OnLine Journal of Biological Sciences 2 (10): 659-661, 2002
ISSN 1608-4127

Genetic Diversity Among Irrigated Traditional and Modern Rice Germplasm

Khaleda Akter, M.K. Bashar, [1]K.M. Iftekharuddaula, M.S. Ahmed and E.S.M.H. Rashid
Genetic Resources and Seed Division, [1]Plant Breeding Division, Bangladesh Rice Research Institute,
Gazipur-1701, Bangladesh

Abstract: Forty five rice genotypes originating from Bangladesh, IRRI (Philippines), Japan and China were evaluated under irrigated ecosystem with a view to finding out genetic divergence for 10 characters including yield. The genotypes were constellated into five distinct groups with the range of three genotypes in cluster V and 16 genotypes in cluster III. The inter-cluster distances were larger than the intra-cluster distances in all cases except in cluster III, suggesting wider genetic diversity among the genotypes of different groups. The intra- cluster distance was highest in cluster III and least in cluster V. Maximum inter- cluster distance was observed between genotypes of cluster I and II followed by cluster I and III; II and IV; III and IV and the minimum was found between genotypes of cluster II and III. Plant height, grains/panicle and yield/hill were mainly responsible for genetic divergence while considering mean values. Though grains/panicle, days to flowering and grain length were positive contributors to genetic diversity based on the latent vectors. Clusters with small intra-cluster distances were considered less diverse than those with large distances. The mean yield, grains/panicle, plant height and days to flowering was lowest in cluster I and therefore, crosses involving the genotypes from this cluster with those from cluster II and III may exhibit high heterosis for earliness and grains/panicle. Crosses could also be made between clusters IV with that of II and III for evolving high yielding and early maturing varieties. Closer affinity of Bangladeshi traditional varieties was observed though some of them were in different clusters. Most of the breeding lines were included in cluster III indicating homogeneity in their pedigree.

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

Introduction

The demand of cereal is increasing day by day with the increasing population pressure. In Bangladesh, irrigated modern rice contributes 47% of the total rice production and about 35% area of total rice production is cultivated under this eco-system (Anonymous, 2001). Bangladesh possessed the abundance of indigenous rice germplasm, which scatter throughout the country. A total of 12,479 names of local rice germplasms including duplicates are listed Thana wise (Ali *et al.*, 1982). It is important to evaluate the existing rice germplasms preserved in BRRI gene bank for using in the hybridization programme.

Genetic divergence is one of the useful tools for selection and efficient use of parents for hybridization to develop high yield potential cultivars. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining stronger heterosis and gives broad spectrum of variability in segregating generations. Sharma (1998) stated that choice of genetically divergent parents for hybridization under transgressive breeding programme is dependent upon categorizing of breeding materials on the basis of appropriate criteria. However, crossing in moderately diverse parents also showed maximum heterosis (Chauhan and Singh, 1982). With the development of advanced biometrical techniques such as multivariate analysis based on the Mahalanobis' (1936) statistics, quantification of degree 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. Until now nearly 7,439 varieties have been collected and preserved at BRRI from indigenous and exotic sources (Bashar and Sarker, 1997). But due to lack of information on these germplasms, utilization of those varieties is limited. This study was, therefore, undertaken to assess the extent of genetic diversity in 45 varieties/lines selected from traditional, pure lines, pedigree and exotic categories. It will help in classifying those into clusters to select varieties/lines as prospective parents to develop transgressive segregants.

Materials and Methods

The experiment was set up on December 12, 2001 under irrigated ecosystem with 45 entries of home and abroad; preserved at Bangladesh Rice Research Institute, Gazipur. The trial was conducted in a randomized complete block design. Forty days-old seedlings from each entry were transplanted using single seedling/hill in 4 rows in 1 x 2.4 m^2 size plot following 25 and 15 cm space between rows and plants respectively. Fertilizers were applied @ 80:27:60:12 Kg N, P, K and S ha^{-1} respectively. 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 at the time of flowering. The other intercultural operations were done to raise the crop uniformly. Observations were recorded from 10 random plants in each plot for plant height (cm), days to flowering, days to maturity, panicle length (cm), panicles/plant, 1000-grain weight (g), grains/panicle, grain length (mm), grain breadth and yield/plant (g). The data was subjected to principal component analysis (PCA) and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952) using respective programme from computer.

