Journal of Biodiversity and Environmental Sciences (JBES)
ISSN: 2220-6663 (Print) 2222-3045 (Online)
Vol. 8, No. 4, p. 196-208, 2016
http://www.innspub.net

INNSPUB
RESEARCH PAPER
OPEN ACCESS

Morphological characterization and diversity analysis of some selected aromatic rice genotypes in Bangladesh

K.K. Bashar[1*], N.A. Ivy[2], M.A.K. Mian[2], K.M. Iftekharuddaula[3], M.A. Hoque[4]

[1]*Bangladesh Jute Research Institute, Dhaka, Bangladesh*

[2]*Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh*

[3]*Plant Breeding Division, Bangladesh Rice Research Institute, Gazipur, Bangladesh*

[4]*Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh*

Article published on April28, 2016

Key words: Aromatic rice, Morphological characterization, Cluster distance, Hybridization.

Abstract

The improvement of aromatic rice genotypes requires proper characterization of its existing germplasm. For this purpose, twenty four (nineteen aromatic and five non-aromatic fine) rice genotypes were evaluated for twenty qualitative and sixteen quantitative traits at morphological level to identify the suitable genotypes for future hybridization program at Bangabandhu Sheikh Mujibur Rahman Agricultural University. All the genotypes produced same scores in the data for eight qualitative characters *viz.* blade colour, leaf sheath: anthocyanin colour, ligule colour, ligule shape, auricle colour, collar colour, anthocyanin coloration of nodes and stigma colour. Differences were found in the genotypes studied for rest of the qualitative characteristics. The analysis of variance indicated the existence of highly significant variability for all the characters studied. All the genotypes made seven clusters. The highest intra-cluster distance was computed for cluster I (0.75), composed of five genotypes followed by the cluster V (0.72) composed of five genotypes. Only one genotype *viz.* Jhingasail belonged to the cluster IV which had intra-cluster distance 0.00, indicated that this genotype was genetically diversed from other genotypes. The inter-cluster distance was the highest (19.26) between cluster III and V followed by the 17.30 between cluster II and cluster VI and the lowest distance (2.63) was obtained between cluster I and cluster III. Considering the magnitude of genetic distances the cross combination Chinigura and Jhingasail, Basmati 107 and (Jhingasail, Rong-er-gura, Kalijira, Rasmala and Chinisagor), Basmati naret and (Rasmala, Rong-er-gura and Kalijira) and Kataribhog and Chinisagor might be selected for future hybridization program.

***CorrespondingAuthor:**K.K. Bashar✉kazi.khayrulbashar@gmail.com

Introduction

Rice (*Oryza sativa* L.) belongings to the family Graminae or Poaceae and subfamily Bambusoideae or Ehrhartoideae (Hooker, 1979) is a self-pollinated, monocotyledonous cereal crop. Grain quality in rice plays an important role in consumer acceptability. Juliano and Duff (1991) concluded that grain quality is second after yield as the major breeding objective for crop improvement. Aroma quality of scented rice is a major character which increases the value of rice in international market (Nayak*et al*., 2002). Most of the scented rice varieties in Bangladesh are of traditional type, photoperiod sensitive and cultivated during the Aman season. Majority of these indigenous aromatic rice cultivars are small and medium grained (Singh *et al*. 2000a,b; Kovach *et al*., 2009; Li *et al*., 2010 and Ray *et al*., 2013) low yielding but its higher price and low cost of cultivation generate higher profit margins compared to other varieties.

Like other parts of the world, Bangladesh has already lost a large number of aromatic rice genotypes and many at the verge of extinction (Singh *et al*., 2000). Rapid adoption of modern varieties is a serious threat for the existence of fine quality rice genotypes for their low yield. The improvement of aromatic rice genotypes requires its collection and evaluation of existing cultivars of Bangladesh. The Himalayan foothill including parts of Bangladesh is considered to be the secondary center of diversity of the genus *Oryza* (Morishima, 1984) but information about the characterization or genetic diversity of aromatic rice is very limited. Systematic study and characterization of such germplasm is not only important for utilizing the appropriate attribute based donors, but also essential in the present era for protecting the unique rice. Thus, there is a need to collect, exploit and evaluate the untapped germplasm (Parikh *et al*., 2012).

Diversity analysis especially the 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 (Zahan*et al*., 2008). Therefore, the study 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

Experimental materials

Twenty four rice genotypes were used in this study. The list of the twenty four rice genotypes including their ecotype, BRRI accession number and place of collection is given in Table 1.

Experimental site

The field experiments for morphological characters of aromatic plants were carried out at the research field of the Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh during June to August 2014.

Experimental design and layout

The field experiment was laid out in a randomized complete block design with three replications. Each replication was divided into twenty four unit plots where twenty four genotypes were allocated at random. Thus total number of unit plots was 72. Size of each units plot was 2.4m² (3m x 0.8m). The spaces between blocks and between plots were 1m and 0.5m, respectively. Plant to plant and line to line distance were 20cm and 25cm respectively. Each plot consists of 24 plants.

Morphological characterization

Data on the agronomical and morphological characters were collected from ten randomly selected hills excluding border rows from each replicated plots. Twenty qualitative and sixteen quantitative traits were recorded using “Germplasm Descriptors & Evaluation Form” by Bangladesh Rice Research Institute (BRRI).

