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GENECTIC VARIABILITY IN SOME MAINTAINER LINES OF HYBRID RICE (*Oryza sativa* L)

A. Ansari, M. G. Rasul[1], P. L . Biswas, A. K. Paul and M. H. Rahman

Plant Breeding Division
Bangladesh Rice Research Institute
Joydebpur, Gazipur1706.

ABSTRACT

Twelve maintainer lines of rice were evaluated for 19 agronomic characters in a randomized complete block design to study the genetic divergence through multivariate analysis. Genotypes were grouped into three different clusters. Cluster I comprised maximum number of genotypes (ten) and II and III contain only single genotype each. PCA showed 70.29% variation against first three eigen values. The highest inter genotypic distance was observed between the genotype BRRI 1B and IR 73328B (2.278) followed by BRRI 3B and IR 68890B (2.229) and the lowest distance was observed (0.752) between genotypes BRRI 10B and IR 78355B followed by the distance (0.920) between genotypes BRRI 3B and IR 58025B. The inter cluster distance was larger than the intra cluster distances. The highest inter-cluster distance was observed between cluster II and III (7.113). The lowest inter-cluster distance was observed between cluster I and II (4.445) followed by cluster I and III (4.509). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. Among the characters anther length (0.00651), stigma length (0.00150), days to maturity (0.03018), number of tillers per hill (0.07890) and panicle weight (0.12713) were major characters that contribute to the genetic divergence.

Key words: Rice, maintainer line, genotype, genetic divergence, D^2

INTRODUCTION

Rice is the staple food of almost half of the world's population, employs millions in jobs and has enormous impact on the environment. About 90% of the world's rice is produced and consumed by small-scale farmers in low-income developing countries (Anon, 2003) and in Bangladesh it is 43504000 tons (FAO, 2008). Rice is the staple food of about 135 millions people of Bangladesh. It provides nearly 48% of rural employment, about two-third of total calorie supply and about one-half of the total protein intakes of an average person in the country. Rice sector contributes one-half of the agricultural GDP and one-sixth of the national income in Bangladesh. China is the first country to produce hybrid rice commercially. Hybrid rice was initiated in 1964 and the genetic tool essentials essential for breeding hybrid rice varieties, such as male sterile rice (A line), the maintainer line (B line) and restorer line (R line), were developed by 1973. Bangladesh Rice Research Institute (BRRI) has organized research program on

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[1] **Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur 1706, Bangladesh**

hybrid in June 1996 with the collaboration of International Rice Research Institute (IRRI). A good number of Hybrid rice out yielded the standard check variety of the same growth duration by more than 1 t/ha (Julfiquar, 1999).

By this time Bangladesh Rice Research Institute (BRRI) has developed two hybrid rice varieties like BRRI hybrid rice 1 and BRRI hybrid rice 2. To strengthen the hybrid rice development program, IRRI provided several component lines (A, B and R lines). For sustainable development of hybrid rice variety locally those component lines should be utilized properly. Study of diverse genotypes of a crop is necessary to evaluate their performances which help to develop a new variety suitable for commercial cultivation. Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them.

Selection of suitable parental lines (CMS, maintainer and restorer) to develop heterotic combinations can be facilitated by determining genetic divergence among them. Very limited work has been done on analysis of the genetic divergence in rice in relation to hybrid rice breeding. The study was undertaken a classifactory analysis on the rice genotypes through multivariate analysis, which will enable us to classify the available genotype into distinct clusters on the basis of their genetic diversity. The information, thus obtained, will be helpful to develop an effective hybrid rice breeding programme.

MATERIALS AND METHODS

Twelve maintainer lines were grown in a randomized complete block design with three replications at the experimental farm of Bangladesh Rice Research Institute, Gazipur during July to December 2008. The experimental site was at 24.00° N latitude and 90.25° E longitude with an elevation of 8.4 meter from the sea level. Three rows constituted of each experimental unit ($2m^2$). Adequate soil fertility was ensured by applying additional quantities of Urea- TSP-MP- Gypsum- $ZnSO_4$ @ 150:100:70:60:10 kg/ha, respectively. Total TSP, MP, Gypsum and $ZnSO_4$ were applied in final land preparation. Total Urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 45 DAT. Twenty one (21) days old seedlings of maintainer lines were transplanted in separate strips with spacing of 20 cm x 20 cm spacing between plant to plant and row to row, respectively were maintained. Necessary intercultural operation was taken during cropping period for proper growth and development of the plants.

