

## Genetic divergence in landraces of rice (*O. sativa* L.) of West Bengal, India

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### ABSTRACT

The assessment of genetic divergence was done for 51 landraces of rice based on 18 agromorphological traits following Mahalanobis's  $D^2$  analysis with the grouping of 51 rice genotypes into 11 clusters. The grouping showed 6 multigenotypic, 3 digenotypic and two monogenotypic clusters. With 16 genotypes, cluster II came to be the largest cluster. The maximum intra cluster  $D^2$  value ( $D^2 = 76.867$ ) was shown by cluster X followed by cluster IX, III and I, while the inter-cluster value was maximum between cluster IX and X ( $D^2 = 316.296$ ). The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. Among the genotypes, maximum contribution towards genetic divergence came from the characters viz., culm length, culm diameter and grain length. Cluster VII recorded highest mean value for plant height, ligule length, culm length, culm diameter, culm number, panicle length and maturity. Hybridization among the genotypes from the cluster I, III, IX and X which had maximum inter-cluster distances and desirable values for flag leaf angle, grain breadth, grain weight, kernel weight, number of primary branches panicle<sup>-1</sup> and number of grains panicle<sup>-1</sup> is likely to produce heterotic combinations and wide variability in segregating generations.

**Key words:** Agromorphological characters, cluster mean,  $D^2$  analysis, landraces, rice

Being the most important food crops in the world, rice (*Oryza sativa* L.) supports over half of the global population and is central in human nourishment for the past 10,000 years (Cordain, 1999). In comparison with the wheat and maize, rice crops conduct more food energy and protein supply per hectare (Lu and Chang, 1980). However, alarming threats for rice breeders and agricultural scientists are coming from increase in global population, projected to be 9.2 billion by 2050, predicted increase in water scarcity and decrease in arable land, and the constant battle against new emerging pathogens and pests and reduced quality due to possible adverse effects from climate change (Khush, 2005). Being staple food, improving productivity and quality traits of rice always remains crucial. The quality, along with morphology 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  $F_1$ s and broad spectrum of variability in subsequent generations (Vivekanandan and Subramanian, 1993). Variability 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.

### MATERIALS AND METHODS

The experimental material comprised of 51 diverse landraces of rice grown in a randomized block design with three replications (during *kharif* season of three consecutive years of 2006, 2007 and 2008) at the Zonal Adaptive Research Station, Krishnagar, Nadia (23°24'N latitude and 88°31'E longitude with an altitude of 9.75 meters above mean sea level). The experimental soil was gangetic alluvial type, sandy loam in texture (having pH of 6.0, organic carbon content 0.57% and 0.056% available nitrogen).

The experimental site belongs to tropical humid climate having the average rainfall of 1464 mm, with maximum rainfall between June and September. Temperature ranged from 7.6° to 41°C. The minimum temperature reached 7.6° in the month of January and the maximum 41°C in the month of May. It was observed that the 74.7% of the annual rainfall was obtained during June to September and more than 83.6% during June to October. Maximum temperature reached 41°C during May to September.

Twenty one days old seedlings were transplanted in 3.0×2.85 m<sup>2</sup> plots. Plant to plant distance was 15 cm; row to row distance was 20 cm and plot to plot distance 50 cm. The recommended

(Hartman *et al.*, 1962) 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. Eighteen productive and quantitative characters *viz* leaf length (C1), leaf breadth (C2) plant height(seedling) (C3), flag leaf angle (C4), ligule length (C5), culm length (C6), culm diameter (C7), culm number (C8), panicle length (C9), grain length (C10), grain breadth (C11), grain length/breadth ratio (C12), grain weight(1000) (C13), kernel weight (1000) (C14), maturity (C15), sterile lemma length (C16), number of primary branches panicle<sup>-1</sup> (C17) and number of grains panicle<sup>-1</sup> (C18) were recorded. The genetic diversity among the landraces was worked out using Mahalanobis's D<sup>2</sup> statistics and grouping of the genotypes into clusters was carried out following Tocher's method (Rao, 1952).

### 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. 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 test of significance for multiple measurements using V- statistic (1665.75) which utilized Wilk's criterion confirmed significant differences among the rice cultivars and suggested the adequacy of continuing of D<sup>2</sup> analysis.

