Bangladesh J. Agri. 2025, 50(2): 120-131 *DOI: https://doi.org/10.3329/bjagri.v50i2.86179*

RESPONSE OF BORO RICE (*Oryza sativa* L.) GENOTYPES TO GENETIC DIVERSITY AND CHARACTER ASSOCIATION FOR YIELD ASSOCIATED TRAITS

T. Islam[1], K. M. K. Huda[2], M. Harun-Ur- Rashid[2], F. T. Johora[3], S. Parveen[2], M. Z. Islam[3] R. Rahmatullah[4] and R. Islam[5]*

[1]Soil Science Division, Bangladesh Rice Research Institute (BRRI), Gazipur; [2]Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka; [3]Genetic Resources & Seed Division, Bangladesh Rice Research Institute (BRRI), Gazipur; [4]Department of Industrial and Systems Engineering, College of Engineering, Lamar University, Texas, USA and [5]Department of Forestry and Environmental Science, Rangamati Science and Technology University, Rangamati.

Abstract

An experiment was conducted at the research field of Sher-e-Bangla Agricultural University, Dhaka-1207 during the Boro season (December 2020 to May 2021) using twenty-three Boro rice genotypes to evaluate genetic variability, heritability, genetic advance, correlation, path analysis and genetic diversity for yield-related traits. The experiment followed a randomized complete block design (RCBD) with three replications. Significant variation among genotypes were observed for all fourteen studied traits. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed (48.90% and 47.72%, respectively) for the number of unfilled grain per panicle. High heritability along with high genetic advance in percentage of mean was recorded for leaf sheath length, number of unfilled grain per tiller, number of primary branches per panicle, panicle length and thousand grains weight, suggesting these traits are governed by additive gene action. Yield per hill was positively and significantly correlated with the number of filled grains per tiller, unfilled grains per tiller and thousand grain weight. Traits such as leaf blade length, stem length, effective tillers, panicle length and branching showed positive direct effects on yield. The genotypes were grouped into four clusters. Based on cluster means and genetic parameters, G20 (BRRI dhan96), G1 (BR 1), G3 (BR 5) and G5 (BR 14) were identified as promising lines. Crosses among clusters I, II, III and IV especially involving cluster IV are recommended for future hybridization to exploit heterosis in breeding programs.

Keywords: Cluster analysis, Genetic variability, Heritability, Path analysis, Yield associated traits.

Introduction

Rice (*Oryza sativa* L.) commonly said "Dhan" in Bangladesh, forms the basic staple food of Asia. It is grown in a variety of cultural environments and over vast

---

* Corresponding author: tanjinatanwi92@gmail.com

geographical ranges. Asia produces and consumes most of the world's rice. Rice is the staple food of nearly 165,000,000 people in Bangladesh mand it is predicted that in 2050 about 44.6 MT of clean rice will be required for 215.4 million population (Kabir *et al*., 2015). It provides about 48% employment for rural people contributing about one-sixth of the national income and one-half of the agricultural GDP in Bangladesh. In 2021, total production of rice was 518.8 million tons covering the area of 165.25 million hectares all over the world (FAO, 2022). Bangladesh placing third in rice production and in 2021, the production was about 35.5-million tones on 11.42 million hectares (BBS, 2022). Rice productivity is growing by 1% a year, but that needs to be 2.4% to meet the demand in 2050 (Rejeth *et al*., 2020). Boro season in Bangladesh covers the most area as opposed to the other two (Aus and Aman). Therefore, it will be necessary to develop some Boro rice cultivars that will be suitable to fulfill our demand.

There are different qualitative and quantitative characters that contribute to the yield of crops. The association of different characters and existence of genetic variability in a population is pre-requisite for a breeding program. A breeding program can only be so efficient by gathering the knowledge of genotypic and phenotypic co-efficient of variation and heritability with genetic advance among the genotypes for the desired character (Islam *et al.,* 2020). Genetic divergence is necessary for the development of elite recombinants which is the basis of any crop improvement program (Remme *et al.*, 2024). So, genotype choice among the clusters could be based on the largest areas of the favorable attributes, which would then be utilized for the improvement through interparietal hybridization (Banumathy *et al.,* 2010). Therefore, the investigation was carried out to generate information on genetic diversity, variability, heritability, genetic advance, character association and path analysis for improving the Boro rice genotypes.

