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

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ABSTRACT

Genetic diversity in 40 traditional boro rice genotypes was studied under irrigated condition through Mahalanobis D^2 statistic for grain yield and yield contributing characters. The genotypes were grouped into five clusters. The inter-cluster distances were higher than intra-cluster distances indicating wider genetic diversity among the clusters. The intra-cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the clusters. The cluster IV contained the highest number of genotypes (22) and the cluster II and V contained the lowest (1). The highest intra-cluster distance was noticed for the cluster III and lowest for cluster II and V. The highest inter-cluster distance was observed between cluster II and III followed by cluster II and V, cluster I and II and the lowest between cluster I and IV. Regarding inter-cluster distance, the genotypes of cluster II showed high genetic distance from all other clusters. The genotypes from cluster II could be hybridized with the genotypes of other clusters for producing transgressive segregants. Based on positive value of vector 1 and vector 2, panicle/hill had maximum contribution towards genetic divergence. The highest cluster means for yield, flag leaf length and grain length breadth ratio were obtained from cluster IV. The highest 1000-grain weight, shortest growth duration and grain breadth were found in cluster II while the lowest mean value for yield, flag leaf length, filled grains and 1000 grain weight were found in cluster V. Therefore, more emphasis should be given on cluster II, III and cluster IV for selecting genotypes as parents for crossing with the genotypes of cluster V which would be used to produce new recombinants with desired traits.

Key words: Genetic diversity, D^2 analysis, cluster analysis, rice (*Oryza sativa* L)

INTRODUCTION

Rice is considered as a major crop in Bangladesh as it constitutes 91.8% of the total food grain (rice, wheat & maize) production (Anonymous, 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 increasing demand for food. Among different ecosystems, irrigated boro is the most suitable for growing rice in this country. Area under boro is the second highest which is about 39.80% of total rice land and contributes 52.07% of the total rice production (Anonymous, 2011-12).

Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which is used to select appropriate parents for hybridization to develop high yielding potential variety (Bhatt, 1970). With the development of advanced biometrical techniques such as multivariate analysis based on the Mahalanobis (1936) statistics, quantification of divergence among the biological population and assessing the relative contribution of different components to the total divergence at intra and inter-cluster levels have now become possible. Such a study also permits to select the genetically diverse parents to obtain the desirable recombinant in the segregating generations upon crossing. 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. Inclusion of more diverse parents (within a limit) is believed to increase the chances 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).

About 8700 rice germplasm have been preserved in BRRI gene bank. But information on this aspect is scanty. The present study was, therefore undertaken to assess the extent of genetic diversity in 40 traditional Boro rice genotypes. This will help in classifying those into clusters to select genotypes as prospective parents to develop transgressive segregants which will be ultimately used for developing modern variety.

MATERIALS AND METHODS

Forty boro rice genotypes selected from the germplasm bank of Bangladesh Rice Research Institute (BRRI), Gazipur were grown under irrigated condition (boro) in 2011-12. The trial was conducted in a randomized complete block design with three replications. Thirty days-old seedlings from each entry were transplanted using single seedling per hill in 2.4 m^2 plot following 25 cm and 20 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. Ten hills from each entry were randomly selected for recording data on flag leaf length (cm), flag leaf width (mm), plant height (cm), days to 50% flowering, days to maturity, panicle/hill (no.), panicle length (cm), grain length (mm), grain breadth (mm), length-breadth ratio, 1000 grain weight (g), filled grains/panicle (no.), unfilled grains/panicle (no.) and yield/hill (g). Grain yield (g/hill) was taken and adjusted at 14% moisture level. The data were analyzed following principal component analysis (PCA) and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Intra and inter cluster distances were calculated by the methods of Singh and Chaudhary (1985). All statistical analyses were carried out using Genstat 5.5.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the 40 genotypes for all of the 14 characters under study indicating the presence of notable genetic variability among the genotypes. The principal component analysis showed that the first two components accounted for 77.57% of the total variation.