Results and Discussion

The analysis of variance showed significant differences among genotypes for all the characters studied. The principal component analysis (PCA) showed that the first two components accounted for 89.7% of the total variation and a two dimensional scatter diagram was constructed using component 1 as X axis and component 2 as Y axis, reflecting the relative position of the genotypes (Fig. 1). As per scatter diagram the genotypes were apparently distributed into five groups. After comparing D^2 values for all possible 990 pairs of populations the 45 entries were grouped into five clusters (Table 1). The clustering pattern reflected by principal component analysis has been confirmed by D^2 analysis. Same trend was reported by Masud *et al.* (1995). Clustering pattern showed that maximum number of genotypes (16) was included in cluster III, while cluster V included the minimum (3). Cluster I, II and IV included 7, 6 and 13 genotypes, respectively. The clustering pattern also revealed that the

Corresponding Author: Khaleda Akter, Scientific Officer, Genetic Resources and Seed Division, Bangladesh Rice Research Institute, Gazipur-1701, Bangladesh

Table 1: Distribution of 45 rice genotypes in different clusters obtained by divergence analysis

Clusters	Accession and serial number (in bracket) of genotypes	Number of genotypes in cluster	Name of genotypes with origin
I	4578 (16), 3404 (20), 3400 (21), 4685 (36), 4459 (41), 3396 (44), 3387 (45)	7	Deshibiplob (Bangladesh), Chinese Var # 1 (China), Ozora (Japan), BR6161-R1-4 (Bangladesh), IR58 (IRRI), Kinki No. 33 (Japan), Musashikogane (Japan)
II	3797 (11), 3969 (12), 4537 (13), 4538 (14), 4540 (15), 2240 (22)	6	BR 824-121-8-8 (Bangladesh), IR184-88-50-1 (IRRI) Banshful (Bangladesh), Madlai (Bangladesh), Kalijira (Bangladesh), Boroi, 120 (Bangladesh)
III	2203 (1), 2206 (2), 2224 (3), 2213 (4), 3956 (10), 4556 (17), 4539 (18), 3745 (19), 2242 (23), 2243 (24), 2227 (26), 4797 (33), 4595 (34), 4536 (40), 4535 (42), 4522 (43)	16	Kali Boro 576 (Bangladesh), Boro 6/2 (Bangladesh), Boro 134/1 (Bangladesh), Boro 34/1 (Bangladesh), Moghal Ssail (Bangladesh), Bagra (Bangladesh), Khoia boro (Bangladesh), Dumsia-81 (Bangladesh), Boroi 275 (Bangladesh), Dhali boro 7/2 (Bangladesh), Boro 209 (Bangladesh), ARCII321 (Bangladesh), Unknown (Bangladesh), Jagli boro (Bangladesh), Shingri boro (Bangladesh), Biroin (Bangladesh)
IV	4409 (5), 4421 (6), 4458 (7), 3839 (8), 3794 (9), 2287 (25), 3790 (27), 3791 (28), 3783 (29), 3765 (31), 4669 (35), 4663 (38), 4460 (39)	13	BRRI dhan28 (BRRI), II-32B (China), IR 43 (IRRI), IR9729-272-2 (IRRI), BR827-35-2-1 (BRRI), IR36 (IRRI), BR808-1-4-1-1 (BRRI), BR802-118-3-1 (BRRI), IR9129-192-2-3-5-3 (IRRI), BR 285-18-2-3-1 (Bangladesh), IR 2053-375-1-1-5 (IRRI), BR 9108-R1-5(BRRI), BR 6107-R1-2 ((BRRI), IR60 (IRRI)
V	3772 (30), 4591 (32), 4594 (37)	3	BR-169-69-2 (BRRI), Sonali Irri (Bangladesh), Blue pajam (Bangladesh)

Table 2: **Average intra (diagonal) and inter-cluster distances (D^2) for 45 rice genotypes**

Clusters	I	II	III	IV	V
I	1.996	12.082	11.075	5.061	9.953
II		1.107	1.962	10.775	4.613
III			3.579	10.606	5.526
IV				2.676	7.017
V					0.332

