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GENETIC DIVERSITY OF LOCAL RAINFED RICE (*Oryza Sativa* L.)

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ABSTRACT

Genetic diversity of 58 traditional local rice genotypes was studied under rainfed condition through Mahalanobis D^2 statistic for grain yield and yield contributing characters. The genotypes were grouped into nine 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 clusters. The cluster III contained the highest number of genotypes (13) and the cluster I contained the lowest (2). The highest intra-cluster distance was noticed for the cluster I and the lowest for cluster VII. The highest inter-cluster distance was observed between cluster I and IV followed by cluster IX and IV, cluster I and VI and the lowest between cluster V and III. Regarding inter-cluster distance, the genotypes of cluster IV showed high genetic distance from all other clusters. The genotypes from cluster IV could be hybridized with the genotypes of other characters of other clusters for producing transgressive segregants. Based on positive value of vector 1 and vector 2, flag leaf length, plant height, panicle length and grain breath had maximum contribution towards genetic divergence. The highest cluster means for yield, 1000 grain weight and grain breath were obtained from cluster VIII. The highest plant height, flag leaf width and panicle length were found in cluster II while the lowest mean value for yield, days to flowering and maturity, unfilled grain and the highest mean value for grain length breadth ratio were found in cluster II. Therefore, more emphasis should be given on cluster IV and cluster VIII, cluster I and cluster IV for selecting genotypes as parents for crossing with the genotypes of cluster II 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 96% of the total food grain (rice and wheat) production of 28.93 million metric tons (Anonymous, 2008). 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 different ecosystems, rainfed condition is the most suitable for growing T. Aman rice in this country. Area under T. Aman is the highest which is about 49.40% of total rice land and contributes 37.06% of the total rice production (Anonymous, 2010). Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which used to select appropriate plant genotypes 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 changes for obtaining stronger heterosis and gives broad spectrum of variability in segregating generations (Joshi and Dhawan, 1966 and 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 and Pathan *et al.,* 1993). About 8000 rice germplasms 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 58 traditional rice varieties. This will help in classifying those into clusters to select varieties as prospective parents to develop transgressive segregants.

MATERIALS AND METHODS

Fifty eight rice genotypes including one salt tolerant variety selected from the germplasm bank of Bangladesh Rice Research Institute (BRRI), Gazipur were grown under rainfed condition (T. Aman) in 2009. 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. 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 50% flowering, days to maturity, panicle length (cm), grain length (mm), grain breadth (mm), length-breadth ratio, 1000 grain weight (g), filled grains $panicle^{-1}$, unfilled grains $panicle^{-1}$ and yield $hill^{-1}$ (g). 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 58 genotypes for all 13 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 69.28% of the total variation. Based on the degree of divergence 58 genotypes were grouped into nine clusters on the basis of cluster analysis (Table 1). The maximum 13 entries were grouped into the cluster III followed by 10 in cluster IV, seven in cluster V and VI, six in clusters VIII and IX, four in clusters II and three in cluster VII. The cluster I contained the lowest (2) number of genotypes.

Intra and inter-cluster distance are presented in Table 2. All the inter-cluster distances was larger than the intra-cluster distance indicating presence of wider diversity among genotypes of distance groups. Most of the germplasm are traditional but 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 1.555 and the highest inter-cluster value was 13.006, which clearly indicated variability existed in the germplasm of different clusters. However, lower values in clusters VII (0.602) and V (0.615) was observed due to lower variation in all morpho-agronomic data within these groups.

Table 1. Distribution of 58 rice genotypes in different clusters grown in T. Aman 2009.

