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GENETIC DIVERSITY OF BORO RICE (*Oryza sativa* L.) LANDRACES IN BANGLADESH

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ABSTRACT

Genetic diversity of 45 traditional Bangladeshi boro rice genotypes was studied through Mahalanobis D^2 statistics and was grouped into six clusters. The inter-cluster distances were higher than intra-cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra-cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the cluster. The cluster V contained the highest number of genotypes (14) and the cluster I and VI contained the lowest (4) number. The highest intra-cluster distance was noticed for the cluster VI and the lowest for cluster V. The highest inter-cluster distance was observed between cluster I and VI followed by cluster II and VI, cluster I and V and the lowest between cluster II and IV. The genotypes from cluster VI could be selected as parents for hybridization for producing transgressive segregants. The highest cluster means for yield, grains per panicle and grain length-breadth ratio were obtained from cluster I; whereas higher yield, grain breadth, 1000 grain weight, flag leaf area, shortest growth duration were obtained from cluster V. Therefore, more emphasis should be given on cluster I, cluster V and cluster VI for selecting genotypes as parents to produce new recombinants with desired traits.

Key words: Rice (*Oryza sativa* L.); D^2 analysis; cluster analysis;

INTRODUCTION

Rice is considered as a major crop in Bangladesh as it constitutes 90.56% of the total food grain (rice, wheat & maize) production (Anonymous, 2015). 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 ecosystem, irrigated (Boro rice) is the most suitable for growing rice in this country. Area under Boro is the second highest which is about 42.39% of total rice land and contributes 55.29% of the total rice production (Anonymous, 2015).

Tomooka (1991) reported that evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm. Genetic

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diversity is a powerful tool to determine the genetic discrimination among the genotypes which is used to select appropriate plant genotypes for hybridization to develop high yielding potential variety (Bhatt, 1970). Biometrical techniques such as multivariate analysis based on the Mahalanobis (1936) statistics is used to quantify divergence among the biological population and assess the relative contribution of different components to the total divergence at intra and inter-cluster levels. Such techniques also used to select genetically diverse parents to obtain desirable recombinant in the segregating generations. Hybridization is a common practice for combining the desirable characters of two or more lines or varieties into a single variety. In several cases, the progenies become far superior to the parents in vigor *i.e.* hybrid vigor or heterosis. Inclusion of more diverse parents (within a limit) is believed to increase the changes for obtaining stronger heterosis and gives broad spectrum of variability in segregating generations (Joshi and Dhawan, 1966; Ananda and Murty, 1968). In addition, crossing in moderately diverse parents also showed maximum heterosis (Chauhan and Singh, 1982). The necessity of principal component analysis (PCA), principal coordinate analysis (PCO), non-hierarchical clustering and canonical vector analysis (CVA) for measuring the degree of divergence has been established by several investigators in rice and other crops (Selvakumar *et al.*, 1989; De *et al.*, 1988; Pathan *et al.*, 1993).

More than 8000 rice germplasm have been registered in BRRRI genebank (BRRRI Annual Report, 2015-16). But information on grain yield and yield contributing characters in traditional rice is scanty. More information is required on this aspect. Keeping this in view, the present study was focused to assess the extent of genetic diversity in 45 land races of boro rice.

MATERIALS AND METHODS

Forty five rice genotypes collected from the genebank of Bangladesh Rice Research Institute (BRRRI), Gazipur were grown under irrigated condition (Boro) in 2015-16. The trial was conducted in a randomized complete block design with three replications. Forty days-old seedlings from each entry were transplanted using single seedling per hill in 2.4 m² plot following 25 cm and 15 cm space between rows and plants, respectively. Fertilizers were applied @ 80:60:40: 12 kg N, P, K and S per hectare. All the fertilizers except N were applied at final land preparation. Nitrogen was applied in three equal splits, at 15 days after transplanting (DAT), at 35 DAT and just before flowering. Intercultural operations and pest control measures were done as and when necessary. At maturity, grain yield (g/hill) was taken and adjusted at 14% moisture level. Ten plants from each entry were randomly selected for recording data on flag leaf length (cm), flag leaf width (cm), plant height (cm), days to flowering, days to maturity, panicle length (cm), effective tiller no., filled grains per panicle (no.), unfilled grains per panicle (no.), grain length (mm), grain breadth (mm), length-breadth ratio, 1000 grain weight (g) and yield/hill (g). The data were analyzed following principal component analysis (PCA) and Mahalanobis (1936) generalized distance (D^2) extended by Rao (1952). Intra and inter cluster distances were calculated by the methods of Singh and Chaudhury (1985). All statistical analyses were carried out using GENSTAT 5.13.

RESULTS AND DISCUSSION

Eigen values (latent roots) and percentage of total variation accounted for them obtained from principle component analysis are offered in Table 1. The result exposed that the first five components in the PCA with eigen values >1, contributed 77.68 % of the total variations among the genotypes for 14 morphological characters. Islam *et al.*

(2016) observed that the first nine axes accounted about 90% of the total variations by PCA in 113 aromatic and fine grain rice landraces. Chakravarty *et al.* (2013) observed the contribution of 76.7% of the first six components to the total variation of rice.

