

# Genetic Divergence of *Balam* Rice (*Oryza sativa* L.) Germplasm of Bangladesh

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## ABSTRACT

Forty genotypes of *Balam* rice germplasm of Bangladesh were studied for 17 morpho-physicochemical characters at BRRI during 2009-11. The cluster analysis using Mahalanobis' D<sup>2</sup> statistics, grouped the genotypes into seven clusters, where no duplicate germplasm was found for the studied characters. The highest number of genotypes (8) was constellated into clusters I, III and V and the lowest (2) was in cluster IV. The intra- and inter-cluster distances were maximum (1.17 and 21.16) in cluster VII and between clusters II and IV and minimum (0.27 and 2.23) in cluster IV and between clusters II and VII respectively. Based on the values of principal component score, the two-dimensional scatter diagram (Z<sub>1</sub>-Z<sub>2</sub>) also distributed the genotypes into seven groups. The genotype of cluster IV, produced the highest flag and penultimate leaf area (1136 cm<sup>2</sup>), culm diameter (7.2 mm), days to maturity (152 days), primary and secondary branches per panicle (63), grain yield per panicle (4.9 g), 1000-grain weight (29.3 g), grain yield per hill (31.3 g), cooking time (19 min) and amylose content (24.1%). Similarly, the genotype of cluster I, produced the tallest plant (148 cm), maximum straw yield per hill (40.0 g) and protein content (9.6%), while the genotype of cluster VI, produced the highest panicle per plant (21) and the genotype of cluster III, produced the longest grain (8.8 mm). Therefore, it may be possible to obtain the highest mean values for the maximum studied characters, if the genotypes of cluster IV are crossed with the genotypes of cluster I, cluster III and cluster VI respectively. Besides, the canonical variate analysis showed that the grain length, cooking time, straw yield per hill, days to maturity, plant height and grain yield per panicle contributed maximum to the genetic divergence of the studied germplasms. Finally, the study revealed that the *Balam* rice germplasm can offer a diverse valuable gene reservoir to utilize in hybridization programmes for the improvement of *Balam* rice.

**Key words:** Genetic divergence, *Balam* rice, Bangladesh

## INTRODUCTION

*Balam* is an indigenous landrace varieties developed over time, by adaptation to its natural and cultural environment and is used to grown in the southern regions especially in Barisal district of the country. Among the fine varieties, *Balam* tops the list and was known as '*Bashool Balam*'. Because it was so fine that it could percolate through one's nose, hence they called it '*Bashool*'. There was a time, when *Balam* used to be cultivated in huge acres of farmland but now gradually leading to extinction and lost their commercial value in the wake of huge demand for high yielding modern rice. As a result, *Balam*, once adored throughout the subcontinent, was included in the extinct list of

Bangladesh Rice Research Institute (BRRI), with the strains now only preserved in the Gene bank.

Rice germplasm is not only endowed with genetic diversity but also represents a wealth of valuable genes (Sarma *et al.*, 2003). Exploring diversity in a landrace collection is very important for identifying new genes and further improvement of the germplasm (Jayamani *et al.*, 2007). However, Bangladesh had abundant rice germplasms from time immemorial. But, now rice diversity in Bangladesh is threatened all over the country due to extensive cultivation of modern varieties (MVs) along with various intervention of rice habitat (Ahmed *et al.*, 2010). Rice germplasm need to be utilized for maintaining its diversity in rice field.

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Genetic diversity is the foundation for an efficient choice of parents for the variety development programme. Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes, which is used to select appropriate parents for hybridization to develop high yielding potential variety (Bhatt, 1970). But limited work has been done on analysis of the genetic divergence for *Balam* rice of Bangladesh.

The present study was, therefore, undertaken to assess the extent of genetic diversity in *Balam* rice germplasm of Bangladesh for selecting genotypes as prospective parents to develop transgressive segregants.

