Journal of Crop and Weed 7(1):26-29 (2011)

Genetic divergence of local germplasms of rice (*Oryza sativa* L.) in red and laterite tracts of West Bengal, India

A. DUTTA[1], P. D. GHOSH[2], F. HOSSAIN[3] AND R. SADHUKHAN[3]

[1] *Pulses and Oilseed Research Station, Berhampore- 742101, West Bengal*
[2] *Department of Botany, Kalyani University, Nadia, West Bengal*
[3] *Department of Genetics & Plant Breeding, BCKV, Mohanpur -741252, West Bengal*

Received: 04.01.2011, Revised: 22.03.2011, Accepted: 30.03.2011

ABSTRACT

A two year field study on the genetic divergence among 60 traditional rice (Oryza sativa L.) germplasms promising for red and laterite tract of West Bengal, India and two released varieties was conducted using Mahalanobis D^2 statistics. The 62 genotypes were grouped into eight clusters where, cluster I was largest containing 38 genotypes followed by cluster II with 9 genotypes. Based on the inter cluster distance, the entries viz. Pankey, 60-Chali, Dudheswar, Sitabhog, Kalonunia, MTU-7029, Netaisail, Bhutmuri (Kelias) were selected which could be intercrossed to obtain high heterotic effect and also to recover desirable transgressive segregants.

Key words: D^2 statistics, genetic divergence, rice

The state West Bengal ranks first (Bhowmick *et al.*, 2009) in rice production in India where rice is grown under diverse agro ecological condition. The western tract of this state is drought prone and in most of the places rice is grown during rainy season only. There are several scented and non scented traditional varieties in this tract which are low in yield potentiality but have high values from quality as well as economic point of views. This necessitated for development of high yielding quality rice varieties. For efficient hybridization programme, selection of genetically diverse parents and superior genotypes are pre requisite criteria, which ensures high heterosis and exhibit a gamut of transgressive segregants in order to reach desired goal. The present investigation was an attempt to know the magnitude of diversity present in different traditional rice germplasms.

MATERIALS AND METHODS

The field experiment was conducted with 60 traditional varieties and two high yielding varieties of rice during *kharif* (wet) season of 2006 and 2007 at Rice Research Station, Bankura (latitude $23^0 5'$N, longitude $87^0 10'$E). The materials were collected from farmers field in different blocks of two drought prone districts of West Bengal, namely Bankura and Purulia during 2004-05. The experimental plots were fairly uniform and homogeneous. Seedlings of each entry were sown in 3.0 x 2.85m^2 plot in *kanali* (semi deep) type of land and there were three replications for each entry. All entries in each replication were planted randomly. Plant to plant distance was 15 cm., row-to-row distances was 20 cm. and plot-to-plot distance was 50 cm. Ten plants were selected at random from each plot for recording observations on various characters. The data on number of panicles m^{-2}, plant height (cm), days to 50% flowering, number of filled grain $panicle^{-1}$, number of primary branches $plant^{-1}$, panicle length (cm), brown rice length and width (mm), bown-rice length-width ratio, shoot and root biomass (g), root density (ml), 1000 grain weight (g) and yield (kg/ha) were recorded using standard evaluation system for rice by IRRI (1996). Analysis of data was made using Mahalanobis D^2 statistics (Mahalanobis, 1936). Average intra and inter cluster distances were estimated as per procedure outlined by Singh and Choudhary (1977).

RESULTS AND DISCUSSION

A meaningful classification of experimental materials depending upon the different characters helps to distinguish genetically close and divergent genotype which is a prerequisite for any genetical study. Genetic divergence has been worked out in rice by several workers like Bui Chi Buu and Tran Minh Tuan (1989), Sarma *et al.* (1997), Soni *et al.*(1999), Singh *et al.* (1999), Bansal *et al.* (1999), etc, considering yield and other ancillary characters at harvest.

Clustering pattern in the present study (Table 1) indicated that the genotypes collected from different places are grouped in different clusters. The two HYVs were in cluster V and VI. Other traditional tall varieties were in different clusters. Thus the sixty two germplasms could be grouped into eight clusters. The cluster no. I included 38 entries reflecting narrow genetic diversity among them. It is interesting to note that the origin / area of cultivation of the varieties within a cluster are localized within a particular pocket of the district. For example, in cluster no. IV all the four varieties *viz.* Badsabhog, Tulsibhog, Kalonunia, Sitabhog are cultivated in Bishnupur only. It is true for other varieties also. The cluster no. V, VI, VII and VIII have only solitary entry indicating their distinctness or dissimilarity from the germplasm accessions with respect to traits considered.

