

## Studies on Genetic Diversity in Rice (*Oryza sativa* L.)

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### ABSTRACT

#### Keywords

Divergence,  
D<sup>2</sup> analysis, Intra  
cluster, Inter  
cluster and  
heterosis.

#### Article Info

Accepted:  
21 July 2017  
Available Online:  
10 September 2017

The present investigation was conducted at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University during 2015 – 2017. The experiment was carried out to explore the extent of divergence in 48 rice genotypes for nine characters. In D<sup>2</sup> analysis, the 48 genotypes were grouped into nine clusters. The clustering pattern indicated that there was no parallelism between genetic diversity and geographical origin as the genotypes from different origins were included in same clusters and *vice versa*. The maximum intra cluster distance was registered in cluster VIII (35.87). The maximum inter cluster distance was found between Cluster VI and Cluster VIII (54.23) followed by Cluster VIII and IX (51.01), cluster V and VIII (50.26) and cluster III and VIII (45.60). Genetically distant parents from those clusters could be able to produce higher heterosis in progenies on hybridization. Grain yield per plant and thousand grain weight were the major contributors towards the total genetic divergence among the genotypes studied. Selection could be made based on grain yield per plant and thousand grain weight for the progenies identified.

### Introduction

Rice (*Oryza sativa* L.), native of India or Africa, is commonly known as arisi, nellu or chawal in India. The cultivated species are diploid with  $2n=24$  whereas the wild species are tetraploid with  $2n=4x=48$ . It is a self-pollinated crop with mechanism of cleistogamy. It is one of the very few crop species endowed with rich genetic diversity which account over one lakh landraces and improved cultivars (Samal *et al.*, 2014). In India, the overall rice production by the year 2015 - 2016 was 104.4 million tons whereas by the year 2014 – 2015 the production was estimated as 105.5 million tons and productivity as 2391 kg ha<sup>-1</sup> under 44.1 million ha (Indiastat, 2017).

Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which can be used to select appropriate parental genotypes for hybridization to develop high yielding potential variety (Bhatt, 1970). Diversity not only results in inducing genetic variation but also provides new recombination of genes in gene pool.

Using advanced biometric techniques such as multivariate analysis based on Mahalanobis D<sup>2</sup> statistic (Mahalanobis, 1936), it has now become possible to quantify the degree of genetic divergence amongst biological populations and assessing the relative

contribution of various desirable attributes of breeding and agronomic value to the total divergence. The investigation was about estimation of magnitude of genetic divergence of 48 rice genotypes and to identify diverse genotypes for the future study.

### **Materials and Methods**

Seeds of forty eight genotypes were sown in raised nursery beds during February, 2016. In each genotype, one seedling per hill was transplanted in the main field after 25 days with spacing of 20 cm X 20 cm. The experiments were conducted at Experimental Farm of Plant Breeding (11<sup>0</sup>24' N latitude and 79<sup>0</sup>44' E longitude, + 5.79 MSL), Annamalai University, Tamil Nadu, India. The experiment was carried out in Randomized Block Design with three replications. As recommended, agronomic and plant protection measures were followed during the crop period.

A uniform population of 12 plants in a row was maintained. The experiment was conducted to explore the extent of divergence in 48 rice genotypes for nine characters *viz.*, days to first flower, plant height, number of tillers per plant, number of panicles per plant, number of grains per panicle, panicle length, thousand grain weight, grain L/B ratio and grain yield per plant. The analysis of genetic divergence was done using Mahalanobis (1936) D<sup>2</sup> statistics. The genotypes were grouped into different clusters, inter and intra cluster distances and mean performances for characters were also computed.

