Bangladesh J. Pl. Breed. Genet., 25(2): 33-40, 2012

GENETIC DIVERSITY IN LOCAL AROMATIC RICE (*Oryza sativa* L.) GENOTYPES

M. Ali, M. A. K. Mian, M. G. Rasul, M. A. Aziz Miah[1], M. Z. Alam[2] and M. A. Hossain[3]

Department of Genetics and Plant Breeding
Bangabandhu Sheikh Mujibur Rahman Agricultural University
Gazipur 1706, Bangladesh

ABSTRACT

Genetic diversity was assessed for 66 local aromatic rice genotypes to identify parental genotypes having distant relationship through Mahalanobis's D^2 statistic. First six principal component axes above unity contributed 90.88% for variation among the genotypes. Yield per plant showed the highest contribution to total divergence followed by grain breadth, days to maturity and others. The genotypes under study were grouped into ten clusters. Clusters III and VII comprised of the maximum number (11) of genotypes when Cluster X possessed single genotype. The lowest inter genotypic distance was recorded between Kalijira-7 and Chinigura when the highest distance was observed between Elai and Rajbhog-2. The highest inter cluster distance was observed between clusters I and V while the shortest distance was carried by the clusters VII and IX. It revealed that the genotypes belonging to cluster I was far diverse from the genotypes under cluster V whereas the genotypes belonging to clusters VII and IX were least diverse. Among the genotypes, Oval Tapl, Sakkorkhora, Black, Dubsail, Rajbhog-2, Badshahbhog-8, Guamori, Elai, Kataribhog and BRRI dhan-38 might be selected from different clusters for different characters for future breeding program.

Key words: Aromatic rice (*Oryza sativa* L.), PCA, PCO, CVA, D^2 analysis, Bangladesh

INTRODUCTION

Among the major cereal crops, is unique for its adaptation. It can be grown in a wide range of agro ecological conditions from 53^0N to 40^0S latitude and from sea level to over 3000 m in the Himalayas (Lu and Chang, 1980). Domestication of wild rice probably started about 9000 years ago (Khush, 2000). Asian and African farmers, mostly women selected different types to suit local condition and needs (Singh *et al*., 2000).

Aromatic rice constitutes a special group of rice which is considered best in quality. Though local aromatic rice varieties are low yielder, a good number of aromatic rice genotypes with appreciable grain quality and taste are present in Bangladesh. These could be excellent source of sound breeding program for aromatic rice in the country. However, increasing yield of aromatic rice through plant breeding techniques has several

[1] Former CSO, Biotechnology Division, Bangladesh Rice Research Institute, Gazipur 1701; Department of Entomology, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706; 3Plant Breeding Division, Bangladesh Rice Research Institute, Gazipur 1701, Bangladesh

problems; one of them is genetic diversity, extensive use of small and medium grain aromatic rice provides viable alternatives to diversify aromatic rice gene pool.

Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Precise information on the nature and degree of genetic divergence of the parents is the prerequisites of an effective breeding program. Genetic diversity could help to sustain long term selection gain (Chowdhury *et al*. 2002). But information on genetic diversity in Bangladeshi aromatic rice is not sufficient. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra- and inter-cluster levels (Jatasra and Parada, 1978; Zahan *et al.* 2008). Therefore, this research program was undertaken to assess genetic diversity in Bangladeshi local aromatic rice genotypes and to select suitable diverse parents for future breeding program.

MATERIALS AND METHODS

The experiment was conducted at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur during T. Aman season (June to December) of 2007. Sixty six Bangladeshi local aromatic rice genotypes were used in the study. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Size of each plot was 2.4 m^2. Data were collected from each replication on number of tillers per plant, days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of primary branches per panicle, number of spikelets per primary branch, number of secondary branches per panicle, number of spikelets per secondary branch, number of total spikelets per panicle, number of filled grains per panicle, 1000 grain weight (gm), yield per plant (gm), harvest index, grain length (mm), grain breadth (mm) and grain length-breadth ratio. Analysis of variance was done by computer using MSTAT-C software. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through different techniques viz. principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis and canonical vector analysis (CVA).

