DIVERSITY ANALYSIS IN BORO RICE (*Oryza sativa* L.) ACCESSIONS

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Abstract

An experiment was conducted with 36 accessions of traditional (local) Boro rice germplasm accessions of three different groups (20 accessions as Kaliboro, 12 as Jagliboro and 4 as Tepiboro) during Boro season 2004 at BRRI farm to identify the duplicates with the help of morph-agronomic characters. On the basis of D^2 values, the 36 genotypes were grouped into six clusters with a range of intra (0.00 for cluster II to 1.78 for cluster I) and inter cluster (1.99 between cluster I and III to 21.20 between cluster II and III) distances. Cluster I comprised the highest number of genotypes (10) and cluster II the lowest (1), while cluster III, IV, V, and VI included 6, 7, 5, and 7 genotypes, respectively. Differences in cluster means existed for almost all the characters. The highest mean value for seedling height (21.68 cm), 1000-grain weight (20.97 g) and grain yield/hill (6.87 g) were observed in cluster I, II for days to 50% flowering (116), panicle length (22.80 cm), grains/panicle (74), and grain length (8.35 mm), cluster IV for tillers/hill (16.44) and panicles/hill (14.17), cluster V for harvest index (0.32) along with cluster I and VI, and cluster VI for plant height (117.17 cm) and flag leaf area (30.68 cm^2). None of the 12 characters had the highest mean value under cluster III. The canonical variate analysis showed in general that the important characters for the differentiation in the descending order of importance were grain length, days to 50% flowering, grains/panicle, grain yield/hill, panicle length, flag leaf area, plant height, seedling height, 1000-grain weight, panicles/hill, harvest index, and tillers/hill, but the similar name group accessions are not duplicate mainly due to dissimilarity of grain length, days to 50% flowering, grains/panicle and grain yield/hill characters. It is apparent from the results that the same name group accessions were quite different from each other.

Keywords : Duplicate sorting, rice *(Oryza sativa* L.), germplasm.

Introduction

Bangladesh had abundance indigenous rice (*Oryza sativa* L.) varieties from time immemorial. A total of 12,487 local variety names including duplicates were listed season and thana-wise by Hamid *et al.* (1982). Farmers used to cultivate these local cultivars as their main crop due to its good adaptability in different ecosystems, low input requirement, and pest resistance. But, now rice diversity in Bangladesh is threatened due to extensive cultivation of Modem Varieties (MVs) all over the country along with various intervention of rice habitat.

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Tomooka (1991) reported that evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm. In both cross and self pollinated crops, genetic diversity is one of the most important tools to quantify genetic variability (Griffing and Lindstrom, 1954 and Murty and Arunachalam, 1966).

At present, more than six thousands accessions are preserved in short and medium terms Genebank of Bangladesh Rice Research Institute. Here, it should be mentioned that the germplasms were collected from all over Bangladesh at different places and in different times including duplicates. For example, more that 36 germplasms under three different groups (20 germplasm as Kaliboro, 12 as Jagliboro, and four as Tepiboro) of Boro rice variety were collected. Therefore, to develop the 'core collection' of germplasm for BRRI Rice Genebank, these duplicate named germplasm need to be sorted out. Keeping this in mind, an experiment was conducted for sorting out whether the same name group accessions (Kaliboro, Jagliboro, Tepiboro) are same variety or not through diversity analysis.

Materials and Method

An experiment was conducted during Boro season 2004 at BRRI farm to identify the duplicate(s) germplasm preserved in BRRI Genebank that have same names but collected from different places of Bangladesh for the last two to three decades. For this, a total of 36 accessions of traditional (local) duplicate named Boro rice germplasm of three different groups (20 germplasm as Kaliboro, 12 as Jagliboro, and four as Tepiboro) were grown under transplanted condition with four replications using single row of 5.4 m long each per entry and 45 days old single seedling per hill with a spacing of 25 cm × 20 cm between rows and plants, respectively. Fertilizers were applied @ 80:60:40 kg NPK/ha. Appropriate control measures for pest, disease, and weeds were taken whenever necessary. The data were collected from individual plant for seedling height (cm), days to 50% flowering, tillers/hill, panicles/hill, panicle length (cm), plant height (cm), 1000-grain weight (g), flag leaf area (cm^2), grains/panicle, grain length (mm), harvest index, and grain yield/hill (g). Genetic diversity and sorting the duplication of accessions based on their morpho-agronomic characters were studied following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Clustering of genotypes was done according to Tocher's method (Rao, 1970). All the statistical analyses were done by GENSTAT 5 and SPSS programme.