### **Results and Discussion**

Analysis of variance for different characters is presented in table 1. Using advanced biometric techniques such as multivariate analysis based on Mahalanobis D<sup>2</sup> statistic (Mahalanobis, 1936), it has now become

possible to quantify the degree of genetic divergence amongst populations and assessing the relative contribution of various desirable attributes of breeding and agronomic value to the total divergence by the clustering pattern. The grouping of genotypes into so many clusters had suggested the presence of high degree of diversity in the materials evaluated. Earlier workers had also reported presence of substantial genetic diversity in rice (Kumar *et al.*, 2014; Ahmed *et al.*, 2014; Sandhya *et al.*, 2015).

Among the nine clusters, cluster I accommodated maximum of 19 genotypes followed by cluster IX of 10 genotypes and cluster VIII of 7 genotypes. The remaining clusters *i.e.* II, III, IV, V, VI and VII were accommodated with two genotypes. The genotypes included in cluster I originated from different origins indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes (Nayak *et al.*, 2004). Distribution of rice genotypes in different clusters was furnished in table 2.

Intra (bold) and inter cluster (unbold) D<sup>2</sup> values and D (unbold) values in rice are tabulated in tables 3 and 4 and in figure 1. The highest intra cluster distance was registered in cluster VIII (35.87) followed by cluster IX (32.82) and cluster I (28.70). Thus the genotypes from those clusters had high degree of divergence that would produce more desirable segregants for achieving greater genetic advance.

The least intra cluster distance was revealed in cluster II (4.63) followed by cluster III (7.75) and cluster IV (9.22) indicating homogenous nature of the genotypes with less deviation between the genotypes. Parallel findings were found by Nirosha *et al.*, (2016), Mamta Kumari *et al.*, (2016) and Hossain *et al.*, (2015).

**Table.1** Analysis of variance for nine characters in rice genotypes

Sl.No.	Source	df	Days to first flower (days)	Plant height (cm)	No. of tillers per plant	No. of panicles per plant	No. of grains per panicle	Panicle length (cm)	Thousand grain weight	Grain L/B ratio	Grain yield per plant (g)
			MSS								
1.	Replication	2	75.55	4.98	4.32	3.31	297.28	1.77	0.36	0.02	0.46
2.	Genotype	47	448.13**	788.95**	292.72**	146.37**	17721.09**	24.31**	29.30**	0.90**	450.35**
3.	Error	94	19.73	7.23	2.85	3.01	938.31	2.26	0.10	0.01	0.37

\*\* Significant at 1% level

**Table.2** Distribution of rice genotypes in different clusters based on D<sup>2</sup> analysis

Cluster No	Number of genotypes	List of the genotypes
<b>I</b>	19	ADT 47, ADT 41, ADT 37, ADT 36, ADT 45, ADT 48, ADT 43, ADT 42, ASD 16, ASD 18, IR 66, IR 64, IR 72, IR 50, TPS 5, CO 51, CO 47, Jaya Mathi, MTU 1156
<b>II</b>	2	IET 14348, MTU 7029
<b>III</b>	2	STBN 18, Bhavani
<b>IV</b>	2	MDU 5, PY 3
<b>V</b>	2	Geetanjali, Sama Mashuri
<b>VI</b>	2	AVT 1320, AVT 1321
<b>VII</b>	2	MTU 1121, MTU 1010
<b>VIII</b>	7	TRY 2, TKM 9, PMK 3, AVT 1303, Dhanya Lakshmi, IR 20, Super Amman
<b>IX</b>	10	Angur Selam, ASD 1, PLA 1100, K. Sona, AVT 1302, Kullakar, Pooughar, IR 36, NLR 34449, Akshaya

**Table.3** Intra (bold) and inter cluster (unbold) D<sup>2</sup> values of various clusters in rice

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>823.66</b>	1296.21	1345.02	667.38	1760.43	2033.09	1166.63	1138.41	1998.20
II		<b>21.40</b>	49.83	329.83	155.52	426.51	71.33	1988.60	615.30
III			<b>59.98</b>	407.21	175.14	334.87	141.25	2079.67	662.27
IV				<b>85.08</b>	736.41	918.62	267.05	1194.36	997.33
V					<b>122.00</b>	440.03	275.38	2526.30	638.02
VI						<b>144.65</b>	564.37	2940.36	846.72
VII							<b>156.11</b>	1791.71	699.23
VIII								<b>1286.55</b>	2602.09
IX									<b>1076.80</b>