Data were collected from 10 randomly selected hills of each genotype on individual plant basis for plant height, number of tillers per hill, number of panicles per hill, flag leaf area, anther length, anther breadth, stigma length, stigma breadth, stigma exertion rate, panicle exertion rate, days to flowering, days to maturity, phenotypic acceptability at vegetative and maturity stage. Genetic diversity was studied following the Mohalanobis's generalized distance (D^2) method extended by Rao (1952). Clustering of genotypes was done according to Tocher's Method (Rao, 1952) and principle component analysis was according to Jager *et al.* (1983). The statistical analyses were done by the GENSTAT computer based software.

RESULTS AND DISCUSSION

Principal component analysis was carried out with 12 maintainer lines of rice. First five eigen values for three principal coordination axes of genotypes accounted for 86.29% variation.

Table 1. Eigen values and percentage of variation for corresponding 19 component characters in 12 maintainer lines of rice

Sl	Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
1	Anther length (μ)	5.5259	29.08	29.08
2	Anther breadth (μ)	4.8759	25.66	54.74
3	Stigma length (μ)	2.9545	15.55	70.29
4	Stigma breadth (μ)	1.7794	9.37	79.66
5	Stigma exertion rate	1.2606	6.63	86.29
6	Spikelet fertility percent	0.8391	4.42	90.71
7	Days to 50% flowering	0.6804	3.58	94.29
8	Days to maturity	0.4115	2.17	96.46
9	Plant height (cm)	0.3577	1.88	98.34
10	Flag leaf area (cm^2)	0.1868	0.98	99.32
11	Number of tillers per hill	0.1282	0.67	99.99
12	Number of panicles per hill	0	0	99.99
13	Panicle length (cm)	0	0	99.99
14	Number of total spikelets per panicle	0	0	99.99
15	Number of filled spikelets per panicle	0	0	99.99
16	Spikelet sterility percent	0	0	99.99
17	Panicle weight	0	0	99.99
18	1000 grain weight (g)	0	0	99.99
19	Grain yield per hill (g)	0	0	99.99

Table 2. Five highest and lowest inter genotypic distance among the 12 maintainer lines of rice

Sl. No.	Genotypic combination	Distances
A.	Five highest inter genotypic distances	
01	BRRI 1B - IR 73328B	2.278
02	BRRI 3B - IR 68890B	2.229
03	Gan 46B - IR 73328B	2.219
04	IR 58025B - IR 68890B	2.147
05	BRRI 1B - IR 78355B	2.145
B.	Five lowest inter genotypic distances	
01	BRRI 10B - IR 78355B	0.752
02	BRRI 3B - IR 58025B	0.920
03	BRRI 1B - IR 75608B	0.947
04	BRRI 1B - BRRI 9B	0.985
05	IR 75608B - IR 80156B	1.023

The computations from covariance matrix gave non-hierarchical clustering among 12 maintainer lines and grouped them into three clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 3 represents the clusters occupied by 12 maintainer lines of rice. Cluster I contained the highest number of genotypes (ten), cluster II and III constitute by one genotype. Cluster II was composed of BRRI 3B. Among the genotypes of cluster II, BRRI 3B was local genotype.

Table 3. Distribution of 12 maintainer lines of rice in three clusters

Cluster	Number of members	Maintainer lines
I	10	BRRI 1B, BRRI 9B, BRRI 10B, Gan 46B, IR 58025B, IR 73328B, IR 78355B, IR 75608B, IR 80156B, Z.S 97B
II	1	BRRI 3B
III	1	IR 68890B

The highest inter-cluster distance was observed (Table 4) between cluster II and III (7.113). The intra cluster distance was the highest (1.499) in cluster I. The lowest inter-cluster distance was observed between cluster I and II (4.445) followed by cluster I and III (4.509). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. Sarawgi and Rastogi (2000), Roy *et al.* (2002) and Naik *et al.* (2004) also found similar trends in rice.

Differently originated genotypes found in same cluster or genotypes from same origin were dispersed in different clusters indicated that no parallel relationship was found between genetic and geographic divergence, which might be due to continuous exchange of germplasm from one place to another. It was observed that group I formed with ten genotypes originated in IRRI and Bangladesh and group II and III occupied by a single genotype originated from BRRI and IRRI origin respectively. Genotypes from IRRI and Bangladesh being in different clusters indicated the broad genetic variability.