Materials and Methods

Twenty-three Boro rice genotypes (Table 1) were collected from BRRI (Bangladesh Rice Research Institute) and Dept. of Genetics & Plant Breeding, SAU. Sprouted seeds were sown in the seedbed. Single seedlings of thirty-nine days aged per hill having 20 cm×20 cm spacing were transplanted to the experimental plot. Each plot size is $8m^2$. Fertilizers were applied 150:60:60:10 kg N:P:K:S per hectare (Ahmmed *et al.,* 2018). All fertilizers were applied at final land preparation except the urea. Urea was splitted into three portions (one portion during final land preparation and other two doses were applied in 30 and 45 DAT, respectively. Data recorded on days to 50% flowering, flag leaf length (cm), leaf blade length (cm), leaf sheath length (cm), stem length (cm), number of effective tillers, number of total tillers, number of filled grain per tiller, number of unfilled grain per tiller, number of primary branches per panicle, number of secondary branches per panicle, panicle length (cm), thousand grain weight (g) and grain yield per hill (g).

Table 1. List of the genotypes used in the study and their sources of collection

Genotypes	Varieties	Source	Genotypes	Varieties	Source
G1	BR1	BRRI	G13	BRRI dhan67	GEPB, SAU
G2	BR2	GEPB, SAU	G14	BRRI dhan68	GEPB, SAU
G3	BR5	GEPB, SAU	G15	BRRI dhan74	GEPB, SAU
G4	BR9	GEPB, SAU	G16	BRRI dhan81	GEPB, SAU
G5	BR14	BRRI	G17	BRRI dhan88	GEPB, SAU
G6	BR16	BRRI	G18	BRRI dhan89	GEPB, SAU
G7	BRRI dhan28	GEPB, SAU	G19	BRRI dhan92	BRRI
G8	BRRI dhan29	GEPB, SAU	G20	BRRI dhan96	BRRI
G9	BRRI dhan50	GEPB, SAU	G21	BRRI dhan97	BRRI
G10	BRRI dhan55	GEPB, SAU	G22	BRRI dhan99	BRRI
G11	BRRI dhan63	GEPB, SAU	G23	SAU Purple 1	GEPB, SAU
G12	BRRI dhan64	GEPB, SAU	-	-	-

Statistical analysis

Significant difference among the genotypes was computed by using statistix 10 software program. Analysis of variance was found by the F test. The significant differences among the genotypes achieved at 5% level of probability by the least significant difference (LSD) test (Gomez and Gomez, 1984). The variance was estimated by the formula of Johnson *et al.* (1955). According to Burton's (1952) PCV and GCV were conducted. Broad sense heritability was computed by using the formula provided by Singh and Chaudhary (1985). For computing genetic advance, Allard’s (1999) formula was used. Genetic advance (% mean) was estimated by the procedure given by Comstock and Robinson (1952). Correlation co-efficient analysis was done by the formula of Al-Jibouri *et al.* (1958). Path analysis was obtained by following Dewey and Lu’s (1959) method. Multivariate analysis, biplot analysis, cluster distance and cluster mean performance were analyzed by using Origin Pro 2023(b) software.

Results and Discussion

Analysis of variance (ANOVA) presented in Table 2. revealed a highly significant level of variation (at 1% significance) among twenty-three rice genotypes across fourteen quantitative traits. The presence of such significant differences indicating considerable genetic variability within the genotypes, which was essential for the improvement of desired traits through selection and hybridization.

Table 2. Analysis of variance for 14 characters of 23 rice genotypes

Source of variation	Replication	Genotype	Error	CV (%)
df	2	22	44	
FFL	0.10	68.02**	1.07	1.62
FLL	6.18	11.92**	5.47	9.15
LBL	126.57	25.79**	10.74	10.23
LSL	9.06	27.43**	2.36	5.99
SL	134.00	161.18**	21.57	7.82
NET	0.41	8.62**	3.28	16.65
NTT	0.88	8.14**	2.75	9.07
NFG	3.96	290.51**	42.81	5.77
NUnFG	3.93	108.64**	1.79	11.22
NPB	0.93	94.49**	2.96	9.43
NSB	10.01	16.54**	5.38	5.98
PL	0.22	78.33**	3.61	12.01
TGW	4.01	40.58**	4.96	9.79
YPH	4.07	92.78**	31.52	20.03

*= Significant at 5 % level of probability, **= Significant at 1 % level of probability and df=Degree of freedom

Here, PCV= Phenotypic co-efficient variation, GCV= Genotypic co-efficient variation, GA= Genetic Advance, h^2b= Broad sense heritability and GA (%) = Genetic Advance in percent of mean FFL=50% flowering; FLL= Flag leaf length (cm); LBL= Leaf blade length (cm); SL= Stem length (cm); NPB= Number of primary branches per panicle; NSB= Number of secondary branches per panicle; PL =Panicle length (cm); TGW= Thousand grain weight (g); YPH= Yield per hill (g); NET= Number of effective tillers; NTT= Number of total tillers; NFG= Number of filled grain per tiller; NUnFG= Number of unfilled grain per tiller and LSL= Leaf sheath length (cm);