Results and Discussion

Significant variations were recorded among the accessions for all the characters studied except grains/panicle and harvest index (Table 1) indicating the existence

of variation among the genotypes. The pattern of variation generated by the statistical analysis was demonstrated by Principal Component Analysis (PCA) and cluster analysis. The PCA produced eigen values of principal component axes for coordination of genotypes in which the first two axes accounted for 83.75 % of the total variation. On the basis of the principal axes I and II, a two dimension scatter diagram was prepared showing the groups into six clusters of varieties.

Table 1. Mean sum of squares of 12 characters studied in 36 Boro rice genotypes.

Factor	Mean square											
	SH	PH	TPH	FLA	DF	PL	PPH	GL	GPP	TGW	HI	GYPH
Genotype (d.f.35)	6.01**	387.82**	22.27**	54.06**	41.32**	8.76**	15.05**	0.37**	181.67^{ns}	6..01**	0.007^{ns}	5.26**
CV(%)	4.42	4.94	15.80	13.53	1.76	5.52	15.22	3.92	22.52	5.65	14.03	25.31

SH= Seedling height, PH= Plant height, TPH= Tiller/hill, FLA= Flag leaf area, DF= Days to 50% flowering, PL= Panicle length, PPFI= Panicles/hill, GL= Grain length, GPP= grains/panicle, TGW= 1000-grain weight, HI= Harvest index and GYPH= Grain yield/hill, NS= not significant, ** significant at 1% level.

On the basis of D^2 values, by the application of non-hierarchical clustering using covariance matrix, the 36 genotypes were grouped into six clusters (Table 2) indicating that all these varieties though have similar name group but variation are existed within the group. Cluster I comprised the highest number of genotypes (10) and cluster II has the minimum number of entries (1), while cluster III, IV, V, and VI included 6, 7, 5, and 7 genotypes, respectively, and cluster IV covered maximum number of regions (5). The clustering pattern of the genotypes indicated that all the genotypes collected from similar ecological region did not form a single cluster. This also indicates that genetic divergence is not related with geographical or ecological diversity. Genetic drift and human selection in different environments have caused greater genetic diversity than the geographical distance (Murty *et al.,* 1966; Sinha *et al.,* 1991, and De *et al.,* 1988). However, the similar name group accessions not formed a single solo cluster rather than two or more. These results confirmed the clustering pattern of the varieties according to principal component analysis. Simultaneously, a two dimensional chart (Z_1 -Z_2) of the genotypes is presented in Fig. 1 .The clustering pattern confirmed the results obtained by divergence analysis.

Inter cluster distance were greater than intra cluster distance with a range of intra (0.00 to 1.78) and inter (1.99 to 21.20) cluster distances (Table 3) suggesting wider diversity among the accessions of different groups. The maximum inter cluster distance was observed between cluster II and III (21.20) followed by cluster I and 11(19.54), cluster II and VI (18.72), cluster II and IV (17.80), cluster II and V (17.49), and the minimum between cluster I and 111(1.99), while the maximum intra cluster distance was observed in cluster

1(1.78) followed by IV (1.40), VI (0.98), III (0.68), V (0.54) and the minimum in cluster II (0.00), since it consisted with one genotype (Table 3). Therefore, it is important that though all the rice gennplasm accessions were local Boro variety, but no single cluster having two or more genotypes was observed with minimum genetic distance (0.00) for indicating the duplicate(s) since lower intra cluster distances indicating lower variability within the cluster.

Table 2. Distribution of 36 genotypes of Boro rice in different clusters grown in Boro season 2004.