#### MATERIALS AND METHODS

Forty genotypes of *Balam* rice germplasm of Bangladesh were selected and collected from BRRI Genebank, Gazipur and were studied for 13 agro-morphological and four physico-chemical characters (Table 1). Thirty-day-old single seedling was transplanted per hill of each

genotype for agro-morphological study during T. Aman 2009 and 2011 seasons. Spaces within and between rows were 20 and 25 cm respectively. The chemical fertilizer dose of 50-40-10 kg PKS per hectare along with 60 kg N per hectare was applied. Total amount of TSP, MP and gypsum were applied at the final land preparation. Urea was applied in three installments at 15, 30 and 45 days after transplanting (DAT). Nine plants from each entry were randomly selected for recording data on seedling height, flag and penultimate leaf area, plant height, culm diameter, effective tiller number per hill, days to maturity, primary and secondary branch number per panicle, average filled grain number per primary and secondary branches, grain yield per panicle, grain length, 1000-grain weight, straw and grain yield per hill. Besides, milling outturn, cooking time, protein and amylose content were measured according to the laboratory manual, GQND, BRRI during 2011. Genetic diversity was worked out following Mahalanobis' (1936) generalized distance ( $D^2$ ) analysis extended by Rao (1952). Multivariate analyses were performed using GENSTAT 5.13 programme.

**Table 1. The list of 40 *Balam* rice germplasm with BRRI accession number.**

Common/ Local name	Code name	Accession number	Place of collection	Growing season
Balam	B1	1430	Dhaka	T. Aman
Balam	B2	995	Khulna	Aus
Balam	B3	516	Rangpur	T. Aman
Balam	B4	841	Sylhet	Aus
Balam	B5	4050	M.Bazar	T. Aman
Balam	B6	692	Comilla	T. Aman
Balam	B7	853	Khulna	Aus
Balam	B8	3643	Pabna	T. Aman
Balam	B9	843	Sylhet	T. Aman
Balam	B10	3516	Rajshahi	Aus
Balam	B11	683	Comilla	T. Aman
Balam	B12	720	Comilla	B. Aman
Balam	B13	855	Sylhet	Aus
Balam	B14	4045	Kushtia	Aus
Balam	B15	842	Sylhet	T. Aman
Balam	B16	823	Sylhet	T. Aman
Balam	B17	1013	Khulna	T. Aman
Balam	B18	839	Sylhet	Aus
Banaful Balam	B19	4164	Jessor	T. Aman
Baulam	B20	3565	Barisal	Aus
Baulam	B21	3730	Barisal	Aus
Beti Balam	B22	1011	Khulna	T. Aman
Bhua Balam	B23	878	Sylhet	T. Aman
Boilam	B24	3538	Noakhali	Aus
Boilam	B25	4608	Noakhali	Aus

Boislam	B26	3201	Dhaka	Aus
Boislam	B27	3497	Chittagong	Aus
Bola Balam	B28	4836	Satkhira	T. Aman
Jesso Balam TAPL	B29	2456	PB, BRRI	T. Aman
Kabra Balam	B30	240	Mymensingh	T. Aman
Kartik Balam	B31	696	Comilla	B. Aman
Khud Balam	B32	3668	Sherpur	T. Aman
Khud Balam	B33	2089	Jamalpur	Aus
Lal Balam	B34	2115	Dhaka	Aus
Lona Balam	B35	4789	Satkhira	T. Aman
Makai Balam	B36	4158	M. Bazar	T. Aman
Mogai Balam	B37	965	Khulna	Aus
Murki Balam	B38	771	Chittagong	T. Aman
Patni Balam	B39	4838	Satkhira	T. Aman
Samriti Balam	B40	3670	Jamalpur	T. Aman

## RESULTS AND DISCUSSION

Table 2 presents eigen values (latent roots) and percentage of total variation accounted for them obtained from principal component analysis (PCA). The result revealed that the first five components in the PCA with eigen values >1, contributed 77.43% of the total variations among the genotypes for 17 morpho-physicochemical

characters. Sohrabi *et al.* (2012) and Chakravorty *et al.* (2013) observed the contribution of 76.7 and 75.9% of the first six and four components respectively to the total variation in rice. On the other hand, Hossain (2008) observed that the first eight axes accounted for about 90% of the total variations by PCA in 78 aromatic and fine grain rice landraces.