Table 1. Latent roots (Eigen Values) and their variation in 14 quantitative characters in 45 landraces

Principal component axes	Latent roots	Variation (%)	Cumulative % of variation
I	3.692	26.37	26.37
II	2.686	19.18	45.55
III	2.189	15.64	61.19
IV	1.337	9.55	70.75
V	0.969	6.93	77.68
VI	0.809	5.78	83.46
VII	0.673	4.81	88.27
VIII	0.549	3.92	92.19
IX	0.455	3.25	95.44
X	0.274	1.96	97.40
XI	0.199	1.43	98.83
XII	0.120	0.86	99.69
XIII	0.039	0.28	99.97
XIV	0.005	0.03	100

Based on the degree of divergence 45 boro rice genotypes were grouped into six clusters on the basis of cluster analysis (Table 2). Islam *et al.* (2016) reported ten clusters, Ahmed *et al.* (2010) and Islam *et al.* (2014) reported six clusters and Siddique *et al.* (2013) reported five clusters in rice genotypes. The distribution pattern of the genotypes indicated that maximum 14 entries were grouped into the cluster V followed by 11 in cluster IV, 7 in cluster III and 5 in cluster II. The cluster I and VI contained the lowest (4) number of genotype.

Intra and inter-cluster distance are presented in Table 3. The inter-cluster distances in almost all of the cases was higher than the intra-cluster distance indicating that wider diversity was present among genotypes of distant groups. The germplasm are traditional and they showed high variability between them which was revealed from the results of intra and inter-cluster distance values. The highest intra-cluster value was 1.347 and the highest inter-cluster value was 17.815, which clearly indicated variability's in the germplasm of different clusters (Table 3). However, lower values in clusters IV (0.813) and V (0.755) was observed due to lower variation in all morpho-agronomic data within these groups. The intra-cluster distances were low for all the six clusters with the range of 0.755 in cluster V to 1.347 in cluster VI which indicated homogeneous nature of the genotypes within the clusters. The results were supported by the findings of Siddique *et al.* (2010 and 2011) in rice. The inter-cluster distances ranged from 4.732 to 17.815 and PCoA scores also indicated a high degree of genetic diversity among the genotypes. Regarding inter-cluster distance, cluster I showed maximum genetic distance (17.815) from cluster VI followed by cluster II (13.859), from cluster VI, Cluster I (13.334) from cluster V and so on. It is obvious that in most of the cases cluster VI produced the highest inter-cluster distances (D^2 values) with all other clusters except V suggesting wide diversity between the genotypes.

Table 2 . Distribution of 45 rice genotypes into six clusters

Cluster	No. of Genotypes	% of total Genotypes	Name of genotypes with BRRI Accession no.
I	04	8.89	Gatu (NC), Chini sail (NC), Lafaia (7675), Sada boro (7679)
II	05	11.11	Chini kuri (NC), Porbat jira (NC), Bash ful (NC), Boro habji (NC), Khanni dhan (7661)
III	07	15.55	Soto babu (NC), Rashian jira (NC), Khato bhojon (7656), Black bhojon (7659), Sada bhojon (7660), Ayla binni (7666), Subal lata (7680)
IV	11	24.45	Kabar balam (NC), Unknown (NC), Rata boro (NC), Gocha dhan (NC), Kali boro (7657), Abdul hai (7662), Begun bichi (7664), Ayna sail (7665), Lakhain (7670), Dholi boro (7674), Rata (7676)
V	14	31.11	Gagli boro (NC), Gochi (NC), Boro (NC), Bairage sail (NC), IA-37 (NC), IA-38 (NC), Lati boro (NC), Lal bhojon (7658), Kalo boro (7663), Asami boro (7667), Khaiya boro (7671), Kalo boro (7673), Kakhai biruin (7677), Kala irri (7678)
VI	04	8.89	Jagli (NC), Pabda for (7668), Amania (7669), Kali boro (7672)

NC-New Collection

The genotypes in these clusters could be used as parents in hybridization program for getting transgressive segregants (Saini and Kaiker, 1987). Moderate inter-cluster distance was observed between cluster VI and IV (10.025), followed by cluster V and II (9.428), cluster IV and I (8.475). The minimum inter-cluster diversity was observed between cluster V and VI (5.151) and cluster V and IV (4.732) indicating that the genotypes of these clusters were genetically closed. The results were supported by the findings of Islam *et al.* (2014) in Sada jira rice germplasm.

