.75	19.27	22.37	19.48
GY	4.71	4.66	4.10	5.43	3.69

Yield rank: Cluster IV > Cluster V > Cluster I > Cluster II > Cluster III

Note: PH= plant height, DF= days to flowering, MD= days to maturity, TM^{-2}= tiller per m^2, PM^{-2}= panicle per m^2, GP^{-1}= grain per panicle, TH^{-1}= tiller per hill, PH^{-1}= panicle per hill, PL= panicle length, TGW= thousand grain weight, GY= grain yield

4. SUMMARY

The purpose of the study was to find short duration, high yielding rice genotypes among 20 rice genotypes. Keeping in mind this concept, the field performance of examined genotypes and the association between various morpho-physiological and yield contributing traits were analyzed under field condition. The investigation was undertaken at Bangladesh Rice Research Institute (BRRI), Regional Station, Shyampur, Rajshahi, from July to December 2020 in aman season. The results of the investigation had been summarized as follows:

Analyses were conducted on the yield and many yield-contributing parameters of 20 rice genotypes and significant differences were detected across genotypes for eleven studied parameters. Maximum plant height (149.67 cm) was observed in genotype BRRI dhan34 which was followed by BR5, BRRI dhan40 and BRRI dhan37, while minimum (98.33 cm) in genotype BRRI dhan51. Rice plant height is a complex trait that results from a number of genetically regulated elements (Cheema et al., 1987). Reducing the height of the plant can potentially boost its resistance to lodging and minimize the severe yield losses caused by this trait (Abbasi et al., 1995). Considering days to flowering, the genotype BRRI dhan57 was earliest which was followed by BRRI dhan33 and BRRI dhan56. All of these three genotypes were earlier than the other varieties. Considering days to maturity, genotypes exhibited range (107.33 to 148.33 days) with an average of 131.37 days. The genotype BRRI dhan57 had the smallest maturity period i.e.107.33 days representing earliness which was followed by BRRI dhan56 and BRRI dhan39 i.e. 112.33 days. Variations in crop length may be employed directly under diverse agro-ecological conditions and breeding program. In case of number of tillers per m2, maximum value (275.00) was obtained in genotype BRRI dhan52 followed by BR10 and BRRI dhan30. The minimum value was 193.67 which was obtained in BRRI dhan37 followed by BRRI dhan32 and BRRI dhan54. Regarding number of panicles per m2, maximum value (261.33) was obtained in genotype BR5 followed by BRRI dhan52 and BRRI dhan31. The minimum value was 172.67 which was obtained in BRRI dhan37 followed by BRRI dhan32 and BRRI dhan38. The maximum value of grains per panicle (220.33) was found in genotype BRRI dhan51 that was followed by BRRI dhan38 and BRRI dhan41, while minimum value of grain panicle-1 (145.00) was observed in genotype BR22 which was followed by BR10 and BRRI dhan39. Because a higher number of filled grains panicle-1 is one of the primary factors that contribute to a higher grain production, this might be used in subsequent programs.

The maximum value of tillers per hill (12.87) was observed in genotype BRRI dhan38 which was followed by BRRI dhan57 and BRRI dhan53, while minimum value of tillers per hill (8.60) was observed in genotype BRRI dhan31 which was followed by BRRI dhan41 and BRRI dhan54. The maximum value of panicles per hill (12.87) was observed in genotype BRRI dhan52 which was followed by BRRI dhan40 and BRRI dhan30, while minimum value of panicles per hill (8.13) was observed in genotype BR5 which was followed by BRRI dhan34 and BRRI dhan57. Regarding the panicle length, maximum value (25.87 cm) was obtained in genotype BRRI dhan52 followed by BRRI dhan40 and BRRI dhan30. The lowest panicle length was obtained in genotype BR5 (20.13 cm) followed by BRRI dhan34 and BRRI dhan57. The maximum value of thousand grains weight (23.63 gm) was observed in genotype BRRI dhan40 which was followed by BRRI dhan30 and BRRI dhan52, while minimum value of thousand grains weight (13.93 gm) was observed in genotype BRRI dhan34 which was followed by BRRI dhan37 and BR5. Maximum value for the grain yield (tha-1), (5.43) was obtained in genotype BRRI dhan51 followed by BRRI dhan52 and BRRI dhan40. The lowest value for the grain yield (tha-1), (2.58) was obtained in genotype BR5 followed by BRRI dhan38 and BRRI dhan37. The mean value was 4.47 ton per hectare. Eigen values from principal component analysis are typically employed to determine the number of retained factors. In the principal component analysis (PCA), Eigen values for the first four components of the total variance were found 89.46% (Table 6), indicating that these components were mostly responsible for the genetic diversity in the present materials.

Cluster I was the largest cluster, containing seven rice genotypes. Clusters II and V contained five and four genotypes of rice, respectively. Clusters III and IV were the smallest, with only two genotypes each. The pattern of distribution of genotypes among different clusters demonstrated the genotypes high genetic diversity, which may be

the result of adaptation to certain environmental factors. The largest value of inter cluster distance indicated that cluster III genotypes were far diversed from cluster IV genotypes. Similarly, the greater inter cluster values between clusters I and III, clusters II and III, clusters IV and V and clusters II and IV indicated that the genotypes belonging to each pair of clusters were far diversed. Negative values in both vectors for tiller per hill suggested that this attribute contributed the least to the total diversity among twenty rice genotypes. Panicles per hill, panicle length, 1000 grain weight and grain yield had positive values in both vectors. According to these findings, the most significant contributors to the diversity that existed among the twenty rice genotypes were these four characteristics.

5. CONCLUSION

The genotype BRRI dhan57 had the smallest maturity period i.e. 107.33 days representing earliness and was followed by BR5, BR6 and BR22 in terms of grain per panicle length. The maximum value of grains per panicle (220.33) was found in genotype BRri dhan51 and the minimum value (145.00) was observed in BR22. The maximum value of tillers per hill (12.87) was observed in genotype BRRI dhan38 and the lowest value for the grain yield (tha-1) was 4.47 ton per hectare. Panicle-1 is one of the primary factors that contribute to a higher grain production, this might be used in subsequent programs. Rice plant height is a complex trait that results from a number of genetically regulated elements. Eigen values from principal component analysis determined the retained factors. Clusters I was the largest cluster, containing seven rice genotypes. Clusters II and V contained five and four genotypes of rice, respectively. Panicles per hill, panicle length, 1000 grain weight and grain yield had positive values in both vectors. Negative values for tiller per hill suggested that this attribute contributed the least to the total diversity.

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