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Research Note

Genetic divergence analysis of traditional rice cultivars of West Bengal, India

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Abstract
Genetic divergence was assessed among 51 landraces of rice genotypes using Mahalanobis's D^2 analysis. The 51 rice genotypes were grouped into 11 clusters. Cluster II was found to be the largest comprising 16 genotypes followed by cluster III having 8 genotypes and cluster I included 7 genotypes. Cluster VI and XI had single genotype each. The pattern of distribution of genotypes from different ecogeographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters viz. culm diameter, culm length, grain length contributed maximum towards genetic divergence among the genotypes and supposed to play important role in the improvement of rice. On the basis of cluster mean, intra and inter cluster distance and per se, cluster XI, X, XI, VI and VII may be used for their desirable characters in breeding programme of rice. Entries like, Sarkele aman, Annada and Jhingasal were selected which could be intercrossed to obtain high heterotic effect and also to recover desirable transgressive segregants.

Keywords: Agromorphological traits, D^2 analysis, traditional rice

Rice (Oryza sativa L.) (2n =24) is the most important food crops in the world and feeds over half of the global population. Rice has played a central role in human nutrition and culture for the past 10,000 years On the basis of mean grain yield, rice crops produce more food energy and protein supply per hectare than wheat and maize. Hence rice can support more people per unit land than the two other staple (Lu and Chang, 1980). However increase in global population, projected to be 9.2 billion by 2030, predicted increase in water scarcity and decrease in arable land, the constant battle against new emerging pathogens and pests and reduced quality due to possible adverse effects from climate change will pose greater challenges for rice breeders and agricultural Scientists (Khush, 2005). Being staple food, improving productivity and quality traits of rice always remain crucial. The quality of rice is a complex trait involving many physicochemical properties, and thus it has been a challenge to accurately evaluate quality for selection in rice breeding programs. To accomplish this, crop improvement programmes should necessarily aim at broadening the genetic base of the breeding stock (Vanaja and Babu, 2004).Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. The nature and magnitude of genetic divergence would help the plant breeder in choosing right choice of parents for choosing programme in order to obtain high amount of heterotic expression in F1s and broad spectrum of variability in subsequent generations (Vivekanandan and Subramanian, 1993). Variabiity studies in grain quality characters for high yielding rice varieties of different ecogeographical origins are limited.

India has tremendous biodiversity for the landraces of rice. The number of landraces cultivated locally is rapidly replaced by improved varieties, which is causing narrowing of genetic base (Guei, 2000). Thus, reduced genetic variability underscores the need to collect landraces for ex- situ conservation and to characterize them for future rice breeding programmes based on agromorphological traits because the evaluation of phenotypic diversity usually reveals important traits of interest to plant breeders. Keeping in view, the present investigation was undertaken to study the nature and degree of genetic divergence among the rice land races grown in gangetic alluvium zone of West Bengal, India. This information can be exploited in future for varietal improvement programme of rice.

The experimental material consisted of 51diverse landraces of rice genotypes which were grown in a randomized block design with three replications (durng *kharif* season of three consecutive years of 2006, 2007 and 2008) at the Zonal Adaptive Research Station, Krishnagar, Nadia.Twenty one days old seedlings were transplanted in 3.0×2.85m^2 plot. Plant to plant distance was 15cm, row to row distance was 20cm and plot to plot distance 50cm.The experimental soil was gangetic alluvial type and sandy loam in texture (having pH of 6.0, organic carbon content 0.57% and 0.056% available nitrogen).The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomly selected plants in each replication from the two centre rows. 18 productive and quantitative characters *viz* leaf length (cm), leaf breadth (cm), plant height (cm)(seedling), flag leaf angle (degree), ligule length (cm), culm length (cm), culm diameter (cm), culm number, panicle length (cm), grain length (mm), grain breadth (mm), grain length/breadth ratio, 1000-grain weight (g), 1000-kernel weight(g), maturity, sterile lemma length (cm), number of primary branches per panicle and number of grains per panicle were recorded. The genetic diversity between the genotypes was worked out using Mahalanobis's D^2 statistics and grouping of the genotypes into clusters was carried out following Tocher's method (Rao, 1952).

A remarkable variation has been found among all the traits studied (Table-1). The test of significance for multiple measurements using V- statistics (1665.75) which utilized Wilk's criterion confirmed significant differences among the rice cultivars and suggested the adequacy of continuing of D^2 analysis. A meaningfull classification of experimental material depending upon the different characters helps to distinguish genetically close and divergent genotype which is a prerequisite for any genetical study.

The analysis of variance revealed a significant difference among 51 traditional rice cultivars for all the 18 quantitative characters indicating the existence of high variability among the genotypes for all the traits (Table-1). The D^2 values of the genotypes ranged from 69.116 to 349.489 indicating that the material was quite diverse (Table-2). Based on genetic distance, the 51 traditional rice cultivars were grouped into eleven clusters (Table-2).

