

## Genetic divergence analysis for quantitative traits in rice (*Oryza sativa* L.)

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### Abstract

The present investigation was conducted with 64 exotic rice germplasm to investigate the nature and magnitude of genetic divergence during *Kharif* 2011. The analysis of variance showed significant differences for all the characters studied among the genotypes. Based on the analysis, the genotypes were grouped into 9 clusters. Maximum number of 27, 17, 10 and 5 genotypes were grouped under cluster III, I, II and IV respectively, while clusters V, VI, VII, VIII, and IX had only one genotypes each. Maximum inter cluster distance was observed between cluster IV and IX (2091.48) followed by cluster VII and IX (1893.05) indicates wider the genetic diversity between genotypes. Cluster VI showed highest mean for seed yield per plant (25.67 g) followed by cluster IX, cluster VII and cluster III. The maximum inter cluster distance exhibited by cluster IV – IX and cluster IV also identified for selecting parents for incorporating the two traits *viz.*, short plant structure and harvest index whereas cluster IX also identified for selecting parents for incorporating the three traits *viz.*, early number of panicles per plant, flag leaf length and seed yield per plant. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. Among the traits studied, number of spikelets per panicle had maximum contribution towards the genetic divergence followed by plant height, panicle length and harvest index whereas number of panicle per hill and panicle length had no contribution towards the genetic divergence.

**Keywords:** Cluster distance, genetic diversity, rice, yield

### 1. Introduction

Rice (*Oryza sativa* L.) is one of the most important food crops of the world for more than half of the global populations. It is primary food source for more than one third of world's population. India is the second largest producer and consumer of rice next to China. As the population is increasing alarmingly, in order to meet the indispensable demand, improvement through genetic manipulation is the only way. The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent (Daniel, 2000) [2]. Even though self-pollinated crops are highly homozygous there is every possibility of genetic variation among the parents collected from different eco-geographical regions. In the present study, an attempt was made to assess the genetic divergence using Mahalanobis D<sup>2</sup> statistics and different clustering procedures, based on yield and quality characters and assessing the relative contribution of different components to total divergence. In order to meet the food requirement of growing population, development of high yielding varieties are essential. The success of any breeding programme depends on the selection of parents for hybridization. The germplasm provides immense scope for wide variability. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekananda and Subramaniam, 1993) [7]. Keeping this in view, the present study was focused to assess the genetic diversity among 64 exotic rice germplasm using Mahalanobis D<sup>2</sup> statistics.

### 2. Materials and Methods

The experimental material for the present study comprised of 64 exotic rice germplasm laid in randomized block design (RBD) with three replications at the Field Experimentation Center, Department of Genetics and Plant Breeding,

Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, U.P., during *Kharif*, 2011. The genotypes were raised in plot of 6 rows with each row of 5 meters length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. All the recommended agronomic practices were followed. Five compataive plants were selected at random for each genotype in each replication to record the data on all yield and yield attributing characters (except days to flowering and days to maturity) *viz.*, plant height, tillers per plant, panicles per plant, flag leaf length, flag leaf width, panicle length, spikelets per panicle, test weight, biological yield per plant, harvest index and seed yield per plant. Days to 50 percent flowering and days to maturity were recorded on plot basis. The genetic distance between the genotypes was worked out using Mahalanobis D<sup>2</sup> analysis (1936) [3] and grouping of varieties into clusters was done following the Tochers method suggested by Rao, 1952.