Statistical analysis for quantitative traits

Mean data of quantitative traits for the morphological characters were subjected to both univariate and multivariate analysis. Univariate analysis of the individual character (analysis of variance) was done by computer using STATISTIX 10 software. The test of significance was done by F-test. Mean, range and coefficient of variation (CV%) were also estimated using STATISTIX 10. Multivariate analysis was done by computer using GENSTAT 5.5 and Microsoft Excel software through four techniques *viz.* Prinicipal Component Analysis (PCA), Principal Coordinate Analysis (PCoA) Cluster Analysis (CA) and Canonical Vector Analysis (CVA) as suggested by Anderson (1957).

Results and discussion

Morphological characterization through qualitative traits

All the genotypes produced same scores in the data for eight qualitative characters *viz.* blade colour, leaf sheath: anthocyanin colour, ligule colour, ligule shape, auricle colour, collar colour, anthocyanin coloration of nodes and stigma colour. These result revealed that there was no variation for these traits among all the test genotypes. All the test genotypes were characterized (Table 2) on the basis of the rest twelve qualitative characters.

Table 1. List of 24 test rice genotypes with their different characters.

SL. No.	BRRI Access No.	Variety Name	Ecotype	Aroma	Place of collection
1	4867	Chinigura	T. Aman	Aromatic	Naogaon
2	7413	Basmati India	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
3	7082	Kataribhog	T. Aman	Aromatic	Dinajpur
4	5347	Sakkorkhora	T. Aman	Aromatic	Barguna
5	4497	Basmati Porder	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
6	4904	Basmati 370	T. Aman	Aromatic	Pakistan
7	4496	Basmati Naret	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
8	4495	Basmati IRGC 27782	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
9	4500	Basmati 1	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
10	4501	Basmati 107	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
11	4502	Basmati 134	T. Aman	Aromatic	GRSD, BRRI, Gazipur
12	4503	Basmati 372	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
13	-	Kamarang	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
14	5950	JamaiAduri	T. Aman	Aromatic	GRSD*, BRRI, Gazipur
15	416	Jhingasail	T. Aman	Non-aromatic	Rajshahi
16	4109	Khutichikon (3)	T. Aman	Aromatic	Comilla
17	4108	Khutichikon (2)	T. Aman	Non-aromatic	Comilla
18	247	Kalijira	T. Aman	Aromatic	Khulna
19	315	Binnaphul	T. Aman	Aromatic	Gaibandha
20	-	Rong-er-gura	T. Aman	Non-aromatic	Bhola
21	245	Chinisagor	T. Aman	Aromatic	Mymensingh
22	-	Rasmala	T. Aman	Non-aromatic	Sherpur
23	7063	SugandhiDhan (2)	T. Aman	Non-aromatic	Nawabganj
24	4490	Basmati T_3	T. Aman	Aromatic	GRSD*, BRRI, Gazipur

GRSD*= Germplasm Resources and Seed Division, BRRI*= Bangladesh Rice Research Institute.

Morphological characterization through quantitative traits

Morphogenetic variation in rice genotypes based on univariate analysis

Analysis of variance (Table 3) of sixteen quantitative characters based on individual sample means showed highly significant differences among the genotypes for all the characters studied indicated wide variation

among the genotypes. The coefficient of variation ranged from 2.5 - 34.38% which indicated considerable variation in the characters studied. Among the sixteen characters unfilled grain per panicle, harvest index, yield per hill and filled grain per panicle were found to have relatively higher coefficient of variation (34.28, 15.22, 11.63 and 11.06 percent, respectively) than the other characters.

Table 2. Classification of rice genotypes based on qualitative characteristics.

Sl. No.	Characters	Classification of genotypes
1	Blade pubescence	(i) intermediate (2): 1, 5 – 12 (ii) pubescent (3): 2 - 4, 13 – 24
2	Leaf angle	(i) Erect (1): 5 - 12 and 22 – 23 (ii) Horizontal (5): 1 - 4, 13 - 20 and 24 (iii) Drooping (9): 21
3	Flag leaf angle	(i) Erect (<30^0) (1): 22 and 23 (ii) Intermediate or semi erect (<30 - 45^0) (3): 1 - 21 and 24
4	Culm angle	(i) Erect (1): 2,15, 17 and 21 – 23 (ii) Intermediate (3): 1, 3 - 12, 14, 16, 18 - 20 and 24 (iii) Spreading (7): 13
5	Internode colour	(i) Green (1): 1 – 12 (ii) Light gold (2): 13 – 24
6	Culm strength	(i) Intermediate (most plants moderately lodging) (5): 3, 20 and 22 - 24 (ii) Weak (most plants nearly flat) (7): 1 - 2, 4 - 19 and 21
7	Panicle type	(i) Compact (1): 22 and 23 (ii) Intermediate (5): 1 - 21 and 24
8	Panicle secondary branching	(i) Light (1): 1 and 4 – 24 (ii) Heavy (2): 2 and 3
9	Panicle exertion	(i) Well Exerted (1): 1 – 4 (ii) Moderately well exerted (3): 5 – 24
10	Awns in the spikelet	(i) Absent (1): 1 - 2, 4 - 14 and 16 – 23 (ii) Present (9): 3, 15 and 24
11	Apiculuscolour	(i) White (1): 14 and 16 (ii) Straw (2): 1 - 12, 15, 17 and 19 - 24 (iii) Purple (6): 13 and 18
12	Stigma exertion	(i) Low (5 - 20%) (3): 3, 13, 15 and 20 – 21 (ii) Medium (21 - 40%) (5): 1 - 2, 4 - 12, 14, 16 - 19 and 22 – 24

Legend:

1 = Chinigura, 2 = Basmati India, 3 = Kataribhog, 4 = Sakkorkhora, 5 = Basmati Porder, 6 = Basmati 370, 7 = Basmati Naret, 8 = Basmati IRGC 27782, 9 = Basmati 1, 10 = Basmati 107, 11 = Basmati 134, 12 = Basmati 372, 13 = Kamarang, 14 = JamaiAduri, 15 = Jhingasail, 16 = Khutichikon (3), 17 = Khutichikon (2), 18 = Kalijira, 19 = Binnaphul, 20 = Rong-er-gura, 21 = Chinisagor, 22 = Rasmala, 23 = SugandhiDhan (2) and 24 = Basmati T_3.

