Genetic Diversity of Drought Tolerant Upland Rice (*Oryza sativa* L.) Genotypes

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Abstract

Genetic divergence of thirty three drought tolerant rice (*Oryza sativa* L.) genotypes were studied through Mohalanobis's D^2 and principal component analysis for twelve characters. The genotypes were grouped into seven clusters. The cluster I and II were comprised of the maximum number of genotypes (eight) in each followed by cluster V containing five genotypes. The highest inter-cluster distance was in between cluster III and I (368.64) indicating a wide genetic diversity between these two clusters followed by clusters VII and III (346.04). The lowest inter-cluster distance was in between cluster IV and II (42.46) followed by cluster VI and IV (63.29) indicating that the genotypes of these clusters were genetically close. The intra cluster distance in the entire seven clusters was less, which indicate that the genotypes within the same clusters were closely related. Considering the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance, BR 7391-2B-7, BR 7392-2B-25, BR 6855-2B-11-3-4, BR 6855-2B-11-3-5 from cluster I, genotypes BR 6976-2B-15, and Morichbati from cluster III, genotypes BR 7187-2B-2-5 from cluster IV, genotype BR 7187-2B-2-3 and BR 7181-2B-35-2 from cluster V and genotypes BR 6855-2B-11-3-7 and BRRI dhan 42 from the cluster VII are likely to perform better if used in hybridization program.

1. Introduction

Rice (*Oryza sativa* L.) is considered as a major crop in Bangladesh as it constitutes 91.79% of the total food grain (rice, wheat and maize) production of 37.5 million metric tons (Anonymous, 2013). Rice is the staple food and it ranks first in production among cereals in Bangladesh. Although Bangladesh is now on the verge of attaining self sufficiency in cereal production, there is still a large gap between its production and demand. We need to produce more rice per unit area. Achieving self-sufficiency in rice production and maintaining price stability are important in countries where rice provides food security and generates employment and income for people (Hossain, 1995). About half of the world's rice area is under rainfed culture where drought is the major limiting factor to rice production globally. Rainfed area includes 13% upland ecosystem, 11% deepwater ecosystem and 25% rainfed

lowland ecosystem of the total rice area (Fukai and Cooper, 1995). Drought is the second most sever limiting factor (Caldo *et al.*, 1996). In upland rice, depth of rooting, root thickness and root-shoot dry weight ratio are related to drought resistance (Fukai and Cooper, 1995).

An understanding of association between yield and yield contribution traits has a great importance in Plant Breeding. For any crop, to setup a suitable breeding program, information about interrelationship among and between yield contributing characters is necessary. The genetic variations constitute a high proportion of the total variation for these traits. Thus, selection for these characters is expected to be highly effective (Abdel-Ghani *et al.*, 2005). High variability, heritability and genetic advance for number of grains per panicle, grain yield per plant, harvest index and kernel L/B ratio, while days to maturity, fertility percentage, hulling recovery and kernel elongation ratio had high heritability coupled with low genetic advance indicating the need for emphasis on these traits during selections for yield improvement (Madhavilatha *et al.*, 2005).

Estimation of genetic diversity is an important factor to know the source of genes for a particular trait within the available genotypes. Genetic diversity among the segregating population also helps to select suitable types as parents and also for commercial cultivation. Therefore, the present study was undertaken to determine the genetic diversity of thirty three drought tolerant upland rice genotypes.

2. Materials and Methods

The experiment was conducted in the research field of Agronomy department of BSMRAU, during 2011 and data were recorded for different agronomical traits. Thirty three genotypes of rice including three check varieties were collected from Genetic Resources and seed Division (RSO) of Bangladesh Rice Research Institute (BRRI), Gazipur. The genotypes were BR 7177-2B-27, BR 7391-2B-7, BR 7392-2B-25, BR

