

Genetic Diversity in Modern T. Aman Rice Varieties of Bangladesh (*Oryza sativa* L.)

(Kepelbagaian Genetik dalam Varieti Beras Modern T. Aman Bangladesh (*Oryza sativa* L.))

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ABSTRACT

A field experiment was conducted from June to December, 2013 to study the genetic diversity of 15 modern T. Aman rice varieties of Bangladesh (Oryza sativa L.) with a view to assess the superior genotype in future hybridization program for developing new rice varieties that is suitable for the target environment. Analysis of variance for each trait showed significant differences among the varieties. High heritability associated with high genetic advance in percent of mean was observed for plant height and thousand seed weight which indicated that selection for these characters would be effective. Hence, thrust has to be given for these characters in future breeding program to improve the yield trait in rice. Multivariate analysis based on 10 agronomic characters indicated that the 15 varieties were grouped into four distant clusters. The inter cluster distance was maximum between cluster II and cluster IV. The highest intra-cluster distance was found in cluster IV. Based on positive value of vector 1 and vector 2, plant height and 1000-seed weight had maximum contribution towards genetic divergence. From the results, it can be concluded that the varieties BRRI dhan40, BRRI dhan44, BRRI dhan46, BRRI dhan49 and BINA dhan7 may be selected for future hybridization program.

Keywords: Cluster analysis; genetic divergence; multivariate analysis; rice (Oryza sativa L.)

ABSTRAK

Kajian ini dijalankan pada bulan Jun hingga Disember, 2013 untuk mengkaji kepelbagaian genetik 15 varieti padi moden Bangladesh (Oryza sativa L.) T. Aman dengan tujuan untuk menilai genotip unggul dalam program penghibridan masa depan bagi membangunkan varieti padi baru yang sesuai untuk persekitaran sasaran. Analisis varians bagi setiap sifat menunjukkan perbezaan yang signifikan antara jenis trait. Pewarisan tinggi yang berkaitan dengan kemajuan genetik yang tinggi dalam peratus min diperhatikan pada ketinggian tumbuhan dan seribu berat benih yang menunjukkan pemilihan untuk sifat yang berkesan. Oleh itu, teras perlu diberikan untuk sifat ini dalam program pembiakan masa depan untuk meningkatkan ciri beras. Analisis multivariat berdasarkan 10 aksara agronomi menunjukkan bahawa 15 jenis telah dikumpulkan ke dalam empat kelompok jauh. Jarak kelompok inter maksimum adalah antara kelompok II dan kelompok IV. Jarak antara kelompok yang paling tinggi didapati dalam kelompok IV. Berdasarkan nilai positif vektor 1 dan vektor 2, ketinggian dan berat 1000 biji mempunyai sumbangan maksimum terhadap perbezaan genetik. Daripada keputusan dapat disimpulkan bahawa jenis BRRI dhan40, BRRI dhan44, BRRI dhan46, BRRI dhan49 dan BINA dhan7 boleh dipilih untuk program penghibridan pada masa hadapan.

Kata kunci: Analisis kelompok; analisis multivariat; beras (Oryza sativa L.); perbezaan genetik

INTRODUCTION

Rice (*Oryza sativa* L.) is considered as the major crop in Bangladesh as it constitutes 91.8% of the total food grain (rice, wheat & maize) production of 37.50 million metric tons (BBS 2012-2013). Although Bangladesh is now on the verge of attaining self sufficiency in cereal production, there is still a large gap between the production and demand. Among other ecosystems, rainfed condition (T. Aman) is the most suitable for growing rice in this country. Area under T. Aman is the highest which is about 49.63% of total rice land and contributes 40.57% of the total rice production (BBS 2011-2012).

Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which can be used to select appropriate parental genotypes for

hybridization to develop high yielding potential variety (Bhatt 1970). A clear understanding of genetic diversity is essential for the effective conservation and utilization of rice genetic resources (Tu et al. 2007). Genetic diversity is a source of variation, the raw material for crop improvement work, essential to decrease crop vulnerability to abiotic and biotic stresses, ensure long-term selection gain in genetic improvement and promote rational use of genetic resources (Messmer et al. 1993).

Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin 1985). The study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations as it estimate the extent

of diversity existed among selected genotypes (Mondal 2003).

This genetic diversity is essential to decrease crop vulnerability to abiotic and biotic stress, ensure long-term selection gain in genetic improvement and promote rational use of genetic resource (Cortese et al. 2010). Genetically distant parents usually able to produce higher heterosis. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Devi et al. 2006). Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Ahmadzadeh et al. 2011; Arega et al. 2007; Daniel et al. 2011; Haydar et al. 2007; Shekhawat et al. 2001). Therefore, the present investigation was undertaken to identify the contribution of character to genetic diversity and to identify divergent genotypes for hybridization program expecting to provide superior segregates.

MATERIALS AND METHODS

Fifteen rice varieties were collected from the genebank of Bangladesh Rice Research Institute (BRRI) (Table 1). The experiment was conducted at the experiment field of Gazipur during T. Aman 2012 using randomized complete block design with three replications. The soil type of the experimental field belongs to the shallow red brown terrace type under Salna Series of Madhupur Tract of Agro ecological Zone (AEZ)-28 which is characterized by silty clay with pH value of 5.92. Twenty six days old seedlings from each entry were planted in 5 × 4 m plot with 25 × 15 cm spacing using single seedling per hill. All necessary cultural operations and management practices were employed whenever needed. At maturity, 10 m² area was harvested for estimating grain yield excluding border area and yield was adjusted at 14% moisture level. Observations were made from ten randomly selected plants and data

were taken on plant height (cm), flag leaf blade length (cm), tillers per hill (no.), panicle length (cm), primary branches per panicle (no.), secondary branches per panicle (no.), panicle per m² (no.), filled grains per hill (no.), 1000 seed weight (g) and grain yield (t/ha). Mean data for each character were subjected to both univariate and multivariate analysis. For univariate analysis, analysis of variance was done individually by F test. Genetic diversity was worked out following principal component analysis (PCA) (Rao 1964), principal coordinate analysis (PCO) (Digby et al. 1989) and cluster analysis was performed by D² analysis (originally outlined by Mahalanobis (1936) and extended by Rao (1952). Multivariate analysis viz. principal component analysis, principal coordinate analysis, cluster analysis were performed using GENSTAT 5.13 program and Microsoft Excel 2007 software.

RESULTS AND DISCUSSION

The analysis of variance showed that the genotypes differed significantly for all the characters studied indicating the presence of notable genetic variability among them. This implied that it would be judicious to classify the population on the basis of degree of divergence. First 3 Eigen values for 3 principal coordination axes of genotypes accounted for 69.46% variation (Table 2). A two dimensional scattered diagram (Figure 1) was developed on the basis of the principal component score.

PRINCIPAL COORDINATE ANALYSIS (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between BRRI dhan46 and BRRI dhan49 (1.8221) followed by BRRI dhan34 and BRRI dhan46 (1.7335) and the lowest distance was observed (0.4084) between BRRI dhan37 and BRRI dhan38 followed by the distance (0.4426) between BRRI dhan44 and BRRI dhan52 (Table 3). The difference between the highest and the lowest