Morphogenetic variation in rice genotypes based on multivariate analysis

Multivariate analysis were done using D^2 statistics, canonical roots and vectors following the principle of Mahalanobis generalized distance as per the procedure obtained by Rao (1952). Moreover, methods of multivariate analysis i.e. Principal Component Analysis (PCA) and Principal Coordinate Analysis (PCoA) were also performed to find out the nature and magnitude of rice diversity.

Principal component analysis (PCA)

Eigen values (latent roots) of 16 principal component axis and percentage of total variation accounted for them obtained from principal component analysis are presented in Table 4. The result revealed that the first axis largely accounted for the variation among the genotypes (36.43%) followed by the second axis (19.39%). The first six axes accounted for about 90% of the total variations among the 16 characters describing test rice genotypes where only 56%

variation was accounted for the first two axes. Hossain (2008) and Islam (2011), found similar findings in determining the variation among 78 and 47 rice genotypes, respectively.

Principal coordinates analysis (PCoA)

Inter-genotypic distance D^2 was obtained from principal coordinate analysis for all possible combinations between pairs of genotypes. Ten highest and 10 lowest inter-genotypic distances between 24 rice genotypes are shown in Table 5.

Table 3. Analysis of variance of sixteen quantitative characters of rice genotypes.

Sources of variation	Df	Mean sum of square								
		LL (mm)	FLA (cm^2)	CD (mm)	TT	ET	PL (cm)	PH (cm)	DF (days)	DM (days)
Replication	2	0.011	0.154	0.266	0.017	3.305	5.443	113.345	1.931	2.667
Genotypes	23	0.596**	59.702**	1.052**	4.616**	2.730**	12.402**	518.442**	507.932**	453.197**
Error	46	0.007	4.708	0.090	0.759	0.935	2.647	27.918	5.684	9.043
CV (%)		4.63	5.65	6.34	7.18	8.81	5.89	3.75	2.65	2.50

Table 3. (contd ....)

Sources of variation	Df	Mean sum of square						
		FG/P	UFG/P	GL (mm)	GB (mm)	1000 grain wt. (g)	Y/hill	HI
Replication	2	80.35	315.551	0.120	0.010	39.926	44.104	0.008
Genotypes	23	5544.25**	97.800**	6.485**	0.092**	49.353**	41.157**	0.018**
Error	46	236.96	167.226	0.150	0.016	3.930	6.440	0.002
CV (%)		11.06	34.28	4.78	5.48	10.10	11.63	15.22

**significant at 1% level

Legend: LL = Ligule Length, FLA = Flag Leaf Area, CD = Culm Diameter, TT = Total Tiller, ET = Effective Tiller, PL = Panicle Length, PH = Plant Height, DF = Days to 50% Flowering, DM = Days to Maturity, FG/P = Filled Grain per Panicle, UFG/P = Unfilled Grain per Panicle, GL = Grain Length, GB = Grain Breadth, Y/hill = Yield per hill, HI = Harvest Index.

The highest inter-genotypic distance was 1.94, which was observed between the genotypes Chinigura and Jhingasail followed by the distance 1.91 (Basmati 107 and Jhingasail). The lowest distance (0.33) was observed between the genotypes Basmati 370 and Basmati 372 followed by the distance 3.38 (Kalijira and Chinisagor). Most of the inter-genotypic distances were obtained between Basmati and non-Basmati group of rice germplasm which may be due to the cause of different genetic background. The difference between the highest and the lowest inter-genotype distance indicated the prevalence of variability among the test genotypes.

Table 4. Latent roots (Eigen Value) and their variation in 16 morphological quantitative traits in 24 test rice genotypes.

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
I	5.830	36.43	36.43
II	3.102	19.39	55.82
III	1.600	10.00	65.82
IV	1.306	8.16	73.98
V	1.087	6.80	80.78
VI	1.012	6.32	87.10
VII	0.819	5.12	92.22
VIII	0.441	2.76	94.98
IX	0.254	1.59	96.57

X	0.203	1.27	97.84
XI	0.176	1.10	98.94
XII	0.073	0.46	99.40
XIII	0.036	0.23	99.63
XIV	0.036	0.22	99.85
XV	0.014	0.09	99.94
XVI	0.010	0.06	100

Table 5. Ten highest and 10 lowest inter-genotypic distances between 24 rice genotypes.

