GENETIC DIVERSITY OF AROMATIC RICE IN BANGLADESH

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ABSTRACT

The nature and magnitude of diversity in 53 aromatic rice genotypes was evaluated in rain fed condition at BRAC Agricultural Research and Development Centre, Gazipur in 2012. The Euclidian method of divergence analysis indicated the presence of appreciable amount of genetic diversity in the material. These aromatic rice genotypes were grouped into six clusters where cluster I was the largest. Inter-cluster distances were larger than the intra-cluster distance revealed that there situated considerable genetic diversity among the genotypes. Based on positive value of vector I and II days to 50% flowering, seed length, and grain yield per hill had maximum contribution towards genetic divergence. Maximum yield contributing traits were accumulated in cluster V and as a result higher grain yield (42.0 g/hill) was obtained in this cluster. The genotypes of cluster V can be used in hybridization program to produce higher yielding breeding materials with all other clusters. The genotypes Cluster IV and cluster V were found most suitable for the respective characters and can be used as potential donor for future breeding programs.

INTRODUCTION

Bangladesh is well known for its native wealth of rice genetic resources and among these, large number of aromatic varieties cultivated in different agro-climatic regions of country (Nayak *et al.* 2004; Pandey *et al.* 2011). Rice landraces of Bangladesh possess tremendous genetic variation. Evaluation of this large genetic diversity is very important for their rational use in diverse needs. Genetic diversity is pre requisite for any crop improvement program, as it helps in the development of superior recombinants by providing necessary gene sources (Naik *et al.*, 2006). Success of hybridization and subsequent selection of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The more diverse the parents, within overall limits of fitness, greater are the chances of obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in segregating generations. Statistical analysis quantifies the genetic distance among the selected genotype and reflects the relative contribution of specific traits towards the total divergence. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Shukla *et al.* (2006) and Sarawgi and Rita Binse (2007). The crosses between parents with suitable genetic divergence are generally the most responsive for yielding the most promising segregants. The present study was, therefore, undertaken to assess the extent of genetic diversity in 53 aromatic rice genotypes which will help to select prospective parents to develop transgressive segregants.

MATERIALS AND METHODS

The present investigation was under taken during rain-fed season (*Aman*) in 2012 at the BRAC Agricultural Research and Development Centre (BARDC), Gazipur, Bangladedsh. Geographically BARDC is located at 23.975°N latitude and 90.399°E longitude and 14 meters above the mean sea level. The genotypes were grown in 5.4 m x 0.6 m plots following randomized complete block design with three replications. The spacing was 20 cm between rows and 15 cm between plants. The data were recorded for yield and yield attributing characters and quality characters of aromatic rice used in this study. Observations were recorded on five randomly selected plants in each replication from the centre row. Different productive and quality characters viz. days to Days to 50% flowering, plant height (cm), tillers per hill, effective tillers per hill, panicle length (cm), filled grains per panicle, unfilled grains per panicle, total grain, sterility percentage, spikelet density, 1000 seed wt (gm), seed length (mm), seed breadth (mm), kernel length (mm), kernel breadth (mm) and grain yield per hill were recorded. The data were analyzed following 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, STAR, version 2.0.1 2014 and PB Tools, version 1.4. 2014 computer software.

RESULT AND DISCUSSIONS

Genetic Distance

All the inter-cluster distances were larger than the intra-cluster distance, indicating presence of wider diversity among genotypes of different groups (Table 1). The germplasm are traditional but they showed high variability between them which was revealed from the results of intra and inter-cluster distances. Basher *et al.* (2007) reported that inter-cluster distances were larger than intra-cluster distances in a multivariate analysis in rice. Intra-cluster distances were low for all clusters indicated homogeneous nature of the genotypes within the clusters. The results were supported by the findings of Iftekharuddaula *et al.* (2002) in rice. Intra cluster distance is highest in cluster II.

Regarding inter-cluster distance, cluster V showed maximum genetic distance (12.004) from cluster I followed by 11.711 of same cluster V from cluster IV (104). It is obvious that in all the cases cluster V produced the highest inter-cluster distances with other clusters suggesting wide diversity of the genotypes within cluster V 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). Lowest inter cluster D^2

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values was recorded between cluster I and III (3.349). Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generation enabling further selection and improvement, which would facilitate successful breeding of rice.

Table 1. Intra and inter cluster average distances of 53 aromatic rice genotypes

Cluster	I	II	III	IV	V	VI
I	**1.177**	6.625	3.349	4.01	12.004	8.245
II		**0.97**	5.245	8.339	10.624	7.231
III			**1.631**	4.295	10.22	6.605
IV				**1.4**	11.711	7.493
V					**5.604**	9.189
VI						**3.143**

Clustering of genotypes

The genotypes fall into six clusters (table 02). The distribution pattern indicated that cluster I, the largest cluster, comprised sixteen genotypes followed by cluster III (11 genotypes), cluster IV (10 genotypes), cluster II (9 genotypes), cluster VI (5 genotypes) and cluster V (2 genotypes). The clustering pattern revealed that the genotypes clustered together indicated there was no association between eco-geographical distribution of genotypes and genetic divergence.