Cluster	No. of genotypes in cluster	Name of genotypes with (accession no.*) (place of collection)
I	10	Tepi Boro (930) (Sylhet), Jagli Boro (3677) (Mymensingh), Kali Boro (735) (Comilla), Kali Boro (1707) (Faridpur), Kali Boro 2/2 (2189), Kali Boro-576 (2203) *(**),* Kali Boro-704 (2205) *(**),* Boro 6/2 (2206) *(**),* Boro 9/2 (2207) (**), Boro 15/1 (2210) (**)
II	1	Jagli (1761) (**)
III	6	Jagli Boro (255) (Mymensingh), Jagli (645) (Noakhali), Jagli (1806) (Kishoregonj), Jagli Boro (4521) (Sunamgonj), Kali Boro-200 (2200) *(**),* Boro 13/2 (2209) (**)
IV	7	Tepi Boro (258) (Mymensingh), Jagli Boro (256) (Mymensingh), Jagli (1705) (Faridpur), Jagli (2253) (Kishoregonj), Jagli (4553) (Netrakona), Kali Boro (1281) (**), Kali Boro (4581) (Tangail)
V	5	Jagli (1704) (Faridpur), Kali Boro (260) (Mymensingh), Kali Boro 41/1 (2192) (**), Kali Boro 109/4 (2196) (**), Kali Boro 139/2 (2198) (**)
VI	7	Tepi Boro (3998) (Habigonj), Tepi Boro (4526) (Sunamganj), Jagli Boro (4536) (Hobiganj), Kali Boro 80/3 (2194) (**), Kali Boro-259 (2201) (**), Kali Boro 600 (2204) (**), Boro 10/3 (2208) (**)

* BRRI rice Genebank accession number, **not available.

Table 3. Average intra (bold) and inter cluster distance (D^2) for 36 genotypes of Boro rice.

Cluster	I	II	III	IV	V	VI
I	**1.78**	19.54	1.99	6.19	2.12	2.44
II		**0.00**	21.20	17.80	17.49	18.72
III			**0.68**	6.09	3.81	4.31
IV				**1.40**	5.39	7.98
V					**0.54**	2.67
VI						**0.98**

Moreover, the similar name group accessions rather situated in quite distance clusters. For example, varieties named Jagliboro were felt into different clusters but not felt in any single cluster, therefore, indicating that they are not duplicates. Similarly, Jagliboro collected from a single location *viz.,* Mymensingh or Faridpur was also not felt in a single cluster. Similar results were also observed in case of Kaliboro and Tepiboro (Table 2). Here it should also be mentioned that genotypes belonging to the clusters with maximum inter cluster distance are genetically more diverged and vise versa. There will be a possibility of obtaining greater variation among segregates by crossing between the genotypes belonging to a divergent cluster which is in agreement with the study of Jagadev *et al.* (1991). Therefore, it is apparent from the result that all the genotypes need to be included in 'core collection' for total conservation of these Boro genotypes in Genebank without making any sorting.
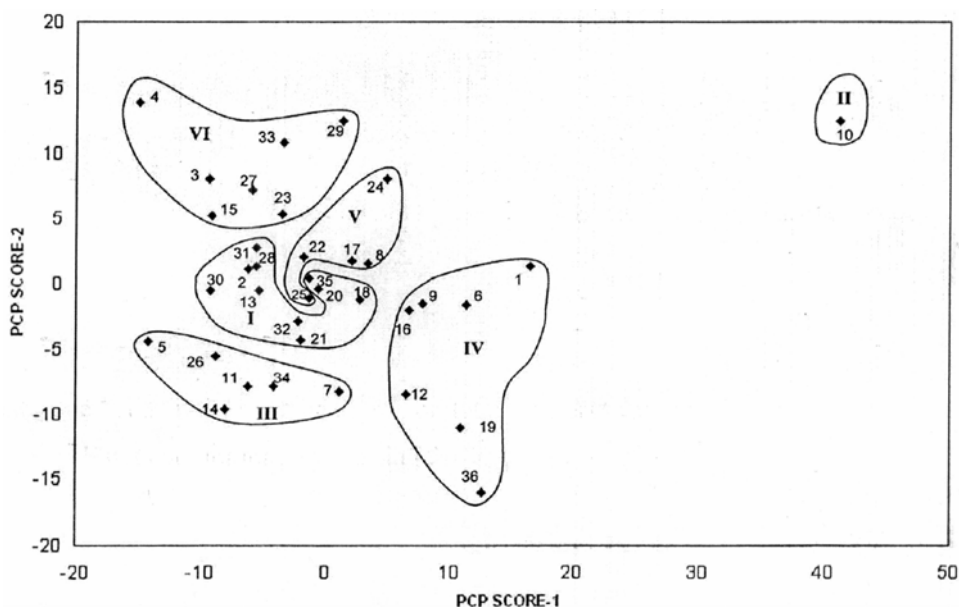