Sl. no.	Genotypic contribution	Distance
A. Ten highest inter genotypic distances		
01	Between Chinigura and Jhingasail	1.9488
02	Between Basmati 107 and Jhingasail	1.9106
03	Between Basmati Naret and Rasmala	1.8364
04	Between Basmati Naret and Rong-er-gura	1.8326
05	Between Basmati 107 and Rong-er-gura	1.8181
06	Between Basmati 107 and Kalijira	1.8120
07	Between Basmati Naret and Kalijira	1.7979
08	Between Basmati 107 and Rasmala	1.7698
09	Between Kataribhog and Chinisagor	1.7592
10	Between Basmati 107 and Chinisagor	1.7433
B. Ten lowest inter genotypic distances		
01	Between Basmati 370 and Basmati 372	0.3330
02	Between Kalijira and Chinisagor	0.3889
03	Between Kamarang and Khutichikon (2)	0.3983
04	Between Jamaiaduri and Khutichikon (2)	0.4165
05	Between Kalijira and Rong-er-gura	0.4221
06	Between Basmati Porder and Basmati Naret	0.4223
07	Between Kalijira and Rasmala	0.4471
08	Between Basmati Porder and Basmati 370	0.4591
09	Between Basmati 370 and Basmati IRGC 27782	0.4661
10	Between Basmati Porder and Basmati 1	0.4666

Canonical variate analysis

Cluster analysis of rice genotypes based on agro-morphological characteristics was reported by many researchers (Ghalain, 2006; Naik *et al*., 2006; Hien *et al*., 2007; Mathure *et al*., 2010, 2011; Sarawgi *et al*., 2012). In this study the cluster VI composed of largest number of genotypes (6), but its intra-cluster distances were not necessarily the highest. The statistical distances represent the index of genetic diversity among the genotypes of a cluster. There were marked variations in intra-cluster distances, which ranged from 0.48 to 0.75 (Table 6). The highest intra-cluster distance was computed for cluster I (0.75), composed of five genotypes followed by the cluster V (0.72) composed of five genotypes. The intra-cluster distances of cluster II, III, IV and VI was 0.48, 0.71, 0.00 and 0.61 consisting of 4, 3, 1 and 6 genotypes, respectively. Only one genotype *viz*.Jhingasail belonged to the cluster IV which represented its intra-cluster distance as 0.00 and indicated that this genotype was genetically diverse from other genotypes. The intra-cluster distances in the entire six clusters were lower than the inter-cluster distances. The lower values of intra-cluster distances in all six clusters indicated genotypes within the same cluster were closely related and wider genetic diversity among the genotypes of different clusters. However, the highest value (0.75) of intra-cluster distance in cluster I indicated that the five genotypes constituted in this cluster might have diverged characters i.e., heterogeneous, which contributed to the formation of this cluster. On the other hand, the lowest value (0.48) of intra-cluster distance in cluster II indicated that the four genotypes constituted in this cluster might have most similarity (homogenous) than the genotypes of the other

remaining clusters. The inter-cluster distance was the highest (19.26) between cluster III and V followed by the distance 17.30 between cluster II and cluster VI and the lowest (2.63) distance was between cluster I and cluster III (Table 6). So the genotypes of the clusters III and V may be used as parents in hybridization programme for obtaining a wide range of variation among the segregants upon crossing. The genotypes between the clusters I and III are closely related as they had the lowest inter-cluster distance.

Table 6. Average intra (bold) and inter cluster distances (D^2) for 24 rice genotypes.

Cluster	I	II	III	IV	V	VI
I	0.7541					
II	3.893	0.4815				
III	2.626	6.432	0.7147			
IV	12.894	10.642	15.259	0.000		
V	17.070	15.170	19.260	4.623	0.7247	
VI	15.506	17.370	15.572	15.464	15.745	0.6112

Table 7. Distribution of 24 rice genotypes in six clusters.

Cluster	Number of genotypes	Genotypes
I	5	Basmati India, Kataribhog, Sakkorkhora, Basmati 1 and Basmati T_3
II	4	Basmati Porder, Basmati Naret, Basmati IRGC 27782 and Basmati 372
III	3	Basmati 370, Basmati 107 and Basmati 134
IV	1	Jhingasail
V	5	Chinigura, Kamarang, Jamai Aduri, Khutichikon (2) and Binnaphul
VI	6	Khutichikon (3), Kalijira, Rong-er-gura, Chinisagor, Rasmala and Sugandhi Dhan (2)

Non-hierarchical clustering of genotypes

The pattern of distribution of 24 rice genotypes were grouped into six different clusters (Table 7). The number of genotypes ranged from 01 to 06 in different clusters. The distribution pattern indicated that the maximum genotypes (06) were included in Cluster VI followed by cluster I and V for five genotypes. Cluster IV was consisted of only one genotype.

Table 8. Average intra (bold) and inter cluster distances ($D = \sqrt{D^2}$) for 24 rice Genotypes.

Cluster	I	II	III	IV	V	VI
I	0.8683					
II	1.973	0.6939				
III	1.620	2.536	0.8453			
IV	3.590	3.259	3.906	0.000		
V	4.131	3.894	4.388	2.150	0.8512	
VI	3.937	4.167	3.946	3.932	3.967	0.7817

Clustering pattern

With the help of D values (Table 8) within and between cluster, an arbitrary cluster diagram (Fig.1) was constructed, which shows the relationship between different genotypes. However, the diagram was not drawn following the exact scale. It was apparent from the figure that the genotypes included in the cluster I was far diversed from the genotypes of all other clusters where the genotypes belonging to clusters I and III were least diversed (1.62) followed by clusters IV and V (2.15). Genotypes of cluster VI were moderately diversed from those of clusters I, II, III, IV, V, VII and VIII.

Intra-cluster mean

The mean values for all the 16 characters along with the marking of the highest (^{H}) and lowest ($_{L}$) for each of the cluster are presented in Table 9.