RESULTS AND DISCUSSION

A considerable genetic variability was observed among the genotypes after performing analysis of variance and thereby, diversity analysis was carried out through multivariate analysis. Eigen values and percentage of total variation accounted for them obtained from principal component analysis revealed that the first axis largely accounted for the variation among genotypes (51.29 %) followed by the second axis (13.55 %) (Table1). First six eigen values above unity accounted for 90.88% while only first two values accounted for 64.84% variation. Shiv *et al*. (2003) also showed that 64% variation was observed in first two values.

Cluster analysis

By application of non hierarchical clustering using covariance matrix, the sixty six genotypes were grouped into ten different clusters (Table 2). Cluster III and cluster VII contained the maximum number of eleven genotypes followed by cluster VI and cluster IX having eight genotypes each and cluster II having seven genotypes respectively. Cluster X possessed a single genotype. These results were in conformity with the clustering pattern obtained through principal component analysis. Similarly,

Jadhav *et al.* (2003) grouped 49 rice cultivars into nine clusters based on genetic distance. Canonical variate analysis was done to compute the intra and inter cluster distances (Table 2). Result indicated that the inter cluster distance were larger than intra cluster distance in most of the cases suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.* (1987) also reported about the cluster by using D^2 statistics.

Table 1. Eigen values and percentage of variation for 19 principal components axes in 66 local aromatic rice genotypes

Principal component axes	Eigen values	Total variation accounted for (%)	Cumulative variation (%)
A	12.575	51.29	51.29
B	3.322	13.55	64.84
C	2.453	10.01	74.85
D	1.617	6.59	81.44
E	1.203	4.91	86.35
F	1.111	4.53	90.88
G	0.534	2.18	93.06
H	0.482	1.97	95.03
I	0.368	1.5	96.53
J	0.261	1.06	97.59
K	0.198	0.81	98.4
L	0.169	0.69	99.09
M	0.088	0.36	99.45
N	0.059	0.24	99.69
O	0.040	0.16	99.85
P	0.015	0.06	99.91
Q	0.013	0.05	99.96
R	0.006	0.02	99.98
S	0.003	0.01	99.99

Table 2. Distribution of 66 local aromatic rice genotypes into ten clusters

Cluster	Number of genotypes	Name of genotypes
I	06	Badshabhog-6, Badshabhog-8, Doiargura, Guamori, Premful and Rajbhog-2
II	07	Agali, Badshabhog-7, Chinigura, Duksail, Kalijira-7, Kalijira-8 and Uknimadhu
III	11	Awned-1, Benaful, Chinikamini, Dakshahi, Kalijira-5, Kalijira-9, Kalijira-11, Kalijira-12, Radhunipagal-3, Saibail and Thakurbhog
IV	06	Basmati-2, BRRI Dhan-5, Hatishail, Kataribhog, Keora, and Rajbhog-1
V	05	Elai, Kalijira-6, Maloti-2, Kalgochi and Buchi
VI	08	Badshabhog-9, Black, Chinisakkor-2, Dubsail, Jirabhog finer, Kalijira-13, Oval Tapl and Sakkorkhora
VII	11	Badshabhog (colored), Badshabhog-3, Badshabhog-5, Badshabhog-10, Basmati-1, BRRI Dhan-37, Chinisakkor-1, Kalijira finer, Kalijira-10, Sorukamini-2 and Radhunipagal-1
VIII	03	Badshabhog-4, BRRI Dhan-34 and Radhunipagal-2
IX	06	Badshabhog-11, Kalijira-1, Kalijira-2, Kalijira-3, Kalijira-4, Khasa, Maloti-1 and Sorukamini-1
X	01	BRRI Dhan-38

Intra cluster distances were computed by using the values of inter genotype distances from distance matrix of PCO. There were no marked variations in intra-cluster distances which ranged from 0.000 to 0.917 (Table 3). Intra cluster distances in all clusters were more or less low which indicated genotypes within the same cluster were closely related. The highest intra cluster distance was computed for cluster V followed by the cluster IV. The intra-cluster distance in cluster X was zero since it was consisted of single genotype. The genotypes under cluster V were most heterogeneous and genotypes under cluster VIII (with the second lowest intra cluster distance) were comparatively homogenous.