Mean performance, variability, heritability and genetic advance of studied traits

Further statistical estimations including mean, range, variance, PCV and GCV, heritability, genetic advance (GA) and genetic advance as a percentage of mean (GAM) were presented in Table 3. In all the studied traits, the PCV (7.52-48.90%) was consistently higher than the GCV (4.97-47.92%), suggesting that environmental influences play a notable role in the expression of these traits which was earlier reported by Islam *et al.* (2020) found similar results of having high range of PCV (5.74% - 32.77%) than GCV (5.68% - 30.76%). Among the measured traits, the number of unfilled grains per tiller exhibited the highest GCV (47.72%) and PCV (48.90%), indicating substantial variability which was followed by panicle length (31.24% GCV, 33.43% PCV) and number of primary branches per panicle (30.42% GCV, 31.86% PCV), highlighting their potential for selection. Similar results were reported by Beena *et al.* (2021) and Meena *et al.* (2019) having the highest GCV (63.86%), PCV (66.50%) and GCV (74.27%), PCV (74.67%), respectively in case of number of unfilled grains per panicle.

Heritability estimates in the broad sense are important indicators of the proportion of total variation that is genetic in nature. High heritability was observed in most traits, excluding number of primary branches per panicle, total tillers, yield per hill, effective tillers and leaf blades and flag leaf length. Similar observations studied by Akshaya *et al.* (2020) for leaf sheath length, Limbani *et al.* (2017) for number of unfilled grains per tiller, Longjam *et al.* (2019) for number of primary branches per panicle, Surjaye *et al.* (2022) for stem length, Singh *et al.* (2026) for number of filled grain per tiller. Notably, the highest heritability was recorded in 50% flowering (95.42%), while the lowest was in flag leaf length (28.20%). The highest genetic advance as percentage of mean was found in the number of unfilled grains per tiller (95.92%) and the lowest in flag leaf length (6.28%). Traits exhibiting both high heritability (>60%) and high genetic advance (>20%) are likely governed by additive gene effects, making them ideal targets for selection. Such trends were also noticed by Beena *et al.* (2021) for numbers of unfilled grain per tiller and by Islam *et al*. (2020) for 1000 grains weight. In contrast, traits like flag leaf length with low genetic advance despite moderate heritability are likely controlled by non-additive gene actions.

Table 3. Estimation of genetic parameters of 23 rice genotypes for 14 yield associated traits

Character	Mean	Range	Vp	V_g	PCV	GCV	h^2b	GA	GA (%)
FFL	64.27	59.33-76.67	23.39	22.32	7.52	7.35	95.42	9.51	14.79
FLL	25.55	21.37-29.60	7.62	2.15	10.81	5.74	28.20	1.60	6.28
LBL	32.11	28.07-37.70	15.75	5.02	12.36	6.98	31.86	2.60	8.11
LSL	25.62	19.40-31.33	10.71	8.36	12.78	11.29	78.01	5.26	20.53
SL	59.34	46.37-71.83	68.10	46.54	13.91	11.50	68.33	11.62	19.57
NET	11.05	9.00-17.00	5.06	1.78	20.36	12.07	35.15	1.63	14.74
NTT	18.23	14.00-21.33	4.55	1.80	11.70	7.36	39.55	1.74	9.53
NFG	113.61	90.33-144.00	125.37	82.57	9.86	8.00	65.86	15.19	13.37
NUnFG	12.51	7.33-31.00	37.41	35.61	48.90	47.72	95.21	12.00	95.92
NPB	18.16	10.33-24.00	33.47	30.51	31.86	30.42	91.16	10.86	59.83
NSB	38.79	34.67-42.33	9.10	3.72	7.78	4.97	40.89	2.54	6.55
PL	15.97	11.17-24.06	28.52	24.90	33.43	31.24	87.33	9.61	60.14
TGW	22.53	12.05-27.45	16.83	11.87	18.22	15.30	70.51	5.96	26.46
YPH	28.09	14.29-43.17	51.94	20.42	25.66	16.09	39.31	5.84	20.78

Here, PCV= Phenotypic co-efficient variation, GCV= Genotypic co-efficient variation, GA= Genetic Advance, h^2b= Broad sense heritability and GA (%) = Genetic Advance in percent of mean FFL=50% flowering; FLL= Flag leaf length (cm); LBL= Leaf blade length (cm); SL= Stem length (cm); NPB= Number of primary branches per panicle; NSB= Number of secondary branches per panicle; PL =Panicle length (cm); TGW= Thousand grain weight (g); YPH= Yield per hill (g); NET= Number of effective tillers; NTT= Number of total tillers; NFG= Number of filled grain per tiller; NUnFG= Number of unfilled grain per tiller and LSL= Leaf sheath length (cm).