Cluster no.	No. of genotypes	BRRI Accession no. of Genotypes	Name of the Genotypes
I	2	4768, 5121	Kaijhuri, Jamni
II	4	4267, 4271, 4272, 5198	Birpala, Rayda, Dhaki Rayda, Dholeshwar Mota
III	13	4113, 4114, 4118, 4156, 4239, 4773, 5190, 5196, 5213, 5217, 5222, 5289, 5316	Ram Dash, Paizra, Kala Binni, Minki, Binni, Dudhsail, Bushihara Mota, Holde Mota, Koti Jira, Ashkor, Akra, Buri Pagli, Nonamurchi
IV	10	4112, 4155, 4777, 4778, 4792, 4793, 4794, 4849, 5212, 5319	Chata Bazail, Chini Kani, Kashra,Katarangi, Basi, Sada Pankaich, Kalahati, Rayeda, Semmua, Gandhakusturi
V	7	5192, 5193, 5195, 5218, 5219, 5223, 5329	Lohamugra, Chaula Mari, Patjait, Baskor, Hali Sail, Bushi Hara, Gota
VI	7	4149, 4162, 4163, 5194, 5197, 5221, 5298	Beto, Kasrail, Khajur Chari, Kal Gora, Kancha Chikon, Kali Sura, Hari Sankar
VII	3	5327, 5330, 5350	Huglapata, Dorkumur, Beti
VIII	6	4111, 4795, 5199, 5250, 5286, 5300	Gopal Gosh, Khajur Chhori, Calenda Mota, Ashfuli, Rani Salut, Birindee
IX	6	5122, 5220, 5310, 5337, 5345, 5347	Chaula Maghi, Hora Kani, Orgoja, Changi, Rasasail, Sackhorkhana

The intra-cluster distances were low for all the nine clusters with the range of 0.602 in cluster VII to 1.555 in cluster I which indicated homogeneous nature of the genotypes within the clusters. The results were supported by the findings of Iftekharuddaula *et al.* (2001) in rice. The inter-cluster distances ranged from 3.281 to 13.006 and PCA scores also indicated a high degree of genetic diversity among the genotypes.

Table 2. Intra (bold) and inter-cluster distances (D^2) for 58 T. Aman rice genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**1.555**	9.872	7.890	13.006	8.412	10.786	8.430	8.418	7.083
II		**1.301**	4.944	8.519	5.284	5.970	8.969	5.928	9.035
III			**0.847**	7.732	3.281	3.575	6.989	3.568	8.268
IV				**0.990**	5.377	5.321	7.739	7.401	10.990
V					**0.615**	3.582	5.243	3.754	7.081
VI						**0.623**	7.483	4.490	9.894
VII							**0.602**	5.807	5.066
VIII								**0.744**	7.898
IX									**0.847**

Regarding inter-cluster distance, cluster IV showed maximum genetic distance (13.006) from cluster I followed by cluster IX (10.990) from cluster IV, Cluster VI (10.786) from cluster I. It is obvious that in all the cases cluster IV produced the highest inter-cluster distances with other clusters suggesting wide diversity of the genotypes within cluster IV 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 VI and IX (9.894), followed by cluster I and II (9.872), cluster II and IX (9.035). The minimum inter-cluster diversity was observed between cluster III and V (3.281), cluster III and VIII (3.568), cluster III and VI (3.575) and cluster V and VI (3.582) indicating that the genotypes of these clusters were genetically closed.The highest cluster means for yield, 1000 grain weight and grain breadth were obtained from cluster VIII (Table 3). The highest plant height, flag leaf width and panicle length were found in cluster II while the lowest mean value for yield, days to 50% flowering and maturity, unfilled grain and highest mean value for grain length breadth ratio were found in cluster I.

