Genetic Diversity in Sadajira Rice (*Oryza sativa* L.) Germplasm

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Abstract

Genetic diversity of 40 traditional Bangladeshi rice genotypes was studied under rainfed condition through Mahalanobis D^2 statistic for grain yield and yield contributing characters. The genotypes were 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 clusters. The cluster VI contained the highest number of genotypes (18) and the clusters I and II contained the lowest (1). The highest intra-cluster distance was noticed for the cluster IV and lowest for cluster VI. The highest inter-cluster distance was observed between cluster I and IV, followed by cluster I and II, cluster I and III and the lowest between cluster III and IV. 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 clusters for producing transgressive segregants. Based on canonical vector analysis, panicle number per plant and 1000 grain weight had maximum contribution towards genetic divergence. The highest cluster means for yield, filled grains panicle^{-1} and grain breadth were obtained from cluster VI. The highest means for plant height, flag leaf area, unfilled grains panicle^{-1}, harvest index and the lowest growth duration were found in cluster I, while the lowest mean value for yield, grain length, 1000 grain weight, plant height and highest mean value for days to flowering and maturity were found in cluster II. The crosses between the genotypes/parents of cluster VI and cluster II, cluster VI and cluster V would exhibit high heterosis as well as higher level of yield potential. Therefore, more emphasis should be given for selection of the genotypes from clusters I, VI and V for future breeding program.

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

1. 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 (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 demand. Among other ecosystems, rainfed

(T. Aman) rice 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 (Anonymous, 2011-12).

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). 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 (Bashar *et al*., 2007). 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 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 between 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 8000 rice genotypes are preserved in Bangladesh Rice Research Institute (BRRI) gene bank. Classifying those into clusters to select varieties as prospective parents to develop transgressive segregants is necessary. However, information on this aspect is scanty. The present study was, therefore, undertaken to assess the extent of genetic diversity in 40 traditional Sadajira rice genotypes.

2. Materials and Methods

Forty Sadajira rice genotypes selected from the gene bank of Bangladesh Rice Research Institute (BRRI), Gazipur were grown under rainfed condition (T. Aman) during 2010. 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 area (cm^2), plant height (cm), days to flowering, days to maturity, panicle length (cm), panicle number/plant, grain length (mm), grain breadth (mm), 1000 grain weight (g), filled grains/panicle, unfilled grains/panicle, harvest index (%) and yield (g/hill). Flag leaf area was estimated according to Gomez (1983). The data were analyzed following principal component analysis (PCA) and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Intra and inter-luster distances were calculated by the methods of Singh and Chaudhary (1985). All statistical analyses were carried out using Genstat 5.5.

3. Results and Discussion

Analysis of variance showed significant differences among the 40 Sadajira rice genotypes for all of the 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 65.31% of the total variation. Based on the degree of divergence, 40 genotypes were grouped into six clusters on the basis of cluster analysis (Table1). Maximum 18 entries were grouped into the cluster VI followed by 10 in cluster V, 5 in cluster III and IV. The cluster I and II contained the lowest (1) number of genotypes.

Table 1. Distribution of 40 Sadajira rice genotypes in different clusters grown in T. Aman 2010

Cluster no.	No. of genotypes	BRRI Accession no. of Genotypes	Genotypes
I	1	2685	Sadajira Tapl 266
II	1	2715	Sadajira Tapl 299
III	5	2686, 2688, 2689, 2695, 2712	Sadajira Tapl 267, Sadajira Tapl 269, Sadajira Tapl 270, Sadajira Tapl 277, Sadajira Tapl 296
IV	5	2701, 2704, 2708, 2711, 2713	Sadajira Tapl 284, Sadajira Tapl 287, Sadajira Tapl 292, Sadajira Tapl 295, Sadajira Tapl 297
V	10	2687, 2690, 2699, 2700, 2705, 2706, 2719, 2720, 2724, 2727	Sadajira Tapl 268, Sadajira Tapl 271, Sadajira Tapl 282, Sadajira Tapl 283, Sadajira Tapl 288, Sadajira Tapl 289, Sadajira Tapl 304, Sadajira Tapl 306, Sadajira Tapl 312, Sadajira Tapl 315
VI	18	2691, 2692, 2693, 2697, 2698, 2702, 2703, 2707, 2710, 2716, 2718, 2721, 2685, 2723, 2725, 2726, 2728, 2729	Sadajira Tapl 272, Sadajira Tapl 273, Sadajira Tapl 247, Sadajira Tapl 279, Sadajira Tapl 280, Sadajira Tapl 285, Sadajira Tapl 286, Sadajira Tapl 291, Sadajira Tapl 294, Sadajira Tapl 300, Sadajira Tapl 302, Sadajira Tapl 307, Sadajira Tapl 310, Sadajira Tapl 311, Sadajira Tapl 313, Sadajira Tapl 314, Sadajira Tapl 316, Sadajira Tapl 317

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

Cluster	I	II	III	IV	V	VI
I	**0.00**	11.745	10.867	12.485	9.324	10.504
II		**0.00**	10.450	9.803	9.284	9.241
III			**0.3828**	3.998	4.892	5.480
IV				**0.6636**	4.831	4.019
V					**0.4157**	4.306
VI						**0.2615**

Intra and inter-cluster distances are presented in Table 2. The inter-cluster distances in almost all of the cases was larger than the intra-cluster distance indicating that wider diversity was present among genotypes of distance groups. Most of the germplasms are traditional but they showed high variability among them which was revealed from the results of intra and inter-cluster distance values. Here the highest intra cluster value was 0.6636 and the highest inter-cluster value was 12.485, which clearly indicated variability in the germplasms of different clusters. However, lower values in clusters VI (0.2615) and II (0.3828) 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 0.2615 in cluster VI to 0.6636 in cluster IV which indicated homogeneous nature of the genotypes within the clusters.