Correlations of measured attributes

Correlations for yield and yield components at both genotypic and phenotypic level were shown in Table 4. Thousand grains weight (r_g= 0.821, r_p=0.673), number of filled grains (r_g = 0.504, r_p = 0.379) and unfilled grains per tiller (r_g = 0.604, r_p = 0.365) showed positively significant association with yield per hill at genotypic along with phenotypic level. These traits should be given priority for rice improvement because of their major influence on yield. This finding was in accordance with Chakrabarty *et al.* (2019) and Islam *et al.* (2020). Furthermore, leaf sheath length and flag leaf length showed significant but negative association with yield per hill at genotypic level.

Table 4. Genotypic (rg) and phenotypic (rp) correlation co-efficient for 14 yield-associated traits of 23 rice genotypes

Character		FFL	FLL	LBL	LSL	SL	NET	NTT	NFG	NUnFG	NPB	NSB	PL	TGW
FLL	r_g	0.246*												
	r_p	0.098												
LBL	r_g	0.765**	0.748**											
	r_p	0.380**	0.522**											
LSL	r_g	0.397**	0.737**	0.905**										
	r_p	0.347**	0.382**	0.506**										
SL	r_g	0.513**	0.327**	0.819**	0.853**									
	r_p	0.392**	0.287*	0.600**	0.693**									
NET	r_g	-0.023	-0.759**	-0.252*	-0.579**	-0.471**								
	r_p	0.007	-0.259*	-0.267*	-0.252*	-0.278*								
NTT	r_g	-0.529**	0.067	-0.165	-0.255*	-0.125	0.184							
	r_p	-0.320**	0.101	-0.006	-0.182	0.002	0.041							
NFG	r_g	-0.232	0.315**	-0.190	-0.028	0.005	-0.586**	0.399**						
	r_p	-0.213	0.255*	0.162	0.025	0.080	-0.297*	0.201						
NUnFG	r_g	-0.396**	0.013	-0.508**	-0.322**	-0.404**	-0.060	0.521**	0.853**					
	r_p	-0.381**	-0.001	-0.220	-0.281*	-0.311**	-0.055	0.327**	0.721**					
NPB	r_g	0.212	0.143	0.023	0.166	0.002	-0.143	-0.249*	0.219	0.278*				
	r_p	0.207	0.089	-0.028	0.135	-0.002	0.028	-0.100	0.177	0.260*				
NSB	r_g	-0.641**	-0.491**	-0.846**	-0.651**	-0.688**	0.580**	0.791**	0.092	0.497**	-0.581**			
	r_p	-0.386**	0.023	-0.127	-0.256*	-0.305*	0.077	0.360**	0.098	0.329**	-0.411**			
PL	r_g	-0.149	-0.016	0.142	-0.028	0.114	-0.075	0.153	-0.212	-0.369**	-0.981**	0.423**		
	r_p	-0.155	-0.030	0.102	-0.000	0.103	-0.089	0.045	-0.161	-0.348**	-0.958**	0.307*		
TGW	r_g	-0.092	-0.439**	-0.039	0.048	0.259*	-0.350**	0.117	0.304*	0.147	-0.017	-0.057	0.039	
	r_p	-0.072	-0.148	-0.046	0.054	0.178	-0.071	-0.021	0.223	0.117	-0.007	-0.055	0.020	
YPH	r_g		-0.654**	-0.280*	-0.380**	-0.102	-0.019	0.461**	0.504**	0.604**	0.037	0.388**	-0.154	0.821**
	r_p	-0.118	-0.162	-0.167	-0.148	-0.071	0.535**	0.113	0.379**	0.365**	0.8126	0.047	-0.146	0.673**

In a column, values having *, ** indictaes significant at 5% and 1% levels, respectively,

Here, PCV= Phenotypic co-efficient variation, GCV= Genotypic co-efficient variation, GA= Genetic Advance, h^2b= Broad sense heritability and GA (%) = Genetic Advance in percent of mean FFL=50% flowering; FLL= Flag leaf length (cm); LBL= Leaf blade length (cm); SL= Stem length (cm); NPB= Number of primary branches per panicle; NSB= Number of secondary branches per panicle; PL =Panicle length (cm); TGW= Thousand grain weight (g); YPH= Yield per hill (g); NET= Number of effective tillers; NTT= Number of total tillers; NFG= Number of filled grain per tiller; NUnFG= Number of unfilled grain per tiller and LSL= Leaf sheath length (cm).

