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Research Note

Studies on genetic divergence in rice germplasm (*Oryza sativa* L.)

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Abstract
Genetic divergence of 50 rice genotypes was studied for thirteen quantitative plant growth and yield related traits was estimated using Mahalanobis's statistics (D^2) analysis. The genotypes were grouped into 8 clusters. The cluster VII was the largest with 12 genotypes followed by cluster III with 8 genotypes, cluster V & VI with 7 genotypes each, while cluster I & IV with 6 genotypes each, cluster VIII with 3 genotypes and cluster II with 1 genotype of rice. The inter cluster distances were higher than the average intra-cluster distance reflecting wider genetic diversity among the genotypes of different groups than those of the same cluster. The highest inter-cluster distance was observed between cluster V & VI1 whereas the highest intra-cluster distance was found in the cluster VI indicated that the highly divergent types existed in these clusters. This study concluded that the genotypes UR-28 followed by UR-3 and DRR-11 were the best genotypes for grain yield as for as characters concerned for harvest index, no. of spikelet per panicle, no. of tillers per plant. The present study registered high GCV along with high genetic advance for no. of panicles per plant, no. of tillers per plant. So these genotypes with grain yield traits should be given top priority during selection of the genetically divergent parents for further utilization as parents in breeding programme.

Key words
Rice, Genetic divergence, Cluster, genotype

Rice (*Oryza sativa* L.), is one of the most important staple food crops of *Graminae* family catering to the 50 per cent of the world population. world. India is a major rice growing country of the world with an area, production and productivity of 43 M. ha, 105.31 million tons and 21.30 q/ha respectively and it contributes 20 per cent to the world production. Rice offers a great wealth of materials for genetic studies because of its wide ecological distribution, wider adaptability and enormous variation encountered for morphological and physiological characters. In order to obtain higher productivity genetic improvement of the crop is prime need which has been started more than a century back. Since the 1960s, food security has been achieved largely due to improved yields (Nguyen, 2002). However, more recently it has become obvious that the current rate of increase in yield (down to around 1% per annum) and the small increase in rice area will not be sufficient to meet growing demand. This yield plateau is because of the narrow range of variability. In order to cope with the ever increasing population and to break the yield plateau in rice production as well as for maintaining price stability there is need for genetic improvement of the crop.

The systematic breeding programme involves creation of genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. The large spectrum of genetic variability in segregating populations depends on the level of genetic diversity among parental genotypes, which can offer better scope for selection. Genetic diversity is pre-requisite for any crop improvement programme as it helps in the development of superior recombinants. (Arunachalam, 1981). The selection of agronomically suitable diverse parents for hybridization is important for getting desired recombinants segregating generations. Hybrids showing strong heterosis are developed from the parental lines that are diverse in relatedness, ecotype, geographic origin *etc* (Lin and Yaun, 1980).

Genetic divergence among the genotypes is estimated by the D^2 analysis and principle component analysis using morphological traits. The D^2 technique is based on multivariate analysis developed by Mahalanobis (1936) who has found it to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely

divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation. Moreover, the relative contribution of different yield components to total divergence using Mahalanobis D^2 technique helps in the identification of selection parameter to be used as criteria for the improvement in the yield. Study of D^2 statistics are expected to provide reliable basis for selecting desirable elite and diverse parents for hybridization and exploitation of variability.

In India rice is grown under four ecosystems: irrigated, rain fed lowland, rainfed upland and flood prone. More than half of the rice area (55%) is under rainfed and distribution wise 80 per cent of the rain fed rice is in eastern India. The area, production and productivity in the study area, *i.e.*, Uttar Pradesh is 5.19 M. ha, 10.81 million tons and 20.84 q/ha respectively (Ministry of Agriculture, 2011-2012). making its cultivation vulnerable to vagaries to monsoon. Hence, this study was undertaken to evaluate and to run a classificatory analysis on the rice genotypes for rainfed conditions by means of Mahanlobis D^2 statistic, which would enable us to classify the available germplasm into distinct groups on the basis of their genetic diversity. Grouping of genotypes finally provides a clear picture about the inter relationship of genotypes and helps to pick up appropriate divergent genotype/parents to be used in future hybridization programme.