The D<sup>2</sup> 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 landraces of rice were grouped into eleven clusters (Table-2). Cluster-II, the largest cluster comprised of sixteen genotypes, followed by cluster-III with eight genotypes, cluster I with 7 genotypes (Table-2). The cluster VII, IX and X comprised 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), Shanmugasundaram *et al.* (2000) and Sharma *et al.* (2011). The clustering pattern revealed that the genotypes from different sources clustered together indicated that there may have association between ecogeographical distribution of genotypes and divergence. Murty and Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances. Cluster II was characterized by 16 genotypes with medium or average leaf length, leaf breadth, flag leaf angle, culm diameter and sterile lemma length reflecting narrow genetic diversity among them. Cluster number VI and XI having only solitary entry, *viz*, Annada and Majhisal respectively, indicated their distinctness or dissimilarity from the germplasm accessions with respect to the traits, like, leaf length, leaf breadth and maturity with maximum value in Annada and with maximum flag leaf angle, grain length and sterile lemma length in Majhisal.

**Table 1: Mean, S.E, critical difference and coefficient of variation of 18 quantitative traits of 51 traditional rice cultivars**

	Traits	Mean ± S.E	Range	LSD (0.05)	CV%
C1	Leaf length (cm)	47.47± 1.11	31-61	2.58	2.35
C2	Leaf breadth (cm)	1.51± 0.05	1.1-2.5	0.13	3.79
C3	Seedling height (cm)	29.40± 2.14	24-43	4.94	7.26
C4	Flag leaf angle	2.37± 0.24	1°-4°	0.70	14.85
C5	Ligule length (cm)	1.82± 23.02	0.90-3.5	0.53	12.64
C6	Culm length (cm)	133.9± 10.26	94- 151	23.7	7.65
C7	Culm diameter (cm)	0.49± 3.53	0.3-0.9	0.08	5.08
C8	Culm number	8.97± 0.58	6-15	1.34	6.49
C9	Panicle length (cm)	24.80± 1.12	21.0-30.5	2.59	4.52
C10	Grain length (mm)	8.30± 0.58	3.9-11.2	1.34	7.02
C11	Grain breadth (mm)	3.06± 0.02	2.05-4.2	0.05	0.79
C12	Grain L / B ratio	2.85± 0.51	1.73-4.96	1.19	18.17
C13	Grain weight (1000)(g)	21.41± 0.09	10.34-29.9	0.22	0.46
C14	Kernel weight (1000)(g)	18.19± 0.42	8.00-25.0	0.97	2.31
C15	Maturity (Days)	139.94±3.86	116-172.5	8.92	2.76
C16	Sterile lemma length(cm)	1.23± 0.31	0.1-0.2	0.72	25.49
C17	No. of primary branches panicle <sup>-1</sup>	11.85± 0.47	5.5-17	1.10	4.04
C18	No. of grains panicle <sup>-1</sup>	169.50±0.003	30-318.5	80.68	20.60

**Table 2: Average inter and intra cluster D<sup>2</sup> values among eleven clusters in 51 traditional rice cultivars**

Cluster	Genotypes in each cluster			Cluster										
	Number of land races	Names of the Genotypes		I	II	III	IV	V	VI	VII	VIII	IX	X	XI
<b>I</b>	7	Sankarsal, Asanlaya(red), Laldhula, Nagra, Kalamkathi, Danaguri,Dhuri	57.63											
<b>II</b>	16	Ranisal,Machkata,Danga,Kalma Rajabadsa,Badhabna,Manikanchan, Majhisal, Malliksal, Mahishladan, Badhsabhog, Jhulur, Pubalgara, Keralasundari, Lalhusri, Dhuladhan	115	55.61										
<b>III</b>	8	Basmotilocal, Baidjhulur, Jhuli, Chandrakanta, Netaisal, Nakrasal, Sunganagra, Asanlaya(White)	212.8	117.8	57.8									
<b>IV</b>	3	Tulsibhog, Kabirajsal, Kalonunia	170.3	122.1	138.3	55.77								
<b>V</b>	5	Punjabsal, Agnisal, Sankarkalma, Asanlaya, Baloramsal	305.2	206.9	117.4	234.8	52.21							
<b>VI</b>	1	Sungakalma	115.3	69.11	137.4	170.1	211	0						
<b>VII</b>	2	Lalhusri, Annada	133.1	73.96	116.9	94.67	211.4	104.7	26.1					
<b>VIII</b>	4	Sitasal, Rupsal, Suakalma, Daharnagra	207.9	121.6	93.95	194.2	120.8	106.2	150.4	38.58				
<b>IX</b>	2	Jhingasal, Sarkele	313.7	225.4	164.6	287.6	101.2	206.8	242.3	119.8	60.55			
<b>X</b>	2	Muktasal, Dudhkalma	114.8	141.5	214.4	118.6	315.4	174.8	123.1	245	349.5	76.85		
<b>XI</b>	1	Behalsal	316.3	217.3	116.8	206.5	87.33	238.9	211	162.2	169.1	304.5	0	

Diagonal values indicate intra cluster while off-diagonal values indicate inter cluster distances respectively