Path coefficient analysis

Path coefficient analysis (Table 5) helps the assessment of the net effect that one attribute has on another. The results depicted in the table showed that panicle length had the highest positive direct effect (16.929) and the least positive direct effect of the number of secondary branches in a panicle was found (0.698). It also stated that positively direct effect on yield per hill exists between stem length, leaf blade length, number of effective tillers per hill, number of unfilled grains per tiller, number of primary branches per panicle, number of secondary branches per panicle and panicle length. The results are consistent with Islam *et al.* (2020). The analysis revealed that 4.4% (residual effects = 0.044) out of total variation for yield was not reported in the present study for fourteen yield contributing traits.

Table 5. Partitioning of genotypic into direct (bold) and indirect effects of morphological characters of 23 rice genotypes by path co-efficient analysis

Traits	FFL	FLL	LBL	LSL	SL	NET	NTT	NFG	NUnFG	NPB	NSB	PL	TGW	Genotypic correlation with YPH
FFL	-0.535	-0.619	1.325	-0.423	0.686	-0.018	0.021	0.414	-1.749	3.591	-0.447	-2.524	0.068	-0.210
FLL	-0.131	-2.521	1.296	-0.784	0.437	-0.571	-0.003	-0.563	0.058	2.420	-0.342	-0.273	0.323	-0.654**
LBL	-0.409	-1.885	1.733	-0.962	1.096	-0.190	0.007	0.340	-2.240	0.381	-0.590	2.412	0.029	-0.280*
LSL	-0.213	-1.859	1.568	-1.064	1.142	-0.435	0.010	0.049	-1.420	2.807	-0.454	-0.477	-0.035	-0.380**
SL	-0.274	-0.824	1.419	-0.908	1.338	-0.354	0.005	-0.010	-1.781	0.026	-0.480	1.931	-0.190	-0.102
NET	0.013	1.914	-0.438	0.616	-0.631	0.751	-0.007	1.047	-0.263	-2.418	0.405	-1.265	0.257	-0.019
NTT	0.283	-0.170	-0.285	0.271	-0.167	0.139	-0.040	-0.712	2.298	-4.216	0.552	2.594	-0.086	0.461**
NFG	0.124	-0.795	-0.330	0.029	0.007	-0.441	-0.016	-1.786	3.765	3.701	0.064	-3.596	-0.224	0.504**
NUnFG	0.212	-0.033	-0.880	0.342	-0.540	-0.045	-0.021	-1.524	4.413	4.695	0.347	-6.255	-0.108	0.604**
NPB	-0.114	-0.361	0.039	-0.177	0.002	-0.107	0.010	-0.391	1.225	16.909	-0.406	-16.606	0.013	0.037
NSB	0.343	1.237	-1.465	0.692	-0.920	0.436	-0.031	-0.165	2.193	-9.829	0.698	7.157	0.042	0.388**
PL	0.080	0.041	0.247	0.030	0.153	-0.056	-0.006	0.379	-1.630	16.586	0.295	16.929	-0.029	-0.154
TGW	0.049	1.108	-0.068	-0.051	0.346	-0.263	-0.005	-0.544	0.649	-0.292	-0.040	0.666	-0.736	0.821**
	Residual effect = 0.04434													

In a column, values having *, ** indictaes significant at 5% and 1% levels, respectively,

Here, PCV= Phenotypic co-efficient variation, GCV= Genotypic co-efficient variation, GA= Genetic Advance, h2b= Broad sense heritability and GA (%) = Genetic Advance in percent of mean FFL=50% flowering; FLL= Flag leaf length (cm); LBL= Leaf blade length (cm); SL= Stem length (cm); NPB= Number of primary branches per panicle; NSB= Number of secondary branches per panicle; PL =Panicle length (cm); TGW= Thousand grain weight (g); YPH= Yield per hill (g); NET= Number of effective tillers; NTT= Number of total tillers; NFG= Number of filled grain per tiller; NUnFG= Number of unfilled grain per tiller and LSL= Leaf sheath length (cm).