Based on the degree of divergence 40 genotypes were grouped into five clusters on the basis of cluster analysis (Table 1). Maximum 22 entries were grouped into the cluster IV followed by 8 in cluster I and III. The cluster II and V contained the lowest (1) number of genotype.

Table 1. Distribution of 40 rice genotypes in different clusters grown in boro 2011-12

Cluster no.	No. of genotypes	BRRI Accession no. of Genotypes	Name of the Genotypes
I	8	178,180,181,262,1405,1713,1791,1863	Cunail, Dholi boro, Ghuni boro, Kaikka boro, Deshi boro, Soloi, Sada boro
II	1	2195	Kali boro 80/9
III	8	933,936,1809,1813,1814,1818,1971,1819	Jhatisail, Khaia boro, Boro jagli, Begun bitchi, Bana jira, Bash boro, Gochi, Rajasail
IV	22	645,929, 1704,1708, 1804,1806,1811,1865,1969,1970,1972,2190,2196,2198,2199,2200,2201,2203,2204,2218,2221,2222	Jajli, Poshusail, Jagli, Bawoi, Bogra boro, Jagli boro, Tupa, Borya, Lafai, Sail boro, Biron, Kali boro 4/1, Kali boro 109/4, Kali boro 139/2, Kali boro 200, Kali boro 208, Kali boro 259, Kali boro 576, Kali boro 600, Boro, Boro, Boro 102/3
V	1	2197	Kali boro 138/2

Intra and inter-cluster distances are presented in Table 2. All the inter-cluster distances were larger than the intra-cluster distance indicating presence of wider diversity among genotypes of distance groups. The genotypes are traditional but they showed high variability among them which was revealed from the results of intra and inter-cluster distance values. The highest intra cluster value was 0.6327 and the highest inter-cluster value was 36.45, which clearly indicated the variability in the germplasm of different clusters. However, lower values in clusters IV (0.5306) and I (0.6032) was observed due to lower variation in all morpho-agronomic data within these groups. The intra-cluster distances were low for all the five clusters with the range of 0.5306 in cluster IV to 0.6327 in cluster III which indicated homogeneous nature of the genotypes within the clusters. The results were supported by the findings of Siddique *et al.* (2011) in rice. The inter-cluster distances ranged from 5.45 to 36.45 and PCA scores also indicated a high degree of genetic diversity among the genotypes. Regarding inter-cluster distance, cluster II showed maximum genetic distance (36.45) from cluster III followed by cluster II (34.71) from cluster V, Cluster II (34.60) from cluster I. It is obvious that in all the cases cluster II produced the highest inter-cluster distances with other clusters suggesting wide diversity of the genotype within cluster II with the genotypes of other clusters and 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 III and V (13.46), followed by cluster I and III (10.32), cluster IV and V (8.24). The minimum inter-cluster diversity was observed between cluster I and IV (5.45) and cluster I and V (7.46) indicating that the genotypes of these clusters were genetically closed.

Table 2. Intra (bold) and inter-cluster distances (D^2) for 40 boro rice genotypes

Cluster	I	II	III	IV	V
I	**0.6032**	34.60	10.32	5.45	7.46
II		**0.0000**	36.45	33.78	34.71
III			**0.6327**	6.34	13.46
IV				**0.5306**	8.24
V					**0.0000**

The highest cluster means for yield, flag leaf length and grain length-breath ratio were obtained from cluster IV (Table 3). The highest grains/panicle, days required to maturity and panicle length were found in cluster III while the lowest mean value for yield, grains/panicle, 1000-grain weight and the highest mean value for plant height, panicle/hill and grain length were found in cluster V.

Mean performance of different clusters for the characters revealed that dwarf stature, short growth duration, the highest1000-grain weight, lower panicle/hill and higher yielding varieties were clubbed into cluster II whereas the lowest flag leaf length and width, grain breath and the lowest growth duration rice were obtained from cluster I.