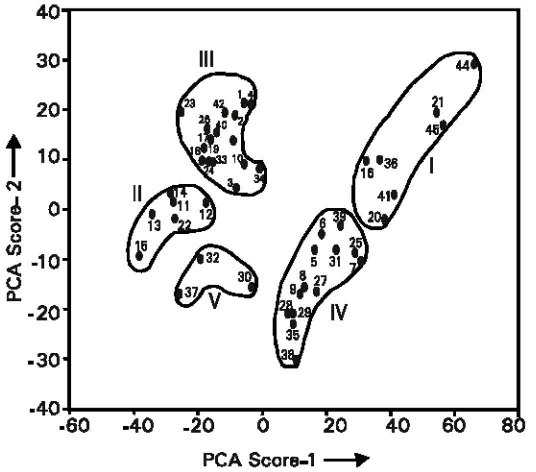

Fig. 1: **Distribution of 45 rice genotypes in a two-dimensional scatter diagram based on PCA scores superimposed with clusters (I, II, III, IV, V)**

genotypes constellated in single cluster were not originated from same country or geographic region. This indicated that genetic divergence is not directly related to geographical distribution, which might be due to continuous exchange of genetic material among the countries of the world. Similar results were reported by Sheriffa and Shivashankar (1992) and Shew *et al.* (1972).

The inter-cluster distances in all cases were larger than the intra-cluster distances except between II and III suggesting wider diversity among the genotypes of the distant group (Table 2). The intra-cluster divergence was maximum in cluster III and minimum in cluster V indicating the genotypes in cluster III were more heterogeneous and those in cluster V were closely related. The intra cluster distances were comparatively low for all the 5 clusters with the range of 0.332 in cluster V to 3.579 in cluster III, that indicated homogeneous nature of the genotypes within the clusters. These results were agreed with Iftekharudddaula *et al.* (2002a). Regarding inter cluster distance, cluster I showed maximum genetic distance from cluster II followed by from cluster III suggesting wider diversity between them (Saini and Kaicker, 1987) and the genotypes in these clusters could be used as parents in hybridization programme for getting transgressive segregants.

Cluster I, having 7 genotypes, contained one variety and advanced line from Bangladesh, one variety each from IRRI and China and the rest three from Japan (Table 1). Divergence among them is not high but cluster I showed high divergence from clusters II, III and V and low divergence from IV. It may be possible to obtain heterotic segregants if the varities/lines of cluster I are crossed with the varieties/lines of cluster II and III. Cluster II, consists of an advanced line each developed from BRRI and IRRI and four Bangladeshi varieties, showed maximum divergence with IV but lowest with cluster III. This might be due to larger panicle length, higher grains/panicle and high yielding ability in cluster II. Most of the genotypes including 7 traditional boro pure lines were constellated in cluster III which had high D^2 values with I and IV but low with II and V. Except one Chinese variety most of the breeding lines developed at BRRI and IRRI were constellated in cluster IV leaving other genotypes in cluster V (Table 1). This might be due to homogeneity in parental source or pedigree of the breeding lines. Bansal *et al.* (1990) also reported that clustering pattern was influenced by the pedigree of the breeding lines.

Cluster V consisting of 3 genotypes had low D^2 values with II and III indicating the genotypes in these clusters to be close in genetic make-up. This might be due to most of the genotypes in these clusters belong to Bangladeshi traditional category. Vairavan *et al.* (1973) reported such closer affinity in Assam and Himalayan local rice cultivars. However, cluster V showed high degrees of inter-cluster divergence with cluster IV and I.

The relative contribution of different characters towards divergence has been demonstrated by CV (%) values at inter-cluster level (Sharma, 1998). In this study, the plant height, grains/panicle and grain yield were the potential contributors to genetic divergence among the genotypes (Table 3). Selvakumar *et al.* (1989) and De *et al.* (1988), reported maximum contribution of grains/panicle and plant height towards the genetic divergence between rice genotypes. Mean performance of different clusters for the characters studied revealed that dwarf stature, lower grains/panicle and low yielding genotypes were clubbed into cluster I, whereas cluster IV and V included late maturing genotypes having relatively taller plant and higher grains/panicle with the highest yield and yield components. On the other hand cluster II showed highest mean value of plant height, panicle length and grains/panicle indicating maximum contribution of these characters towards the divergence of cluster II with I and IV (Table 3). Similarly cluster IV had high divergence with cluster II and III for distant mean values of plant height, grains/panicle and yield/hill that were almost similar with the results of Iftekharudddaula *et al.* (2002b). Endang *et al.* (1971) have stated that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits.