Genetic diversity among rice genotypes

The genetic structure of the studied genotypes based on the hierarchical cluster analysis of 14 yield associated traits was described in fig. 1. Multivariate analysis revealed four closely related groups among 23 rice genotypes. There were about seven genotypes in cluster 1 demonstrating 36.36% of total genotype in the study area, cluster 2 had about thirteen genotypes (56.52%) and the study area was represented by only one genotype in cluster 3 that is 4.35% while cluster 4 had about two genotypes making 8.70% of the total genotypes. Cluster 2 was the largest positioned cluster, while 1 was the smallest. This finding was recognized by Akhtar *et al.* (2022) and Diploma and Khanna (2018) found the similar result for cluster 2 positioning the highest one.

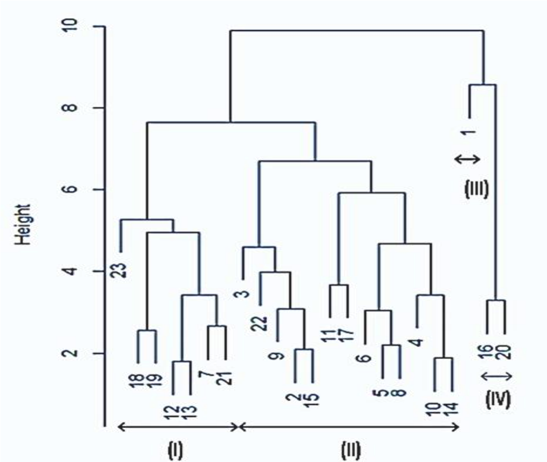

Fig. 1. Dendogram generated using multivariate analysis among 23 rice genotypes.

Principal component analysis

From the biplot analysis (Fig. 2) it was obtained that yield had significant positive correlations with number of total tillers per hill, number of filled grains per tiller, number of unfilled grains per tiller, length of the leaf blade, length of the leaf sheath, length of plants stem, length of flag leaf, 1000 grains weight and days to flowering at 50% level as those lines with arrow were close to the yield. And yield had negative correlations with number of secondary branches per panicle, panicle length (cm) and number of effective tillers. Besides that, the first two coordinates PC1 and PC2 explained 30.17% and 19.60% variations, respectively and in total both contribute 49.77% variation. The contribution of two dimensions in together also supported the work done by Khalequzzaman *et al.* (2023).

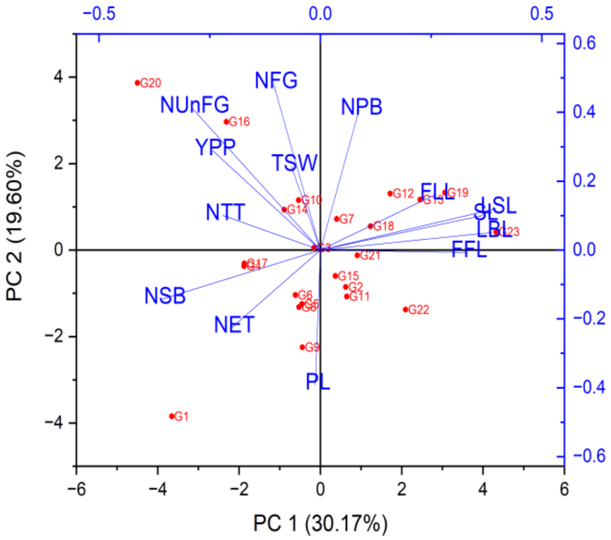

Fig. 2. Biplot analysis of the first two principal components (PC1 and PC2).

Here, FFL=days of 50% flowering; FLL= Flag leaf length (cm); LBL= Leaf blade length (cm); LSL= Leaf sheath length (cm); SL=Stem length (cm); NET= Number of effective tillers; NTT= Number of total tillers; NFG= Number of filled grain per tiller; NUnFG= Number of unfilled grain per tiller; NPB= Number of primary branches per panicle; NSB= Number of secondary branches per panicle; PL = Panicle length (cm); TGW= Thousand grain weight and YPH = Yield per hill (g).

The genetic distance within and between clusters, as shown in Table 6 revealed substantial genetic divergence among the twenty-three rice genotypes. The greatest inter-cluster distance was recorded between Cluster III and Cluster IV (61.46), followed by Cluster II and Cluster IV (54.02), and Cluster I and Cluster IV (52.02), highlighting the significant genetic dissimilarity among these groups. Similar findings were also reported by Takar *et al.* (2024), who observed maximum divergence between Cluster III and Cluster IV. The lowest inter-cluster distance was observed between Cluster I and Cluster II suggesting this group was genetically almost similar. Among the intra-cluster distances, the highest value was found in Cluster III (32.61) indicating high genetic variability within this cluster.

