

## GENETIC BASIS OF VARIABILITY AND DIVERSITY PRESENT IN FINE RICE AVAILABLE IN BANGLADESH

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### ABSTRACT

A set of thirty genotypes of fine rice collected from different parts of Bangladesh were integrated in the investigation to assess variability and diversity pertained among themselves. The experiment was conducted in the experimental field, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh and laid out at RCBD with three replications during July to December, 2006. Analysis of variance revealed significant variation for each of the characters that instigated to study variability and diversity present in the materials. High heritability was estimated for panicle length followed by spikelets/panicle, yield /ha and tillers/plant but high heritability coupled with high genetic advance was estimated for panicle length and spikelets/panicle. The genotypes fell into 7 different clusters based on  $D^2$  statistics. Cluster I contained the highest number of genotypes viz. Katari, Zira, Badshabhong, Zethakatari, Philippinekatari, Neniya, Chinigura, Shadakatari, Dudshar and Bolder. The popular known primitive cultivar, Kalazira was included in cluster II along with Shilkamal and Shitabhog. The only variety, BRRI 34 had fallen under cluster VI containing Darkashail too. Moulata alone was included alone in cluster V. The genotypes under cluster I produced the highest yield (3.307 t/ha). The contribution of spikelets/panicle alone exerted maximum load (19.58%) to evolve genetic diversity, and the ultimate end product yield/ha contributed only 5.38% to the genetic diversity.

**Keywords:** *Fine rice, cluster, variability, diversity.*

### INTRODUCTION

Most of the rice farmers, particularly in northern part of Bangladesh are resource poor and are not able to use recommended package of production. So, improved varieties developed have not been fully adopted by the farmers. The local rice cultivars with desirable characters can withstand stress conditions, though their yield is less than the modern varieties. The modern varieties are not responsiveness to low management. The farmers of this belt grow heterogeneous rice fields for different end uses. Different varieties fulfill different livelihood functions like food, livestock, fodder, thatching, cash etc. For example, farmers like varieties with long fine aromatic grains because these are used as special rice in different social and religious occasions and have high market value.

It has been proved that fine rice is more preferable and costly than that of conventionally edible rice cultivars. It has great potentiality because fine rice cultivars is preferred for its aroma and therefore utilized in different popular/elite functions held in a society. Also it can bring off huge foreign money through export. The farmers of our country are always compelled to grow the available traditional fine rice cultivars for their own family interest. At present no systematic efforts have been paid for selection of superior aromatic rice cultivars with high. Even the popular aromatic rice cultivars of a particular locality are still remaining out of reach to the farmers of other parts of Bangladesh. Therefore, there remains immense scope to exploit the fine and aromatic rice genotypes in Bangladesh for improvement through fruitful breeding approaches.

Keeping these in view, the investigation was under taken to study in details the available fine rice cultivars in Bangladesh.

## Objectives

The objectives of the research are:

- i) To assemble different fine rice genotypes available in Bangladesh.
- ii) To evaluate the genotypes on qualitative and quantitative traits.
- iii) To estimate variability and diversity pertained in the genotypes.
- iv) To identify the traits for improving the fine quality of the genotypes.
- v) To select the appropriate genotypes with quality grain and high aroma content.

## MATERIALS AND METHODS

The experiment was conducted at the experimental field of the Dept. of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur during July to December, 2006. The experiment was laid out in randomized complete block design with three replications. Each replication contained 200 plants of 30 genotypes having 20 x 15 cm spacing. Each plot was 3 m in length and 2 m in breadth. The present experimental material comprised of 30 fine rice local germplasms including BRRI 34 collected from different parts of Bangladesh. The list of genotypes with their respective local name and sources of collection is presented in Table 1. Eleven characters were considered for the study and the data were recorded from 10 randomly selected plants/plot on plant height, tillers/plant, panicle length, spikelets/panicle and sterility percent. Thousand grains weight was estimated in three replications for each entry. Chlorophyll content was measured from appropriate leaves and grain length breadth ratios were estimated with the help of a digital slide calipers. Days to 50% flowering and days to maturity were obtained from the field and yield/ha was the conversion value of yield/plot.