Table 3. Average intra (Diagonal) and inter cluster D^2 values for 66 local aromatic rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**0.393**									
II	10.347	**0.728**								
III	13.790	5.469	**0.679**							
IV	15.108	7.12	5.54	**0.913**						
V	18.647	9.826	6.718	5.359	**0.917**					
VI	8.537	3.641	6.139	8.294	11.243	**0.70**				
VII	8.066	4.424	6.876	7.906	11.622	3.658	**0.588**			
VIII	5.384	8.654	11.665	12.258	15.846	6.763	5.828	**0.358**		
IX	6.127	5.064	8.671	10.295	13.712	4.365	3.545	5.501	**0.469**	
X	12.282	10.669	10.984	11.428	14.957	8.942	8.545	10.674	9.995	**0.0**

Statistical distances obtained through canonical vector analysis represented the index of genetic diversity among the clusters. Inter-cluster distance was maximum between clusters I and V (18.647) and minimum between clusters VII and IX (3.545) (Table 2). The maximum value of inter cluster distance indicated that genotypes belonging to cluster I was far diverged from those of cluster V. The inter cluster distances in all the clusters were higher than the intra cluster distances reflecting wider diversity among genotypes of different clusters. The results are in agreement with Singh et *al*. (1996) and Bashar *et al*. (2007). Genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregates (Mokate *et al.,* 1998). It is more beneficial if crossing might be carried out between genotypes belonging to different groups if their genetic distances (D^2) are greater than 12.5 (Wei *et al*., 1994).

Cluster means for the characters

The mean performances of 19 characters in ten clusters are shown in table 4. Most of the characters showed distinct difference among the clusters. In cluster I, it contained the highest mean values for the character number of total spikelets per panicles, number of filled grains per panicle and harvest index. While it produced the lowest mean for the characters number of tiller per plant, number of productive tillers per plant, 1000 grain weight, yield per plant and grain breadth. Cluster II produced the highest cluster mean for the character plant height with no lowest cluster mean value. Cluster III had the maximum cluster mean for the character days to first flowering, days to 50% flowering and days to maturity and the lowest for the character harvest index.

Cluster IV comprised the highest cluster mean for grain length-breadth ratio and the lowest cluster mean for days to first flowering, days to 50% flowering and panicle length. Cluster V had the maximum range of variability for the characters 1000 grain weight, yield per plant, grain length and grain breadth where as it gave the lowest cluster.

Table 4. Cluster mean for nineteen characters in 66 local aromatic rice genotypes

Character	Cluster									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Number of tillers per plant	14.58	16.38	16.07	15.69	016.41	16. 65	16.45	15.71	16.25	24.17
Days to 1st flowering	105.05	107.52	110.27	103.28	107.27	108.29	107.61	106.44	105.08	108.00
Days to 50% flowering	109.56	112.24	115.70	108.06	111.80	113.71	112.57	111.44	110.58	113.33
Days to maturity	144.78	146.81	150.18	144.61	147.87	148.46	146.55	145.55	145.92	144.33
Plant height (cm)	141.18	148.50	143.07	121.19	135.39	140.57	130.93	128.83	144.69	107.11
Number of productive tillers per plant	9.72	11.46	11.17	10.55	10.94	11.30	11.58	11.03	11.32	13.93
Panicle length (cm)	26.98	26.41	27.30	22.91	26.17	28.47	23.78	24.11	25.29	26.50
Number of primary branches per panicle	11.77	11.98	11.82	10.52	10.05	12.06	10.29	11.21	11.65	10.87
Number of spikelets per primary branch	29.45	25.19	20.85	21.64	19.05	27.51	25.60	36.58	28.36	18.00
Number of secondary branches per panicle	56.86	55.10	45.63	40.11	37.05	60.29	46.54	55.07	49.30	48.30
Number of spikelets per secondary branch	5.80	05.22	04.42	04.44	3.83	5.23	5.33	6.10	6.06	3.87
Number of total spikelets per panicle	232.64	196.42	166.68	166.23	141.36	198.89	199.47	215.23	211.29	188.43
Number of filled grains per panicle	192.40	144.11	138.11	129.82	116.91	159.52	160.19	181.32	165.62	165.83
1000 grain weight (g)	11.94	16.38	17.20	18.47	25	15.72	13.56	12.09	13.18	12.65
Yield per plant (g)	21.97	26.45	25.91	24.25	30.84	26.94	24.14	23.24	24.42	29.96
Harvest index	0.50	0.44	0.42	0.47	0.49	0.48	0.46	0.5	0.49	0.44
Grain length (mm)	5.606	6.745	6.413	7.651	7.963	5.957	5.945	5.57	6.03	5.397
Grain bredath (mm)	2.250	2.676	2.703	2.488	3.054	2.787	2.355	2.373	2.411	2.424
Grain length-breadth ratio	2.460	2.517	2.425	3.184	2.687	2.164	2.56	2.35	2.506	2.227