Average intra and inter cluster D^2 values among 62 genotypes (Table 2) revealed that cluster IV

Email: amitavapors@gmail.com

had the minimum intra cluster D^2 value (9.93) indicating that genotypes within this cluster were similar. While cluster II showed maximum intra cluster D^2 value (12.05) followed by cluster I (10.78) indicating existence of diverse genotypes that fell in these clusters. The inter cluster D^2 value ranged from 14.58 to 54.09. Minimum inter cluster D^2 value was obtained between III and V indicating close relationship among the genotypes included in these clusters. Maximum inter cluster D^2 value was observed between III and VII (54.09) followed by III and IV (46.22), V and VII (44.32) revealing that genotypes included in these clusters are genetically diverse and may give rise to high heterotic response (Rama, 1992). Similar results were also found by Qian and He (1991), Rao and Gomanthinayagam (1997).

The picture of contribution to divergence (Table 4) revealed that maximum percentage of contribution came from the trait- days to 50% flowering (38.02%), followed by yield (29.56%), 1000-seed weight (8.25%), shoot biomass (7.03%) and root biomass (5.71%). Relative importance of some of those characters in inter varietal divergence in rice was reported by number of workers like Mahapatra *et al.* (1995), Pravin *et al.* (2003) and Pradhan and Mani (2005). The rest traits had very low or negligible contribution (below 1%) to genetic divergence. Yield is an economical trait and it shows maximum divergence. Selection for yield may be emphasized as there is genetic divergence that may give scope for better performances.

Table 1: Distribution of 62 germplasms into eight clusters based on D^2 values

Cluster	No. of accessions	Accessions	Origin & number
I	38	Ranisail, Badhabana, Machkata, Raghusail, Laldhula, Dhuladhan, Kalamkathi (white), Suakalma, Murgibadam, Lal Lakra, Nakrasail, Asanlaya(red), Pubalgara, Daharnagra, Mahisladan, Radhunipagal, Dudhkalma, Sankarsail, Agnisail, Chandrakanta, Suryakanta or Muktasail, Punjabsail, Rabansail, Sitasail, Behalsail, Kabirajsail, Laldhusri, Mailliksail, Manikanchan , Nagra, Majhisail, Basmati, Sankar kalma, Jhingasail, Sungakalma, Kalma, Sunga Nagra, Baloramsail	Hura (17) Bankura (21)
II	9	Kalamkathi (red), Asanlaya(white), Durgasail, Baid Jhulur, Jhulur, Rupsail, Debasis, Rajabadsa, Laxmi Chura	Hura (6) Khatra (3)
III	7	Pankey, 60-Chali, 90-Chali, Dudheswar, Bhutmuri/ Kelias (Black), Bhutmuri/ Kelias (White), Jhuli	Hatwara (4) Khatra (3)
IV	4	Badsabhog, Tulsibhog, Kalonunia, Sitabhog	Bishnupur (4)
V	1	IR-64	HYV
VI	1	MTU-7029	HYV
VII	1	Netaisail	Indpur
VIII	1	Danaguri	Indpur

Table 2: Average intra & inter cluster distances (D^2values)

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	10.776							
II	21.651	12.055						
III	41.008**	23.675	9.946					
IV	18.151	28.515*	46.221**	9.934				
V	31.276**	16.027	14.577	36.013**	0.000			
VI	17.532	24.620*	41.043**	18.828	29.826**	0.000		
VII	18.836	34.427**	54.086**	21.715	44.316**	23.937*	0.000	
VIII	17.716	25.693*	42.919**	19.950	33.945**	24.058*	17.963	0.000

** & ** significant at 5% and 1% level of significance respectively*

Bold figures indicate intra cluster distances; other figures indicate inter cluster distances