Table 6. Inter and Intra (bold) cluster distance

	Cluster			
Cluster	1	2	3	4
1	25.00			
2	31.08	19.80		
3	42.18	40.12	32.61	
4	52.02	54.02	61.46	18.77

Based on cluster means (Table 7), Cluster I exhibited the highest mean values for key yield-related traits, including grain yield (37.63 g/hill), 1000 grain weight, number of secondary branches per panicle, number of filled grains per tiller and total tillers per hill. Conversely, Cluster IV showed the lowest mean values for most traits, including yield and yield-contributing parameters. In summary, Cluster I emerged as the most desirable for selecting high-yielding genotypes. For maximum heterosis in breeding programs, crosses between genotypes from Cluster I and Cluster IV are promising, particularly for traits like the number of effective tillers per plant, 1000 grain weight and number of filled grains per tiller, hybridization between Clusters I and IV may produce beneficial outcomes.

Table 7. Mean cluster values for fourteen yield contributing traits

	FFL	FLL	LBL	LSL	SL	NET	NTT	NFG	NUnFG	NPB	NSB	PL	TSW	YPH
Cluster I	60.33	25.4	29.83	23.28	52.52	12.58	20	138.16	9.5	21.83	41.66	11.32	24.92	37.63
Cluster II	63.25	26.11	33.27	27.37	63.31	10.24	18.29	112.75	9.5	11.54	39.75	22.26	23.57	27.21
Cluster III	66.26	26.1	33.28	27.37	63.31	10.7	17.81	112.33	10.03	23.11	36.63	11.86	23.37	27.95
Cluster IV	61.91	24.37	29.58	22.27	49.57	10.83	18.41	104.16	12	18.91	40.33	14.15	18.71	25.05

Conclusion

The study revealed significant variability among 23 Boro rice genotypes. High heritability with high genetic advance was observed for leaf sheath length, unfilled grains per tiller, primary branches per panicle, panicle length and 1000 grain weight, indicating potential for effective selection. PCV exceeded GCV for all traits, suggesting environmental influence. Yield per hill showed a highly significant positive correlation with filled grains per tiller, unfilled grains per tiller and 1000-grain weight. These traits are key contributors to yield. Crosses between genetically divergent genotypes may result in maximum heterosis. However, crosses among genotypes from Cluster I and Cluster IV are more suitable for hybridization, as they are expected to exhibit high heterotic potential and serve as valuable breeding materials.

Acknowledgement

We acknowledge the immense financial support of National Science & Technology (NST) and Genetics & Plant Breeding Department of Sher-e Bangla Agricultural University, Dhaka for successfully completing this research work.

Authors' contribution

Conceptualization was carried out by TI, KMKH, and SP. TI was responsible for methodology, investigation, and preparation of the original draft. Supervision was provided by TI and MHR. Formal analysis was performed by TI, FTJ, MZI, and RI. Data curation was undertaken by KMKH, MZI, and RI. Writing-review and editing were contributed by TI, KMKH, MHR, SP, RR, and RI.

References

Allard, R. W. (1999). *Principles of Plant Breeding*. John Wiley and Sons Inc., New York. p. 36.

Al-Jibouri, H., Miller, P. A., & Robinson, H. F. (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of interspecific origin. *Agron. J.* 50(10):633-636.

Ahmmed, S., *et al.* (2018). *Fertilizer Recommendation Guide-2018*. Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka-1215. p. 223.

Akhtar, R., Iqbal, A., Jana, M., and Dasgupta, T. (2022). Agro-morphological characterization and genetic diversity in a mini core collection of aromatic rice (*Oryza sativa* L.). *Curr. J. Appl. Sci. Tech.* 41(10):12-19.

Akshaya, M., Thirumurugan, T., Chitra, S., Nithila, S., and Jeyaprakash, P. (2020). Genetic variability in rice (*Oryza sativa* L.) land races for seedling vigor traits. *Electron. J. Plant Breed.* 11(1):91–96.

Banumathy, S., Manimaran, R., Sheeba, A., Manivannan, N., Ramya, B., Kumar, D., and Ramasubramanian, G. V. (2010). Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electron. J. Plant Breed.* 1(4):500-504.

BBS (Bangladesh Bureau of Statistics). (2022). *Yearbook of Agricultural Statistics of Bangladesh*. Ministry of Planning, Government of Bangladesh, Sher-e-Bangla Nagar, Dhaka. p. 156.

Beena, R., Veena, V., Jaslam, M. P. K., Nithya, N., and Adarsh, V. S. (2021). Germplasm innovation for high-temperature tolerance from traditional rice accessions of Kerala using genetic variability, genetic advance, path coefficient analysis and principal component analysis. *J. Crop Sci. Biotech.* 24:555–566.