**Table 2. Latent roots (Eigen value) and their variation for 17 morpho-physicochemical characters of 40 Balam rice germplasms.**

Principal component axes	Latent root	Variation accounted (%)	Cumulative variation
I	6.5278	38.40	38.40
II	2.0587	12.11	50.51
III	1.7933	10.55	61.06
IV	1.4885	8.76	69.82
V	1.2940	7.61	77.43
VI	0.9941	5.85	83.28
VII	0.7496	4.41	87.69
VIII	0.5897	3.47	91.16
IX	0.4392	2.58	93.74
X	0.3143	1.85	95.59
XI	0.2457	1.45	97.04
XII	0.1478	0.87	97.91
XIII	0.1184	0.70	98.61
XIV	0.0899	0.53	99.14
XV	0.0701	0.41	99.55
XVI	0.0526	0.31	99.86
XVII	0.0262	0.15	100.00

The 40 genotypes of *Balam* rice germplasm were grouped into seven clusters on the basis of non-hierarchical clustering method using Mahalanobis' D<sup>2</sup> statistics for 17 morpho-physicochemical characters (Table 3). Sohrabi *et al.* (2012) reported six clusters in 50 Malaysian upland rice accessions for 12 growth traits, yield and yield components. Roy *et al.* (2004) found

five clusters from 35 Aman rice cultivars for 10 traits during Kharif season and Datt *et al.* (2003) observed four clusters from 61 elite Basmati rice genotypes by using Mahalanobis' D<sup>2</sup> statistics. But, Mahalingam *et al.* (2012) observed 13 clusters in 31 Indian and exotic germplasm lines.

The distribution pattern of cluster indicated that the highest number of genotypes (8) included in clusters I, III and V, followed by clusters VI and VII respectively, while the lowest number of genotypes (2) included in cluster II. It also revealed that no duplicate existed among the genotypes for the studied characters. Fukuoka *et al.* (2006), Hossain (2008), Sarhadi *et al.* (2009) and Nascimento *et al.* (2011) earlier also found no duplicates from cluster analysis using Mahalanobis' D<sup>2</sup> statistics in rice. The clustering pattern also revealed that the genotypes constellated in the cluster were not originated from the same geographic region. Chakravorty *et al.* (2013) by evaluating 51 rice land races, Hosan *et al.* (2010) by studying 20 landraces,

Rajesh *et al.* (2010) by assessing 29 land races and Medhabati *et al.* (2013) by studying 37 wild and cultivated rice also found no parallel relationship between genetic and geographical divergence. Based on the values of principal component score 1 and 2 obtained from the PCA, a two-dimensional scatter diagram (Z<sub>1</sub>-Z<sub>2</sub>) (Fig. 1) using component score 1 as X-axis and component score 2 as Y-axis was constructed. The position of the genotypes in the scatter diagram was apparently distributed into seven groups indicating the existence of considerable diversity among the genotypes. The clustering pattern confirmed the results obtained by divergence analysis.

**Table 3. Distribution of 40 Balam rice germplasms into seven clusters for 17 morpho-physicochemical characters.**

Cluster	No. of genotype	Name of genotype
I	8	B3, B5, B11, B22, B29, B36, B38, B39
II	4	B9, B10, B28, B35
III	8	B1, B4, B12, B13, B19, B23, B34, B37
IV	2	B17, B18
V	8	B7, B16, B20, B24, B25, B26, B27, B40
VI	5	B2, B6, B8, B30, B32
VII	5	B14, B15, B21, B31, B33

Table 4 presents the average intra-(bold) and inter-cluster distances (D<sup>2</sup>). The intra-cluster distance was maximum (1.17) in cluster VII and minimum (0.27) in cluster IV, denoting that the genotypes under cluster VII were the most diverse and those of cluster IV were comparatively similar or less diverse than the genotypes of other clusters. Regarding the inter-cluster distance, maximum genetic distance (21.16) was observed between the clusters II and

IV indicating wide range of diversity, while the minimum inter-cluster distance (2.23) was observed between the clusters II and VII. Mahalingam *et al.* (2012) found inter cluster distance ranged from 6.14 to 24.84, higher than intra cluster distance that ranged from 0.0 to 12.11 for Indian and exotic rice. Hossain (2008) reported intra- and inter-cluster distance ranged from 0.0 to 1.02 and 2.21 to 21.59 respectively on aromatic and fine grain land races of rice.