7397-2B-10, BR 7662-2B-44, BR 6855-2B-11-3-4, BR 6855-2B-11-3-5, BR 7178-2B-19, BR 7178-2B-19, OM 1490, BR 7383-2B-23, BR 7384-2B-24, BR 7381-2B-15, BR 7181-2B-35-3, BR 7384-2B-5, BR 6976-2B-15, BR 7385-2B-13, BR 7187-2B-2-5, BR 7587-2B-3, BR 7187-2B-2-3, BR 7187-2B-2-5, BR 7662-2B-22, BR 7181-2B-35-2, BR 7181-2B-35-7, BR 7381-2B-2, BR 7586-2B-27, BR 6976-2B-11-1, 7181-2B-35-6, BR 6855-2B-11-3-7, BR 7134-2B-19-3. The three check varieties were BRRI dhan 42 (rice color is white, life duration is 100 days, coarse grain and drought tolerant, yield is 3.5 to 4.0 t/ha), BRRI dhan 43 (rice color is white, life duration is 100 days, medium coarse grain and drought tolerant, yield is 3.5 t/ha), and Morichbati (yield 3.0 t/ha, life duration is 98 days, drought tolerant).

The experiment was laid out in a randomized completed block design (RCBD) with three replications. The field was divided into three blocks; they were subdivided into thirty three plots where the genotypes were randomly assigned. The unit plot size was 8 m × 2.5 m. The genotypes were distribution to each plot within each block randomly. The land was prepared thoroughly by 3-4 times ploughing followed by laddering to attain a good puddled condition. Weeds and stubbles were removed and the land was finally prepared by the addition of basal dose of fertilizers. The experimental plots were fertilized by applying urea, TSP, MoP and Gypsum @ 180-100-70-60 kg/ha respectively. Total TSP, MoP and Gypsum were applied at final land preparation. Total urea was applied in three installments, at 15 days after sowing (DAS), 30 DAS and 50 DAS as recommended by BRRI (Anonymous, 1999).

Data were collected from 5 hills for each genotype on individual plant basis. Data on 12 quantitative traits such as plant height, Days to 50% flowering, Number of tillers per plant, Days to harvesting, No of panicles per hill, Panicle length, No. of primary branches per panicle, No. of secondary branches per panicle, No. of grains per panicle, No. of unfilled grains per panicle,

100 grain weight (g), Yield per hill (g) were calculated. Mean data of each character was subjected to multivariate analysis viz. Principal Coordinate Analysis (PCO), Principal Component Analysis (PCA), Cluster Analysis, and Canonical Variate Analysis using GENSTAT 513 (Mahalanobis, 1936; Digby *et al.,* 1989; Jager *et al.*, 1983).

3. Results and Discussion

The analysis from distance matrix gave non-hierarchical clustering among 33 drought tolerant genotypes and varieties. All genotypes were grouped into seven clusters (Table 1). The cluster I and II included eight genotypes in each which were the highest, followed by cluster V containing five genotypes, Cluster III, IV, VI, VII contained two, three, four, and three genotypes, respectively. The cluster III contained two genotypes, which was the smallest among the seven clusters. Based on the percentage, the distribution of genotypes into different clusters, each of cluster I and II included 24.24% and cluster V contained 15.15%. The cluster III being the smallest cluster had 6.06 % of genotypes (Table 1).

Two varieties BRRI dhan 42 and BRRI dhan 43 were locally developed and one Morichbati was a local cultivar for upland. Grouping of all genotypes from different sources indicated that there was no association between clustering pattern and eco-geographical distribution of the genotypes. De and Rao (1987) and Singh *et al.* (1987) also revealed that geographical diversity is not necessarily related to genetic diversity. Intra and inter cluster distances are presented in Table 2. The inter cluster distances in almost all of the cases were larger than the intra cluster distances indicating that wider diversity was present among the genotypes of distance groups.

The intra-cluster distances were low for all the range of 16.36 in cluster IV to 94.64 in cluster VII, which indicate homogeneous nature of the genotypes within the clusters (Table 2). These results are in agreement with those reported by Iftekharuddaula *et al.* (2002) and Kulsum *et al.* (2011) in rice.