The canonical analysis revealed that, values in both vectors for days to flowering (0.4037, 0.1388), grain length (0.4672, 0.398) and grains/panicle (0.0202, 0.0769) were found positive (Table 4). Such results indicated that these characters contributed maximum towards divergence of the genotypes. Almost similar results

Table 3: Cluster means with inter-cluster CV (%) for ten characters in 45 rice genotypes

	Clusters					
Characters	I	II	III	IV	V	% CV
Plant height (cm)	66.48	137.54	126.66	88.99	123.90	27.43
Days to flowering	125.67	129.89	125.37	140.13	141.22	5.83
Days to maturity	155.43	154.83	150.25	166.97	168.00	4.98
Panicles/plant	14.54	15.58	17.13	16.83	13.60	9.63
Grains/panicle	60.65	102.99	81.33	90.12	101.48	19.84
Panicle length (cm)	19.55	25.51	22.85	23.23	24.73	9.91
1000-grains weight (g)	19.98	18.45	19.38	21.41	22.85	8.50
Grain length (cm)	7.80	7.85	7.55	8.53	8.74	6.33
Grain breadth (cm)	2.98	2.76	2.79	2.60	2.87	5.02
Grain yield, (t ha^{-1})	16.93	27.00	25.11	31.34	32.03	22.95

Table 4: Relative contribution of the ten characters to the total divergence in rice

	Vectors	
Characters	I	II
Plant height (cm)	-0.2107	+0.0294
Days to flowering	+0.4037	+0.1388
Days to maturity	-0.2181	+0.0066
Panicles/plant	+0.1367	-0.0233
Grains/panicle	+0.0202	+0.0769
Panicle length (cm)	+0.2938	-0.3106
1000-grains weight (g)	-0.0301	+0.1305
Grain length (cm)	+0.4672	+0.3098
Grain breadth (cm)	+0.4210	-0.8078
Grain yield (t ha^{-1})	-0.0837	+0.0349

were shown by Murty *et al.* (1967) and Sisoda *et al.* (1983) that the number of grains/panicle, panicle length and days to flowering contributed maximum to the genetic divergence. It is encouraging that the greater divergence in the present material due to the characters like grains/panicle, days to flowering and grain length will offer a good scope for improvement of yield through rational selection. The major contribution of these characters to divergence was well confirmed by their cluster mean, where the ranges varied indicating the major role of these characters as differentiative at inter cluster level. The cluster means for grains/panicle were 60.65 for cluster I and 103.0 for cluster II with a difference of about two times. This was also confirmed by the largest inter-cluster distance (12.08) between these two clusters. Similar results were obtained by Amiruzzaman *et al.* (1997).

However, the objective of a plant breeder is not only to get high heterosis but also to achieve high level of production and reducing the life span of the variety so that, it can be fitted in existing cropping pattern. In this study maximum distance existed between cluster I and II; followed by I and III; II and IV and III with IV. The mean yield, grains/panicle, panicle length and days to flowering was lowest in cluster I and therefore, crosses involving the genotypes from this cluster with those from cluster II and III may exhibit high heterosis for earliness in maturity and grains/panicle. Arunachalam *et al.* (1984), Mian and Bhal (1989) and Gadheri *et al.* (1979) reported that the parents separated by medium magnitude of divergence generally showed higher heterosis. Keeping this idea in view, it appears that the crosses between the genotypes belonging to cluster I with that of cluster III; between cluster IV with that of II and III would exhibit high heterosis as well as earliness and high yield in segregating generation.

References

Ali, H., M. Nasiruddin, M. Haque and E. Haque, 1982. Deshi Dhaner Jaat (written in Bengali). Bangladesh Rice Research Institute, Joydevpur, Dacca, Bangladesh, pp: 117.

Amiruzzaman, M., M.A.Y. Akhond, M.A.Z. Chowdhury and M.M. Hoque, 1997. Genetic divergence in grain sorghum (*Sorghum bicolor* (L) Moench). Bangla. J. Pl. Breed. Genet., 10: 45-49.