The results are supported by those of Iftekharuddaula *et al*. (2002) in rice. The inter-cluster distances ranged from 3.998 to 12.485 and PCA scores also indicated a high degree of genetic diversity among the genotypes. Regarding inter-cluster distance, cluster IV showed maximum genetic distance (12.485) from cluster I followed by cluster II (11.745 from cluster I, Cluster III (10.867) from cluster I and so on. It is obvious that in most of 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 characters. 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 IV and II (9.803), followed by cluster V and I (9.324), cluster V and II (9.284). The minimum inter-cluster diversity was observed between cluster III and IV (3.998), cluster IV and VI (4.019), cluster VI and V (4.306) and cluster V and IV (4.831) indicating that the genotypes of these clusters were genetically close.

The highest cluster means for yield, filled grain per panicle and grain breadth were obtained from cluster VI (Table 3). The highest plant height, flag leaf area, unfilled grains per panicle , harvest index and lowest growth duration were found in cluster I, while the lowest mean value for yield, grain length, 1000 grain weight, plant height and highest mean value for days to flowering and maturity were found in cluster II.

Mean performance of different clusters for the characters studied revealed that dwarf stature, higher growth duration, lower panicle length and low yielding (t/ha) genotypes were clubbed into cluster II whereas higher yield, filled grains per panicle and other second highest yield contributing characters (taller plant, panicle length, flag leaf area) were obtained in cluster VI.

Table 3. Cluster means for thirteen characters of 40 Sadajira rice genotypes

Characters	I	II	III	IV	V	VI	CV
Flag leaf area (cm^2)	27.71	22.17	23.24	20.79	23.99	27.58	11.73
Days to 50% flowering	103.00	114.67	103.87	102.60	104.17	105.63	4.30
Days to maturity	133.00	144.00	133.80	134.40	134.90	136.28	2.97
Plant height (cm)	118.33	90.00	109.59	100.97	106.74	111.37	9.18
Panicle number/plant	10.36	10.90	11.86	12.37	11.60	11.46	6.22
Panicle length (cm)	25.56	24.73	25.92	25.66	26.36	26.16	2.23
Filled grains/panicle	85.33	84.93	67.87	80.20	83.60	93.31	10.16
Unfilled grains/panicle	58.53	33.33	25.61	18.77	34.38	23.56	23.65
Grain length (mm)	9.46	8.63	9.50	9.41	9.73	9.39	4.01
Grain breadth (mm)	2.30	2.56	2.62	2.67	2.66	2.70	5.72
1000 grain weight (g)	22.48	20.33	23.65	23.06	23.76	23.45	5.67
Harvest index (%)	20.56	15.39	17.81	20.13	14.63	19.35	13.88
Yield/hill (g)	11.10	7.16	10.74	11.06	8.65	12.10	18.23

Maximum good characters were accumulated in cluster VI and as a result higher yield (12.10 g/hill) was obtained in this cluster. It was interesting that considering cluster distances, the cluster IV roduced comparative higher estimates of inter cluster-values 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 chances 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 II which may produce new recombinants with desired traits. Cluster II had the lowest cluster mean value for grain length, 1000 grain weight and also lower grain yield. The lowest filled grains/panicle was constelled in cluster III. However, yield was comparatively higher due to

higher grain length, 1000 grain weight and lower unfilled grains. It was also noticed that yield performance in six clusters was highly variable. On the other hand, cluster V showed moderate plant height, highest grain length, panicle length and 1000 grain weight but yield was comparatively lower due to more unfilled grains and lower harvest index. Such results reflected that all these aman 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 number per plant and 1000 grain weight were positive. Such result indicated that these two characters contributed maximum towards divergence. It is interesting that the greater divergence in the present materials due to these two characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic rice hybrids.