The data revealed that different clusters exhibited different mean values for almost all the characters.

The genotype of cluster IV produced the highest mean for days to 50% flowering, days to maturity, grain length and 1000 grain weight. On the other hand, the lowest means of this cluster for the characters were ligule length, total tiller, effective tiller, filled grain per panicle and harvest index. Golam*et al*., (2011) reported that the number of effective tillers and filled grains per panicle has the positive contribution to grain yield.

Table 9. Cluster mean for 16 quantitative characters of 24 rice genotypes.

Characters	I	II	III	IV	V	VI
Ligule length (cm)	2.12	2.27	2.28^{H}	1.41$_{L}$	1.44	1.52
Flag leaf area (cm^2)	38.07	42.22^{H}	40.83	38.93	37.01	35.81$_{L}$
Culm diameter (cm)	5.30^{H}	5.21	5.18	4.46	4.23$_{L}$	4.55
Total tiller	13.14^{H}	12.18	11.60	11.13$_{L}$	12.58	11.37
Effective tiller	12.27^{H}	11.13	11.13	9.70$_{L}$	11.03	10.08
Panicle length (cm)	27.11	26.66$_{L}$	30.39^{H}	29.20	27.14	28.82
Plant height (cm)	130.90$_{L}$	145.48	157.53^{H}	145.17	138.84	137.52
Days to 50% flowering	81.00	78.75	71.33$_{L}$	105.00^{H}	103.20	102.33
Days to maturity	111.40	106.50$_{L}$	108.00	140.00^{H}	133.40	133.17
Filled grain per panicle	125.81	89.22	120.27	59.20$_{L}$	139.45	214.65^{H}
Unfilled grain per panicle	28.77	30.35	26.53$_{L}$	73.53	28.73	66.05^{H}
Grain length (mm)	9.16	9.64	9.50	9.72^{H}	7.07	6.43$_{L}$
Grain breadth (mm)	2.55^{H}	2.39	2.26	2.29	2.49	2.22$_{L}$
1000 grain weight (g)	22.77	20.62	17.73	24.80^{H}	17.76	12.46$_{L}$
Yield per hill (g)	24.46	22.78	19.37	27.09^{H}	19.67	16.10$_{L}$
Harvest index	0.34	0.33	0.40^{H}	0.30$_{L}$	0.37	0.33

The genotypes of cluster III produced the highest mean for ligule length, panicle length, plant height and harvest index, but 50% flowering and unfilled grain per panicle showed the lowest mean values for the genotype in this cluster.

The genotypes of cluster I gave the highest mean for culm diameter, total tiller, effective tiller and grain breadth but lowest mean for only one character plant height.

The genotypes of cluster VI gave the highest mean for filled grain per panicle and unfilled grain per panicle, but flag leaf area, grain length, grain breadth, 1000 grain weight and yield per hill was found with the lowest mean values.

The genotypes of cluster II gave the highest mean for only one character flag leaf area but lowest mean for panicle length and days to maturity.

The genotypes of cluster V produced no highest mean value for any character lowest mean for only one character culm diameter.

In general, the cluster producing the highest mean values for a particular trait not necessarily possessed the genotypes with the highest value for that specific trait in the same cluster. For example, the highest cluster mean for grain length possessed by cluster IV,

but the genotypes with the longest grain fall under cluster I (Table 9 and Table 10). Similar result was observed for ligule length, flag leaf area, panicle length, days to 50% flowering, days to maturity, unfilled grain per panicle, 1000 grain weight, yield per hill and harvest index. These results indicated the less contribution of those traits in the formation of the cluster.

Table 10. Mean of 24 test genotypes for 16 quantitative characters.