The D^2 value ranged from 42.46 to 368.64 and PCA scores also indicated a high degree of genetic diversity among the genotypes (Table 2). Regarding the cluster distance, the highest inter-cluster distance was observed between cluster III and I (368.64) indicating the wider genetic divergence between the clusters. It was followed by clusters VII and III (346.04). The lowest inter-cluster distance was observed between cluster IV and II (42.46) followed by cluster VI and IV (63.29). The maximum value of inter cluster distance indicate that the genotypes belonging to cluster III was far diverged from those of cluster I. Similarly, the higher inter cluster values between clusters V and III (254.66), cluster VI and III (163.46), cluster III and II (153.56) and cluster VII and III (151.06) indicate genotypes belonging to each pair of clusters were far diverse (Table 2).

It was observed that in all cases, the cluster III produced the highest D^2 values (368.64) among the all clusters. It revealed that wider diversity among them and crossing among the genotypes would yield the maximum heterosis. These results are supported by Saini and Kaicke (1987). The minimum inter cluster divergence was observed between cluster IV and II (42.46) indicating that the genotypes of these cluster were genetically closed. However, genotypes within the other pair of clusters indicate that they were less diverged (Table 2).

The selection of diverge genotype from cluster would produce a broad spectrum of variability for morphological and quality traits studied which may enable further selection and improvement. The hybrid developed from the selected genotypes within the limit of compatibility of these clusters may produce high magnitude of heterosis. This would be rewarded in hybrid rice breeding program. The results reported by Roy *et al.* (2002) and Naik *et al.* (2004) were agreement with these findings.

Table 1. Distribution of 33 advance rice genotypes in different clusters based on various yield and yield contributing characters

Cluster no.	No. of genotypes	Percent (%)	Name of genotypes
I	8	24.24	BR 7177-2B-27, BR 7391-2B-7, BR 7392-2B-25, BR 7397-2B-10, BR 7662-2B-44, BR 6855-2B-11-3-4, BR 6855-2B-11-3-5, BRRI dhan 42
II	8	24.24	BR 7178-2B-19, BR 7178-2B-19, OM 1490, BR 7383-2B-23, BR 7384-2B-24, BR 7381-2B-15, BR 7181-2B-35-3, BR 7384-2B-5
III	2	6.06	BR 6976-2B-15, MORICHBATI
IV	3	9.09	BR 7385-2B-13, BR 7187-2B-2-5, BR 7587-2B-3
V	5	15.15	BR 7187-2B-2-3, BR 7187-2B-2-5, BR 7662-2B-22, BR 7181-2B-35-2, BR 7181-2B-35-7
VI	4	12.12	BR 7381-2B-2, BR 7586-2B-27, BR 6976-2B-11-1, 7181-2B-35-6
VII	3	9.09	BR 6855-2B-11-3-7, BR 7134-2B-19-3, BRRI dhan 43

Table 2. Intra (Diagonal) and intercluster distances (D^2) of 33 advance rice genotypes including 3 check varieties

Cluster	I	II	III	IV	V	VI	VII
I	**50.94**	116.81	368.64	115.53	94.50	111.90	125.17
II		**40.65**	153.56	42.46	80.28	69.09	101.90
III			**86.14**	124.22	254.66	163.46	346.04
IV				**16.36**	82.02	63.29	130.46
V					**83.73**	105.86	136.21
VI						**43.21**	151.06
VII							**94.64**

Table 3. Cluster mean values for yield and yield contributing in 33 advance rice genotypes including 3 check varieties

Characters	I	II	III	IV	V	VI	VII
Plant height (cm)	122.15	109.83	100.37	109.14	114.08	118.79	118.66
No. of tiller per hill	16.71	18.08	19.00	18.44	21.20	14.08	18.00
Days to 50% flowering	73.12	72.79	72.17	72.00	71.80	74.91	75.89
Days to harvesting	93.79	94.62	92.66	92.00	94.33	95.58	97.55
No. of panicle per hill	12.50	14.12	14.16	12.33	12.87	10.58	14.55
Panicle length (cm)	26.18	22.34	18.61	22.04	22.06	23.58	24.62
No. of primary branches	11.96	10.63	9.20	11.79	10.98	10.02	11.92
No. of secondary branches	28.79	23.36	15.91	25.72	26.28	24.87	26.83
No. of grain per panicle	99.86	66.50	45.40	65.90	87.28	76.64	72.95
No. unfilled grain per panicle	29.19	33.06	20.33	27.98	27.32	26.65	43.78
100 grain wt.(g)	2.69	2.57	2.70	2.63	2.47	2.48	2.86
Yield per hill(g)	30.97	25.83	13.91	21.94	30.69	20.24	32.00