Table 4. Relative contributions of the thirteen characters to the total divergence in 40 Sadajira rice genotypes

Trait	Vector 1	Vector 2
Flag leaf area	-0.4085	-0.0744
Days to flowering	-0.3954	-0.3635
Days to maturity	-0.3839	-0.3672
Plant height (cm)	-0.2171	-0.0374
Panicle number/plant	0.0046	0.3683
Panicle length (cm)	-0.1475	-0.2830
Filled grains/panicle	-0.3835	0.0223
Unfilled grains/panicle	0.1911	-0.2726
Grain length (mm)	0.1554	-0.1860
Grain breadth (mm)	-0.2712	0.1234
1000 grain weight (g)	0.0638	0.1088
Harvest index (%)	-0.2266	0.4207
Yield/hill (g)	-0.3509	0.4438

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 IV and I. However, considering the yield and filled grain numbers, crosses involving the genotypes of cluster III and cluster VI may exhibit high heterosis for yield. Again, considering growth duration and plant height, crosses between the genotypes of cluster I and II may exhibit higher heterosis for earliness and dwarf stature. Similarly, the genotypes of cluster VI might be crossed with the genotypes of cluster II to get higher grain yield. Mian and Bahe (1989) reported that the parents separated by medium magnitude of inter-cluster distance generally showed higher heterosis in chickpea. Similar findings were also reported by Habib *et al.* (2005) and Khalequzzaman *et al.* (2008) for rice.

4. Conclusions

The crosses involving parents belonging to maximum divergent clusters were expected to manifest maximum heterosis and also wide genetic variability. A higher heterosis could be produced from the crosses between genetically distant parents (Ghaderi *et al.*, 1984). Keeping this in view, it appeared that crosses between the genotypes belonging to cluster VI and cluster II, cluster VI 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 VI and cluster V might be selected for future breeding program.

References

Ananda, I. J. and Murty, B. R. 1968. Genetic divergence and hybrid performance in linseed. *Indian Journal of Genetics and Plant Breeding,* 28: 178-185.

Anonymous, 2013. Bangladesh Economic Review. Ministry of finance. Govt. of Bangladesh. 92 p.

Anonymous, 2011-12. Department of Agriculture Extension, Ministry of Agriculture, Govt. of Bangladesh.

Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents of hybridization aiming at yield improvement in self-pollinated crops. *Australian Journal of Agricultural Research,* 21: 1-7.

Bashar, M. K., Mian, M. A. K., Nasiruddin, M., Elahi, Nur-E., Julfiquar, A. W. and Rasul, M. G. 2007. Genetic divergence based on morphophysiological characters of some maintainer and restorer lines in rice (*Oriza sativa* L.). In Proce. of the 7th Biennial Conference of Plant Breeding and Genetics Society of Bangladesh held on May 26, 2007 at Bangladesh Rice Research Institute, Gazipur. 72 p.

Chauhan, V. S. and Singh, B. B. 1982. Heterosis and genetic variability in relation to genetic divergence in soybean. *Indian Journal of Genetics and Plant Breeding,* 42 (2): 324-328.

De, R. N., Seetharaman, R., Sinha, M. K. and Banerjee, S. P. 1988. Genetic divergence in rice. *Indian Journal of Genetics and Plant Breeding,* 48(2): 189-194.

Ghaderi, A., Shishegar, M., Regai, A. and Ehdaie, B. 1984. Multivariate analysis of genetic diversity for yield and its components in mungbean. *Journal of American Society for Horticultural Science,* 104: 728-732.

Gomez, K. A. 1983. Technique of yield experiments with rice. International Rice Research Institute, Philippines.

Habib, S. H., Bashar, M. K., Khalequzzaman, M., Ahmed, M. S. and Rashid, E. S. M. H. 2005. Genetic Analysis and Morpho-physiological Selection Criteria for Traditional Biroin Bangladesh Rice Germplasms. *Journal of Biological Sciences,* 5(3): 315-318.

Iftekharuddaula, K. M., Akter, K., Bashar, M. K. and Islam, M. R. 2002. Genetic parameters and cluster analysis of panicle traits in irrigated rice. *Bangladesh Journal of Plant Breeding and Genetics*, 15 (1): 49-55.

Khalequzzaman, M., Islam, M. Z., Akter, K. and Bashar, M. K. 2008. Genetic diversity in local rainfed lowland rice (*Oryza sativa* L.) in Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics,* 21(1): 49-54.

Joshi, A. B. and Dhawan, N. L. 1966. Genetic improvement of yield with special reference to self fertilizing crops. *Indian Journal of Genetics and Plant Breeding,* 26 A: 101-113.

Mahalanobis, P. C. 1936. On the generalized distance in Statistics. Proceedings of the National Institute of Sciences., India 2: 49-55.

Mian, M. A. K. and Bahe, P. N. 1989. Genetic divergence and hybrid performance in chickpea. *Indian Journal of Genetics,* 49 (1): 119-124.

Rao, C. R. 1952. Advanced Statistical method in biometries research. John Wiley and Sons. New York. 390 p.

Pathan, M. S., Haque, E., Miah, N. M. and Miah, M. A. A. 1993. Genetic diversity in rice varieties released and recommended by BRRI. *Bangladesh Journal of Botany,* 22 (2): 161-166.

Saini, H. C. and Kaiker, U. S. 1987. Genetic diversity in opium poppy. *Indian Journal of Genetics,* 91-296.

Selvakumar, K. S., Soundrapandian, G. and Amirthadevarathinam, A. 1989. Genetic divergence for yield and yield components in cold tolerant rice. *Madras Agricultural Journal,* 76 (12): 688-694.

Singh, R. K. and Chaudhury, B. D. 1985. Biometrical methods in quantitative genetic analysis. Kalayoni publishers. New Delhi. 318 p.