Tree Diagram for 51 Varieties  
Complete Linkage  
Mohalnobis Distance

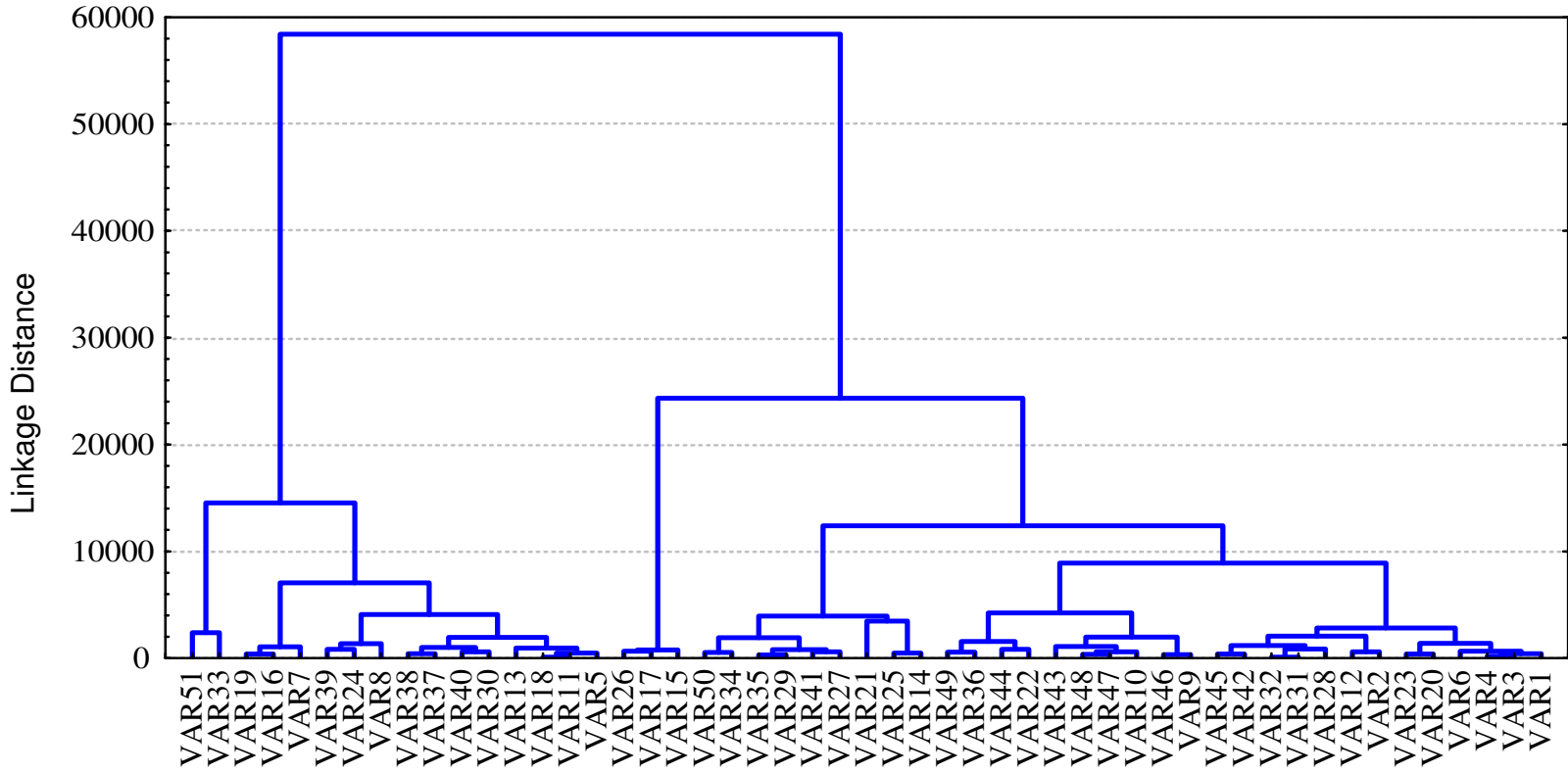


Fig. 1: Dendrogram of 51 landraces of rice

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 followed by clusters IX (60.55), Cluster III (57.8) and I (57.63); the lines included in clusters I, III, IX and X were relatively more diverse than those in the other clusters. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses. Nevertheless, the genetic divergence for the expression of the heterotic effect has a limit (Arunachalam and Bandyopadhyay, 1984). 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).

The inter cluster  $D^2$  value ranged from 69.116 in between clusters II and VI to 349.489 between cluster IX and X 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 ( $D^2=302.481$ ). This indicated greater divergence between the clusters IX and X, followed by cluster I and XI. Parental lines selected from these clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama, 1992). Such recommendations were also made by Qian and He (1991) and Rao and Gomanthinayagam (1997). The greater distance between two clusters the wider the genetic diversity between their genotypes.

