

## Assessment of Genetic Diversity in Rice

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**ABSTRACT:** A set of 76 rice genotypes were subjected to Mahalanobis  $D^2$  analysis to assess genetic diversity among them. All these genotypes were grouped into nine clusters with maximum inter cluster distance between cluster VI and cluster IX (5805.13) and minimum inter cluster distance was observed between cluster I and cluster II (374.05). Among the ten characters studied days to 50 per cent flowering contributed maximum towards genetic divergence (41.58 per cent) followed by number of unfilled grains per panicle (12.49 per cent) and number of filled grains per panicle (11.16 per cent).

### INTRODUCTION

Rice (*Oryza sativa* L.) is the prime food crop of the world for more than half of the global populations. India is the second largest producer and consumer of rice next to China. As the population is increasing alarmingly, it is projected that the demand of rice in 2025 A.D. would be 140mt as against the production of about 131.9 mt. Hence, 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). Even though self pollinated crops are highly homozygous there is every possibility of genetic variation among the genotypes.

The genetic diversity which is the basis of crop improvement is produced due to inherent genetic differences in plant species and hence, it is necessary to evaluate extent of genetic divergence in genotypes. There are many approaches for selection of parents for hybridization programme *viz.*, selection of parents based on *per se* performance, ecogeographic diversity, regression analysis, multivariate analysis and combining ability. But, Mahalanobis  $D^2$  analysis has the ability to estimate genetic divergence and to access the relative contribution of each character towards genetic divergence. Bhatt (1973) has demonstrated the usefulness of  $D^2$  statistics for choosing parents in wheat. The study of genetic divergency among genotypes will, therefore, help to plan hybridization programme to develop varieties or hybrids with high yield.

### MATERIALS AND METHODS

The material taken for this study consisted of 76 rice genotypes collected from different research stations (Table 1). All genotypes were grown in randomized block design with three replications during 2011-2012. The seedlings were transplanted to main field 20cm apart between rows and 15cm with in row. Recommended agronomic practices and need based plant protection measures were taken up. Observations were recorded on ten qualitative characters *viz.*, days to 50 per cent flowering, plant height, number of tillers per plant, panicle length, number of filled grains per panicle, number of unfilled grains per panicle, total grains per panicle, 1000-grain weight, spikelet sterility percentage and grain yield per plant. Genetic diversity analysis was done following the  $D^2$  statistics proposed by Mahalanobis (1936).

### RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating existence of variability among the genotypes for the characters studied. Based on the relative magnitude of  $D^2$  values, 76 genotypes were grouped into nine clusters (Table 2). The cluster II was the biggest consisting of 22 genotypes followed by 17 in cluster V, 12 in cluster I, 8 in cluster III, 7 in cluster VIII, 6 in cluster VII, 1 in cluster VI and IX.

The maximum intra cluster distance was observed in cluster VII (369.139) followed by cluster I (357.677)

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indicating limited genetic diversity among genotypes representing these clusters (Table 3). The cluster VI and IX consisted of only one genotype hence, they lack intra-cluster distance (0.000). The relative divergence of each cluster from other cluster (inter-cluster) indicated greater divergence between cluster VI and IX (5805.13), followed by IV and IX (3193.751). The minimum inter-cluster distance was recorded between cluster I and II (37.057). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield, which may enable further selection and genetic improvement.

The average cluster wise mean values for different characters are presented in table 4 which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster IV recorded highest plant stature with longer panicle length and higher 1000-grain weight. Cluster VII exhibited superior mean performance for total grains per panicle. Cluster VIII had the desirable mean for grain yield per plant and number of filled grains per panicle. The results indicated that none of the clusters

contained the genotypes with all the desirable characters for direct selection and exploitation. Similar results were reported by Bose and Pradhan (2005).

The characters contributing maximum to the divergence need greater emphasis for deciding on the clusters for purpose of further selection and choice of parents for hybridization. Among the nine characters studied, days to 50% flowering contributed maximum of 41.58 per cent, followed by unfilled grains per panicle (12.49 per cent), filled grains per panicle (11.16 per cent) and panicle length (10.42 per cent) to the divergency. Similar results were observed by Subudhi *et al.* (2008) and Deepak *et al.* (2006). Hence, these characters could be given due importance for selection of genotypes for further improvement. There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environment influences over the character. Regarding the least contribution, total number of grains and plant height contributed the least. The minimum contribution by this traits reveal that this traits were least affected in course of evolution.