SL No.	Genotypes	LL (mm)	FLA (cm^2)	CD (mm)	TT	ET	PL (cm)	PH (cm)	DF	DM	FG/P	UFG/P	GL (mm)	GB (mm)	1000.0 Gwt.(g)	Y/hill(g)	HI
1	Chinigura	2.1	41.3	4.6	12.3	11.0	24.8	127.8	95.0	122.0	167.0	16.7	6.1	2.7	15.8	19.3	0.5
2	Basmati India	1.7	51.1	5.4	12.0	11.3	29.9	113.0	72.0	97.0	140.3	29.7	11.4	2.7	20.1	24.6	0.3
3	Kataribhog	2.2	35.1	4.8	15.0	13.5	25.2	119.3	86.0	119.0	110.0	32.5	8.5	2.5	30.9	32.3	0.3
4	Sakkorkhora	2.5	30.4	5.2	14.0	13.0	20.8	131.4	91.0	118.0	125.0	30.0	6.5	2.7	19.3	24.8	0.1
5	Basmati porder	2.2	42.2	5.4	14.0	13.4	26.6	144.8	88.0	107.0	92.2	27.4	9.6	2.1	20.6	23.2	0.4
6	Basmati 370	2.3	42.0	4.8	11.8	10.6	30.5	178.9	72.0	111.0	99.4	28.2	9.6	2.2	20.3	20.3	0.3
7	Basmati Naret	2.4	44.2	5.3	12.8	10.4	25.3	135.5	74.0	104.0	89.6	22.0	9.5	2.5	20.5	24.5	0.3
8	Basmati IRGC 27782	2.3	42.1	4.9	11.3	10.1	25.7	139.7	83.0	108.0	92.1	38.4	9.5	2.5	20.6	21.1	0.3
9	Basmati 1	2.2	37.3	5.6	13.4	12.8	31.3	143.6	72.0	111.0	125.0	24.8	9.8	2.4	20.3	25.1	0.6
10	Basmati 107	2.2	39.4	5.2	10.0	9.8	31.0	165.5	72.0	107.0	136.8	15.2	9.1	2.3	16.7	18.1	0.4
11	Basmati 134	2.4	41.1	5.6	13.0	13.0	29.7	167.4	70.0	106.0	124.6	36.2	9.9	2.2	16.2	19.7	0.4
12	Basmati 372	2.2	40.4	5.2	10.6	10.6	29.0	161.9	70.0	107.0	83.0	33.6	10.0	2.5	20.7	22.3	0.4
13	Kamarang	1.4	33.7	4.3	10.7	9.6	26.8	147.1	108.0	142.0	112.7	43.7	7.1	2.4	19.0	23.1	0.4
14	Jamaiaduri	1.1	35.9	4.0	12.7	10.9	26.4	140.3	104.0	136.0	154.1	29.6	8.0	2.2	18.3	20.8	0.4
15	Jhingasail	1.4	38.9	4.5	11.1	9.7	29.2	145.2	105.0	140.0	59.2	73.5	9.7	2.3	24.8	27.1	0.3
16	Khutichikon (3)	1.5	38.3	4.0	10.4	9.1	26.9	128.9	105.0	137.0	193.3	62.3	7.2	2.3	15.6	19.2	0.4
17	Khutichikon (2)	1.5	33.4	3.8	12.4	10.8	28.4	139.5	105.0	140.0	121.3	33.5	6.6	2.7	18.8	19.8	0.4
18	Kalijira	1.7	41.4	4.5	10.9	9.6	28.7	135.9	102.0	131.0	226.1	77.8	6.5	2.2	10.6	18.4	0.3
19	Binnaphul	1.1	40.7	3.9	14.7	12.8	29.4	139.4	104.0	127.0	142.1	20.1	7.5	2.4	17.0	15.3	0.2
20	Rong-er-gura	1.2	32.7	5.4	12.5	11.0	29.1	135.2	100.0	131.0	221.0	71.1	5.8	2.0	9.6	18.4	0.3
21	Chinisagor	2.0	36.8	5.0	10.7	9.8	29.2	148.5	104.0	121.0	194.0	74.1	6.2	2.1	10.1	14.0	0.3
22	Rasmala	1.4	31.5	4.3	11.9	10.6	29.7	142.7	100.0	130.0	262.3	69.5	6.1	2.3	12.9	15.4	0.4
23	Sugandhidhan (2)	1.4	34.1	4.1	11.8	10.4	29.3	133.9	103.0	131.0	191.2	41.4	6.8	2.5	16.0	11.3	0.3
24	Basmati T_3	2.1	36.5	5.6	11.3	10.7	28.4	147.3	84.0	112.0	128.7	26.9	9.6	2.4	23.3	15.5	0.4

The genotypes produced either highest or lowest mean values at least for six morpho-quantitative characters by the particular clusters and either of the clusters also possessed their respective genotypes having the highest or lowest values of the characters. It may be mentioned that the genotypes with the highest mean values and the individual mean values for the most of the characters *viz.* culm diameter, total tiller, effective tiller, plant height, filled grain per panicle and grain breadth were the same (Table 7, 9 and 10**)** which indicated that these traits may have some positive contribution to the formation of the clusters.

Contribution of characters towards divergence

Contribution of characters towards divergence obtained from canonical variate analysis is presented in Table 11 and Table 12. In this method vectors or canonical roots were calculated to represent the variates in the graphical form (Rao, 1952). This is helpful in cluster analysis as it facilitates the study of group constellations and also serves as a pictorial representation of the configuration of various groups. The absolute magnitude of the coefficients in the first

two canonical vectors also reflects to a great extent, the importance of characters for primary and secondary differentiation. The character, which gives high absolute magnitude for vector 1, is considered to be responsible for primary differentiation. If the same character gives equal magnitude for both the vectors then that character is considered responsible for primary as well as secondary differentiation.

Table 11. Values of canonical roots and the percentage of variation absorbed by them.

Canonical roots	Values of canonical roots	% of variation absorbed by the canonical roots
1	66.94	53.46
2	44.49	35.53
3	8.55	6.83
4	3.15	2.51
5	2.09	1.67
Total	125.22	100

Table 12. Relative contribution of 16 moroho-quantitative traits of 24 test genotypes of total divergence in rice.

Characters	Vector I	Vector II
Ligule length (cm)	0.3186	-0.0872
Flag leaf area (cm^2)	0.2202	-0.1820
Culm diameter (cm)	0.2773	-0.1917
Total tiller	0.1385	0.3728
Effective tiller	0.2147	0.2487
Panicle length (cm)	-0.0464	-0.4157
Plant height (cm)	0.0626	-0.3864
Days to 50% flowering	-0.3599	0.2107
Days to maturity	-0.3492	0.1745
Filled grain per panicle	-0.3077	-0.0806
Unfilled grain per panicle	-0.2909	-0.0991
Grain length (mm)	0.3372	-0.1551
Grain breadth (mm)	0.1474	0.2942
1000 grain weight (g)	0.2761	0.2335
Yield per hill (g)	0.2403	0.2499
Harvest index	0.0406	-0.2844

In the present study, it appeared from the canonical analysis that 53.46% of the total variation was accounted for canonical root 1 and 35.53% by canonical root 2 (Table 11). Since the two canonical roots absorbed about 89% of the variability, a two dimensional representation of relative positions of the genotypes in the Z_1 and Z_2 graph was considered to be adequate. The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 11.