Arunachalam, V., A. Bandyopadhyay, S.N. Nigam and R.W. Gibbons, 1984. Heterosis in relation to genetic divergence and specific combining ability in ground nut (*Arachis hypogaea* L.). Euphytica, 33: 33-39.

Anonymous, 2001. Bangladesh Bureau of Statistics. Ministry of Planning, Govt. of Bangladesh.

Bansal, M.P., D.V.S. Panwar and M.R. Naidu, 1990. Genetic divergence among the breeding lines of diverse crosses of rice. Research and Development Reporter, 7: 90-96.

Bashar, M.K. and H.C. Sarker, 1997. Rice genetic resources conservation and utilization in Bangladesh. In: Hossain, M.G., R.K. Arora and P.N. Mathur (Eds.). Plant Genetic Resources–Bangladesh Perspective. Proceedings of a National Workshop on Plant Genetic Resources, 26-29 August. BARC. Dhaka, Bangladesh, pp: 66-70.

Chauhan, V.S. and B.B. Singh, 1982. Hetrosis and genetic variability in relation to genetic divergence in soybean. Indian J. Genet. Pl. Breed., 42: 324-328.

De, R.N., R. Seetharaman, M.K. Sinha and S.P. Banerjee, 1988. Genetic divergence in rice. Indian J. Pl. Breed. Genet., 48: 189-194.

Endang, S., S. Andani and H. Nasoetion, 1971. Multivariate classification of some rice (*Oryza sativa* L.) varieties and strain on yield components. Int. Rice Comm. Newsl., 20: 26-34.

Gadheri, A., M. Shishegar, A. Regai and B. Edaie, 1979. Multivariate analysis of genetic diversity for yield and morphological traits in dry edible bean and faba bean. Crop Sci., 24: 37-42.

Iftekharuddaula, K.M., Khaleda Akter, M.K. Bashar and M.R. Islam, 2002a. Genetic parameters and cluster analysis of panicle traits in irrigated rice. Bangladesh J. Pl. Breed. Genet., 15: 49-55.

Iftekharuddaula, K.M., Khaleda Akter, M.S. Hassan, K. Fatema and A. Badshah, 2002b. Genetic divergence, character association and selection criteria in irrigated rice. Online J. Biol. Sci., 2: 243-246.

Mahalanobis, P.C., 1936. On the Generalized Distance in Statistics. Proc. Natl. Inst. Sci., India, 2: 49-55.

Masud, M.A.T., M.A.Z. Chowdhury, M.A. Hossain and S.M.M. Hossain, 1995. Multivariate analysis in pumpkin *(Cucurbita moschata* Duch ex poix). Bangladesh J. Pl. Breed. Genet., 8: 45-50.

Mian, M.A.K. and P.N. Bhal, 1989. Genetic divergence and hybrid performance in chickpea. Indian J. Genet., 49: 119-124.

Murty, B.R., J.B.L. Mathur and V. Arunachalam, 1967. Factor analysis of diversity in the genus sorghum. Indian J. Genet., 27: 123-135.

Rao, C.R., 1952. Advanced Statististical Method in Biometrics Research. John Wiley and Sons, New York, pp: 390.

Saini, H.C. and U.S. Kaicker, 1987. Genetic diversity in opium poppy. Indian J. Genet., 291-296.

Selvakumar, K.S., G. Soundrapandian and A. Amirthadevarathinam, 1989. Genetic divergence for yield and yield components in cold tolerant rice. Madras Agril. J., 76: 688-694.

Sharma, J.R., 1998. Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited, Puna, India, pp: 432.

Sheriffa, R.A. and G. Shivashankar, 1992. Genetic divergence in foxtail millet (*Setaria italica* B.) Indian J. Gent. Pl. Breed., 52: 29-32.

Shew, W.H., B.R. Murty, H.B. Sing and V.M.B. Rao, 1972. Genetic divergence in recent elite strains of soybean and groundnut. Indian J. Genet., 32: 35-37.

Sisoda, N.S., A. Henry and Y.K. Gupta, 1983. Genetic divergence in grain sorghum. Madras Agric. J., 70: 678-680.

Vairavan, S., E.A. Siddiq, V. Arunachalam and M.S. Swaminathan, 1973. A study on the nature of genetic divergence in rice from Assam and North East Himalayas. Theor. Appl. Genet., 43: 213-221.