### 3. Results and Discussion

Analysis of variance showed significant differences for all the characters studied among the genotypes (Table 1). This suggested that the genotypes were genetically diverse and considerable amount of variability existed among them. Thus indicated the better scope for selection of different parents for further hybridization programme to get the high heterotic combinations in terms of various quantitative characters. Based on D<sup>2</sup> values, all the genotypes were grouped into 9 clusters (table-1) Maximum number of genotypes (26 genotypes) was grouped in cluster III. It was followed by cluster I (17 genotypes), cluster II (10 genotypes) and cluster IV (5 genotypes). while remaining clusters *viz.*, cluster VI, VII, VIII and IX were consists only one genotypes each. The intra and inter cluster distance are presented in (Table 2.) The

maximum inter cluster distance was observed between cluster IV and cluster IX (2091.48) followed by cluster VII and cluster IX (1893.05), Cluster IV and cluster VII (1819.94) and Cluster IV and cluster VIII (1783.75), indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would be desirable. The minimum inter cluster distance was found between cluster V and cluster VII (153.74) indicating that closeness and hence, hybridization among the varieties will not give effective results. The maximum intra cluster distance was observed for cluster IV (362.126) followed by cluster III (238.259), cluster II (148.08) and cluster I (78.43), indicating the considerable variation present within the clusters.

The diversity in the present material was also supported by the appreciable amount of variation among cluster means for different characters (Table 3), which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster VI showed highest mean for seed yield per plant (25.67 g) followed by cluster IX (25.33 g), cluster VII (24.00 g) and cluster III (22.73 g). None of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Most of the minimum and maximum mean values were distributed in relatively different clusters. Cluster IX exhibited maximum cluster mean value for seed yield per plant as well as number of panicles per plant and flag leaf length; cluster VIII for early flowering; cluster VII for flag leaf width, panicle length and number of

spikelets per panicle; cluster VI for biological yield per hill; cluster V for test weight; cluster IV for harvest index. Thus, based on cluster means, the various these clusters have been identified for selecting parents for future hybridization programme. The maximum inter cluster distance exhibited by cluster IV – IX and cluster IV also identified for selecting parents for incorporating the two traits viz., short plant structure and harvest index whereas cluster IX also identified for selecting parents for incorporating the three traits viz., early number of panicles per plant, flag leaf length and seed yield per plant. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety and also suggested to create variability for developing the varieties involving a large number of different lines instead of closely related ones. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. The contribution of each trait to total divergence is presented in table 4. Among the traits studied, number of spikelets per panicle had maximum contribution towards the genetic divergence (47.47%) followed by plant height (24.40%), panicle length (4.46%) and harvest index (4.27%) whereas number of panicle per hill and panicle length had no contribution towards the genetic divergence.

**Table 1:** Clustering pattern of 64 rice genotypes based on D<sup>2</sup> statistics

S. No	No. of cluster	No. of genotypes	Name of the genotypes
1	I Cluster	17	44 IRR1197, 46 IRR1199, 1 IRR1153, 60 IR78537-32-1-2-1, 43 IRR1196,50 IRR1203,63 IR77512-2-1-2-2, 49 IRR1202, 47 IRR1200, 38 IRR1191, 27 IRR1180,36 IRR1189, 39 IRR1192, 26 IRR1179, 48 IRR1201, 34 IRR1187, 54 HO-14-1-1-6
2	II Cluster	10	29 IRR1182, 32 IRR1185, 28 IRR1181, 45 IRR1198, 33 IRR1186, 14 IRR1167, 30 IRR1183, 31 IRR1184, 16 IRR1169, 20 IRR1173
3	III Cluster	27	37 IRR1190, 53 HO-12-5-3-B4, 62 IR77298-14-1-2, 61 IR78554-145-1-3-2, 9 IRR1161, 58 JR77736-54-3-1-2, 5 IRR1157, 40 IRR1193, 2 IRR1154, 8 IRR1160, 41 IRR1194, 52 PT9882-16-4-2-3-2P-M-2, 42 IRR1195, 17 IRR1170, 56 JP78006-55-2-3-3, 19 IRR1172, 18 IRR1171, 64 IR77629-72-2-1-3, 23 IRR1176, 24 IRR1177, 22 IRR1175, 6 IRR1158, 60 IR78537-32-1-2-1, 21 IRR1174, 57 JP77734-03-2-3-2, 4 IRR1156, 7 IRR1159
4	IV Cluster	5	12 IRR1165, 13 IRR1166,3 IRR1155, 15 IRR1168, 55 JR-60080-46A
5	V Cluster	1	11 IRR1164
6	VI Cluster	1	35 IRR1188
7	VII Cluster	1	10 IRR1163
8	VIII Cluster	1	25 IRR1178
9	IX Cluster	1	51 88023-RE

