

## Original Research Article

# Genetic Divergence in Indigenous and Exotic Genotypes of Rice (*Oryza sativa* L.)

Shama Parveen<sup>1\*</sup>, Lakshman Singh<sup>1</sup> and Amit Kanawjia<sup>2</sup>

<sup>1</sup>School of Agriculture, ITM University, Gwalior, India

<sup>2</sup>KVK, Jalaun, U.P., India

\*Corresponding author

## ABSTRACT

Genetic divergence of 216 rice (*Oryza sativa* L.) genotypes from indigenous and exotic collection was investigated using Mahalanobis  $D^2$  statistic. Based on 11 agro-morphological characters, these genotypes were grouped into 15 clusters. Out of 216 genotypes, 45 genotypes were grouped in cluster I; cluster II comprised only two genotypes, cluster III had 23 genotypes, cluster IV consisted 82 genotypes, cluster V and VI comprised of 25 and 14 genotypes respectively. Geographical origin was not found to be a good parameter of genetic divergence. Clusters V, IX, XI and XIII exhibited high values for most of the characters. Plant height, days to maturity, days to 50% flowering and leaf length contributed relatively maximum to genetic divergence to the formation of clusters. Cluster XIII recorded high values for number of effective tillers per plant and yield per plant. The genotypes belonging to clusters V, VIII, IX, XI and XIII could be used in hybridization programme to obtain better recombinants.

### Keywords

Genetic variability,  
Cluster analysis,  
Genetic diversity;  
Inter-cluster  
distance, Crop  
diversity

## Introduction

Assessment of variability, heritability, character association and contribution of characters to yield is prerequisite of the exploitation of genetic potential. Further,  $D^2$  analysis given by Mahalanobis is an efficient statistical tool for assessing diversity among genotypes differing for multiple traits. Genetic divergence among the parents is important because a cross involving genetically diverse parents is likely to produce high heterotic effect and also more variability could be expected in segregating generations (Khush *et al.*, 1979). Therefore, a meaningful classification of genotypes will enable the breeders to identify the best parents with sufficient genetic diversity and to utilize them for

hybridization programme. Mahalanobis  $D^2$  statistics measures inter-se genetic distance amongst the genotype. Their clustering based on the genetic distance finally provides a clear picture about the inter-relationship of the genotypes and helps to pick up appropriate genotype for utilization in the hybridization programme.

## Materials and Methods

The experimental seed material for the present investigation consisted of 216 genotypes of rice received from NBPGR and six check varieties. All the 216 genotypes were sown in the nursery on 21<sup>th</sup> June 2012; 25 days old seedlings were used for transplanting in the field. All entries were

raised in an augmented design. Whole experimental field was divided into 4 blocks and each block was further divided into 60 sub plots. All the genotypes including checks are randomized in such a way that each block receives 54 test genotypes and 6 check varieties. Same checks were replicated in each blocks i.e. four replications, but test genotype is different for each block. All the genotypes were grown with a spacing of 20 x 15 cm between row to row and plant to plant respectively. Cultural practices like weeding and irrigation were followed to maintain good crop growth apart from controlling of diseases and pests with suitable control measures. Recommended fertilizer dose were applied to obtain the good crop growth. The performance of the genotypes was evaluated by recording observations on 11 yield and yield related attributes *viz.* seedling height, leaf length, leaf width, days to 50 per cent flowering, days to maturity, number of effective tillers per plant, panicle length, yield per plant, 100 seed weight and kernel L/B Ratio. Five plants were selected randomly from the each genotype and observations were recorded for all characters except days to 50% flowering and days to maturity, whereas the latter two characters were recorded on plot basis. Assessment of genetic diversity was made using Mahalanobis's  $D^2$  analysis. Tocher's method of grouping is most widely used procedure of clustering.

### **Intra and inter-cluster $D^2$ values**

All the 222 genotypes were grouped into fifteen clusters by using Tocher's method (Singh and Choudhary, 1977). The distribution of genotypes into fifteen clusters was presented in Table 1. Cluster I had 45 genotypes, cluster II had 2 genotypes, cluster III had 23 genotypes, cluster IV had 82 genotypes, cluster V had 25 genotypes, cluster VI had 14 genotypes. Single

genotype was included in the clusters VII, VIII, IX, X, XI, XII, XIII, XIV and XV. The intra-cluster distance was found minimum for cluster I and maximum for cluster VI while it was zero for VII, VIII, IX, X, XI, XII, XIII, XIV and XV as these clusters consisted of only single genotype. The inter-cluster distance was minimum between cluster VII and cluster IX indicating close relationship and similarity for most of the characters of rice genotypes falling in these clusters. The maximum inter-cluster distance was recorded between cluster II and cluster IX suggesting highest genetic divergence existing between the genotypes of these clusters. Hybridization among these genotypes drawn from widely divergent clusters with high yield potential is likely to produce more heterotic effect. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents. Similar results of inter and intra cluster distances in rice were reported by Vaithiyalingan (2005), Singh *et al.* (2006) and Kuchanur *et al.* (2009).

### **Cluster mean analysis**

The cluster means for each of 11 characters are presented in Table 1. The cluster means for seedling height ranged from 9.53 (Cluster VII) to 17.31 (Cluster IX) leaf length ranged from 30.25 (Cluster II) to 73.61 (Cluster VIII). For leaf width, cluster means ranged from 0.59 (Cluster XII) to 1.28 (Cluster IX). Days to 50% flowering ranged from 74.03(Cluster II) to 158.83 (Cluster XI). Days to maturity ranged from 99.31 (Cluster II) to 184.71 (Cluster XI). Similarly, plant height ranged from 72.41 (Cluster II) to 171.51 (Cluster V), whereas the number of effective tillers per plant ranged from 5.96 (Cluster II) to 8.77 (Cluster XIII) and panicle length ranged from 21.37 (Cluster XII) to 28.34 (Cluster V).

