

**GENETIC DIVERSITY AND PARENTS SELECTION FROM EXOTIC RICE
(*Oryza sativa* L.) GERMPLASM**

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ABSTRACT

Genetic divergence among fifty exotic rice genotypes along with two check varieties were estimated using D^2 and principal component analysis. The study was undertaken to select suitable donor parents for use in improved breeding program of Bangabandhu Sheikh Mujibur Rahman Agricultural University in 2009. Principal component analysis (PCA) revealed that the first five axes accounted for 58.10% of the total variation. As per cluster analysis, the genotypes were grouped into seven clusters consisting 11, 16, 7, 11, 1, 2 and 4 genotypes which revealed that there exist considerable diversity among the genotypes. Considering the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters, the genotypes RG-BU-08-057, 61, 65, 67, 69, 71, 85, 86, 88, 94, 96, 98 and 99 might be selected as a suitable parent for future hybridization program.

Key words: Rice (*Oryza sativa* L.), genetic variability, parents, hybridization.

INTRODUCTION

Rice (*Oryza sativa* L.) is the second largest cereal in the world. With the increasing population pressure, the demand of cereal is increasing day by day. Bangladesh agricultural economy predominantly based on rice production. Rice occupies about 75% of the total cropped area and constitutes 94% of cereals production (Anonymous, 1999). Although Bangladesh is now on the verge of attaining self-sufficiency in cereal production, there is still a major gap between the production and demand. Two-third of Bangladesh populations is engaged in livelihood activities related to rice. (<http://asiarice.org/asiarice/demosite/sections/chapters/Bangladesh/BRF>). Production potentiality of rice does not only depend on cultural practices and management, but also on the suitability of rice varieties. Development of potential rice varieties depends on existing germplasm collected and conserved by genetic resources centers (Ng *et al.*, 1988). The progress of breeding is conditioned by the magnitude and nature of inter-relationship among the characters and variation of different characteristics. Knowledge about genetic control of the characters is essential in formulating an efficient breeding scheme as it provides not only a basis for selection but also some valuable indication relating selection of parents to be hybridized. Exotic species present potential donor sources for complex traits such as yield and would help to realize the dream of sustained food security. However, the utilization of these rice

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genetic resources had been limited to only adaptable genotypes (Caldo *et al.*, 1996). Genetic diversity is a useful tool in quantifying the degree of divergence in a biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Jatasara and Paroda, 1978). Cluster analysis is also carried out to detect divergent parents for hybridization purposes and to attain meaningful group constellations of a collection of genotypes. Considering the availability of genetic variability, its scope of yield improvement and export potential, the present investigation was undertaken to search suitable diverse germplasm as suitable donor parents for the utilization in future breeding program.

MATERIALS AND METHODS

A total of fifty exotic rice genotypes and two varieties, collected from Department of Genetics and Plant Breeding of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur namely: RG-BU-08-051 to RG-BU-08-100, BRR1 dhan28 and BRR1 dhan29, were grown at the experimental farm of BSMRAU, Gazipur following randomized block design with three replications in 2009. The field was divided into three blocks, the blocks were subdivided into 52 plots where genotypes were randomly assigned. The unit plot size was 12.5m × 2.5m. Each plot had two lines. Row to row and plant to plant distances were 25cm and 20cm respectively. Standard agronomic practices were followed to raise a good crop. Observations were recorded on days to first flowering (DFF), days to 50% flowering (50%DF), days to harvesting (DH), anther length (AL), anther breadth (AB), stigma length (SL), stigma breadth (SB), pollen sterility (PS), pollen fertility (PF), spikelet sterility (SS), out crossing rate (OCR), filled grains per panicle (FGP), unfilled grains per panicle (UGP), grain length (GL), grain breadth (GB) and grain yield per hill (GYH). Data were subjected to both univariate and multivariate analysis. Under multivariate analysis Principal Component Analysis (PCO), Principal Coordinate Analysis (PCA), Cluster Analysis (CA) and Canonical Vector Analysis were done by using GENSTAT 5.5 program.

RESULTS AND DISCUSSION

Analysis of variance showed significant variations among the tested genotypes for all the characters studied indicating a wide range of genotypic variation among the genotypes. Estimated eigen values of principal component indicated that the first five axes accounted for 58.10% of the total variation while the former two accounted for 27.07%. These results are in agreement with the findings of Ogunbayo *et al.* (2005). On the basis of principal axes I and II, a two dimension chart (Z_1 - Z_2) of the genotypes are presented in Fig. 1. As per the scattered diagram the genotypes were apparently distributed into seven clusters.