Table 3: Cluster means of fourteen characters in D^2 analysis

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Panicles m^{-2}	313.4	362.2	423.8	301.4	353.3	366.0	283.0	375.3
Plant height	159.5	142.4	116.3	173.2	125.3	101.7	125.0	152.3
Days to 50% flowering	111.5	96.2	79.3	114.6	87.7	102.7	122.0	112.7
Filled grains $panicle^{-1}$	117.0	86.4	74.6	179.9	82.7	94.3	101.7	120.0
Primary branch $panicle^{-1}$	10.8	11.4	8.7	11.1	5.7	10.3	13.3	10.00
Panicle length	26.3	26.2	22.9	30.0	18.0	19.7	29.3	27.3
Brown rice length	6.3	6.2	5.6	4.6	6.3	6.0	6.7	4.2
Brown rice width	1.9	1.9	1.9	1.8	1.7	2.1	2.1	1.5
Brown rice L-W ratio	3.3	3.3	3.0	2.5	3.7	2.9	2.9	2.8
1000 seed wt.	21.9	20.8	19.1	11.1	18.3	18.8	17.6	9.6
Root biomass	8.1	6.5	5.6	8.9	2.4	2.8	21.4	19.4
Root density	13.1	11.9	9.9	12.7	9.3	7.3	20.0	18.7
Shoot biomass	13.9	14.4	11.3	16.0	14.5	12.7	17.7	17.7
Yield	2975.0	2418.5	2116.7	3010.4	2686.7	4733.3	3650.0	2700.0

Bold faces denote highest value for the particular character

Table 4: Relative character contribution to the genetic divergence

Character	Times ranked first	% Contribution to divergence	Cumulative
Panicles m^{-2}	2	0.11	0.11
Plant height	9	0.48	0.58
Days to 50% flowering	719	38.02	38.60
Filled grains $panicle^{-1}$	40	2.12	40.72
Primary branch $panicle^{-1}$	5	0.26	40.98
Panicle length	8	0.42	41.41
Brown rice length	57	3.01	44.42
Brown rice width	52	2.75	47.17
Brown rice L-W ratio	3	0.16	47.33
1000 seed wt.	156	8.25	55.58
Root biomass	108	5.71	61.29
Root density	40	2.12	63.41
Shoot biomass	133	7.03	70.44
Yield	559	29.56	100.00
Total	**1891**	**100**	

Cluster means of fourteen characters presented in table-3 revealed that cluster III represented highest number of panicles m^{-1}(423.81) followed by cluster VIII (375.3). Cluster IV comprised maximum plant height (173.17 cm.), number of filled grains $panicle^{-1}$ (179.92) and panicle length (30.0cm.). Cluster VI represented shortest plant height (101.67). Cluster VII comprised longest days to 50% flowering (122.0 days) and cluster III comprised shortest days to 50% flowering (74.57 days). Highest number of primary branch /panicle was in cluster VII (13.33) followed by cluster II (11.41). Highest value of brown rice length (6.33) brown rice length width ratio (3.70) was in cluster V highest brown rice width (2.13) fell in cluster VII. Cluster I represented highest value of 1000 seed weight (21.97) followed by cluster II (20.79). Highest value of root biomass (21.4), root density (20.0) and shoot biomass (17.71) was in cluster VII. Cluster VI represented highest seed yield (4733.3 kg ha^{-1}) followed by cluster VII (3650.0 kg ha^{-1}). Therefore, hybridization among members of the distant clusters is suggested to get desirable recombinants. Thus, there is a scope of isolating recombinants out of crossing involving MTU-7029 and Netaisail, Sitabhog, Tulsibhog, Kalonunia with Bhutmuri or Kelias (white) or 60-Chali and Dudheswar.

The results obtained in the present study have great relevance to the future breeding programme of drought tolerant germplasm. Members of different cluster having high genetic distance may be intercrossed for improvement of the germplasm. Characters like days to 50% flowering, 1000-seed weight, root biomass, shoot biomass and yield contributed maximum amount towards genetic divergence. So, these characters would be useful as

selection parameters. Cluster VII contains traditional variety Netaisail, in which most of the desirable characters for drought tolerant type is present except days to 50% flowering. Pankey, 60-Chali, Dudheswar may be crossed with Netaisail for transfer of this character to get desirable progenies.

Data on inter cluster distance and per se performance of genotypes indicated that MTU 7029 (cluster VI) may be intercrossed with Netaisail (cluster VII) and Sitabhog (highest number of filled grains panicle^{-1} and panicle length). Tulsibhog and Kalonunia of cluster IV may be hybridized with Bhutmuri or Kelias (white) of cluster III which had highest panicles m^{-2} or 60-Chali, Pankey, Dudheswar(early flowering) to expose desirable variability. The progenies derived from such crosses are expected to show wide variability, providing greater opportunity for isolating transgressive segregants in the advanced generations.