Fig.1. Distribution of 36 genotypes of Boro rice in a two-dimensional scatter diagram based on PCA scores superimposed with clusters.

The cluster means were shown in Table 4. The highest mean value for seedling height (21.68 cm), 1000-grain weight (20.97 g), and grain yield/hill (6.87 g) were observed in cluster I, cluster II for days to 50% flowering (116), panicle length (22.80 cm), grains/panicle (74), and grain length (8.35 mm), IV for tillers/hill (16.44) and panicles/hil (14.17), cluster V for harvest index (0.32) along with cluster I and VI and cluster VI for plant height (117.17 cm) and flag leaf area (30.68 cm^2). None of the 12 characters had the highest mean value under cluster III. Similarly, the lowest mean value for seedling height (16.70 cm), plant height (70.30 cm), panicles/hill (10.50), 1000-grain weight (19.30 g) and

grain yield/hill (6.03 g) were observed in cluster II, cluster III for grains/panicle (53), and harvest index (0.30), cluster IV for panicle length (20.04 cm), and flag leaf area (22.56 cm²), cluster V for days to 50% flowering (103), cluster VI for tillers/hill (11.94), and grain length (7.70 mm), and none of the 12 characters had the lowest mean value under cluster I. From the cluster mean, it was also observed that the varieties situated in different clusters were different from each other though having the same name. However, mean differences among the clusters are relatively low as most of the cultivars were originated from almost similar climatic condition. Similar result was also found by Choudhury *et al.* (1999) in indigenous rice.

Table 4. Cluster means for 12 characters in 36 genotypes of Boro rice.

Characters	Cluster mean					
	I	II	III	IV	V	VI
Seedling height (cm)	21.68	16.70	21.00	20.97	21.18	21.26
Tillers/hill	13.30	12.60	12.50	16.44	13.50	11.94
Days to 50% flowering	107	116	105	104	103	107
Plant height (cm)	114.04	70.30	116.63	101.10	110.48	117.17
Flag leaf area (cm²)	28.34	24.12	27.85	22.56	23.38	30.68
Panicles/hil	12.34	10.50	11.43	14.17	12.36	10.81
Panicle length (cm)	21.38	22.80	21.30	20.04	20.12	21.96
Grains/panicle	60	74	53	57	65	69
Grain length (mm)	7.93	8.35	7.88	8.00	8.11	7.70
l000-grain weight (g)	20.97	19.30	19.94	20.73	20.15	19.95
Harvest index	0.32	0.31	0.30	0.31	0.32	0.32
Grain yield/hill (g)	6.87	6.03	6.19	6.11	6.42	6.83

Contribution of characters towards divergence was estimated through canonical variate analysis. The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 5. The data showed in general that the important characters for the differentiation in the descending order of importance were grain length, days to 50% flowering, grains/panicl, grain yield/hill, panicle length, flag leaf area, plant height, seedling height, 1000-grain weight, panicles/hill, harvest index, and tillers/hill[-1]. From the positive absolute values of these two vectors, it appear that grain length was the most responsible for differentiation followed by days to 50% flowering, grains/panicle and grain yield/hill. On the other hand, the negative values for the two vectors of 1000-grain weight indicated the least responsibility of both the primary and secondary differentiations. However, the positive absolute values of vector 1 and negative values for vector 2 for the traits panicle length, seedling height, and

tillers/hill[-1] indicated the responsibility of primary differentiation. On the contrary, the negative absolute values of vector 1 and positive values for vector 2 for the traits flag leaf area, plant height, panicles/hill and harvest index indicated the responsibility of secondary differentiation.