**Table.4** Average intra (bold) and inter cluster D (unbold) values in rice

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>28.70</b>	36.00	36.67	25.83	41.96	45.09	34.16	33.74	44.70
II		<b>4.63</b>	7.06	18.16	12.47	20.65	8.45	44.59	24.81
III			<b>7.75</b>	20.18	13.23	18.30	11.89	45.60	25.74
IV				<b>9.22</b>	27.14	30.31	16.34	34.56	31.58
V					<b>11.05</b>	20.98	16.59	50.26	25.26
VI						<b>12.03</b>	23.76	54.23	29.10
VII							<b>12.49</b>	42.33	26.44
VIII								<b>35.87</b>	51.01
IX									<b>32.82</b>

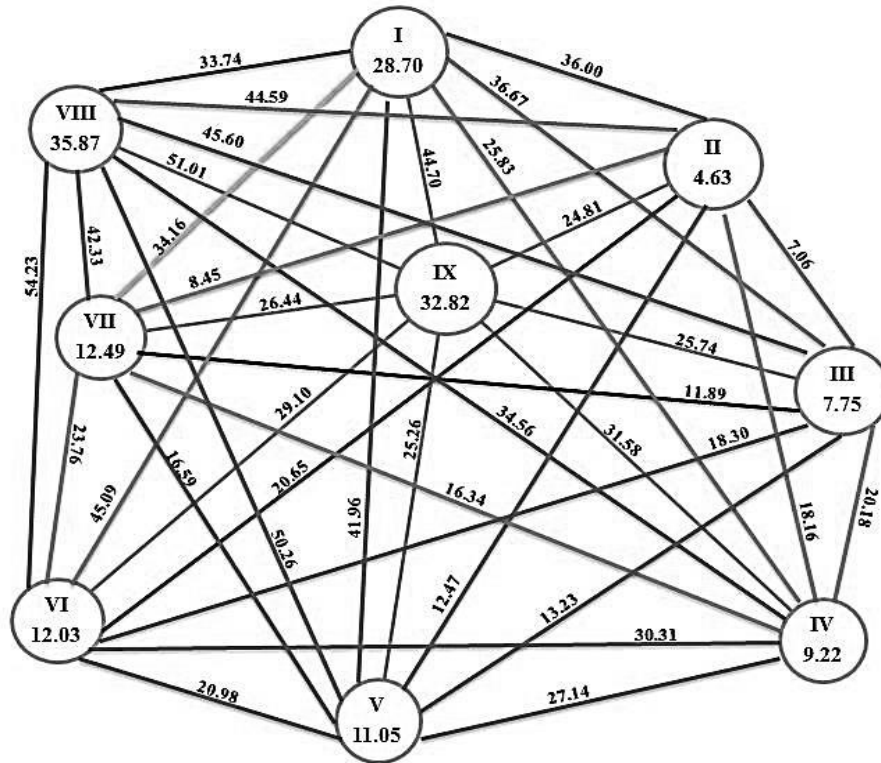
**Table.5** Cluster means of rice genotypes for different traits