**Table.1** Average intra (bold) and inter cluster D2 values for 15 clusters (Tocher's method)

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster	11 Cluster	12 Cluster	13 Cluster	14 Cluster	15 Cluster
<b>1 Cluster</b>	<b>221.77</b>	14371.41	6997.13	733.84	939.70	3706.34	848.51	1067.50	732.92	4099.02	1938.48	10589.48	4659.02	3174.43	765.81
<b>2 Cluster</b>		<b>306.99</b>	1738.20	12775.19	17182.59	5438.51	19692.54	20525.20	18891.71	4901.17	21811.30	584.50	5655.93	8664.58	13213.40
<b>3 Cluster</b>			<b>474.67</b>	6118.45	9075.84	1914.84	10930.36	11516.90	10342.84	1832.99	12781.57	857.92	2591.47	4206.13	6466.90
<b>4 Cluster</b>				<b>590.99</b>	2041.48	3636.36	1186.98	1461.44	1181.30	2714.22	1828.63	8916.39	3115.39	1800.31	1136.13
<b>5 Cluster</b>					<b>931.12</b>	4950.14	1814.36	1575.71	1711.85	6542.64	3193.83	13527.01	7611.14	5869.45	1749.77
<b>6 Cluster</b>						<b>1496.33</b>	6844.35	7160.58	6340.89	2323.92	8736.46	3788.70	3222.60	3840.79	3698.69
<b>7 Cluster</b>							<b>0.00</b>	339.41	151.13	6024.24	347.91	14748.87	6197.58	3735.51	1356.88
<b>8 Cluster</b>								<b>0.00</b>	680.35	6532.82	524.15	15657.82	7332.72	4631.24	1775.78
<b>9 Cluster</b>									<b>0.00</b>	5863.53	715.44	14159.28	5834.23	3629.57	1119.05
<b>10 Cluster</b>										<b>0.00</b>	6687.12	2424.65	358.16	739.29	3788.09
<b>11 Cluster</b>											<b>0.00</b>	16339.41	6814.67	3889.00	2263.24
<b>12 Cluster</b>												<b>0.00</b>	2877.78	5105.19	9640.78
<b>13 Cluster</b>													<b>0.00</b>	474.49	4218.29
<b>14 Cluster</b>														<b>0.00</b>	2735.62
<b>15 Cluster</b>															<b>0.00</b>

The cluster mean for yield per plant ranged from 4.86 (Cluster XI) to 23.73 (Cluster XIII). The cluster mean for 100-seed weight ranged from 1.76 (Cluster XV) to 2.74 (Cluster V) and for kernel L/B ratio ranged from 2.69 (Cluster IX) to 3.64 (Cluster XII).

The cluster means for different characters indicated differences between the clusters for all the characters. The cluster V recorded high mean values for plant height, panicle length and 100-seed weight. Cluster VIII recorded high value for leaf length. Cluster IX recorded high values for seedling height and leaf width. Cluster XI recorded high values for days to 50% flowering and days to maturity. Cluster XIII recorded high values for number of effective tillers per plant and yield per plant. The genotypes belonging to clusters V, VIII, IX, XI and XIII could be used in hybridization programme to obtain better recombinants.

#### **Relative contribution of characters towards diversity**

The relative contribution of different plant characters to the total genetic divergence estimated by  $D^2$  analysis indicated that plant height, days to maturity, days to 50% flowering and leaf length contributed relatively maximum to genetic divergence. Apart from the divergence, the performance of genotypes and the character with maximum contribution towards divergence should also be given due consideration which appear as desirable for improvement of rice. Plant height, days to 50% flowers, days to maturity were the important traits contributing maximum towards divergence whereas L/B ratio and leaf width had no

contribution towards divergence. Similar results in rice were also reported by Kuchanur *et al.* (2009) and Sravan *et al.* (2013) for days to 50% flowering and leaf width, Vennila *et al.* (2011) and Saravanan and Pachiyappan (2013) for plant height.

#### **References**

- Khush G.S., Phule C.M. and Delacruz N.M. 1979. Rice grain quality evaluation and improvement at IRRI. In: Chemical aspects of rice gain quality. IRRI, pp. 21-31.
- Kuchanur, P. H., Naresh Dronavalli and Vijaykumar, A. G. (2009) Genetic variability and divergence in ' New Plant Type' genotypes. *Crop Improvement*, 36 (1):20-24.
- Saravanan, K. and Pachiyappan, R. (2013). Genetic divergence analysis in rice. *International Journal of Agricultural Sciences*. 9(1):197-200.
- Singh, R.K. and Choudhary, B.D. (1977). Study of genetic variability and correlation coefficient analysis in mid landraces of rice. *Annals of Agri. Research*, 25 (1):1-3.
- Sravan, T. Rangare, N. R. Suresh, B. G. Reddy, G. E. Reddy, P. A. (2013). Genetic divergence in upland rice germplasm (*Oryza sativa* L.). *Trends in Biosciences*. 6(5): 583-585.
- Vaithiyalingan, M. (2005). Genetic divergence in rice (*Oryza sativa* L.). *J. of Ecobiology*, 17(4): 393-395.
- Vennila, S., Anbuselvam, Y. And Palaniraja, K. (2011).  $D^2$  analysis of rice germplasm for some quantitative and quality traits. *Electronic Journal of Plant Breeding*, 2: 392-396.