Burton, G. W. (1952). Quantitative inheritance in grass pea. *Proc. 6th Grassl. Cong.* 1:277-283.

Comstock, K., and Robinson, P. R. (1952). Estimation of genetic advance. *Indian J. Hil.* 6(2):171-174.

Chakrabarty, T., Islam, M. Z., Akter, N., and Khalequzzaman, M. (2019). Variability, traits association and path coefficient of yield and yield contributing traits of selected boro rice (*Oryza sativa* L.) germplasm. *SAARC J. of Agric.* 17(2): 103-115.

Dewey, D. R., and Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51:515-518.

Diploma, D., and Khanna, V. K. (2018). Intervarietal hybridization and genetic diversity of rice by molecular markers. *Curr. Invest. Agric. Curr. Res.* 3(4):394-403.

FAO. (2022). *FAOSTAT*. Food and Agriculture Organization of the United Nations.

Gomez, K. A., and Gomez, A. A. (1984). *Statistical Procedures for Agricultural Research* (2nd ed.). John Wiley and Sons, New York. p. 680.

Islam, M. Z., Akter, N., Prince, M. F. R. K., Monir, N., and Khalequzzaman, M. (2020). Genetic variability and inter-relationship between yield and yield components in jhum rice (*Oryza sativa* L.) genotypes of Khagrachhari district. *SAARC J. Agric.* 16(1):193-203.

Johnson, H. W., Robinson, H. F., and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* 47:314-318.

Kabir, M. S., Salam, M. U., Chowdhury, A., Rahman, N. M. F., Iftekharuddaula, K. M., Rahman, M. S., Rashid, M. H., Dipti, S. S., Islam, A., Latif, M. A. A., Islam, K. M. S., Hossain, M. M., Nessa, B., Ansari, T. H., Ali, M. A., and Biswas, J. K. (2015). Rice vision for Bangladesh: 2050 and beyond. *Bangladesh Rice J.* 19(2):1-18.

Khalequzzaman, M., Chakrabarty, T., Islam, M. Z., Rashid, E. S. M. H., Prince, M. F. R. K., and Siddique, M. A. (2023). Deciphering genetic variability, traits association, correlation and path coefficient in selected Boro rice (*Oryza sativa* L.) landraces. *Asian J. Biology*. 19:33-45.

Limbani, P. L., Gangani, M. K., and Pandya, M. M. (2017). Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Int. J. Pure Appl. Biosci*. 5(6):1364-1371.

Longjam, S., and Singh, N. B. (2019). Assessment of heritability and genetic advance for yield contributing characters in hill rice (*Oryza sativa* L.) genotypes of Manipur. *Pharma Innov. J.* 8(4):07-11.

Meena, S., Kumar, R., Maurya, V., Bisen, P., Loitongbam, B., Rathi, S. R., Upadhyay, S., and Singh, P. K. (2019). Estimation of variability parameters, correlation and path coefficient for yield and yield associated traits in rice (*Oryza sativa* L.). *Int. J. Agric. Environ. Biotech.* 867-873.

Remme, R. N., Joti, S., and Islam, M. Z. (2024). Agro-morphological characterization and genetic diversity assessment of nineteen BRRI-released rice varieties. *Khulna Univ. Stud.* 21(1):84-97.

Rejeth, R., Manikanta, C. L. N., Beena, R., Roy, S., Manju, R. V., and Viji, M. M. (2020). Water stress-mediated root trait dynamics and identification of microsatellite markers associated with root traits in rice (*Oryza sativa* L.). *Physiol. Mol. Biol. Plants.* 26(6):1225-1236.

Singh, R. K., and Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. p. 56.

Singh, S. K., Sirohi, V., Bisane, R. D., Krishna, V. A., Poudel, A. P., and Singh, A. (2026). Deciphering Genetic Variability, Correlation and Path Analysis for Yield and Yield Related Traits in Early Rice (*Oryza sativa*) Genotypes Under the Direct-Seeded Rice (DSR) System. *Agril. Res.* 1-11.

Surjaye, N., Singh, Y., Singh, S. K., Rahangdale, S., and Mehta, A. K. (2022). Genetic variability, correlation and path coefficient study for various yield and quality traits in NPT lines of rice (*Oryza sativa* L.). *Environ. Ecol.* 40(1):115-122.

Takar, G., Kumar, M., Sandhya, D. L., Yadav, B. K., Patidar, T. G., and Rajesh, N. (2024). Study of genetic diversity in rice (*Oryza sativa* L.) genotypes for yield and related traits using D^2 analysis in the south-eastern plain zone of Rajasthan. *Biological Forum. Int. J.* 16(6):89-92.