### Statistical analysis

The collected data on eleven characters were analyzed for variance, different components of phenotypic and genotypic variance, heritability and genetic advance and then genetic divergence. Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.*, (1955). Genotypic and phenotypic coefficients of variations were estimated following the standard formulae used by Burton (1952). The expected genetic advances for different characters under investigation were estimated according to the formula used by Johnson *et al.*, (1955) and Allard (1960). Genetic advance expressed as percentage of mean were estimated by using the formula as described by Comstock and Robinson (1952). The Mahalanobis' distance ( $D^2$ ) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1985). The  $D^2$  values of genotypes were arranged in order of relative distances from each other following the method of Tocher (Rao, 1952). Cluster formation was done by methods of Singh and Chaudhury (1985).

Table 1. List of fine rice cultivars with their respective local name and sources of collection.

Accession No.	local name	Sources
FR 1	Katari	Sadar, Dinajpur
FR 2	Kalazira	Sadar, Kurigram
FR 3	Zira	Birol, Dinajpur
FR 4	Badshabhog	Chirirbandar, Dinajpur
FR 5	Zethakatari	Birol, Dinajpur
FR 6	Philippinekatari	Fulbari, Dinajpur
FR 7	Malshira	Fulbari, Dinajpur
FR 8	Shilkamal	Fulbari, Dinajpur
FR 9	Lal Paijam	Bhola
FR 10	Ranjid	Barisal

FR 11	Zhumur	Barisal
FR 12	Amur	Barisal
FR 13	Moulata	Panchagarh
FR 14	BRRI 34	BRRI, Yoydebpur
FR 15	Neniya	Kurigram
FR 16	Chinigura	Kurigram
FR 17	Uknimodhu	Panchagarh
FR 18	Binnipakri	Chirirbandar, Dinajpur
FR 19	Shadakatari	Chirirbandar, Dinajpur
FR 20	Darkashail	Natore
FR 21	Dudshar	Rajshahi
FR 22	Rajshaisharna	Thakurgoan
FR 23	Boldar	Thakurgoan
FR 24	Lalchicon	Jossore
FR 25	Mala IRRI	Thakurgaon
FR 26	Shadamota	Barisal
FR 27	Shotormota	Barisal
FR 28	Lalmota	Khulna
FR 29	Shitabhog	Barisal
FR 30	Mothamota	Barisal

## RESULTS AND DISCUSSION

The results and discussion on eleven characters are presented below to assess the variability and genetic diversity pertained in 30 genotypes of fine rice.

### Analysis of variance

Analysis of variance was computed on yield and other ten yield related characters. The significant mean squares values articulated remarkable variation against each of the characters in 30 different genotypes of fine rice (Table 2). According to the ANOVA it was noted that major portion of variation for each character proclaimed that differences were inherently dipped into the genotypes.

### Mean Performances

Mean performances of yield and yield contributing characters are presented in Table 3. The mean values of each character have been optioned to separate through lsd test. The genotypes Ranjid required minimum days (70.33 days) to attain 50% flowering and it was significantly different from other 29 genotypes of fine rice. The maximum days to 50% flowering (89.67 days) were needed for Dudshar followed by Shilkamal, Moulata, Binnipakri, Mala IRRI and Shitabhog. Amongst the genotypes, Zhumur was the dwarfest but it was comparable with Ranjid, Badshabhog, Malshira and Mothamota. The tallest genotype Kalazira having 135.65 cm height was statistically similar with Bolder, Shadamota, Shotomota and Lalmota for the trait. It is virtually true that tallest plants are prone to lodging, causing remarkable loss in yield. Zira had the lowest

Table 2. Mean squares (MS) derived from ANOVA -2 model on yield and yield contributing characters in fine rice