Table 4. Intra and inter cluster distances (D^2) for 12 maintainer lines of rice

	I	II	III
I	**1.499**		
II	4.445	**0.000**	
III	4.509	7.113	**0.000**

Among 19 characters, cluster I stood first for seven characters viz. anther breadth (587.7), stigma length (1270.7), stigma breadth (465.2), number of tillers per hill (11.1), umber of panicles per hill (10.2), panicle weight (2.8) and grain yield per hill (10.5). Cluster II was formed by one genotype viz. BRRI 3B, which was collected from BRRI had highest cluster mean for three characters viz. stigma exertion rate (54.5), flag leaf area (43), panicle length (26.7) and spikelet sterility percent (62.3). Genotypes IR 68890B originated from IRRI which was established in cluster III which estimated high cluster mean value for eight characters viz. anther length (2555.6), out crossing rate (80.8), days to 50% flowering (97), days to maturity (109.3), plant height (109.3), number of total spikelets per panicle (188), number of filled spikelets per panicle (152) and 1000 grain weight (27.1). Cluster I was recorded as high yielding group associated with the highest anther breadth, stigma length and stigma breadth. This cluster also produced the highest number of tillers per hill and number of panicles per hill. High yield for the genotypes of this cluster perhaps was due to the increasing panicle weight and grain yield per hill.

Table 5. Cluster mean for 19 characters of 12 maintainer lines of rice

Parameters	**I**	**II**	**III**
Anther length (µ)	2238.3	1782	2555.6
Anther breadth(µ)	587.7	388.3	405.6
Stigma length(µ)	1270.7	1122.7	1122.8
Stigma breadth(µ)	465.2	420.7	429.3
Stigma exertion rate	37.5	54.5	16.1
Spikelet fertility percent	57.3	37.7	80.8
Days to 50% flowering	77.4	73	97
Days to maturity	102.1	101	109.3
Plant height (cm)	93	95.3	109.3
Flag leaf area (cm^2)	36.2	43	38
Number of tillers per hill	11.1	8.7	9.7
Number of panicles per hill	10.2	8	7.7
Panicle length (cm)	24.8	26.7	26.3
Number of total spikelets per panicle	159.7	130	188
Number of filled spikelets per panicle	92.1	49	152
Spikelet sterility percent	42.7	62.3	19.1
Panicle weight	2.8	1.9	2.3
1000 grain weight (g)	23.3	24.7	27.1
Grain yield per hill (g)	10.5	8.3	10

The values of vector I and vector II are presented in Table 6. Vector I obtained from PCA expressed that anther length (0.00651), stigma length (0.00150), days to maturity (0.03018), number of tillers per hill (0.07890) and panicle weight (0.12713) had positive value which were the major contributor to the total genetic divergence. It was the reflection of first axis of differentiation. In vector 2 anther length (0.00373), stigma length (0.00257), days to maturity (0.00331), number of tillers per hill (0.06178) and panicle weight (0.06363) showed their important role toward genetic divergence for having positive value. The value of vector I and vector II revealed that both the Vectors had positive values for anther length, stigma length, days to maturity, number of tillers per hill and panicle weight indicated the highest contribution of this traits towards the divergence among 12 maintainer lines of rice.

Negative values in both vectors as observed for number of panicles per hill, panicle length, number of filled spikelets per panicle and 1000 grain weight had lower contribution towards the divergence. Naik *et al*. (2006) suggested in rice that the cluster analysis is that in the studied population high variability observed between the genotypes in different clusters for different characters.

Table 6. Latent vectors for 19 principal component characters of 12 maintainer lines of rice

Characters	Vectors 1	Vectors 2
Anther length (µ)	0.00651	0.00373
Anther breadth(µ)	-0.00248	0.00375
Stigma length(µ)	0.00150	0.00257
Stigma breadth(µ)	-0.00102	0.00509
Stigma exertion rate	-0.00897	0.00411
Spikelet fertility percent	0.01384	-0.02492
Days to 50% flowering	-0.00448	0.01057
Days to maturity	0.03018	0.00331
Plant height (cm)	0.05830	-0.06746
Flag leaf area (cm^2)	-0.04458	0.00792
Number of tillers per hill	0.07890	0.06178
Number of panicles per hill	-0.05080	-0.02451
Panicle length (cm)	-0.09818	-0.08802
Number of total spikelets per panicle	-0.01087	0.01173
Number of filled spikelets per panicle	-0.00097	-0.00489
Spikelet sterility percent	-0.01383	0.02491
Panicle weight	0.12713	0.06363
1000 grain weight (g)	-0.00119	-0.08696
Grain yield per hill (g)	-0.03082	0.01471

Considering cluster distance and cluster mean, the genotype BRRI 1B, BRRI 9B, IR 73328B and IR 80156B from cluster I, genotype BRRI 3B from cluster II, genotype IR 68890B from cluster III may be considered better parents for future hybridization programme.

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