Maximum good characters were accumulated in cluster IV and as a result higher yield (7.95 g/hill) was obtained in this cluster. But it was interesting that in the entire cases cluster II produced the highest inter cluster-value with all other clusters. Therefore, the genotypes of cluster II and IV can be used in hybridization program to produce higher yielding genotypes.

Table 3. Cluster means for fourteen characters of 40 boro rice genotypes

Characters	Cluster Number				
	I	II	III	IV	V
Flag leaf length (cm)	28.71	34.07	35.04	35.28	29.73
Flag leaf width (cm)	9.53	11.67	11.08	11.28	10.60
Plant height (cm)	89.87	96.20	107.43	106.79	126.80
Days to 50% flowering	118.46	115.00	117.50	118.68	119.67
Days to maturity	147.62	101.53	151.09	147.73	148.67
Panicles/hill	12.42	10.73	11.29	12.16	13.80
Panicle length (cm)	19.66	21.73	24.81	21.51	21.20
Filled grains/panicle	49.38	65.87	91.53	68.19	44.93
Unfilled grains/panicle	6.35	7.67	11.21	8.95	6.47
Grain length (mm)	7.65	7.84	7.51	8.10	8.20
Grain breadth (mm)	2.56	3.08	2.57	2.67	3.05
Length-breath ratio	3.05	2.54	3.02	3.06	2.69
1000 grain weight (g)	20.65	20.73	20.70	20.60	20.00
Yield/hill (g)	6.74	7.69	7.00	7.95	5.71

Joshi and Dhawan (1966) reported that inclusion of more diverse parents (within a limit) is believed to increase the chances for obtaining stronger heterosis and give broad spectrum of variability in segregating generations. Therefore, more emphasis should be given on cluster II and IV for selecting genotypes as parents for crossing with the genotypes of cluster V which may produce new recombinants with desired traits. Cluster V had the lowest cluster mean value for filled grains/panicle which had negative effect on mean value of yield. It was also noticed that yield performance in five clusters was less variable. The results reflected that all these Boro varieties are genetically distant from each other.

Contributions of the characters towards divergence are presented in Table 4. The canonical vector analysis revealed that the vectors (vector I and II) for only panicle/ hill were positive. Such results indicated that this single character contributed maximum towards divergence. It is interesting that the greater divergence in the materials under study was due to this single character, which will offer a good scope for improvement of yield through rational selection of parents.

Table 4. Relative contributions of the fourteen characters to the total divergence in boro rice

Trait	Vector 1	Vector 2
Flag leaf length (cm)	-0.3805	0.1782
Flag leaf width (mm)	-0.3456	0.0165
Plant height (cm)	-0.2733	0.0075
Days to 50% flowering	0.2318	-0.0421
Days to maturity	-0.1259	-0.1802
Panicle/hill	0.1803	0.0661
Panicle length (cm)	-0.4286	-0.0282
Filled grains/panicle	-0.4410	-0.0448
Unfilled grains/panicle	-0.4179	-0.1882
Grain length (mm)	-0.0209	-0.1052
Grain breadth (mm)	-0.0598	0.6236
Length-breath ratio	0.0425	-0.6457
1000 grain weight (g)	-0.0176	-0.1408
Yield/hill (g)	-0.0015	-0.2330

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 to have high heterosis but also to achieve high level of production reducing the growth duration. In the present study, the maximum distances existed between cluster II and III. However, considering the yield, filled grains/panicle, 1000-grain weight, crosses involving the parents of cluster III and cluster V may exhibit high heterosis for yield. Again, considering growth duration, and plant height, crosses between the parents of cluster II and III 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 were also reported by Habib *et al.,* 2005 for rice. Keeping this view in mind, it appears that the crosses between the genotypes/parents of cluster II and cluster III, cluster III and cluster V would exhibit high heterosis as well as higher level of yield potential. Therefore, the genotypes under cluster II, cluster III, cluster V might be selected for future breeding program.

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