Table 4. Relative contribution of the 12 characters of 33 advance rice genotypes including 3 check varieties to the total divergence

Parameters	Vector-1	Vector-2
Plant height(cm)	-0.0170	0.0570
No. of tiller per hill	0.2111	-0.0970
Days to 50% flowering	-0.2554	0.4973
Days to harvesting	0.0380	-0.3015
No.of panicle per hill	0.2366	-0.3127
Panicle length(cm)	0.0957	-0.0642
No. of primary branches	0.4053	-0.3517
No. of secondary branches	-0.1199	0.1305
No. of grains per panicle	-0.1076	-0.1332
No. unfilled grain per panicle	-0.0354	0.1219
100 grain wt.(g)	2.4338	-2.1882
Yield per hill(g)	-0.1977	0.2880

Cluster mean values for 12 characters are presented in Table 3. Difference in cluster means existed for almost all the characters studied. Among 12 characters, cluster I had the highest mean values for five characters viz. plant height (122.15cm), panicle length (126.18cm), no. of primary branches per panicle (11.96), no. of secondary branches (28.79) and no. of grain per panicle (99.86), that means the lines or varieties falling in cluster I having the potentialities to contribute better for maximizing yield of drought tolerant upland rice.

Cluster III had seven characters viz. plant height (103.37cm), panicle length (14.16cm), no. of primary branches per panicle(9.20), no. of secondary branches per panicle (15.91), no. of grain per panicle (45.40), no. of unfilled grain per panicle (20.33), and yield per hill (13.91g) showed the lowest value. Cluster V has two characters viz. days to 50% flowering (71.80) and 100 grain weight (2.47g) which showed the lowest cluster mean value among the characters. In cluster VI, highest cluster mean value was observed but has two character viz. no. of tiller per hill (14.08) and no. of panicle per hill (10.58) which showed the lowest cluster mean value among the characters. Cluster VII showed six highest clusters mean value viz. 50% flowering (75.89), days to harvesting (97.55), no. of panicle per hill (14.55), no. of unfilled grains per

panicle (43.78), 100 grain wt. (2.86g) and yield per hill (32.00g).

It was clear from Table 3 that the highest intra cluster means for yield were obtained from cluster VII and five other most important reproductive and vegetative characters were obtained from cluster I. Therefore, more emphasis should be given on these cluster for selecting genotypes as a variety and as well as parents in crossing with other genotypes.

The character contributing the maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization.

Contributions of characters towards divergence obtained from canonical variant analysis are presented in Table 4. Vectors were calculated to represent the genotypes in the graphical form (Rao, 1952). In vector-I, important characters responsible for genetic divergence in the major axis of differentiation were no. of tiller per hill, days to harvesting, no. of panicle per hill, panicle length (cm), no. of primary branches, and 100 grain wt.(g) having positive vector values. However, the rest of the characters played a minor role in the second axis of differentiation. In vector-II, other important character

responsible for genetic divergence in the major axis of differentiation were plant height (cm), days to 50% flowering, no. of secondary branches, no. of unfilled grain per panicle and yield per hill (g) having positive vector values, while rest of the characters played a minor role in the second axis of differentiation. Negative values in both vectors for the no. of grains per panicle had lower contribution towards the divergence (Table 4).

4. Conclusions

Genetically distant parents are usually able to produce higher heterosis and the clustering pattern could be utilized in choosing parents for cross combinations which are likely to generate the highest possible variability for effective selection of various economic traits. The findings of this study indicate that the cluster I and III, III and VII showed the higher distance. Parental materials selection from these clusters would give the manifestation of heterosis as well as wide spectrum of variation when they are hybridized.

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