The experiential material for the present study comprised of 50 genotypes of rice (table.1) obtained from Directorate of Research and Sam Higginbottom Institute of Agriculture, Technology and Sciences (SHIATS) and laid in randomized block design (RBD) with three replications at the field experimentation centre of Department of Genetics and Plant breeding, Allahabad school of agriculture, SHIATS, Allahabad, Uttar Pradesh. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per plant number of panicles per plant, panicle length (cm), number of spikelets per panicle, flag leaf length (cm), flag leaf width (cm), biological yield per plant (g), harvest index (%), test weight (g), grain yield per plant (g), and observations on days to 50 % flowering and days to maturity were recorded on plot basis. The data was subjected to Mahanlobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

In the present investigation, the genetic divergence among 50 rice genotypes was studied by D^2 statistic of Mahalanobis (1928) followed by clustering of genotypes by Tocher's method. These analyses were carried out to know the extent of divergence in the genotypes, to identify the superior genotypes for utilization in hybridization programme and to find out the contribution of different characters towards genetic divergence in rice. The mean values of 50 accessions were tested for significance by univariate ANOVA and wilk'statistic. Significance of these statistics suggested the existence of considerable divergence

and justified further calculation of D^2 clustering resulted in the grouping of 50 genotypes into eight clusters. The statistical differences among the clusters based on D^2 value area also represented diagrammatically in Fig. 1.

The square of the distance (D^2 value) between any two entries calculated as sum of the difference between the mean values of all 50 genotypes were obtained for further analysis. Total 30 combinations of D^2 value were obtained. Group constellation was carried out following Tocher's method (Rao, 1952) which utilizes the D^2 value. The fifty genotypes under study were grouped into eight clusters using Mahalanobis D^2 analysis (Table 2). Cluster VII constitutes 12 genotypes forming the largest cluster followed by cluster III (8 genotypes) cluster V and VI (7 genotypes) in each, cluster I and IV (6 genotypes) cluster VIII (3 genotypes) and cluster II (1 genotypes). The pattern of group constellation proved the existence of significant amount of variability. The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning clustering with respect to the DRR- and UR- series as per their origin, i.e, the genotypes from different origin were grouped together in the same cluster. This kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions (Kumari and Rangaswamy, 1997 and Gupta *et al*. 1999).

The inter and intra cluster distances among eight clusters were computed and have been given in Table no.3. Maximum intra cluster D^2 value of 4122 was observed for cluster VI followed by cluster V (2737). Cluster VIII had zero inter cluster distance since it was represented by a single genotype. The intra cluster distance ranged from 882 (cluster VII) to 4122 (cluster VI). The inter cluster distance was maximum between cluster V and VIII (58955), followed by cluster II and Cluster III (45395) and between cluster III and cluster VIII (44968) and cluster II and cluster VII (41743). Since these clusters have high inter-cluster distance among them, crossing between

these clusters will result in increased heterosis. The inter-cluster D^2 value was found to be minimum between cluster III and cluster IV (4327), suggesting a close relationship between them and a low degree of diversity among the lines. To realize maximum variability and high heterotic effect, Mishra *et al*. (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance and the selection of genotypes from those lines which has low inter-cluster distances should be avoided.

Cluster mean values of the thirteen characters are provided in Table. 4. Wide range of variations among the clusters were noted. The cluster V exhibited highest mean values for plant height (1152.51 cm) lowest mean value in cluster VIII (115.73). It also recorded highest mean value for panicle length (30.44 cm), biological yield (151.90) and grain yield (118.60 g/plant. Days to 50 % harvesting (80.33) and days to maturity (111.33) was lowest in Cluster VIII. It also recorded highest tillers/plant (72.56), panicles/plant (66.13) and test weight (29.16). Cluster VII recorded highest value for flag leaf length (45.36), flag leaf width (1.98), spikelets/panicle and harvest index (84.77). Cluster IV recorded highest value for days to 50 per cent flowering and days to maturity. Cluster V recorded the highest value for days to 50 % flowering and days to maturity. Considering the mean performance of the clusters, the Cluster VIII (DRR-11, UR-3 and UR-28) had the highest mean values for tillers/plant, panicles/plant and test weight and the lowest mean value for days to 50% flowering, plant height and days to maturity. Genotypes of this cluster could be used in crossing programmes for producing heterotic hybrids and for generating variability for rainfed conditions. In addition to get desirable flag leaf length and width, tillers/plant, spikelet /plant and harvest index the genotypes of Cluster VII (DRR-4, DRR-7, DRR-10, DRR-18, DRR-19, UR-6, UR-17, UR-21, UR-22, UR-23, UR-25, UR-29) can be used. To increase the grain, yield the following genotypes viz., DRR-5, DRR-13, DRR-15, DRR-17, UR-7, UR-10, UR-20 from cluster V can be involved in crossing program.