**Table 1**  
List of rice genotypes studied for genetic diversity

S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes
1	Himalaya 741	20	JGL-18047	39	Lalankanda	58	AC-41038
2	CT-6	21	JGL-384	40	Tomozomachi	59	AC-41028
3	CT-327	22	IR-83222-174	41	CTH-1	60	AC-41037
4	CT-376	23	JGL-1798	42	Rajendra	61	AC-41039
5	ECJ-21	24	Himalaya-2	43	Kakatiya	62	AC-41015
6	IR-64	25	JGL-11118	44	Takari	63	AC-40778
7	Tellahamsa	26	Shanta	45	Pusa superfast	64	AC-41016
8	BPT-5204	27	JGL-17004	46	Kupparalavadlu	65	AC-41009
9	JyothiPrasad	28	AC-3283	47	Varalu	66	AC-41010
10	Kasturi	29	Emergency	48	WGL-14377	67	AC-3569
11	IET-19600	30	JGL-11727	49	JGL-18270	68	AC-38460
12	JGL-17970	31	Bu-Pu-Mui	50	Singadis	69	AC-38453
13	JGL-3828	32	JGL-3855	51	Duppitokalu	70	AC-38459
14	Kahara	33	JGL-11470	52	Gedanzipeton	71	AC-34983
15	CT-19	34	JGL-19621	53	Erramallelu	72	AC-40776
16	BRS-7	35	PusaBasmathi	54	VD-82	73	AC-41043
17	HPR-2177	36	China 988	55	AC-630	74	AC-40779
18	RP-2421	37	Padma	56	WGL-283	75	AC-41022
19	VD-62	38	JGL-1853	57	AC-41036	76	AC-41015

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**Table 2**  
**Distribution of rice genotypes in different clusters**

Cluster	No. of genotypes	Genotypes
I	12	Himalaya741, AC41037, Takari, AC34983, RP2421, VD82, Varalu, AC41016, JGL17004, CTH1, AC40779, WGL14377
II	22	CT6, Pusabasmathi, Kasturi, CT376, AC41038, WGL283, JGL18047, IR83222-174, VD62, AC41028, AC41022, Erramallelu, AC41009, CT19, Jyothiprasad, AC3569, IET19600, Gadonzipeton, BPT5204, AC41039, AC41010, Lalankanda
III	8	CT327, Kahara, AC40778, JGL17970, AC630, Tellahamsa, China988, AC38460
IV	2	AC38459, AC41015
V	17	Shanta, Kakatiya, IR64, BRS7, ECJ21, Padma, Bu-pu-mui, Tomazomachi, Singadis, Duppitokalu, pusauperfast, Kupparalavadlu, AC40776, JGL3855, Rajendra, Emergency, AC41043
VI	1	AC38453,
VII	6	JGL1798, JGL11470, JGL19621, Himalaya2, AC3283, AC41036
VIII	7	JGL11118, JGL1853, JGL18270, AC41015, JGL384, JGL3828, JGL11727
IX	1	HPR2177

**Table 3**  
**Intra cluster (in bold) and inter cluster distance for 10 characters in rice**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>357.677</b>	374.057	549.513	1066.862	891.081	2151.141	840.504	1317.458	2974.966
II		<b>171.915</b>	302.174	654.794	395.85	1864.958	563.762	780.355	2833.759
III			<b>191.498</b>	656.261	358.166	1617.069	646.490	723.290	2901.064
IV				<b>355.485</b>	644.004	1582.964	1036.688	898.323	3193.751
V					<b>235.461</b>	1815.011	677.390	570.941	3090.438
VI						<b>0.000</b>	2684.019	2670.095	5805.130
VII							<b>369.139</b>	488.337	1827.484
VIII								<b>175.616</b>	2739.146
IX									<b>0.000</b>