Non-hierarchical clustering using co-variance matrix among the genotypes grouped the rice genotypes into seven clusters. Singh *et al.* (1987) and Rao *et al.* (1981) reported ten clusters, Anandakummar and Subramanian (1989), and Biswas and Sasmal (1990) reported six clusters and Ratho (1984) reported five clusters in rice genotypes. The clustering pattern is determined by the principal component analysis (Table 1) which represent the composition of different clusters with the genotypes. The distribution pattern of the genotypes indicated that the maximum genotypes (16) were included in cluster II followed by cluster I & IV (11), cluster III (7), cluster VII (4), cluster VI (2) and cluster V (1). Genotypes in seven clusters were ranged from 1 to 16. The distribution

of genotypes into seven clusters revealed that there exists considerable diversity among the genotypes.

Table 1. Distribution of 50 exotic rice genotypes with two check varieties in seven clusters

Cluster	Members	Name of Genotypes
I	11	RG-BU-08-055, 57, 65, 67, 71, 74, 81, 84, 85, 86
II	16	RG-BU-08-053, 54, 58, 60, 61, 63, 64, 69, 70, 72, 78, 89, 91, 92, 96, 97
III	7	RG-BU-08-068, 76, 79, 80, 82, 93, 95
IV	11	RG-BU-08-051, 52, 56, 62, 77, 83, 90, 94, 100, BRR1 dhan28, BRR1 dhan29
V	1	RG-BU-08-099
VI	2	RG-BU-08-088, 98
VII	4	RG-BU-08-059, 73, 75, 87

Intra-cluster distances were estimated using the inter genotypic distance (Table 2) following Singh and Chaudhury (1977). The highest intra-cluster distance was recorded in cluster VII (2.08) containing four genotypes followed by cluster I (1.65) with eleven genotypes. The lowest intra-cluster distance was observed in cluster V (0) having the lowest (1) number of genotype and the cluster II showed the second lowest intra cluster distance (0.13) having the highest (16) number of genotypes. Such results indicated that the genotypes of cluster VII were more heterogeneous as compared to those included in cluster II.

The highest inter-cluster distance was observed between cluster V and VI (36.37) followed by clusters V and VII (36.08) (Table 2). The lowest inter-cluster distance was observed between cluster IV and VI (0.56) followed by cluster II and IV (0.74). The maximum value of inter cluster distance indicated that the genotypes belonging to cluster V was far diverged from those of cluster VI. The minimum inter cluster divergence was observed between cluster IV and VI (0.56) indicating that the genotypes of these clusters were genetically closed. However, genotypes within the other pair of clusters indicated that they were less diverged. The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. The results were in agreement with Rahman *et al.* (1997) and Singh and Chaudhury (1985).

Table 2. Average intra (Diagonal) and intercluster distances (D^2) of 50 exotic rice genotypes with 2 check varieties on the basis of sixteen morphological characters

	I	II	III	IV	V	VI	VII
I	1.65						
II	10.62	0.13					
III	4.34	6.44	1.52				
IV	11.34	0.74	7.12	0.32			
V	34.05	35.53	35.14	35.92	0		
VI	11.16	0.88	6.90	0.56	36.37	1.08	
VII	8.11	2.88	3.78	3.48	36.08	3.17	2.08

Higher inter and intra-cluster distances indicated higher genetic variability among genotypes between and within clusters, respectively. The minimum inter and intra-cluster distance indicated closeness among the genotypes of two clusters and within

the cluster also. These relationships, in respect of genetic distance, were also reflected in the scatter diagram (Fig. 1). Genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregants (Mokate *et al.*, 1998). Crossing might be carried out between genotypes belonging to different clusters having genetic distances (D^2) greater than 12.5 (Wei *et al.*, 1994). Thus parents selected from the distant clusters V, VI and VII may manifest the highest level of heterotic response in crosses.