TABLE 1. List of rice (*Oryza sativa* L.) varieties used in the study

SL. No.	Name of variety	Year of release	Parents/crosses
01	BR11	1980	IR20 × IR5-47-2
02	BR23	1988	DA29 × BR4
03	BRR1 dhan33	1997	BG388 × BG367-4
04	BRR1 dhan34	1997	Selection (Acc. No 4341)
05	BRR1 dhan37	1998	Bashmati (D) × BR5
06	BRR1 dhan38	1998	Bashmati (D) × BR5
07	BRR1 dhan39	1999	BR1185-2B-56-2-1-1×BR1674-28-3-1-1
08	BRR1 dhan40	2003	BR10 × IR4595-4-1-15
09	BRR1 dhan41	2003	BR23 × BR1185-2B-16-1
10	BRR1 dhan44	2005	BR10 × BRR1 dhan31
11	BRR1 dhan46	2007	BR11 × ARC14766 × Swarnolota
12	BRR1 dhan49	2008	BR4962-12-4-1 × IR33380-7-2-1-3
13	BRR1 dhan51	2010	Swarna × IR49830-7-1-2-3
14	BRR1 dhan52	2010	BR11 × IR 40931-33-1-3-2
15	BINA dhan7	2007	Ain guen 250 γ ray

TABLE 2. Eigen value and percent contribution of 10 yield contributing characters of fifteen rice varieties

Principal component axis	Eigen values	% total variation account for	Cumulative percent
Plant height	5.2929	31.13	31.13
Flag leaf blade length	2.5420	14.95	69.46
Tillers per hill	1.1027	6.49	82.99
Panicle length	0.8096	4.76	87.75
Primary branches per panicle	0.4793	2.82	95.22
Secondary branches per panicle	0.2830	1.66	96.88
Panicle / m ²	0.1827	1.07	99.28
Filled grains per hill	0.0766	0.45	99.73
1000 seed weight	0.0007	0.00	100
Grain yield	0.0000	0.00	100

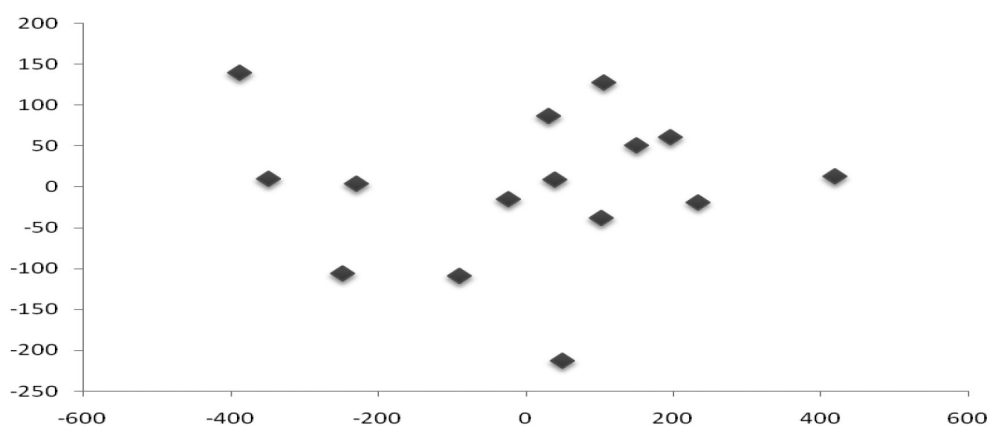


FIGURE 1. Scatter diagram of 15 varieties of rice based on their principal component scores superimposed with cluster

TABLE 3. Ten highest and ten lowest inter genotypic distance among the fifteen rice varieties

Sl. No.	Genotypic combination	Distances
10 highest inter genotypic distance		
01.	BRR1 dhan46 – BRR1 dhan49	1.8221
02.	BRR1 dhan34 – BRR1 dhan46	1.7335
03.	BR23 – BRR1 dhan49	1.7294
04.	BRR1 dhan37 – BRR1 dhan46	1.6880
05.	BRR1 dhan46 – BINA dhan7	1.6547
06.	BRR1 dhan38 – BRR1 dhan46	1.6235
07.	BRR1 dhan46 – BRR1 dhan51	1.5867
08.	BRR1 dhan33 – BRR1 dhan46	1.5704
09.	BRR1 dhan41 – BRR1 dhan49	1.5025
10.	BRR1 dhan49 – BINA dhan7	1.5021
10 lowest inter genotypic distance		
01.	BRR1 dhan37 – BRR1 dhan38	0.4084
02.	BRR1 dhan44- BRR1 dhan52	0.4426
03.	BRR1 dhan40 - BRR1 dhan41	0.5009
04.	BR16 - BRR1 dhan52	0.5026
05.	BR23 - BRR1 dhan41	0.5649
06.	BR16 - BRR1 dhan39	0.5912
07.	BRR1 dhan33 - BRR1 dhan44	0.5999
08.	BRR1 dhan33 - BRR1 dhan52	0.6096
09.	BR16 - BRR1 dhan51	0.6189
10.	BRR1 dhan39 - BRR1 dhan41	0.6223