Table 5: Desirable genotypes for different characters **(Mean of two years)**

Characters	Rank-I	Rank-II	Rank-III
Panicles m^{-2}	Bhutmuri or Kelias (White)	Debasis	Asanlaya(red)
Plant height	Ranisail	Manikanchan	Majhisail
Days to 50% flowering	60-Chali	90-Chali	Dudheswar
Filled grains panicle^{-1}	Sitabhog	Badsabhog	Sankar Kalma
Primary branch panicle^{-1}	Netaisail	Behalsail	Suakalma
Panicle length	Malliksail	Mahisladan	Behalsail
Brown rice length	Pubalgara	Suakalma	Kalamkathi (white)
Brown rice width	Behalsail	Asanlaya (white)	
Brown rice L-W ratio	Suakalma	Sankarsail	Basmati
1000 seed wt.	Pubalgara	Machkata	Punjabsail
Root biomass	Netaisail	Danaguri	Badhabana
Root density	Machkata	Suryakanta	Durgasail
Shoot biomass	Dudheswar	Jhulur	Baid Jhulur
Yield	MTU-7029	Malliksail	Asanlaya (Red)

REFERENCES

Bansal, U.K., Saini, R.G., Rani, N.S and Kaur, A.1998. Genetic divergence in quality rice. *Oryza* **36**: 20-23.

Bhowmick, M. K., Adhikari, B., Bag, M. K. and Ghosh, R. 2009. Modern techniques of rice production for sustaining self-sufficiency in West Bengal, India. *Proceedings*. State Level Seminar on "Role of science in rural development", Raja Rammohun Roy Mahavidyalaya, Radhanagar, Hooghly, West Bengal, August 4, 2009: pp. 107-22.

Bui, C. B. and Cran, M. T.1989. Genetic diversity in rice. *IRRN.* **14**:5.

Choudhary, C. R. 1996. *Standard Evaluation System for rice.* 4th edition, IRRI, Manila, Philippines.

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

Mahapatra, K. C., Mishra, C. H. P. and Acharya, B. 1995. Clustering of rice mutants by different methods of analysis. *Indian J. Genet.* **55**: 138-47.

Murty, B. R. and Arunachalam, V. 1996. The nature of genetic diversity in relation to breeding system in crop plant. *Indian J. Genet.***26**, 188-98.

Naik D., Sao A., Sarawgi A.K.and Singh P. 2006. Genetic divergence in some indigenous scented rice (Oryza sativa L.) accessions of central India. *Asian J. Pl. Sci.,* **5**: 197-200.

Pradhan, S. K. and Mani, S.C. 2005.Genetic diversity in basmati rice. *Oryza*, **42:**150-52.

Pravin, J., Sarangi, A. K. and Mishra, A.K. 2003. Studies on genetic diversity in rice genotypes. *Pl. Arch.,* **3**:15-19.

Qian, Y. W. and He, K. M.1991. Utilization of exotic rice germplasm resources in Guang-dong province. *Crop Genet. Resour.* **2**:36-37.

Rama, T. 1992. Heterosis and inbreeding depression in rice. *IRRI Newsletter,* Los Banos **17**: 7.

Rao, T. P. and Gomathinayagam, P. 1997. Genetic diversity in semi dry rice under different environments. *Madras Agric. J.* **84**: 314-17.

Rao, C. R. 1952. *Advance Statistical Methods in Biometrical Research.* John Wiley & Sons, New York.

Sarma, M. K., Agarwal, R. K. and Richaria, A. K. 1997. Genetic diversity in rice under rainfed upland and irrigated ecosystems. *Oryza.* **34:**19-24.

Singh R.K. and Chowdhary B.D. 1977. Biometrical methods in quantitative genetics analysis. Kalyani Publishers, New Delhi. India.

Singh, S. K. and Haque, M. F. 1999. Heterosis for yield and yield components in rice. *Indian J. Genet.*, **59:** 237-38.

Soni, D. K. Sarawgi, A. K. and Raotogi, N. K. 1999. Genetic divergence in traditional rice accessions of M.P., India. *Oryza*, **36**:118-20.