Cluster-II, the largest cluster consisted of sixteen genotypes, followed by cluster-III with eight genotypes, cluster I with 7 genotypes (Table-2). The cluster VII, IX and X consisted two genotypes each. Cluster VI and XI had single genotype each.
The clustering pattern revealed that the genotypes collected from same geographic origin were found to be distributed in different clusters. Similar findings of non correspondence of genetic divergence with geographic diversity were reported earlier in rice by Vivekanandan and Subramanian (1993), Rahman *et al*. (1997) and Shanmugasundaram *et al*. (2000). Murty and Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances.

The intra cluster average D^2 values ranged from 26.152 to 76.869 (Table-2). The highest intra cluster distance (76.869) was observed in the cluster X, indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce more desirable breeding materials for achieving maximum genetic distance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines (Rahman *et al*., 1997). Therefore genotypes from cluster X should be given emphasis while selection of parents for hybridization programme since most of the elite breeding cultivars were included in this cluster.

The inter cluster D^2 value ranged from 69.116 to 349.489. Minimum inter cluster D^2 value was obtained between clusters II and VI (D^2=69.116) indicating close relationship among the genotypes included in these clusters. Maximum inter cluster D^2 value was observed between cluster IX and X(D^2=349.489), followed by cluster I and XI (D^2=316.296), cluster V and X(D^2=315.427), cluster IX and I(D^2=313.699), cluster I and V(D^2= 305.206), cluster X and XI(D^2=304.544) and cluster II and III(D^2=302.481), 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).

<u>Contribution of the characters towards genetic divergence</u>: The picture of contribution of divergence (Table-3) revealed that maximum percentage of contribution came from the trait culm diameter (8.80%), followed by culm length (8.0%), grain length (7.40%), plant height(seedling) (7.40%) ,grain length/breadth ratio (7.10%), flag leaf angle (6.50%), culm number (6.20%) and panicle length (5.70%) (Table 3). Relative importance of some of those characters in inter varietal divergence in rice was reported by number of workers like Mahapatra *et al*, (1995) and Pravin *et al*. (2003). The other traits had very low contribution to genetic divergence.

The cluster mean values showed a wide range of variation for all the traits under study (Table 3). It is evident from the table that cluster VI was marked for high leaf length (60cm), leaf breadth (1.90cm) and lowest time to days of maturity (122.5). Cluster VII was distinguished for highest seedling height (42cm), culm length (150.50cm), culm diameter (0.85cm), culm number (14.5), panicle length (29cm) and lowest time to maturity (122.5days). On the other hand, cluster VIII was marked for its high duration of maturity in days (159.62). Cluster IX was distinguished for highest flag leaf angle (4˚), grain breadth (3.75mm), grain weight (29.37g), kernel weight (24.25g) and number of primary branches panicle^{-1} (14.25). Cluster X had highest sterile lemma length (1.5cm) along with the number of grains panicle^{-1} (241). The greater the distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the clusters having maximum inter cluster distance can be selected for crop improvement programme.

Considering the importance of genetic distance, relative contributions of characters towards total divergence and yield potential of genotypes, the present investigation suggests that parental lines selected from cluster I (e.g. Sankarsal, Asanlaya(red)) for kernel weight, leaf length, cluster V (e.g. Sankarkalma) for 1000-grain weight, cluster X (e.g. Muktasal, Dudhkalma) for grain length/ breadth ratio, number of grains panicle^{-1} and cluster XI (e.g. Behalsal) for flag leaf angle and grain length could be used in a hybridization programme.

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Table 1. Mean ,S.E, critical difference and coefficient of variation of quantitative traits of traditional rice cultivars

Character	Mean±S.E	Range	CD Value	CV%
Leaf length (cm)	47.47±1.11	31-61	2.58	2.35
Leaf breadth (cm)	1.51±0.05	1.1-2.5	0.13	3.79
Plant height (cm) (Seedling height)	29.40±2.14	24-43	4.94	7.26
Flag leaf angle (degree)	2.37± 0.24	1°-4°	0.70	14.85
Ligule length (cm)	1.82±23.02	0.90-3.5	0.53	12.64
Culm length (cm)	133.9±10.26	94-151	23.7	7.65
Culm diameter (cm)	0.49±3.53	0.3-0.9cm	0.08	5.08
Culm number	8.97±0.58	6-15	1.34	6.49
Panicle length (cm)	24.80±1.12	21.0-30.5	2.59	4.52
Grain length (mm)	8.30±0.58	3.9-11.2	1.34	7.02
Grain breadth (mm)	3.06±0.02	2.05-4.2	0.05	0.79
Grain length/breadth ratio	2.85±0.51	1.73-4.96	1.19	18.17
1000-Grain weight (g)	21.41±0.09	10.34-29.9	0.22	0.46
1000-Kernel weight (g)	18.19±0.42	8.00-25.0	0.97	2.31
Maturity(in Days)	139.94±3.86	116-172.5	8.92	2.76
Sterile lemma length (cm)	1.23±0.31	0.1-0.2	0.72	25.49
Number of primary branches panicle^{-1}	11.85±0.47	5.5-17	1.10	4.04
Number of grains panicle^{-1}	169.50±0.003	30-318.5	80.68	20.60