Source of Variation	df	Days to 50% flowering	Plant height (cm)	Tillers /Plant	Panicle length(cm)	Spikelets /panicle	Sterility (%)	1000-grain weight (g)	Chlorophyll content (mg/g)	Grain length breadth ratio	Days to maturity	Yield/ha (t)
Replication	2	1.283	10.35	0.785	12.082	7.174	11.327	11.92	8.280	3.269	2.878	5.286
Genotype	29	110.121**	659.31* *	63.160**	236.170**	5020.401**	16.142**	116.238 **	0.327**	0.904* *	393.4 78**	1.588**
Error	58	22.965	161.67	9.800	18.273	501.038	4.378	19.153	0.053	0.178	94.21 1	0.201
Non-additivity	1	0.012	0.003	0.010	0.000	0.453	0.685	0.001	0.000	0.000	0.220	0.002
Residual	57	22.953	161.66	9.790	18.273	500.585	3.693	19.152	0.053	0.178	93.99 1	0.199
CV(%)		7.292	9.26	11.286	5.705	14.914	15.026	6.280	3.825	4.283	8.825	10.281

Table 3. The magnitude of heritability projects the degree of transmission of character concerned from parental Continuation

Accession No.	Variety	Days to 50% flowering	Plant height (cm)	Tillers/Plant	Panicle length (cm)	Spikelets/panicle	Sterility (%)	1000-grain weight (g)	Chlorophyll content (mg/g)	Grain length breadth ratio	Days to maturity	Yield/ha (t)
FR 16	Chinigura	79.33	102.47	15.35	19.25	130.28	7.65	21.34	1.732	2.54	110.67	3.29
FR 17	Uknimodhu	83.67	122.44	14.10	21.21	131.25	9.25	19.47	1.503	2.75	119.33	2.75
FR 18	Binnipakri	85.33	116.77	15.35	18.11	125.23	10.25	22.43	1.567	3.00	111.67	2.50
FR 19	Shadakatari	84.33	115.84	17.48	16.54	95.33	11.00	21.79	1.345	2.83	123.67	3.25
FR 20	Darkashail	78.67	118.35	14.95	25.33	125.44	12.36	18.50	1.433	3.25	119.33	2.90
FR 21	Dudshar	89.67	120.34	17.36	29.34	145.35	7.77	18.75	1.733	3.00	133.67	3.43
FR 22	Rajshahisharna	79.33	121.65	19.25	20.58	120.34	6.35	22.50	1.703	3.15	116.33	2.30
FR 23	Bolder	80.00	130.64	20.45	27.67	162.74	7.33	21.35	1.241	2.25	136.67	3.80
FR 24	Lalchicon	81.67	115.53	21.38	25.87	121.12	8.67	19.25	1.321	2.50	125.00	3.25
FR 25	Mala IRRI	88.67	115.25	18.95	26.84	116.13	9.66	18.25	1.243	3.21	133.33	3.51
FR 26	Shadamota	81.33	125.45	18.23	21.72	129.75	10.63	23.50	1.123	3.24	116.00	2.78
FR 27	Shotormota	78.00	130.96	19.45	23.34	135.84	11.00	24.25	1.221	2.50	110.33	2.85
FR 28	Lalmota	79.67	123.66	14.76	24.45	131.28	8.50	24.30	1.543	3.24	113.33	2.74
FR 29	Shitabhog	88.67	119.25	15.48	24.75	99.27	6.33	21.40	1.623	3.29	135.00	3.47
FR 30	Mothamota	77.67	98.44	14.25	25.25	98.33	5.55	23.28	1.432	2.25	114.33	2.50
LSD		4.519	11.99	2.952	4.031	21.018	1.973	4.1127	0.217	0.398	9.153	0.423

Table 4. Genetic variabilities in eleven characters of fine rice.

Parameters	Days to 50% flowering	Plant height (cm)	Tillers/ Plant	Panicle length (cm)	Spikelet s/ panicle	Sterility (%)	1000- grain- weight (g)	Chloro phyll content (mg/g)	Grain length breadth ratio	Days to maturit y	Yield/ ha (t)
Genotypic variance ( $\sigma^2_g$ )	29.052	165.880	17.787	72.632	1506.45 4	3.921	32.362	0.091	0.242	99.755	0.462
Phenotypic variance ( $\sigma^2_p$ )	52.017	327.545	27.587	90.905	2007.49 2	8.299	51.515	0.144	0.420	193.96 7	0.663
Environtal variance ( $\sigma^2_e$ )	22.965	161.665	9.800	18.273	501.038	4.378	19.153	0.053	0.178	94.211	0.201
GCV	6.592	11.205	23.668	35.376	31.468	23.261	29.702	20.012	16.803	8.273	22.247
PCV	8.820	15.745	29.476	39.576	36.326	33.841	37.474	25.157	22.136	11.536	26.648
Heritability (%)	55.851	50.643	64.476	79.899	75.042	47.249	62.820	63.279	57.619	51.429	69.699
Genetic advance (at 5% selection intensity)	8.298	18.881	6.976	15.693	69.262	2.804	9.288	0.495	0.769	14.755	1.169
Genetic advance (as % of mean)	10.148	16.426	39.150	65.139	56.155	32.938	48.495	32.794	26.275	12.221	38.261