inter genotypic distance indicated the moderate variability among the 15 genotypes of rice. The highest intra-cluster distance was recorded in cluster IV (1.3053) containing four genotypes BRR1 dhan40, BRR1 dhan46, BRR1 dhan49 and BRR1 dhan51. The lowest intra-cluster distance was observed in cluster I (0.000) having one genotype BINA dhan7. It favored to decide that intra-group diversity was the highest in cluster IV and the lowest in cluster I. The cluster II comprised six genotypes viz. BRR1 dhan33, BRR1 dhan34, BRR1 dhan37, BRR1 dhan38, BRR1 dhan44, BRR1 dhan52 and had an intra-cluster distance of 0.6772. Cluster III having four genotypes viz. BR16, BR23, BRR1 dhan39, BRR1 dhan41 and had an intra-cluster distance of 0.7144 (Tables 4 and 5; Figure 2).

NON-HIERARCHICAL CLUSTERING

The computations from covariance matrix gave non-hierarchical clustering among fifteen rice genotypes and grouped into four clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA

were confirmed by non-hierarchical clustering represents the clusters occupied by fifteen genotypes of rice (Table 5). It explains that cluster I contained the single number of genotype, cluster II constituted by six genotypes, cluster III constituted by four genotypes and cluster IV constituted by four genotypes. Cluster mean for 45 traits are presented in Table 6. Cluster IV was formed by the genotypes BRR1 dhan40, BRR1 dhan46, BRR1 dhan49 and BRR1 dhan51. These clusters were unable to lead in respect of the highest cluster mean value for maximum characters. Non corresponding genetic diversity and geographic distribution were also reported earlier by Chandra et al. (2007), Choudhury et al. (1999), De et al. (1988), Mannan et al. (1993), Masud et al. (2003) and Sinha et al. (1991). Considering this, parents should be selected on the basis of genetic diversity rather than geographic diversity which are supported by Hasan et al. (2000). Among 10 characters, cluster IV produced the maximum cluster mean for the five characters viz. plant height (121.5), flag leaf blade length (36.2) primary branches per panicle (12.7), secondary branches per panicle (9.8) and number of filled grains per plant (1454.9).

TABLE 4. Distribution of fifteen rice varieties of rice in four clusters

Cluster	Number of varieties	Name of the varieties
I	1	BINA dhan7
II	6	BRR1 dhan33, BRR1 dhan34, BRR1 dhan37, BRR1 dhan38, BRR1 dhan44, BRR1 dhan52
III	4	BR16, BR23, BRR1 dhan39, BRR1 dhan41
IV	4	BRR1 dhan40, BRR1 dhan46, BRR1 dhan49, BRR1 dhan51