However, the selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al*. 2004). The highest contribution in manifestation of genetic divergence was exhibited by spikelet per panicle (56.00 %) followed by biological yield per plant (24.00 %), grain yield per plant (4.41 %) and tillers/plant (4.00%). Other characters like plant height, flag leaf length and width, panicles/plant, days to maturity, days to 50 % maturity, test weight contributed least towards the genetic divergence (Table.5). Roy and Ponwar (1993) Kumari and Rangasamy (1997) Hegde and Patil (2000) Reddy *et al.* (2002) Mishra *et al*., (2003) Awasthi *et al.* (2005) Sankar *et al.* (2005) Senapati and Sarkar (2005) Reddy *et al*. (2006) Sabesan *et al.* (2009) Banumathy *et al*. (2010) Latif *et al.* (2011) Chanbeni *et al.*(2012) and Medhabati *et al.*(2013) reported that the traits like spikelets per panicle, biological yield per plant, grain yield per plant and tillers/plant were the major contributors to genetic divergence and should form the basis of selection for genotypes. In other words, selection for these characters may be rewarding.

This suggests that the genotypes present in the two clusters *i.e.*, cluster VII (DRR-4, DRR-7, DRR-10, DRR-18, DRR-19, UR-6, UR-17, UR-21, UR-22, UR-23, UR-25, UR-29) and cluster V (DRR-5, DRR-13, DRR-15, DRR-17, UR-7, UR-10, UR-20), which has highest mean values for the traits contributing maximum to divergence, can be used as parents for effective crosses in a line X tester fashion to get more heterosis among the hybrids.

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Table 1. List of genotypes used in the experiment

S.NO	GENOTYPES	S.NO	GENOTYPES
1	DRR-2	26	UR5
2	DRR-3	27	UR6
3	DRR-4	28	UR7
4	DRR-5	29	UR8
5	DRR-6	30	UR10
6	DRR-7	31	UR11
7	DRR-8	32	UR12
8	DRR-9	33	UR13
9	DRR-10	34	UR14
10	DRR-11	35	UR15
11	DRR-12	36	UR16
12	DRR-13	37	UR17
13	DRR-14	38	UR18
14	DRR-15	39	UR19
15	DRR-16	40	UR20
16	DRR-17	41	UR21
17	DRR-18	42	UR22
18	DRR-19	43	UR23
19	DRR-36	44	UR24
20	DRR-43	45	UR25
21	DRR-68	46	UR26
22	UR1	47	UR27
23	UR2	48	UR28
24	UR3	49	UR29
25	UR4	50	NDR359 (CHECK)

Table 2. Intra (Diagonal) and Inter Cluster (off diagonal) distance (D^2) in upland rice germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**2403**	4335	4896	4610	14345	9739	25799	30195
II		**2279**	5405	9246	15421	18956	41743	**45395**
III			**2709**	4327	7068	13144	31568	**44968**
IV				**1963**	8281	5561	17164	30394
V					**2737**	18430	35216	**58955**
VI						**4122**	7862	18416
VII							**882**	13336
VIII								**0**

Table 3. Clustering pattern of 50 genotypes of *Oryza sativa L.* on the basis of Mahaanobis D^2 analysis

S. No	Cluster numbers	Number of genotypes	Genotypes included
1	I	6	UR-1,UR-2,UR-11,UR-15,UR-19,NDR-359
2	II	1	DRR-2
3	III	8	DRR-3,DRR-6,DRR-9,DRR-16,DRR-36,DRR-68,UR-5, UR-12
4	IV	6	DRR-8,DRR-12,DRR-14,DRR-43,UR-24,UR-27
5	V	7	DRR-5,DRR-13,DRR-15,DRR-17,UR-7,UR-10,UR-20
6	VI	7	UR-4,UR-8,UR-13.UR-14,UR-16,UR-18,UR-26
7	VII	12	DRR-4,DRR-7,DRR-10,DRR-18,DRR-19,UR-6,UR-17, UR-21,UR-22,UR-23,UR-25,UR-29
8	VIII	3	DRR-11,UR-3,UR-28

Table 4. Cluster mean values of 8 clusters for 13 quantitative characters in rice and their contribution towards Genetic divergence.