mean for number of primary branches per panicle, number of secondary branches per panicle, number of spikelets per secondary branch, number of spikelets per panicle and number of filled grains per panicle. Cluster VI possessed highest cluster mean for panicle length, number of primary branches per panicle and number of secondary branches per panicle and the lowest cluster mean for grain length-breadth ratio.

Cluster VIII produced the highest mean for number of spikelets per primary branch, number of spikelets per secondary branch and harvest index. The highest cluster mean for number of tillers per plant and number of productive tillers per plant was observed in cluster X while this cluster produced the lowest cluster mean for day to maturity, plant height, number of spikelets per primary branch and grain length.

Contribution of characters towards divergence of the genotypes:

Contribution of characters towards divergence of the genotypes is presented in Table 5. Yield per plant, grain breadth, days to maturity, days to first flowering, days to 50% flowering, number of tillers per plant, number of productive tillers per plant and panicle length for vector I and vector II had positive value which indicated that they were the important component having higher contribution to the genetic divergence among genotypes studied. With few exceptions, Bidhan *et al.* (2002), Bashar *et al.* (2007) and Rahim *et al*. (2007) also showed that positive value of vector I and II in case of number of tillers per plant and panicle length.

Selection of parent for future hybridization

The crossed 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 appears that crosses between genotypes belonging to cluster I and V would give high manifestation of heterosis as well as wide spectrum of genetic variation in F_2 generation.

Table 5. Relative contributions of nineteen characters of local aromatic rice genotypes to the total divergence

Character	Vector-I	Vector II
Number of tillers per plant	0.074	0.126
Days to 1st flowering	0.099	0.392
Days to 50% flowering	0.096	0.416
Days to maturity	0.158	0.348
Plant height (cm)	-0.064	0.227
Number of productive tillers per plant	0.029	0.100
Panicle length (cm)	0.038	0.296
Number of primary branches per panicle	-0.084	0.304
Number of spikelets per primary branch	-0.350	-0.012
Number of secondary branches per panicle	-0.271	0.265
Number of spikelets per secondary branch	-0.326	-0.045
Number of total spikelets per panicle	-0.369	0.047
Number of filled grains per panicle	-0.337	0.035
1000 grain weight (gm)	0.361	-0.040
Yield per plant (gm)	0.281	0.056
Harvest index	-0.088	-0.163
Grain length (mm)	0.298	-0.215
Grain breadth (mm)	0.264	0.180
Grain length-breadth ratio	0.102	-0.330

Genotypes included in Cluster I was important for number of total spikelets per panicle, number of filled grains per panicle and harvest index, cluster II for plant height, cluster III for days to first flowering, days to 50% flowering and days to maturity, cluster IV for grain length-breadth ratio, cluster V for 1000 grain weight, Yield per plant, grain length, grain breadth, cluster VI for panicle length, number of primary branches per panicle, number of secondary branches per panicle, cluster VIII for number of spikelets per primary branch, number of spikelets per secondary branch, harvest index and cluster X for number of tillers per plant and number of productive tillers per plant.