Table 2. Clustering pattern of 53 aromatic rice genotypes

Cluster no.	No. of genotypes	Name of the Genotypes
I	1, 6, 11, 12, 14, 19, 20, 21, 23, 24, 25, 34, 40, 41, 43, 44	Badshabhog, Binnaful, Chinikanai-1, Chinikanai-2 Chinigura-PL2, Kalijira (Thin type), Kalijira (Round type), Kalijira (White type), Kalijira-PL3, Kalijira-PL6, Kalijira-PL9, Parbatjira, Tilkapur, Tulshimala, Tulshimala-PL3, Uknimadhu
II	2, 15, 16, 17, 26, 33, 37, 38, 50	Baoi-jhak, Damander-mukh, Gopalbhog, Gandho-kasturi, Kalijira-Japani, Modhumala, Rajbhog, Sabrot, Thai-3PL8-3
III	3, 4, 10, 22, 27, 28, 30, 31, 39, 42, 45	Basmati (Gazipur), Basmati PL90, BRRI dhan 38, Kalijira (Late), Kaloshailla, Kataribhog PL1, Jata Kataribhog, Philippine Kataribhog,Sakkorkhora, Tulshimala-PL1, Shandha
IV	5, 7, 8, 9, 13, 18, 29, 32, 35, 36	Begun bichi, BR5 (Dulabhog), BRRI dhan34, BRRI dhan 37, Chinigura, Kalijira (Normal), Kataribhog PL2, Kaminisharu, Premful, Radhunipagal
V	46, 48	Basmati 370, Jesmine
VI	47, 49, 51, 52, 53	Basmati 386, BRRI dhan50, CNI 9012, GSR 1234, GSR 1242

Cluster Mean

The highest cluster means for grain yield, 1000 seed wt and panicle length were obtained from cluster V (table 03). Highest total grain number, sterility percentage, spikelet density found in cluster IV, whereas the lowest grain yield and number of filled grain per panicle found in cluster III. Mean performance of different clusters for the characters studied revealed that dwarf stature, lower tillers per hill were in cluster VI whereas highest 1000 seed weight, panicle length, tillers number per hill and high yielding genotype were in V. Maximum desirable characters were accumulated in cluster V and as a result higher grain yield (42.0 g/hill) was obtained in this cluster. It was interesting that considering cluster distances, the cluster V showed comparative higher estimates of inter cluster-values with all other clusters.

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Table 3. Cluster means for 53 aromatic rice genotypes

Traits	I	II	III	IV	V	VI
Days to 50% flowering	78	81	79	79	91	90
Plant height (cm)	114	109	114	113	121	87
Tillers/hill	11	9	11	9	13	7
Effective tillers/hill	9	8	10	9	12	6
Panicle length (cm)	24.0	25.1	24.8	25.1	27.5	24.4
Filled grains /panicle	169	112	109	171	157	134
Unfilled grains /panicle	22	12	22	42	28	32
Total grain	191	124	131	214	185	166
% Sterility	11.5	9.8	16.7	20.1	15.2	18.5
Spikelet density	8.0	5.0	5.4	8.6	6.9	6.9
1000 seed wt (gm)	10.6	20.4	15.0	10.9	23.9	19.9
Seed length (mm)	6.0	7.5	7.6	6.6	10.6	10.1
Seed breadth (mm)	2.3	2.8	2.4	2.2	2.5	2.3
Kernel length (mm)	4.3	5.4	5.3	4.6	7.5	7.0
Kernel breadth (mm)	2.0	2.4	2.0	1.9	2.0	1.8
Grain yield/Hill	16.7	16.9	16.3	16.6	42.0	17.2

Table 4. Contributions of the characters towards divergence in 53 aromatic rice genotypes