**Table 2:** Intra and inter cluster average of yield traits in 64 rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>78.434</b>	200.218	331.974	932.541	211.960	234.501	445.130	537.811	900.837
II		<b>148.088</b>	465.870	798.679	308.959	537.406	571.088	973.566	1400.275
III			<b>238.259</b>	765.583	773.742	659.745	1198.510	610.406	718.151
IV				<b>362.126</b>	1221.307	1604.691	1819.939	1783.750	2091.480
V					<b>0.000</b>	280.477	153.743	949.911	1578.145
VI						<b>0.000</b>	429.055	306.986	760.531
VII							<b>0.000</b>	1300.456	1893.048
VIII								<b>0.000</b>	257.371
IX									<b>0.000</b>

**Table 3:** Cluster mean of different yield characters in 64 rice genotypes

Clusters	Days to 50% flowering	Plant height	tillers/ plant	panicles/ plant	Flag Leaf length (cm)	Flag leaf width (cm)	Panicle Length (cm)	spikelets/ Panicle	Days To maturity	Test Weight	Biological yield/ plant (g)	Harvest Index	Seed Yield/ Plant (g)
I	106.686	113.099	15.202	12.951	34.803	1.480	28.493	186.586	132.059	23.549	45.706	34.642	21.275
II	94.700	94.170	13.107	11.527	30.118	1.348	24.319	190.280	128.367	23.083	40.733	31.722	20.467
III	97.284	115.231	17.730	14.919	33.671	1.446	27.650	114.589	124.272	23.019	46.630	38.144	22.728
IV	102.400	90.340	16.187	11.953	28.380	1.361	29.480	107.080	84.867	21.371	46.267	54.529	21.200
V	117.333	105.600	14.060	12.233	41.400	1.620	30.800	244.467	124.333	31.087	42.667	34.307	21.333
VI	106.333	135.567	19.733	16.867	43.933	1.617	24.233	223.807	130.000	26.793	56.667	43.610	25.667
VII	116.333	109.933	14.367	14.567	29.400	1.653	38.067	290.667	137.000	21.840	49.667	36.253	24.000
VIII	93.000	156.567	15.133	11.167	37.333	1.243	20.467	153.533	127.333	31.027	52.667	41.390	21.333
IX	77.333	164.000	20.733	18.533	48.067	1.463	27.867	111.733	132.667	19.040	49.000	36.970	25.333

**Table 4:** Percentage of contribution of each character towards total divergence

Source	Times Ranked 1st	Contribution %
1 Days to 50% flowering	85	4.22
2 Plant height	492	24.40
3 Tillers/ plant	20	0.99
4 Panicles/ plant	0	0.00
5 Flag Leaf length (cm)	49	2.43
6 Flag leaf width (cm)	0	0.00
7 Panicle Length (cm)	90	4.46
8 spikelets/ Panicle	957	47.47
9 Days To maturity	140	6.94
10 Test Weight	72	3.57
11 Biological yield/ plant (g)	23	1.14
12 Harvest Index	86	4.27
13 Seed Yield/ Plant (g)	2	0.10

#### 4. Conclusion

Results of the present study indicated maximum inter cluster distance exhibited by cluster IV – IX and cluster IV also identified for selecting parents for incorporating the two traits viz., short plant structure and harvest index whereas cluster IX also identified for selecting parents for incorporating the three traits viz., early number of panicles per plant, flag leaf length and seed yield per plant. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety.

#### 5. References

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