1000 grain weight (10g) and it was not statistically different from Katari, Kalazira and Zethakatari. The maximum 1000 grain weight (24.30g) was estimated from Lalmota but its was alike with 13 genotypes in statistical sense. The maximum chlorophyll content was recorded in Dudshar (1.733 mg/g) and it was statistically similar with those of 15 other genotypes. The minimum chlorophyll content was obtained from Shadamota (1.23mg/g) and it was not different from 15 genotypes. High chlorophyll content is associated with utmost foliage but delayed leaf senescence development (Bansal *et al.*, 1999).

Out of 30 genotypes, 6 were late maturing and 14 were early maturing and the others were intermediate. The maximum and minimum days to maturity were found in Bolder and Shotomota respectively. Usually prolonged maturity period turns into higher grain yield but does not correlate with high aroma content. In general, the yield potential of the genotypes was low as compared to high yielding varieties of rice. However, the highest yield was obtained from Bolder (3.80 t/ha), followed by Badshabhog, Philippinekatari, Pajam, BRRI 34, Dudshar, Mala IRRI and Shitabhog. The lowest yield was recorded in Rajshahisarna (2.3 t/ha) and it was similar with Shilkamal, Zhumur, Amur, Moulata, Binnipakri and Mothamota. The other genotypes had medium yield potential.

### **Genetic variability**

The phenotypic variance against each character was higher than the corresponding genotypic variance but the latter was higher than the respective environmental variance, suggesting that environment played a substantial role to express the characters (Table 4). The difference between GCV and PCV was maximum for sterility percent followed by 1000-grain weight while minimum difference was observed for days to 50% flowering followed by days to maturity. The higher difference between GCV and PCV indicated prominent effect of environment over the expression of the trait concerned (Falconer, 1981). The highest heritability was estimated for panicle length (79.899%) and the lowest was for sterility percent (47.249). generation to its progenies. However, high heritability coupled with high genetic advance was proclaimed by panicle length and spikelets/panicle. Moreover, genetic advance as percent of mean was also high for the two characters which has lessened the work of identification for traits (Gomez *et al.*, 1986). Therefore, the two characters are indispensable for improvement of yield through discriminant function.

### **Genetic divergence analysis**

The 30 fine rice genotypes fall into seven clusters based on  $D^2$  statistics (Mahalanobis 1936). The cluster I comprised with 10 genotypes, cluster II with 3, cluster III with 7, cluster IV with five, cluster V with a single and both clusters VI and VII possessed two genotypes each (Table 5).

The genotypes under the cluster I did not have same source of collection, so, it might be prognosticated that genetic diversity was independent to ecological diversity. Intra cluster distance was maximum (103.29) in cluster VI, suggesting that both BRRI 34 and Darkashail of the group VI played a fruitful role to create genetic diversity. The ten genotypes under cluster I also showed a considerable intracluster distance (89.35). The genotypes of cluster III were genetically farthest from the genotypes of cluster I and cluster VI (Table 6). Therefore, the genotypes of cluster III may be crossed with the genotypes of cluster VI, and the genotypes of cluster I with the genotypes of cluster III for improving yield and yield contributing characters of fine rice. On the contrary, the genotypes of cluster II showed the minimum distance with genotypes of cluster V, suggesting that crossing between the genotypes under the two groups would not offer any fruitful result. The cluster means of yield and yield contributing characters are presented in Table 7. The genotypes of cluster VII required the minimum days to 50% flowering an