Table 3. Cluster means for thirteen characters of 58 T. Aman rice genotypes

Characters	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
Flag leaf length (cm)	24.83	32.74	33.06	32.62	31.28	36.77	28.87	31.51	29.90
Flag leaf width (cm)	1.24	2.34	1.16	1.40	1.16	1.16	1.46	1.17	1.35
Plant height (cm)	94.28	138.53	128.60	133.80	124.63	135.20	101.64	126.86	95.37
Days to 50% flowering	112.83	118.91	122.92	117.13	120.33	123.43	124.67	123.22	125.22
Days to maturity	144.83	147.50	151.77	145.70	149.28	151.57	154.89	154.78	153.39
Panicle length (cm)	22.53	27.89	26.42	27.21	25.44	26.89	25.88	26.98	25.72
Filled grains/panicle (no.)	71.37	76.59	87.64	131.73	104.73	109.08	118.94	95.74	98.39
Unfilled grains/panicle (no.)	11.63	37.71	12.00	22.27	23.59	13.62	23.53	14.61	45.92
Grain length (mm)	8.38	7.98	8.43	7.53	8.53	8.41	8.73	8.27	8.67
Grain breadth (mm)	2.04	2.85	2.52	2.05	2.15	2.70	2.22	2.87	2.28
Length-breath ratio	4.17	2.88	3.48	3.74	4.02	3.22	3.97	2.94	3.88
1000 grain weight (g)	21.49	28.07	24.01	17.40	22.30	24.40	24.39	32.46	22.08
Yield/hill (g)	13.34	9.20	16.90	19.84	20.17	20.70	20.14	31.24	20.03

Mean performance of different clusters for the characters revealed that dwarf stature, short growth duration, lower panicle length and low yielding varieties were clubbed into cluster I whereas higher yield and other second highest yield contributing characters (tall plant height, panicle length, filled grains panicle^{-1}, grain length and flag leaf area) were obtained from cluster IV. Maximum good characters were accumulated in cluster VIII and as a result higher yield (31.24 g/ hill) was obtained in this cluster. But it was interesting that in the entire cases cluster IV produced highest inter cluster-value with all other clusters. Therefore, the genotypes of cluster IV can be used in hybridization program to produce higher yielding genotypes with all other clusters. 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.

Table 4. Relative contributions of the thirteen characters to the total divergence in Boro rice

Trait	Vector 1	Vector 2
Flag leaf length (cm)	0.2107	0.2536
Flag leaf width (cm)	-0.0847	0.2461
Plant height (cm)	0.2258	0.4290
Days to 50% flowering	0.3360	-0.3670
Days to maturity	0.3679	-0.3735
Panicle length (cm)	0.2742	0.3320
Filled grains/panicle (no.)	-0.1796	0.1275
Unfilled grains/panicle (no.)	-0.1437	-0.0727
Grain length (mm)	-0.0160	-0.4030
Grain breadth (mm)	0.5040	0.0160
Length-breath ratio	-0.4063	-0.2671
1000 grain weight (g)	0.2970	-0.1837
Yield/hill (g)	0.1163	-0.1268

Therefore, more emphasis should be given on cluster VIII and II for selecting genotypes as parents for crossing with the genotypes of cluster I which may produce new recombinants with desired traits. Cluster I had the highest cluster mean value for grain length-breadth ratio and also lower filled grains panicle^{-1} which had negative effect on mean value of yield. It was also noticed that yield performance in nine clusters was more variable. The results reflected that all these T. Aman varieties were 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 flag leaf length, plant height, panicle length and grain breadth were positive. Such result indicated that these four characters contributed maximum towards divergence. It was interesting that the greater divergence in the present materials due to these four characters would offer a good scope for improvement of yield through rational selection of parents for producing heterotic rice hybrids.

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 IV. However, considering the yield, filled grains panicle^{-1}, 1000-grain weight, crosses involving cluster VIII and cluster IV may exhibit high heterosis for yield. Again, considering growth duration, fertile grains and plant height, crosses between cluster I and IV may exhibit higher heterosis for earliness and dwarf stature. Similarly; the genotypes of cluster IV might be crossed with the genotypes of cluster VIII to get higher grain yield. 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 for rice. Keeping this view in mind, it appears that the crosses between the genotypes/parents of cluster IV and cluster VIII, cluster I and cluster IV would exhibit high heterosis as well as higher level of yield potential. So, based on this result, the genotypes under cluster IV and cluster VIII, cluster I and cluster IV might be selected for future breeding program.

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