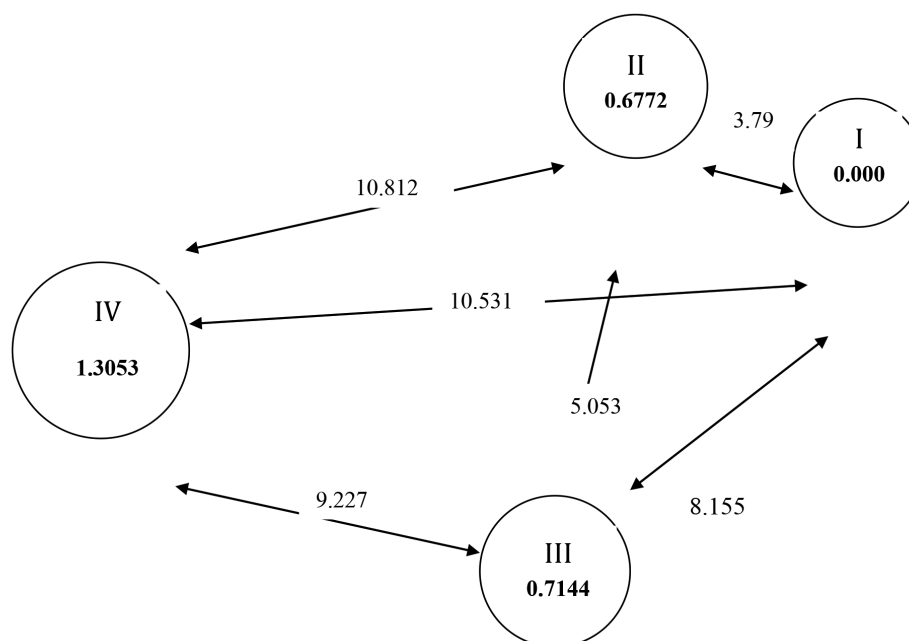


FIGURE 2. Diagram showing the intra and inter cluster distances of 15 rice varieties

TABLE 5. Average Inter and intra cluster distance of fifteen rice varieties

	I	II	III	IV
I	0.000			
II	3.790	0.6772		
III	8.155	5.053	0.7144	
IV	10.531	10.812	9.227	1.3053

TABLE 6. Cluster mean value of 15 rice varieties

Parameter	I	II	III	IV
Plant height	96.5	119.0	120.0	121.5
Flag leaf blade length	31.6	34.3	33.3	36.2
Tillers per hill	14.7	16.2	13.2	14.6
Panicle length	24.5	26.0	26.5	26.2
Primary branches per panicle	10.7	10.6	11.7	12.7
Secondary branches per panicle	7.7	7.7	9.1	9.8
Panicles / m ²	328.0	244.6	240.4	259.3
Filled grains per hill	779.7	1035.3	1198.4	1454.9
1000 seed weight	21.4	24.2	24.3	22.3
Grain yield (t/ha)	4.7	4.0	4.3	4.4

Similarly, cluster III ranked first for panicle length (26.5) and 1000 seed weight (24.3). Cluster I ranked first for panicle per square meter (328.0) and grain yield (4.7). Cluster II ranked tillers per hill (16.2) (Table 6).

CANONICAL VARIATE ANALYSIS

The highest inter-cluster distance was observed between cluster II and IV (10.812) followed by between cluster I and IV (10.531) (Table 4). The intra cluster distance was the highest (1.3053) in cluster IV. The lowest inter-cluster distance was observed between cluster I and II (3.79) followed by cluster II and III (5.053). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program. However, the highest inter-cluster distance was observed between cluster II and IV indicated the genotypes in these clusters were far diverged than those of other clusters. Moderate or intermediate inter-cluster distance was found between cluster I and III (8.155),

cluster III and IV (9.227). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. The results are supported by those of (Siddique et al. 2011) in rice.

The result of different multivariate analysis were superimposed in Figure 2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another. As per scatter diagram the genotypes were apparently distributed into four clusters. Islam et al. (2004) also found similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding, the objective was not only high heterosis but also to achieve high-level production. In the present study, the maximum distance existed between cluster II and IV. But considering the yield and duration crosses involving cluster II and IV, they may exhibit high heterosis for yield. Main and Bahl

TABLE 7. Latent vectors for 10 principal component characters of fifteen varieties of rice

Component characters	Vector I	Vector II
Plant height	0.3644	0.0854
Flag leaf blade length	0.3002	-0.1243
Tillers per hill	-0.1800	0.0394
Panicle length	0.3755	-0.0532
Primary branches per panicle	0.2477	-0.3434
Secondary branches per panicle	-0.0079	-0.3329
Panicles / m ²	-0.3254	-0.1748
Filled grains per hill	0.1710	-0.3350
1000 seed weight	0.3415	0.0924
Grain yield	-0.1279	-0.4116