Therefore, the genotypes from the clusters having maximum intercluster distance can be selected for crop improvement programme.

#### Character contribution towards genetic divergence

Varied contribution of characters towards divergence (Table-3) revealed that maximum percentage of contribution came from the trait (C7) culm diameter (8.80%), followed by (C6) culm length (8.0%), (C10) grain length (7.40%), (G3) plant height(seedling) (7.40%), (G12) grain length/breadth ratio (7.10%), (G4) flag leaf angle (6.50%), (C8) culm number (6.20%) and (C9) panicle length (5.70%) (Table3). 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 Madhan and Mani (2005). The rest traits had very low contribution to genetic divergence.

#### Cluster mean

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, leaf breadth and lowest time to days of maturity (122.5). Cluster VII was distinguished for highest seedling height, culm length, culm diameter, culm number, panicle length and lowest time to maturity. 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, grain breadth, grain weight, kernel weight and number of primary branches panicle<sup>-1</sup>. Cluster X had highest sterile lemma length along with the number of grains panicle<sup>-1</sup>.

**Table 3: Cluster means and percent contribution of 18 quantitative traits for divergence in 51 landraces of rice**

Traits	Cluster											PC%
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	
C1	45.14	45.75	47.56	40.00*	49.50	<b>60.00</b>	53.50	50.62	55.00	50.75	44.00	4.80
C2	1.40	1.41	1.54	1.38*	1.55	<b>1.90</b>	1.55	1.77	1.75	1.70	1.50	6.1
C3	25.78	28.32	30.87	25.00*	32.50	32.50	<b>42.00</b>	27.12	38.50	26.50	26.00	7.4
C4	1.00*	2.00	3.00	2.00	<b>4.00</b>	2.00	2.00	3.00	<b>4.00</b>	1.00*	<b>4.00</b>	6.50
C5	1.98	2.02	1.58	1.96	1.62	1.30	<b>2.50</b>	1.32	2.30	1.50	1.10*	6.50
C6	131.42	129.56	138.43	147.16	128.10*	142.00	<b>150.50</b>	132.75	143.00	130.00	130.00	8.00
C7	0.41	0.47	0.48	0.40	0.56	0.50	<b>0.85</b>	0.37*	0.70	0.50	0.40	8.80
C8	8.14	8.62	9.25	7.16	9.40	11.50	<b>14.50</b>	7.62	12.75	8.25	6.50*	6.20
C9	24.21	24.62	25.00	23.66	25.10	24.00	<b>29.00</b>	24.50	27.50	23.25*	23.50	5.70
C10	9.03	8.56	8.18	5.41*	8.20	8.39	8.41	8.55	7.84	7.80	<b>10.00</b>	7.40
C11	3.20	3.14	3.00	2.60	2.87	3.50	2.85	3.32	<b>3.75</b>	2.32*	3.00	2.10
C12	3.26	2.82	2.88	2.28	2.88	2.39	2.96	2.58	2.13*	<b>3.44</b>	3.33	7.10
C13	23.42	21.94	19.32	12.31*	22.35	26.54	18.56	26.25	<b>29.37</b>	15.48	15.39	1.30
C14	19.92	18.84	16.52	9.36*	19.07	23.75	15.12	22.87	<b>24.25</b>	12.49	12.00	4.60
C15	131.21	136.40	136.12	144.33	156.00	<b>122.50</b>	<b>122.50</b>	<b>159.62</b>	152.50	148.75	125.50*	3.10
C16	1.14	1.31	1.25	1.33	1.20	1.00*	1.00*	1.25	1.00*	<b>1.50</b>	<b>1.50</b>	7.20
C17	11.28	12.15	11.50	11.50	12.10	11.00	13.25	10.00*	<b>14.25</b>	14.00	10.00	3.70
C18	130.64	181.15	189.31	178.16	126.80	169.00	137.00	133.75	165.00	<b>241.00</b>	116.00*	3.60

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

The present investigation suggests that the parental lines selected from cluster I, *i.e.*, Sankarsal, Asanlaya (red) having desired characters like kernel weight and leaf length; from cluster V including Sankarkalma having high value of 1000-grain weight; from cluster X, *i.e.*, Muktasal, Dudhkalma, having high value of grain length/ breadth ratio, number of grains panicle<sup>1</sup> and from cluster XI having Behalsal for lower flag leaf angle and high grain length, can be selected as ultimate parents for inclusion in the hybridization programme. Thus, the crosses resulting from these divergent parents are expected to throw wide spectrum of variability for yield and its component characters in the segregating generations.

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