Table 5. Clustering pattern of 30 fine rice genotypes by Tocher's Method

Clusters	Number of genotypes	Genotypes
I	10	Katari, Zira, Badshabhog, Zethakatari, Philippinekatari, Neniya, Chinigura, Shadakatari, Dudshar, Bolder
II	3	Kalazira, Shilkamal, Shitabhog
III	7	Malshira, Amur, Lalchicon, Shadamota, Mothamota, Lalmota, Shotormota
IV	5	Paijam, Ranjid, Zhumur, Rajshahisharna, Mala IRRI
V	1	Moulata
VI	2	BRR1 34, Darkashail
VII	2	Binnipakri, Uknimodhu

Table 6. Average inter and intra-cluster distance ( $D^2$ ) for 30 fine rice genotypes based on eleven characters.

Clusters	I	II	III	IV	V	VI	VII
I	<b>89.35</b>	138.25	538.18	99.63	83.70	211.56	77.00
II		<b>27.60</b>	440.42	257.12	51.66	65.16	132.19
III			<b>78.05</b>	492.62	40.65	648.88	202.27
IV				<b>52.28</b>	112.98	89.47	205.36
V					<b>0.00</b>	151.32	290.48
VI						<b>103.29</b>	97.07
VII							<b>21.37</b>



Table 7. Clusters' Means of yield and yield characters of fine rice.

Clusters	Days to 50% flowering	Plant height (cm)	Tillers/ Plant	Panicle length (cm)	Spikelets/ panicle	Sterility (%)	1000-grain weight (g)	Chlorophyll content (mg/g)	Grain length breadth ratio	Days to maturity	Yield/ ha (t)
I	82.100	115.821	17.853	24.981	115.479	8.212	17.045	1.6234	2.848	124.167	3.307
II	86.670	125.4166	16.200	26.686	118.606	7.443	18.333	1.530	3.063	122.556	3.113
III	79.572	113.465	17.554	23.421	113.822	9.324	22.058	1.374	2.860	117.760	2.852
IV	79.466	105.918	18.688	24.006	128.122	7.636	19.496	1.391	3.028	119.666	3.032
V	88.330	121.650	21.820	22.360	151.290	9.000	14.350	1.703	2.750	119.670	2.500
VI	80.170	114.595	19.925	23.605	122.255	9.495	20.500	1.567	3.250	119.665	3.200
VII	84.500	119.605	14.725	19.660	128.240	9.750	20.950	1.535	2.875	115.500	2.625

Table 8. Mean performance and contribution towards genetic divergence in fine rice.

Characters	Mean range	Contribution towards diversity (%)
Days to 50% flowering	70.33-89.67	8.95
Plant height (cm)	89.00-135.65	5.26
Tillers/ Plant	14.10-21.82	8.07
Panicle length (cm)	16.54-32.25	10.39
Spikelets/ panicle	80.69-162.74	19.58
Sterility (%)	5.55-11.25	3.65
1000- grain weight (g)	10.00-24.30	14.48
Chlorophyll content (mg/g)	1.123-1.733	2.49
Grain length breadth ratio	2.24-3.33	11.84
Days to maturity	110.33-136.67	9.90
Yield/ ha (t)	2.30-3.80	5.38

lowest number of tillers as compared with other clusters. The genotypes of cluster II produced largest panicle and the smallest panicle was produced by the genotypes under cluster VII. The genotypes of cluster V had the lowest 1000 grain weight. The single genotype, Moulata of cluster V had the highest chlorophyll content (1.703 mg/g) followed by the genotypes of cluster I. The highest yield/ha was estimated in cluster I followed by cluster VI, II and IV (>3t/ha). In general, the yield potential of all the clusters did not show any remarkable variation. Among the eleven characters, spikelets/panicle exerted the maximum contribution towards genetic diversity followed by 1000-grain weight, grain length breadth ratio and panicle length. Sterility percent showed minimum contribution to create genetic diversity. Likewise, plant height and yield/plant contributed insufficient effect on diversity. Days to 50% flowering and days to maturity rendered medium and almost equal contribution towards diversity. Variability and diversity of the investigated fine rice genotypes thus offered a amazing scope of quality and quantity improvement in fine rice.

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