TABLE 8. Mean \pm Standard Deviation for 10 principal component characters of fifteen varieties of rice

Varieties	Characters									
	Plant height	Flag leaf blade length	Tillers per hill	Panicle length	Primary branches per panicle	Secondary branches per panicle	Panicles / m ²	Filled grains per hill	1000 seed weight	Grain yield (t/ha)
BR16	111.7 \pm 2.00	31.25 \pm 0.02	16.67 \pm 0.58	26.47 \pm 0.06	11.33 \pm 0.58	9 \pm 1.00	283.66 \pm 33.70	1126 \pm 245.40	22.8 \pm 0.34	5.00 \pm 0.24
BR23	122.87 \pm 4.33	36.83 \pm 0.57	15.33 \pm 0.58	28.03 \pm 0.05	13 \pm 1.00	8 \pm 1.00	175 \pm 7.21	1183.67 \pm 101.20	26.53 \pm 0.41	4.00 \pm 0.10
BRR1 dhan33	111.33 \pm 2.36	36.97 \pm 0.58	11.67 \pm 0.58	25.87 \pm 0.11	10 \pm 1.00	6.67 \pm 0.58	264 \pm 16.37	984.67 \pm 103.35	24.33 \pm 0.67	4.06 \pm 0.18
BRR1 dhan34	117.13 \pm 0.55	28.16 \pm 0.01	14.33 \pm 0.58	25.5 \pm 0.10	9.33 \pm 0.58	6 \pm 0.005	197.33 \pm 10.01	966.67 \pm 54.84	22.75 \pm 0.25	3.31 \pm 0.03
BRR1 dhan37	126 \pm 0.50	35.32 \pm 1.16	18.66 \pm 1.15	24.5 \pm 0.01	9.66 \pm 1.15	9 \pm 1.00	265.66 \pm 6.65	1020 \pm 32.78	22.97 \pm 0.13	3.49 \pm 0.04
BRR1 dhan38	125.93 \pm 0.60	32.41 \pm 0.005	20.66 \pm 0.58	24.52 \pm 0.04	10.33 \pm 0.58	8.67 \pm 0.58	270.67 \pm 1.52	1026.67 \pm 37.52	23.18 \pm 0.17	3.47 \pm 0.03
BRR1 dhan39	105.67 \pm 0.38	31.83 \pm 0.02	10.33 \pm 0.58	25.48 \pm 0.03	10.67 \pm 0.58	11 \pm 1.00	284.67 \pm 9.07	1200.67 \pm 25.32	23.18 \pm 0.07	4.15 \pm 0.06
BRR1 dhan40	147.6 \pm 3.24	40.82 \pm 0.01	10.33 \pm 0.58	29.76 \pm 0.16	13.67 \pm 0.58	9.67 \pm 0.58	194 \pm 21.28	1445 \pm 216.91	24.46 \pm 0.47	4.11 \pm 0.14
BRR1 dhan41	140.93 \pm 0.90	33.32 \pm 0.005	10.33 \pm 0.58	26.13 \pm 0.41	11.67 \pm 0.57	8.33 \pm 0.58	218.33 \pm 62.45	1283.33 \pm 186.31	24.56 \pm 0.11	4.01 \pm 0.51
BRR1 dhan44	117.3 \pm 3.81	38.34 \pm 0.02	15.33 \pm 0.58	27.95 \pm 0.05	11.67 \pm 0.58	8.33 \pm 0.58	247.66 \pm 10.21	1117.33 \pm 122.07	26.8 \pm 0.26	5.05 \pm 0.18
BRR1 dhan46	138.33 \pm 2.34	40.66 \pm 0.58	15 \pm 1.00	27.98 \pm 0.10	12.66 \pm 2.08	9.33 \pm 0.58	253.67 \pm 24.54	1467 \pm 289.26	25.7 \pm 0.45	3.83 \pm 0.34
BRR1 dhan49	107.76 \pm 1.51	35.53 \pm 0.05	16 \pm 1.00	23.06 \pm 0.05	12 \pm 1.73	10.33 \pm 0.58	320.33 \pm 19.13	1509 \pm 209.98	19 \pm 0.50	5.00 \pm 0.10
BRR1 dhan51	92.36 \pm 2.45	27.76 \pm 0.15	17 \pm 1.00	23.8 \pm 0.17	12.33 \pm 0.58	9.67 \pm 0.58	269.33 \pm 21.36	1398.33 \pm 141.35	19.83 \pm 0.11	4.67 \pm 0.65
BRR1 dhan52	116.3 \pm 3.37	34.36 \pm 0.058	16.33 \pm 0.58	27.93 \pm 0.11	12.33 \pm 0.58	7.67 \pm 0.58	222 \pm 22.06	1096.33 \pm 143.98	25.2 \pm 0.95	4.76 \pm 0.19
BINA dhan7	96.46 \pm 1.51	31.63 \pm 0.11	14.66 \pm 0.58	24.51 \pm 0.07	10.67 \pm 0.58	7.67 \pm 0.58	328 \pm 29.61	779.67 \pm 165.16	21.4 \pm 0.40	4.68 \pm 0.34