Clusters / Characters	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	94.37	96.62	98.96	99.86	94.77	94.04	81.33	80.33
Plant height	135.49	143.42	137.75	138.44	152.51	141.70	133.75	115.73
Flag leaf length	37.34	37.74	41.86	38.75	44.45	39.95	45.36	26.26
Flag leaf width	1.91	1.83	1.79	1.91	1.74	1.67	1.98	1.76
Tillers/plant	32.64	31.96	22.77	25.30	26.77	30.41	28.35	72.56
Panicles/plant	27.06	29.25	17.83	21.18	20.02	23.90	24.00	66.13
Panicle length	23.62	21.94	28.79	25.98	30.44	23.18	23.40	21.80
Spikelets/panicle	179.74	125.37	151.47	213.02	153.04	279.41	372.76	367.33
Days to maturity	124.62	125.08	127.85	130.00	124.77	125.04	114.33	111.33
Biological yield	83.90	77.00	105.01	106.49	151.90	101.11	101.06	68.00
Test weight	21.49	20.87	26.98	23.66	22.61	22.36	23.07	29.16
Harvest index	66.53	69.69	78.14	78.49	78.14	68.26	84.77	56.44
Grain yield/plant	54.91	54.08	81.23	83.58	118.60	69.38	85.90	38.36

Table 5. Percent contribution of different quantitative characters to genetic divergence.

S. No	Source	Times Ranked 1st	Contribution (%)
1	Days to 50% flowering	15	1.22
2	Plant height	23	1.88
3	Flag leaf length	3	0.24
4	Flag leaf width	0	0.00
5	Tillers/plant	49	4.00
6	Panicles/plant	9	0.73
7	Panicle length	31	2.53
8	Spikelets/panicle	686	**56.00**
9	Days to maturity	1	0.08
10	Biological yield/plant	294	24.00
11	Test weight	22	1.80
12	Harvest index	38	3.10
13	Grain yield/plant	54	4.41

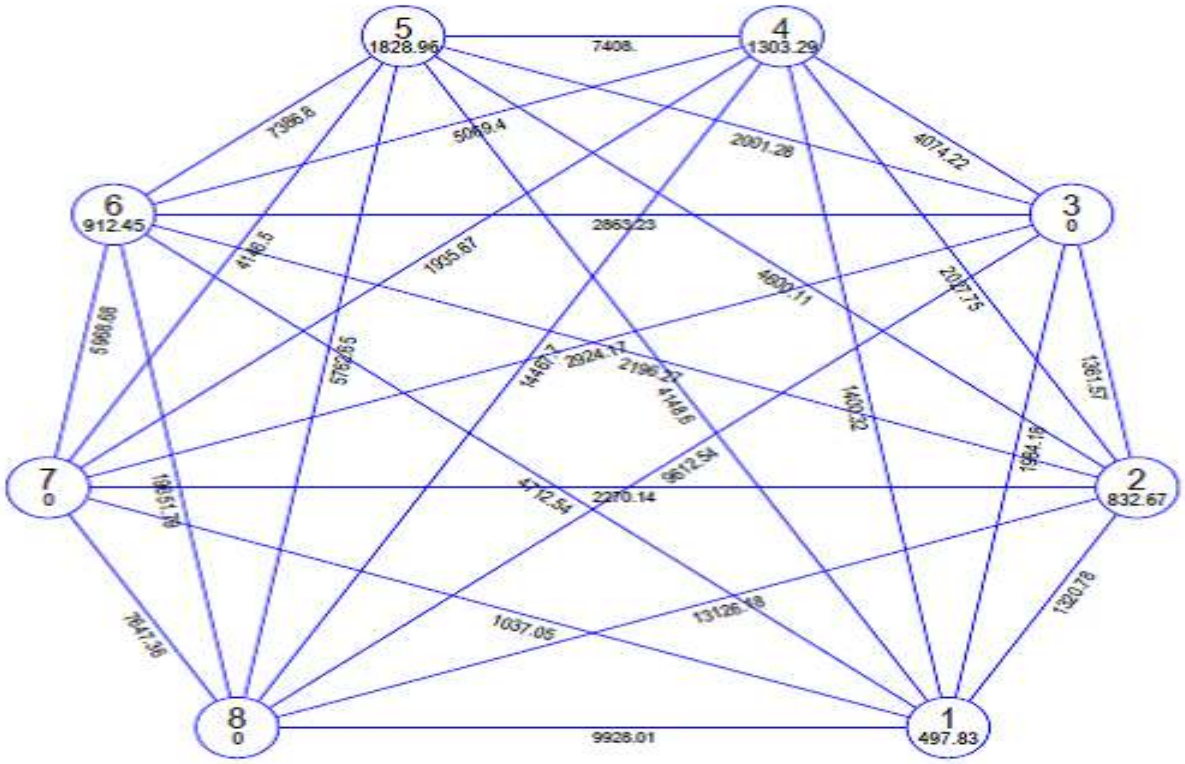

Fig.1. Mahalnobis Euclidean Distance

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