The data (Table 12) in general indicated that the characters for the primary differentiation in the descending order were ligule length, flag leaf area, culm diameter, plant height, grain length and harvest index. From the positive absolute values of the vector 1, it would appear that grain length was the most responsible for primary differentiation followed by ligule length, culm diameter, flag leaf area, plant height and harvest index. On the other hand, the negative values for the two vectors of panicle length, filled grain per panicle and unfilled grain per panicle indicated least responsibility of both the primary and secondary differentiations. However, from the positive absolute values of these two vectors, it would appear that total tiller, effective tiller, grain breadth,

1000 grain weight and yield per hill value were responsible for both primary and secondary differentiation and highest contribution of these traits towards the divergence between twenty four rice genotypes. On the contrary, the negative absolute values for vector I and positive values for vector II for the characters days to 50% flowering and days to maturity indicated the responsibility of secondary differentiation and had lower contribution towards the divergence. From the positive magnitude of results of vector I it was appeared that the contribution of grain length was the highest followed by ligule length, culm diameter, flag leaf area, harvest index and plant height to the total divergence in rice. Hossain (2008) reported that head rice recovery percentage was the highest followed by milling outturn, stem length, elongation ratio, days to flowering and days to maturity to the total divergence in rice. Islam (2011) reported that contribution of kernel breadth was the most responsible for primary differentiation followed by L/B ratio, time of 50% heading, amylose content, number of filled grains/panicle, thousand grain weight, number of tillers per plant, seed yield per plant and panicle length to the total divergence in rice.

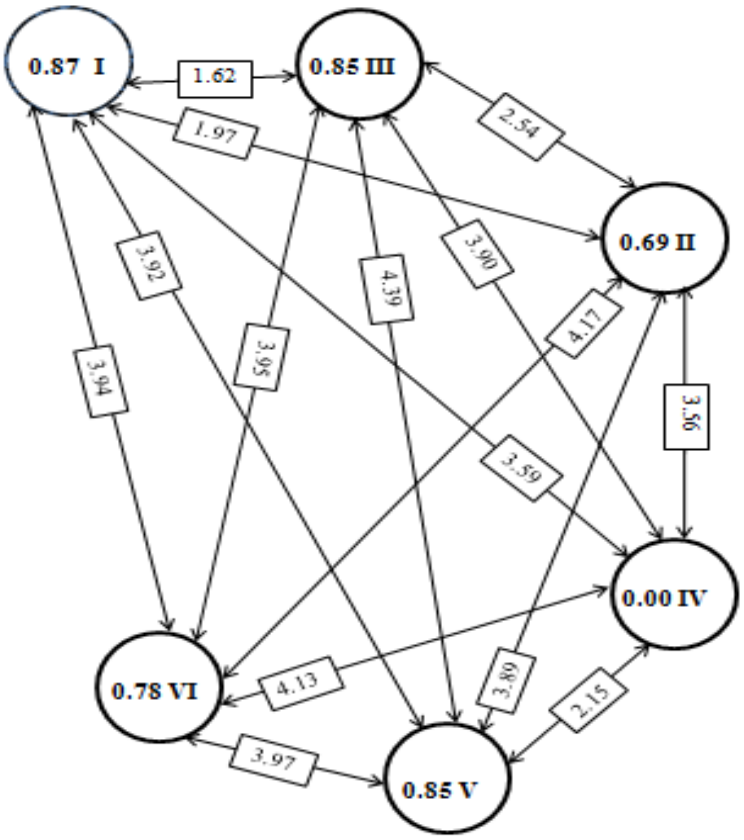

Fig. 1. Cluster diagram showing the inter cluster distance ($D = \sqrt{D^2}$) for 24 rice genotypes.

Conclusion

High heterosis can be obtained from the cross between genetically distant parents (Ghaderi *et al.*, 1984). Counting the magnitude of genetic distance, contribution of different characters toward the total divergence, magnitude of cluster means for different characters, the following genotypes can be selected to perform better if used in hybridization programme. Among the inter-cluster distance, the highest distance was observed between the cluster III and cluster V. Cluster I and cluster III showed lowest inter-cluster distance. Some inter-cluster distance showed

intermediate distance. Intermediate diversed parents have the more chance to contribute heterosis in the subsequent generation.

To select clusters to obtain more heterotic genotypes eleven pairs of clusters can be considered for this purpose. These pair of combinations may be as follows I and IV, I and V, I and VI, II and IV, II and V, II and VI, III and IV, III and V, III and VI, IV and VI and V and VI. Cluster III showed the highest mean for ligule length, panicle length, plant height and harvest index. Panicle length and plant height were important for yield contributing character. In this cluster there were two lowest mean values for unfilled grain per panicle and days to 50% flowering those are more desirable characters. Cluster I had the highest mean value for culm diameter, total tiller, effective tiller and grain breadth. In this cluster culm diameter, total tiller and effective tiller were most important yield contributing characters. In this cluster it also showed lowest mean value for only one but most desirable character *viz.* plant height. Cluster III had been comprised of rice genotype viz. Basmati 370, Basmati 107 and Basmati 134. Cluster I had been comprised of Basmati India, Kataribhog, Sakkorkhora, Basmati 1 and Basmati T_3. Hybridization between the genotypes of cluster I and cluster III by considering Basmati and non-Basmati type will provide maximum heterosis and will create a wide genetic variability.