(1989) reported that the parents separated by D^2 values of moderate generally showed higher heterosis.

CONTRIBUTION OF CHARACTERS TOWARDS DIVERGENCE OF THE VARIETIES

The values of Vector I and Vector II are presented in Table 7. Vector I obtained from PCA expressed that plant height (0.3644), flag leaf blade length (0.3002), panicle length (0.3755), primary branches per panicle (0.2477), number of filled grains per plant (0.1710) and thousand seed weight (0.3415) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II, days to plant height (0.0854), tillers per hill (0.0394) and thousand seed weight (0.0924), showed their important role toward genetic divergence. Negative values in both vectors for secondary branches per panicle, panicles/m² and grain yield had lower contribution towards the divergence.

SELECTION OF VARIETIES AS PARENT FOR HYBRIDIZATION PROGRAMME

Selection of generically diverse parents is an important step for hybridization program. Therefore, the varieties were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer 1960; Ghaderi et al. 1984; Moll et al. 1962; Ramanujam et al. 1974). Considering the magnitude of cluster mean and agronomic performance, the variety BRRI dhan40 for maximum plant height and panicle length from cluster IV; BRRI dhan44 for maximum thousand seed weight and yield from cluster II. Therefore considering group distance and other agronomic performance, the inter varietal crosses between BRRI dhan38 and BRRI dhan44; BRRI dhan38 and BRRI dhan40; BRRI dhan38 and BRRI dhan49; BRRI dhan40 and BRRI dhan44; BRRI dhan40 and BRRI dhan49; BRRI dhan40 and BINA dhan7; BRRI dhan44 and BRRI dhan49; BRRI dhan44 and BINA dhan7; BINA dhan7 and BRRI dhan38; BRRI dhan46 and BRRI dhan49; and BRRI dhan49 and BINA dhan7 may be suggested for future hybridization program (Table 8).

CONCLUSION

There is significant genetic diversity among the tested genotypes that indicates the presence of excellent opportunities to bring about improvement through wide hybridization by crossing genotypes with high genetic distance. Plant height and number of filled grains per plant were the important component characters having higher contribution to the genetic divergence. Wide genetic diversity was observed in 15 varieties of rice, which were grouped into four clusters and most diverse varieties were BRRI dhan46 and BRRI dhan49. That variability could be used for breeding materials of future breeding programme of rice in Bangladesh. High heritability coupled with high genetic advance in percent of mean was observed in plant height and thousand seed weight. Hence, yield

improvement in rice would be achieved though selection of these characters. The varieties of clusters IV were more diverse from the varieties of cluster I.

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