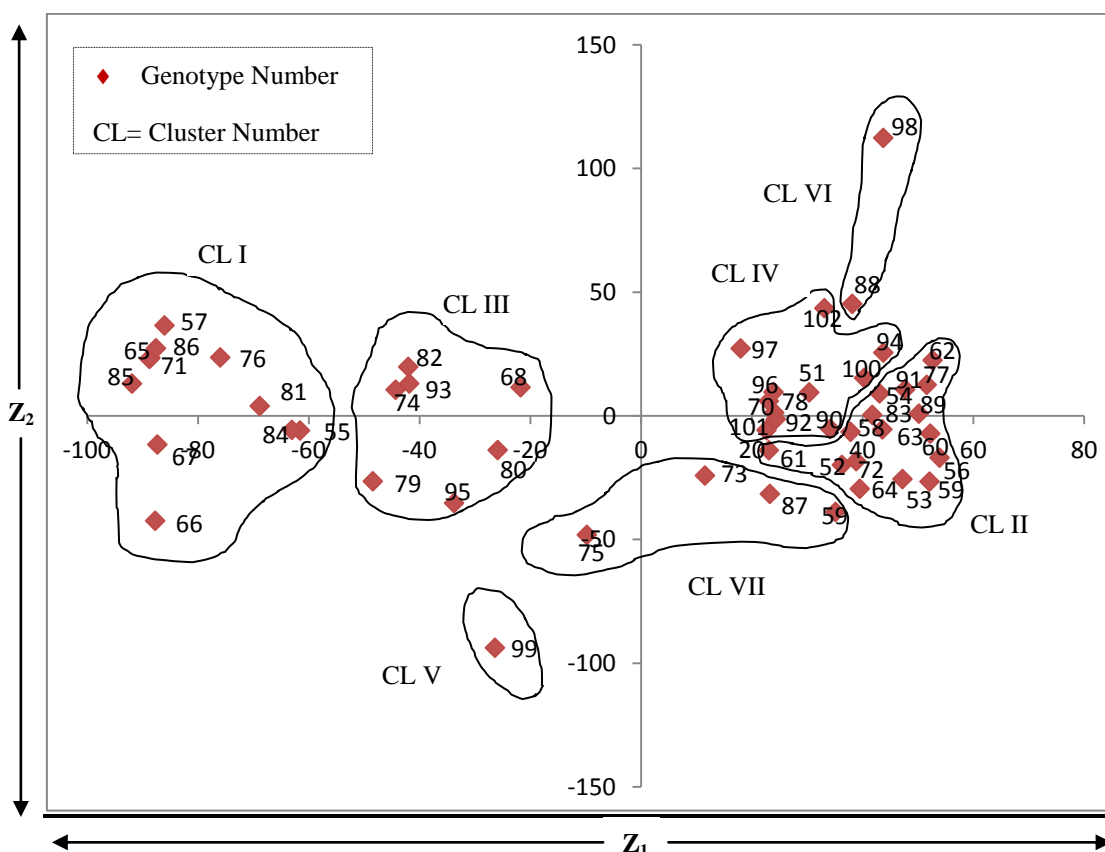


Fig. 1: Relative position of 50 exotic rice genotypes with 2 check varieties in Z_1 - Z_2 graph based on the morphological characters superimposed with clustering.

Results of 10 higher and 10 lower inter genotypic estimated from distant matrix of Principal Coordinate Analysis are shown in Table 3. The highest inter genotypic distance (6.448) was observed between RG-BU-08-085 and RG-BU-08-069 followed by the distance 6.444 observed between RG-BU-08-085 and RG-BU-08-062. Genotypes RG-BU-08-085 and RG-BU-08-069, a high level of pollen fertility with moderate seed length and seed breadth, may be selected as parent. Genotypes RG-BU-08-086, 57, 65 etc. may be selected as parents for hybridization since Chauhan and Singh (1982) reported maximum heterosis observed in those crosses, which were involved moderately diverged parents. Ying *et al.* (1991) also reported the heterobeltiosis from the cross between intermediate distant classes. Buu and Tuan (1989) and Joshi and Dhawan (1966) reported that genetic diversity is very much important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops like rice. Bhatt (1970) inferred that Mahalanobis's D^2 statistic is a powerful tool for choosing diverse parents for hybridization.

Table 3. Ten higher and ten lower inter genotypic distance among the 50 exotic rice genotypes with 2 check varieties from distance matrix in PCO

Sl. No.	Genotypic combination	Distances
A. 10 higher inter genotypic distance		
01	RG-BU-08-085 - RG-BU-08-069	6.448
02	RG-BU-08-085 - RG-BU-08-062	6.444
03	RG-BU-08-084 - RG-BU-08-056	6.310
04	RG-BU-08-085 - RG-BU-08-077	6.222
05	RG-BU-08-086 - RG-BU-08-069	6.004
06	RG-BU-08-086 - RG-BU-08-062	5.968
07	RG-BU-08-069 - RG-BU-08-057	5.931
08	RG-BU-08-086 - RG-BU-08-060	5.915
09	RG-BU-08-086 - RG-BU-08-056	5.865
10	RG-BU-08-069 - RG-BU-08-065	5.852
B. 10 lower inter genotypic distance		
01	RG-BU-08-071 - RG-BU-08-057	0.380
02	RG-BU-08-071 - RG-BU-08-065	0.387
03	RG-BU-08-086- RG-BU-08-065	0.473
04	RG-BU-08-084- RG-BU-08-055	0.502
05	RG-BU-08-063- RG-BU-08-054	0.524
06	RG-BU-08-065 - RG-BU-08-057	0.588
07	RG-BU-08-078- RG-BU-08-070	0.597
08	RG-BU-08-091 - RG-BU-08-063	0.604
09	RG-BU-08-092 - RG-BU-08-070	0.610
10	RG-BU-08-074 - RG-BU-08-068	0.613

Considering the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters the genotypes RG-BU-08-057, 61, 65, 67, 69, 71, 85, 86, 88, 94, 96, 98, & 99 might be selected as parents for efficient hybridization program.

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