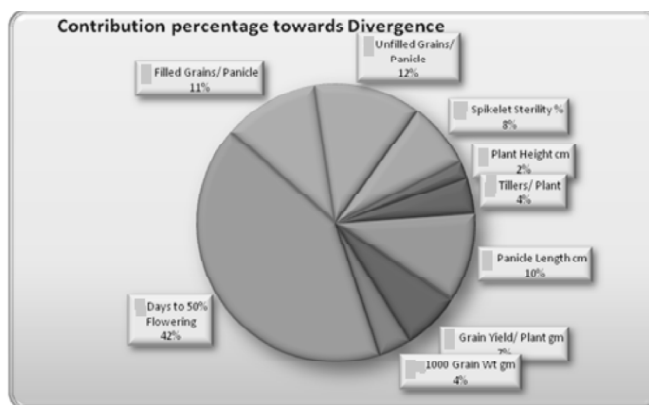
**Table 4**  
**Character means in different clusters of rice genotypes**

Cluster	1	2	3	4	5	6	7	8	9	10
I	71.733	11.632	17.706	16.385	17.722	92.000	91.372	14.061	105.433	13.208
II	76.418	13.837	19.736	21.220	17.889	99.758	90.103	13.893	103.996	13.264
III	67.702	10.578	18.496	10.626	17.110	105.708	75.793	15.683	91.476	16.975
IV	<b>105.475</b>	12.717	<b>25.093</b>	11.217	<b>26.043</b>	106.500	118.512	11.657	130.168	9.755
V	76.808	16.561	20.251	21.170	17.593	110.882	83.552	15.404	98.955	15.648
VI	95.200	12.800	17.800	6.089	25.967	104.000	26.167	39.933	66.100	60.420
VII	74.250	14.806	20.461	23.077	14.219	104.500	121.746	40.275	<b>162.021</b>	26.043
VIII	74.980	12.654	22.542	<b>23.744</b>	12.877	<b>114.429</b>	<b>150.887</b>	28.026	178.913	15.629
IX	103.533	<b>19.133</b>	25.053	10.283	16.587	99.667	67.933	<b>91.713</b>	159.647	<b>57.447</b>

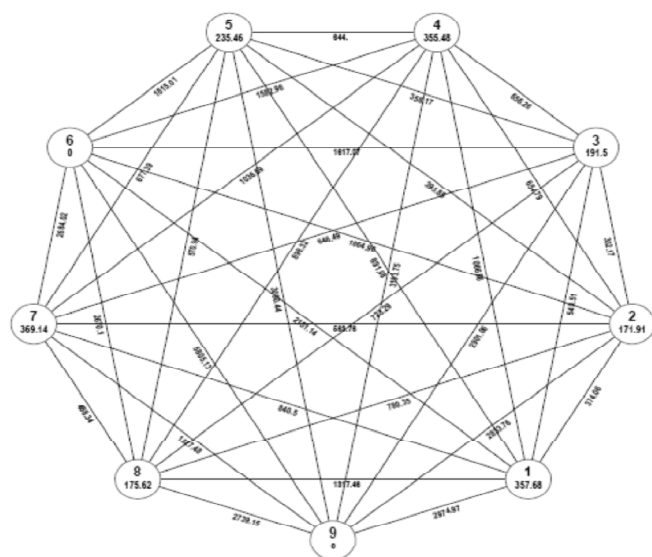
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|-----------------------------------|------------------------------------|----------------------------|
| 1. Plant Height in cm             | 5. 1000 Grain Weight in grams      | 9. Total Grains/ Panicle   |
| 2. Number of Tillers per Plant    | 6. Days to 50 per cent Flowering   | 10. Spikelet Sterility (%) |
| 3. Panicle Length in cm           | 7. No. of Filled Grains/ Panicle   |                            |
| 4. Grain Yield per plant in grams | 8. No. of Unfilled Grains/ Panicle |                            |

**Table 5**

S. No	Source	Times Ranked 1 <sup>st</sup>	Contribution %
1	Days to 50% Flowering	1185	41.58
2	Unfilled Grains/ Panicle	356	12.49
3	Filled Grains/ Panicle	318	11.16
4	Panicle Length cm	297	10.42
5	Spikelet Sterility %	220	7.72
6	Grain Yield/ Plant gm	190	6.67
7	Tillers/ Plant	118	4.14
8	1000 Grain Wt gm	109	3.82
9	Plant Height cm	57	2.00
10	Total Grains/ Panicle	0	0.00



**Figure 2: Contribution of different characters to divergency**



**Euclidean<sup>2</sup> Distance (Not to the Scale)**

**Figure 1: Cluster diagram depicting the genetic distance**

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