Traits	Genotypes	Replication	Error	SE	CV	Mean	Min	Max	LSD	Vector 1	Vector 2	h^2_b
Days to 50% flowering	79.51	15.92	0.40	0.36	0.8	81	71	98	1.0	0.211	0.026	98.5
Plant height (cm)	479.47	19.42	17.23	2.4	3.8	111	74	135	6.7	-0.010	0.003	89.9
Tillers/hill	13.40	4.58	2.42	0.9	15.6	10	6	14	2.5	-0.010	-0.147	60.1
Effective tillers/hill.	11.68	4.47	1.84	0.78	15.2	9	5	13	2.2	-0.724	-0.147	64.1
Panicle length (cm)	10.40	11.09	2.55	0.92	6.5	24.7	21	29	2.6	-0.027	0.142	50.7
Filled grains /panicle	4861.18	91.49	181.54	7.78	9.4	143	71	278	21.8	0.148	-0.110	89.6
Unfilled grains /panicle	499.99	306.84	100.39	5.78	39.7	25	5	61	16.2	0.241	-0.075	57.0
Total grain	6599.48	693.31	222.40	8.61	8.8	169	91	327	24.2	-0.155	0.106	90.5
% Sterility	112.63	52.25	27.05	3	35.4	14.7	5.1	32.7	8.4	-0.239	0.126	51.3
Spikelet density	10.43	0.11	0.59	0.45	11.2	6.9	3.6	11.4	1.3	-1.316	-0.012	84.7
1000 seed wt (gm)	74.86	0.07	0.07	0.16	1.9	14.6	8.9	27.9	0.4	-0.070	-0.251	99.7
Seed length (mm)	6.96	0.54	0.12	0.2	4.7	7.3	5.6	11.2	0.6	0.873	0.689	95.2
Seed breadth (mm)	0.24	0.03	0.01	0.07	5.1	2.4	2	3.5	0.2	-0.487	-0.438	83.3
Kernel length (mm)	3.60	0.09	0.06	0.15	4.9	5.1	3.6	7.6	0.4	-0.838	0.144	94.9
Kernel breadth (mm)	0.16	0.00	0.01	0.05	4.5	2.0	1.5	2.9	0.2	1.661	-3.679	86.4
Grain yield/Hill	113.54	21.04	6.52	1.47	14.6	17.4	9.4	50.1	4.1	0.274	0.181	84.6

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Canonical Vector Analysis

The canonical vector analysis revealed that the vectors (vector I and II) for Days to 50% flowering, seed length, and grain yield per hill were positive (Table 4). Such result indicated that these three characters contributed maximum towards divergence. The greater divergence in the present materials due to these three characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic rice hybrids.

Correlation

50% flowering time had significant positive correlation with sterility percentage, 1000 seed wt (gm), seed length (mm), kernel length (mm), and grain yield per hill while negatively associated with plant height (cm). Plant height showed some sorts of correlation for tillers per hill and effective tillers per hill, while significant negative correlation for seed length, kernel length (table 05). Nofouzil et al. (2008) reported significant and positive correlation between grain yield and plant height. Significant and positive correlation among number of productive tillers per plant and grain yield was also noticed by Ali *et al.* (2008) in wheat. This result is also in consistent with the findings of Dogan (2009) and Gashaw et al. (2007). They reported significant positive correlation between grain yield and 1000-grain weight.

The correlations of tillers/hill were significantly positive with effective tillers per hill and GYP on the other hand effective tillers per hill and panicle length have significantly positive relation with GYP. There is no negative correlation for tillers/hill, effective tillers per hill and panicle length, where total grain showed only negative correlation with 1000 seed wt, seed length, Seed breadth, Kernel length and Kernel breadth. TSW has positively correlated with all characters. Although sterility percentage and kernel breadth showed no significant correlation with any characters but seed length and seed breadth showed significant positive correlation.

Table 5. Phenotypic correlation coefficients estimation between yield and yield component characters

	50F	PH	TILL	ETILL	PL	TG	%S	TSW	SL	SB	KL	KB
PH	-0.335*											
TILL	-0.074	0.286*										
ETILL	-0.142	0.321*	0.893**									
PL	0.127	0.224	-0.002	0.041								
TG	0.063	0.113	-0.148	-0.157	0.164							
%S	0.301*	-0.078	0.002	-0.019	-0.094	0.101						
TSW	0.564**	-0.25	-0.184	-0.202	0.11	-0.481**	0.04					
SL	0.623**	-0.430**	-0.107	-0.095	0.095	-0.328*	0.167	0.772**				
SB	0.218	0.058	-0.007	-0.055	0.163	-0.424**	-0.077	0.626**	0.167			
KL	0.602**	-0.387**	-0.111	-0.119	0.084	-0.356**	0.111	0.803**	0.977**	0.195		
KB	0.093	0.145	-0.045	-0.1	0.037	-0.315*	-0.084	0.470**	-0.075	0.898**	-0.039	
GYP	0.461**	0.091	0.338*	0.384**	0.295*	0.217	-0.067	0.434**	0.444**	0.198	0.437**	0.099

50F=Days to 50% flowering, PH=plant height (cm), TILL=tillers per hill, ETILL=effective tillers per hill, PL=panicle length (cm), TG=total grain, %S=sterility percentage, TSW=1000 seed wt (gm), SL=seed length (mm), SB=seed breadth (mm), KL= kernel length (mm), KB=kernel breadth (mm).

CONCLUSION AND RECOMMENDATION

Evaluated 53 aromatic rice genotypes of the present study are good sources of valuable genes. There is a high degree of diversity existed among the genotypes which needs to be utilized in future varietal improvement and/or development programs. Specifically, the genotypes of clusters V and IV may be selected as parents for hybridization programs to develop high yielding rice varieties with desirable other good characters. Future breeding goal should concentrate on selecting genotypes with high grain yield, long panicle length and more tillers per hill.

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