It was found that different genotypes performed better in desirable direction for different characters. Considering the magnitude of genetic distance, cluster mean and per se performance, Rajbhog-2, Kataribhog, Oval Tapl, Sakkorkhora, Badshabhog-8, Dubsail, Elai, Guamori, Black and BRRI Dhan -38 might be selected for future hybridization program from different clusters. Similarly, after assessing genetic diversity in rice genotypes, Arun *et al.* (2002) and Rahim *et al*. (2007) identified some genotypes as suitable for future breeding program.

REFERENCES

Arun, S., D. V. Yadav, A. K. Singh, Y. Gaurav, G. Surinde, K. R. Gupta, S. Ranghvirendra, P. Deepak, A. Sharma, G. Yadav, S. Gulia, R. Singh and D. Prem. 2002. Genetic divergence in aromatic rice (*Oryza sativa* L.). National Journal of Plant Improvement. 4(2): 46-49.

Bashar, M. K., M. A. K. Mian, M. Nasiruddin., Nur-E-Elahi, A. W. Julfiquar and M. G. Rasul. 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. 72p.

Bidhan, R., A. K. Basu, A. B. Manda and B. Roy. 2002. Genetic diversity in rice (*Oryza sativa* L.) Genotypes under humid tropic of Andaman based on grain yield and seed characters. Indian Journal of Agricultural Sciences. 72(2): 84-87.

Chowdhury, M. A., V. Vandenberg and T. Warkentin. 2002. Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L). Euphytica. 127(3): 317-325.

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

Jadhav, P., A. K. Sarawgi., L. K. Mishra and J. Pravin. 2003. Studied on genetic diversity in rice genotype (*Oryza sativa* L.). Plant Archives. 3(1): 15-19.

Jatasra, D. S. and R. S. Parada. 1978. Genetic divergence in wheat under different environmental conditions. Cereal Research Communication. 6: 307-317.

Khush, G. S. 2000. Taxonomy and origin of rice. In Aromatic rices (Singh, R.K., Singh, U. S., Khush-GS. Eds.). Oxford and IBS publishing Co. Ltd., New Delhi, India. 5-14pp.

Lu, J. and T. T. Chang. 1980. Rice in its temporal and spatial perspectives. In : B.S. Luh (ed). Rice production and utilization. Avi, Davis, California. 1-74pp.

Mokate, A. S., S. S. Mehetre, V. W. Bendale and S. P. Birari. 1998. Genetic divergence in rice. Adv. Sci. 11(2): 189-192.

Rahim, M. A., M. S. Hossain and M. S. R. Bhuiyan. 2007. Characterization and genetic diversity analysis in rice (*Oriza sativa* L.). In Proc. of the 7th Biennial

Conference of Plant Breeding and Genetics Society of Bangladesh held on May 26, 2007 at Bangladesh Rice Research Institute, Gazipur. 50pp.

Shiv, D., S. C. Dani and S. Datt. 2002. Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L.). Indian Journal of Genetics and Plant Breeding. 63(1): 73-74.

Singh, R. P., D. P. Singh and B.D. Chaudhury. 1987. Morphological variation in Indian mustard. Annals of Biology. 3(1): 26-31.

Singh, R. K., P. L. Gautam, S. Sanjcev and S. Singh. 2000. Scented Rice Germplasm: Conservation, evaluation and Utilization. In Aromatic rices (Singh, R.K., Singh, U. S., Khush, G. S. Eds.). Oxford and IBS publishing Co. Ltd., New Delhi, India. 107-134 pp.

Singh, S. K., R. S. Singh and S.M. Singh. 1996. Genetic divergence in scented and fine genotypes of rice (*Oryza sativa* L.) Annals of Agricultural Research. 17(2): 163-166.

Wei, W. X., H. Zhang, F. Y. Lu and S. L. Wei. 1994. Principal component analysis and genetic distance estimation and their application in sesame breeding programme. Acta Agric. Boreali Sinica. 9(3): 29-33.

Zahan, M. I., M. S. R. Bhuiyan, and M. S. Hossain. 2008. Genetic divergence in Oleiferous *Brassica* species. Journal of Shere-Bangla Agricultural University. 2(1): 1-6.