Table 2. Average inter and intra cluster D^2 values among eleven clusters in traditional rice cultivars

Cluster	Genotypes in each cluster		Cluster Distance										
	Number	Names of the Genotypes	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	7	Sankarsal, Asanlaya(red), Laldhula, Nagra, Kalamkathi, Danaguri,Dhuri	57.63										
II	16	Ranisal,Machkata,Danga,Kalma Rajabadsa,Badhabna,Manikanchan, Majhisal, Malliksal, Mahishladan, Badhsabhog, Jhulur, Pubalgara, Keralasundari, Lalhusri, Dhuladhan	114.99	55.61									
III	8	Basmotilocal, Baidjhulur, Jhuli, Chandrakanta, Netaisal, Nakrasal, Sunganagra, Asanlaya(White)	212.83	117.83	57.80								
IV	3	Tulsibhog, Kabirajsal, Kalonunia	170.33	122.12	138.26	55.77							
V	5	Punjabsal, Agnisal, Sankarkalma, Asanlaya, Baloramsal	305.20	206.85	117.44	234.77	52.21						
VI	1	Sungakalma	115.27	69.11	137.38	170.05	211.04	0.00					
VII	2	Lalhusri, Annada	133.14	73.96	116.92	94.67	211.40	104.71	26.1				
VIII	4	Sitasal, Rupsal, Suakalma, Daharnagra	207.89	121.62	93.95	194.16	120.79	106.17	150.36	38.58			
IX	2	Jhingasal, Sarkele	313.69	225.43	164.58	287.55	101.20	206.82	242.25	119.81	60.55		
X	2	Muktasal, Dudhkalma	114.81	141.45	214.42	118.61	315.42	174.83	123.10	244.95	349.48	76.85	
XI	1	Behalsal	316.29	217.34	116.79	206.48	87.33	238.94	211.02	162.2	169.06	304.54	0.00

- **Diagonal figures indicate intra cluster values**

Table 3. Cluster means and percent contribution of quantitative traits for divergence in traditional rice cultivars

Clusters	Leaf length (cm)	Leaf breadth (cm)	Plant height (cm) (Seedling height)	Flag leaf angle (degree)	Ligule length (cm)	Culm length (cm)	Culm diameter (cm)	Culm number	Panicle length (cm)	Grain length (mm)	Grain breadth (mm)	Grain length/breadth	1000-Grain weight (g)	1000-Kernel weight (g)	Maturity(in Days)	Sterile lemma length (cm)	Number of primary branches $^{-1}$	Number of grains panicle^{-1}
I	45.14	1.40	25.78	1.00*	1.98	131.42	0.41	8.14	24.21	9.03	3.20	3.26	23.42	19.92	131.21	1.14	11.28	130.64
II	45.75	1.41	28.32	2.00	2.02	129.56	0.47	8.62	24.62	8.56	3.14	2.82	21.94	18.84	136.40	1.31	12.15	181.15
III	47.56	1.54	30.87	3.00	1.58	138.43	0.48	9.25	25.00	8.18	3.00	2.88	19.32	16.52	136.12	1.25	11.50	189.31
IV	40.00*	1.38*	25.00*	2.00	1.96	147.16	0.40	7.16	23.66	5.41*	2.60	2.28	12.31*	9.36*	144.33	1.33	11.50	178.16
V	49.50	1.55	32.50	**4.00**	1.62	128.10*	0.56	9.40	25.10	8.20	2.87	2.88	22.35	19.07	156.00	1.20	12.10	126.80
VI	**60.00**	**1.90**	35.50	2.00	1.30	142.00	0.50	11.50	24.00	8.39	3.50	2.39	26.54	23.75	**122.50**	1.00*	11.00	169.00
VII	53.50	1.55	**42.00**	2.00	**2.50**	**150.50**	**0.85**	**14.50**	**29.00**	8.41	2.85	2.96	18.56	15.12	**122.50**	1.00*	13.25	137.00
VIII	50.62	1.77	27.12	3.00	1.32	132.75	0.37*	7.62	24.50	8.55	3.32	2.58	26.25	22.87	**159.62**	1.25	10.0*	133.75
IX	55.00	1.75	38.50	**4.00**	2.30	143.00	0.70	12.75	27.50	7.84	**3.75**	2.13*	**29.37**	**24.25**	152.50	1.00*	**14.25**	165.00
X	50.75	1.70	26.50	1.00*	1.50	130.00	0.50	8.25	23.25*	7.80	2.32*	**3.44**	15.48	12.49	148.75	**1.50**	14.00	**241.00**
XI	44.00	1.50	26.00	**4.00**	1.10*	130.00	0.40	6.50*	23.50	**10.00**	3.00	3.33	15.39	12.00	125.5*	**1.50**	10.0*	116.0*
P.C(%)	4.80	6.10	7.40	6.50	6.50	8.00	8.80	6.20	5.70	7.40	2.10	7.10	1.30	4.60	3.10	7.20	3.70	3.60

Bold faces denote highest value and * denote lowest value for the particular character