Table 3. Intra (bold) and inter-cluster distances (D^2) among 45 Boro rice landraces

Clusters	I	II	III	IV	V	VI
I	0.953	5.977	9.502	8.475	13.334	17.815
II		0.871	8.111	4.732	9.428	13.859
III			1.008	5.908	7.095	11.483
IV				0.813	5.567	10.025
V					0.755	5.151
VI						1.347

The highest cluster means for yield, filled grains per panicle and grain length-breath ratio were obtained from cluster I (Table 4). The highest plant height, flag leaf area, days to flowering, days to maturity, and panicle length were found in cluster IV while the lowest mean value for yield, 1000 grain weight and other low to moderate mean value for yield contributing character were found in cluster II. Mean performance of different clusters for the characters studied revealed that dwarf stature, flag leaf area, moderately lower panicle length and comparative low yielding varieties were clubbed into cluster III, whereas higher yield and other higher yield contributing characters (grain breath, 1000 grain weight, flag leaf area) were obtained from cluster V. Maximum desirable characters were accumulated in cluster I and as a result higher grain yield (18.0g/ hill) was obtained in this cluster. Moreover, it was interesting that in the entire cases cluster VI produced the highest inter cluster-value with all other clusters, except cluster V. Therefore, the genotypes of cluster I and VI can be used in hybridization program to produce higher yielding genotypes.

Table 4. Cluster means for fourteen characters in Boro rice genotypes

Characters	I	II	III	IV	V	VI
Flag leaf length (cm)	48.20	48.24	41.43	54.53	48.20	47.20
Flag leaf width (cm)	0.97	0.98	1.13	1.08	0.99	0.90
Plant height (cm)	117.80	127.56	86.74	127.96	119.49	116.05
Days to flowering	131.75	127.60	129.71	135.64	125.71	127.50
Days to maturity	159.75	155.80	158.86	161.91	153.14	155.00
Panicle length (cm)	26.55	27.92	25.51	28.02	23.99	21.20
Effective tiller no.	13.75	9.40	12.14	12.36	14.43	19.00
Filled grains/panicle (no.)	201.00	152.60	122.57	118.91	75.50	32.25
Unfilled grains/panicle(no.)	22.25	18.00	18.57	17.55	12.93	6.50
Grain length (mm)	7.26	6.41	8.79	7.68	8.11	8.00
Grain breadth (mm)	2.29	2.84	2.91	2.85	3.04	2.94
Length-breath ratio	3.18	2.25	3.13	2.75	2.67	2.74
1000 grain weight (g)	19.62	18.40	27.86	24.07	28.76	27.82
Yield/hill (g)	18.01	13.18	16.63	17.61	17.44	14.47

Joshi and Dhawan (1966) reported that inclusion of more diverse parents (within a limit) is believed to increase the changes for obtaining stronger heterosis and give broad

spectrum of variability in segregating generations. Therefore, more emphasis should be given on cluster I and VI for selecting genotypes as parents for crossing with the genotypes of cluster V which may produce new recombinants with desired traits. Cluster II had the lowest cluster mean value for effective tiller, grain length and length-breadth ratio, 1000 grain weight and also lower grain yield. It was also noticed that yield performance in six clusters was moderate and less variable. From the above discussion it can be concluded that all these Boro varieties are genetically distant from each other. Contributions of the characters towards divergence are presented in Table 5. The canonical vector analysis revealed that the both vectors (vector 1 and 2) were found positive for flag leaf area, flag leaf width, days to flowering, days to maturity, plant height and grain yield. Similar findings were obtained by Siddique *et al.* (2011). Such result indicated that these six characters contributed maximum towards divergence. It is interesting that the greater divergence in the present materials due to these six characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic rice hybrids.

Table 5. Relative contributions of the fourteen characters to the total divergence in Boro rice

Traits	Vector 1	Vector 2
Flag leaf length(cm)	0.3197	0.2215
Flag Leaf Width	0.2468	0.2319
Plant height (cm)	0.2246	0.0740
Days to flowering	0.3785	0.2412
Days to maturity	0.3613	0.2194
Panicle length (cm)	0.4070	-0.0211
Effective tiller no.	-0.1821	0.1478
Filled grains per panicle	0.3043	-0.3373
Unfilled grains per panicle	0.2750	-0.2383
Grain length (mm)	-0.2491	0.2372
Grain breadth (mm)	-0.0058	0.4986
Length-breath ratio	-0.1711	-0.2086
1000 grain weight (g)	-0.2247	0.4408
Yield/hill (g)	0.0618	0.2234

It is assumed that, maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production and reducing the life duration. In the present study the maximum distances existed between cluster I and VI. However, considering the yield, filled grains number, crosses involving cluster I and cluster II may exhibit high heterosis for yield. Again, considering growth duration and yield, crosses between cluster I and V may exhibit higher heterosis for earliness and dwarf stature. Mian and Bahl (1989) reported that the parents separated by inter-cluster of medium magnitude generally showed higher heterosis in chickpea. Similar findings also reported by Habib *et al.* (2005) in rice. Keeping this view in mind, it appears that the crosses between the genotypes/parents of cluster I and cluster VI, cluster I and cluster V would exhibit high heterosis as well as higher level of yield potential. So, based on this result, the genotypes under cluster I, cluster V and cluster VI might be selected for future breeding program.

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