Acknowledgement

The authors express their cordial thanks for financial support by the SPGR sub-project of National Agricultural Technology Project (NATP), phase-1, Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka entitled "Genetic enhancement of local rice germplasm towards aromatic hybrid rice variety development in Bangladesh."The author extends special thanks to Md. Zahidul Islam and Md. Abu Syed, Scientific Officer, Bangladesh Rice Research Institute (BRRI) for their sincere cooperation, valuable suggestions and comments for the improvement of the manuscript.

References

Anderson E. 1957. A Semigraphical method for the analysis of complex problems. Proceedings of National Academy of Science. Washington, United States of America, **48,** 923- 927.

Ghaderi A, Shisegar M, Rejai A, Ehdaie B. 1979. Multivariate analysis of genetic diversity for yield and its components in mungbean. Journal of the American Society for Horticultural Science104, 728-731.

Ghalain SS. 2006. Genetic divergence in rice (*Oryza sativa* L.) genotypes grown in Kamaun Himalaya. Indian Journal of Genetics and Plant Breeding **66,** 37- 38.

Golam F, Hui Yin Y, Masitah A, Afnierna N, Majid NA, Khalid N, Osman M. 2011. Analysis of aroma and yield components of aromatic rice in Malaysian trpoical environment. Australian Journal of Crop Science **5,** 1318- 1325.

Hien NL, Sarhadi WA, Hirata Y, Oikawa Y, Hirata Y. 2007. Genetic diversity of morphological responses and the relationships among Asia aromatic rice (*Oryza sativa* L.) cultivars. Tropics **16,** 343- 355.

Hooker JD. 1979. The flora of British India. vol. 2L. Reeve Co. Kent, England, 25.

Hossain Z. 2008. Genetic diversity for morpho-physiochemical characters and microsatellite DNA markers in fine grain and aromatic landraces of rice (*Oryza sativa* L.). PhD thesis, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh.

Islam MS. 2011. Characterization of aromatic rice (*Oryza sativa* L.) germplasm through morphological, biochemical and molecular techniques. PhD thesis, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh.

Juliano BO, Duff D. 1991. Rice grain quality as an emerging priority in National rice breeding programmes. In: rice grain marketing and quality issues. Los Banos, Laguna, IRRI, 55- 64.

Kovach MJ, Calingacion MN, Fitzgerald MA, McCouch SR. 2009. The origin and evolution of fragrance in rice (*Oryza sativa* L.). Proceedings of National Academy of Sciences. United States of America**106,** 14444- 14449.

Li X, Yan W, Agrama H, Hu B, Jia L, Jia M, Jacks on A, Moldenhauer K, McClung A, Wu D. 2010. Genotypic and phenotypic characterization of genetic differentiation and diversity in the USDA rice mini-core collection. Genetica **138,** 1221- 1230. http://dx.doi.org/10.1007/s10709-010-95215

Mathure S, Jawali N, Nadaf A. 2010. Diversity analysis in selected non-basmati scented rice collection (*Oryza sativa* L.). Rice Science **17,** 35- 42. http://dx.doi.org/10.1016/S1672-6308(08)60102-X.

Mathure S, Shaikh A, Renuka N, Wakte K, Jawali N, Thengane R, Nadaf A. 2011. Characterisation of aromatic rice (*Oryza sativa* L.) germplasm and correlation between their agronomic and quality traits. Euphytica **179,** 237–246. http://dx.doi.org/10.1007/s10681-010-0294-9.

Morishima H. 1984. Wild plant and demonstration in biology of rice. Japan Scientific Society Press, Tokyo, 3-30.

Naik D, Sao A, Sarawgi AK, Singh P. 2006. Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of Central India. Asian Journal of Plant Sciences **5,** 197- 200.

Nayak AR, Reddy JN, Pattnaik AK. 2002. Quality evaluation of some Thailand and Vietnam scented rice. Indian Journal of Genetics and Plant Breeding **15,** 125- 127.

Parikh M, Motiramani NK, Pastogi NK, Sharma B. 2012. Agro-Morphological characterization and assessment of variability in aromatic rice germplasm. Bangladesh Journal of Agricultural Research **37,** 1- 8.

Rao CR. 1952. Advance Statistical Methods in Biometrical Research. A Division of Macmillan Publishing Co., Inc. Hafner press. New York, United States of America.

Ray A, Deb D, Ray R, Chattopadhayay B. 2013. Phenotypic characters of rice landraces reveal independent lineages of short-grain aromatic *indica* rice. AoB Plants, **5,** plt032. http://dx.doi.org/10.1093/aobpla/plt03.2

Sarawgi AK, Parikh M, Sharma B. 2012. Morphological and quality characterization of dubraj group from aromatic rice germplasm of Chhattisgarh and Madhya Pradesh. Vegetos- An International Journal of Plant Research**25**, 387- 394.

Singh RK, Gautam PL, Saxena S, Singh S. 2000a. Scented rice germplasm: conservation, valuation and utilization. In: Singh RK, Singh US, Khush CS (eds) Aromatic rices. Kalyani publisher, New Delhi, India, 107- 133.

Singh RK, Singh US, Khush GS, Rohilla R, Singh JP, Singh G, Shekhar KS. 2000b. Small and medium grained aromatic rices of India. In: RK Singh, US Singh, CS Khush (eds) Aromatic rices. Kalyani Publishers, New Delhi, India, 155- 177.