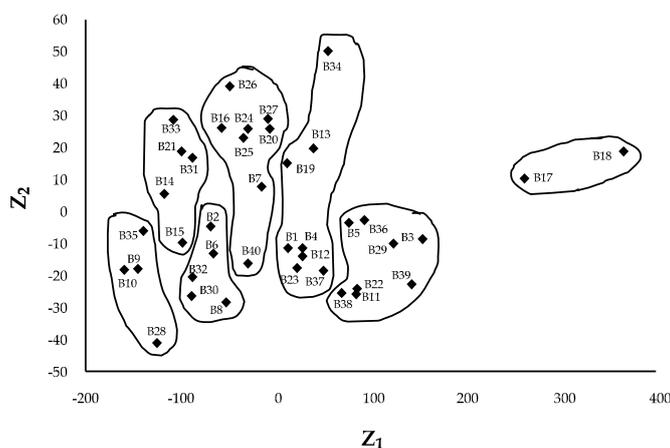


Fig. 1. Two dimensional scatter diagram based on PCA scores for 17 morpho-physicochemical characters of 40 Balam rice germplasms.

**Table 4. Average intra-(bold) and inter-cluster distances (D<sup>2</sup>) for 17 morpho-physico-chemical characters of 40 *Balam* rice germplasms.**

Cluster	I	II	III	IV	V	VI	VII
I	<b>0.69</b>						
II	11.54	<b>1.15</b>					
III	3.95	7.60	<b>1.01</b>				
IV	11.85	21.16	14.74	<b>0.27</b>			
V	8.26	5.61	5.13	15.86	<b>0.99</b>		
VI	8.15	3.54	4.23	18.57	4.64	<b>0.71</b>	
VII	10.19	2.23	6.35	19.12	3.40	3.18	<b>1.17</b>

Table 5 presents the mean values for all the 17 morpho-physicochemical characters. The data revealed that different clusters exhibited the highest and lowest mean values of individual characters and none of the clusters showed the highest or lowest mean values of all the characters. However, the genotype of cluster IV with the cumulative ranking 1, produced the highest flag and penultimate leaf area (1136 cm<sup>2</sup>), culm diameter (7.2 mm), days to maturity (152 days), primary and secondary branch number per panicle (63), grain yield per panicle (4.9 g), 1000-grain weight (29.3 g), grain yield per hill (31.3 g), cooking time (19 min) and amylose content (24.1%). Similarly, the genotype of cluster I with the cumulative ranking 2, produced the tallest plant (148 cm) and maximum straw yield per hill (40.0 g) and protein content (9.6%), while the genotype of cluster VI with the cumulative ranking 3, produced the highest effective tiller number per plant (21) and the genotype of cluster III with the cumulative ranking 4 produced the longest grain (8.8 mm). Therefore, it may be possible to obtain the highest mean values for the maximum studied characters, if the genotypes of

cluster IV are crossed with the genotypes of cluster I, cluster III and cluster VI respectively. Hosan *et al.* (2010), Mahalingam *et al.* (2012), Sohrabi *et al.* (2012) and Medhabati *et al.* (2013) earlier reported similar trend of conclusions on rice using Mahalanobis' D<sup>2</sup> statistics.

In the present study, it was also appeared from the canonical analysis that 73.85% of the total variation was accounted for canonical root 1 and 15.71% by canonical root 2 (Table 6). Table 7 presents the coefficients pertaining to the different characters in the first two canonical roots. It was revealed from canonical variate analysis that grain length, cooking time, straw yield per hill, days to maturity, plant height and grain yield per panicle were the most responsible for both the primary and secondary differentiations and contributed maximum to the genetic divergence for the characters of the germplasm studied. Earlier, Mahalingam *et al.* (2012) and Rajesh *et al.* (2010) found similar results. However, the above result was in agreement with earlier reports in rice by Hossain (2008) and Hosan *et al.* (2010).