From the above results, it appeared that contribution of grain length was the highest followed by days to 50% flowering, grains/panicle and grain yield/hill to the total divergence in Boro rice. Choudhury *et al.* (1999) also found that earliness, plant height, tiller number, grain size, and yield contributes the highest for genetic divergence. Vector 1 obtained from PCA expresses that grain length, tillers/hill, seedling height, and 50 % flowering were the major characters that contribute to genetic divergence whereas in Vector 2, grain length, harvest index and panicles/hill played their role on genetic divergence and the rest of the characters have minor role in determining divergence. Therefore, it can be said that the similar name group accessions are not duplicate mainly due to dissimilarity of grain length, days to 50% flowering, grains/panicle and grain yield/hill.

Table 5. Latent vectors for 12 principle characters of 36 genotypes of Boro rice.

Characters	Vector 1	Vector 2
Seedling height (cm)	+0.3298	-0.6340
Tillers/hill[-1]	+0.4075	-1.7417
Days to 50% flowering	+0.3277	+0.3209
Plant height (cm)	-0.2930	+0.1120
Flag leaf area (cm^2)	-0.2 192	+0.0543
Panicle/shill	-0.8112	+1.5805
Panicle length (cm)	+0.0004	-0.1084
Grains/panicle	+0.1244	+0.2407
Grain length (mm)	+0.7478	+2.5845
1000 grain weight (g)	-0.4681	-0.1801
Harvest index	-2.9264	+1.6066
Grain yield/hill (g)	+0.0211	+0.0688
% total variation accounted for	57.17	26.58

Finally, it can be concluded that all these Boro varieties are not duplicates in spite of having same name. Therefore, all the accessions need to be included in 'core collection' of conservational programme of germplasm in Genebank for total safeguarding of rice gene pool.

References

Choudhury, D. A., A. Hamid, A. Bhowmik, G. U. Mian and M. S. Islam. 1999. Genetic divergence in indigenous rice *(Oryza sativa* L) varieties of Bangladesh. *Bangladesh J. P1. Breed. Genet.* **12**(l&2):33-36.

De, R. N., R. Seetharaman, M. K. Sinha and S.P. Banerjee. 1988. Genetic divergence in rice. *Indian J. Genet.* **48:** 189-194.

Griffing, B. and E. W. Lindstorm. 1954. A study of combining abilities of corn inbreds having varying proportions of corn belt and non-corn belt germplasm. *Agron. J.* **46:** 545-552.

Hamid,A., M. Nasiruddin, M. Haque and E. Haque.1982. Deshi Dhaner Jat (In Bangla). Editated by Taluckdar M.H.R. Published by Bangladesh Rice Research Institute, Joydevpur, Gazipur. pp ix.

Jagadev, P. .N., K. M. Samal and *L.* Lenka. 1991. Genetic divergence in rape mustard. *Indian J. Genet.* **51:** 465-466.

Mahalanobis, P. C. 1936. On the generalized distance in statistics. Proc. NatI. Inst. Sci., India. **2:** 49-55.

Murty, B. R. and V. Arunachalam. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*. **26A:** 188-198.

Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York. p.390.

Rao, C. R. 1970. Advanced Statistical Methods in Biometrical Research. Hafner Publishing Company, Darien, Conn., USA. pp 361-64.

Sinha, P. K., V. S. Chauhan, K. Prashad and J. S. Chauhan. 1991. Genetic divergence in indigenous upland rice varieties. *Indian J. Genet.* **51**(1): 47-50.

Tomooka, N. 1991. Genetic diversity and lanhrace differentiation of mungbean, *Vigna radiata* (L.) Wilczek, and evaluation of its wild relatives (The subgenus Ceratotopics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan No.28. Ministry of Agr., Forestry and Fisheries, Japan. p.1.