Clusters	Days to first flower	Plant height (cm)	Number of tillers per plant	Number of panicles per plant	Number of grains per panicle	Panicle length (cm)	Thousand grain weight (g)	Grain L/B ratio	Grain yield per plant (g)
<b>Cluster I</b>	79.39	90.68	21.47	15.20	156.67	23.13	18.28	4.19	28.38
<b>Cluster II</b>	94.84	100.46	25.30	15.31	220.17	23.12	18.61	4.02	11.19
<b>Cluster III</b>	96.04	98.91	20.96	12.17	287.66	23.20	18.60	4.37	10.67
<b>Cluster IV</b>	79.85	85.96	32.01	22.91	207.72	23.50	19.28	3.97	20.45
<b>Cluster V</b>	90.03	114.43	21.33	11.52	209.30	27.93	16.54	4.18	7.91
<b>Cluster VI</b>	73.01	96.72	26.14	14.57	182.77	25.62	18.12	5.54	6.51
<b>Cluster VII</b>	93.61	100.45	26.59	18.36	137.23	24.88	19.30	4.00	13.07
<b>Cluster VIII</b>	88.36	113.50	28.56	20.43	212.70	24.63	19.24	4.24	32.86
<b>Cluster IX</b>	93.53	112.77	35.46	20.05	211.99	23.19	16.66	4.41	10.10

**Table.6** Relative contribution of different characters to genetic divergence

S. No.	Characters	Per cent contribution
1.	Days to first flower	0.80
2.	Plant height	0.80
3.	Number of tillers per plant	0.80
4.	Number of panicles per plant	4.87
5.	Number of grains per panicle	0.35
6.	Panicle length	0.35
7.	Thousand grain weight	11.26
8.	Grain L/B ratio	3.99
9.	Grain yield per plant	76.78

**Fig.1** Clustering pattern based on D values (not to scale) in rice genotypes



Highest inter cluster distance (54.23) was found between cluster VI and VIII followed by cluster VIII and IX (51.01), cluster V and VIII (50.26), cluster III and VIII (45.60) and cluster I and VI (45.09) indicating the wider genetic diversity among the genotypes between these clusters. This indicated that the genotypes in these clusters had broad spectrum of genetic diversity and could very well be used in hybridization programme. Similar results were reported by Yadav *et al.*, (2011) and Sandhya *et al.*, (2015).

The minimum inter cluster distance was found between cluster II and III (7.06). The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes. Similar results were reported by Banumathy *et al.*, (2010), Toshimenla *et al.*, (2016), Vijay Kumar (2015), Chamundeswari (2016) and Nirosha *et al.*, (2016).

The overall clustering pattern indicated that genotypes developed in same geographical region were distributed in different clusters. Shanmugam and Rangasamy (1982) reported that grouping of material of same geographical origin into different clusters was an indication of the broad genetic base of genotypes belonging to that origin. Similar results of non-association of geographical region with the genetic diversity were reported by Mohan *et al.*, (2015), Vijay Kumar (2015), Toshimenla *et al.*, (2016), Chandramohan *et al.*, (2016) and Thippeswamy *et al.*, (2016).

Cluster mean analysis revealed a wide range of variation for all the traits under study (Table 5). Cluster VI chronicled earliness in flowering and might be utilized as a suitable source for incorporation of earliness in other genotypes. Cluster IV reported minimum cluster mean for plant height. Hence



genotypes from the cluster could be made use in development of dwarf and semi – dwarf lines or the trait could be transferred into other desirable genotypes. Cluster VIII had the maximum cluster mean value for grain yield per plant. Hence the genotypes could be utilized in yield improvement breeding programmes.

The relative contribution of each characters towards  $D^2$  depends upon the inter cluster distances in all combinations (Table 6). The selection and choice of parents mainly depends upon contribution of characters towards divergence. In the present investigation, the highest contribution in manifestation of genetic divergence was exhibited by grain yield per plant (gm) (76.78%) followed by thousand grain weight (gm) (11.26%). Next to the above characters number of panicles per plant (4.87%) and grain L/B ratio (3.99%) had moderately contributed towards the genetic divergence. Hence grain yield per plant and thousand grain weight should be given importance during choice of parents for hybridization and selection in the segregating populations.

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**How to cite this article:**

Sowmiya C. A. and Venkatesan M. 2017. Studies on Genetic Diverity in Rice (*Oryza Sativa* L.). *Int.J.Curr.Microbiol.App.Sci.* 6(9): 1749-1756.  
doi: <https://doi.org/10.20546/ijcmas.2017.609.216>