**Table 5. Cluster means of 40 *Balam* rice germplasm for 17 morpho-physicochemical characters.**

Cluster	Seedling height (cm)	Flag and penultimate leaf area (cm <sup>2</sup> )	Plant height (cm)	Culm diameter (mm)	Effective tiller number per hill	Straw yield per hill (g)	Days to maturity	Primary and secondary branches per panicle	number per primary and	Grain yield per panicle (g)	Grain length (mm)	1000-grain weight (g)	Grain yield per hill (g)	Milling outturn (%)	Cooking time (min)	Amylose content (%)	Protein content (%)	Cumulative ranking*
I	65	924	148	6.2	15	40.0	151	51	7.2	3.4	8.5	23.2	26.0	70	19	22.3	9.6	2
II	66	680	119	4.9	18	26.5	139	34	6.9	2.5	8.5	24.3	23.6	70	18	23.1	8.6	5

III	60	854	127	5.3	15	30.6	142	41	6.9	2.5	8.8	22.4	23.0	68	18	21.7	9.1	4
IV	64	1136	141	7.2	9	34.4	152	63	7.2	4.9	8.3	29.3	31.3	70	19	24.1	8.6	1
V	64	798	110	4.8	14	17.2	133	29	7.4	2.2	8.3	24.1	16.9	69	18	22.1	8.9	7
VI	62	748	131	5.4	21	28.6	147	44	6.9	2.7	8.6	21.2	25.7	68	17	22.6	9.6	3
VII	54	724	104	4.9	13	20.0	133	37	7.5	2.3	8.1	20.1	15.7	70	18	23.5	9.1	6

\*Cumulating the values of all the seventeen characters individually for each cluster and 1 is the most superior or top rank cluster.

**Table 6. Values of canonical roots and percentage of variation of 17 morpho-physicochemical characters of 40 *Balam* rice germplasms.**

Canonical root	Values of the canonical root	% of variation absorbed by the canonical root
1	28.53	73.85
2	6.07	15.71
3	1.96	5.08
4	1.23	3.18
5	0.47	1.21
6	0.38	0.98
Total		100.0

**Table 7. Latent vectors for 17 morpho-physicochemical characters of 40 *Balam* rice germplasms.**

Character	Vector I	Vector II	Combined ranking*
Seedling height (cm)	+0.0089	-0.0743	9
Flag and penultimate leaf area (cm <sup>2</sup> )	-0.0413	-0.0157	8
Plant height (cm)	-0.0228	+0.0940	5
Culm diameter (mm)	-0.6004	+0.0651	14
Effective tiller number per hill	-0.0204	-0.0569	10
Straw yield per hill (g)	+0.0017	+0.1988	3
Days to maturity	+0.0095	+0.0775	4
Primary and secondary branch number per panicle	+0.0074	-0.0556	7
Average filled grain number per primary and secondary branches	+0.0875	-0.6988	16
Grain yield per panicle (g)	-0.1799	+0.1988	6
Grain length (mm)	+0.4411	+0.3270	1
1000-grain weight (g)	-0.0193	-0.2049	13
Grain yield per hill (g)	+0.0321	-0.2122	11
Milling outturn (%)	-0.0148	-0.6437	17
Cooking time (min)	-0.0241	+0.7290	2
Amylose content (%)	+0.0161	-0.1970	12
Protein content (%)	-0.0503	-0.5521	15

\*Combined ranking is estimated by summing the values of vector I and II, then higher (1) is the rank with higher positive value.

## CONCLUSIONS

The highest genetic diversity was existed between the genotypes of clusters II and IV. The genotype of cluster IV produced the highest flag and penultimate leaf area, culm diameter, days to maturity, primary and secondary branches per panicle, grain

yield per panicle, 1000-grain weight, grain yield per hill, cooking time and amylose content. On the other hand, cluster I produced the tallest plant along with maximum straw yield per hill and protein content, while cluster VI produced the highest panicle per plant and cluster III

produced the longest grain. Therefore, it may be possible to obtain *Balam* rice with maximum good characters, if the genotypes of cluster IV are crossed with the genotypes of cluster I, cluster III and cluster VI.

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