

**Studies on Genetic Divergence in High Yielding Rice (*Oryza sativa* L.) Genotypes****G. Bharathi, B. Krishna Veni\*, M. Lal Ahamed and K. Jaya Lalitha**

Department of Genetics and Plant Breeding, Agricultural College, Bapatla.

Scientist, Plant Breeding, RRU, Bapatla ANGRAU.

Department of Crop Physiology, Agricultural College, Bapatla, ANGRAU.

\*Corresponding author: bkv\_lam@yahoo.co.in

Received: 20<sup>th</sup> March, 2016; Accepted: 14<sup>th</sup> October, 2016**Abstract**

Genetic divergence was studied among 32 rice (*Oryza sativa* L.) genotypes using D<sup>2</sup> technique for ten characters. The 32 genotypes were grouped into 9 clusters containing 1 to 12 genotypes. The random distribution of genotypes indicated absence of parallelism between geographical diversity and genetic diversity. Cluster I was the largest with 12 genotypes and cluster III, V, VI, VII and VIII were lowest with one genotype each. In D<sup>2</sup> analysis, filled grains per panicle followed by ear bearing tillers per panicle and days to 50% flowering contributed maximum for the divergence. The inter-cluster distance was maximum between clusters V and IX and between clusters V and VII. Based on these studies, crosses may be made between genotypes of clusters IX (MTU 1010, BPT 2741, and MTU 1001) and V (BPT 1768) followed by clusters VII (RGL 2537) and cluster V (BPT 1768) to obtain new desirable recombinants in rice.

**Keywords:** Clusters, D<sup>2</sup> analysis, Genetic Divergence, Rice (*Oryza sativa* L.)**Introduction**

Rice occupies the enviable prime place among the food crops cultivated around the world and it is the second most staple food crop of the world next to wheat (Abodolereza and Raionzer, 2009). Genetic diversity in crop plants is essential to sustain level of high productivity (Tripathi *et al.*, 2013). Generally, in any breeding programme, based on the objective, the divergent parents are crossed to develop promising breeding lines having sufficient diversity. Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis D<sup>2</sup> statistic has proved to be a powerful technique (Murthy and Arunachalam, 1966). In view of the great importance of genetic diversity to breeding, techniques, present investigation was undertaken to study the diversity between 32 high yielding rice genotypes.

**Materials and Methods**

The experimental material consisted of thirty two genotypes (Table 1) obtained from Rice Research Unit (RRU) Bapatla and RARS, Maruteru. The study was conducted at Agricultural College Farm, Bapatla during *kharif* 2015 in randomized block design with two replications. One month old seedlings were transplanted in thoroughly puddled main field. Each experimental unit consisted of 2.4 m<sup>2</sup> and the spacing adopted was 20 cm between rows and 15 cm between plants. Single plant observations were

recorded on ten plants selected at random per genotype per replication and their means were used for statistical analysis. Mean performance of 32 genotypes of rice for yield components and quality parameters presented in table 6. The components taken for the study are Days to 50% flowering, Plant height (cm), Number of ear bearing tillers per plant, Panicle length(cm), Number of filled grains per panicle, Test weight (g), Grain yield per plant (g), Grain length (mm), Grain breadth (mm) and L/B ratio. Analysis of variance was carried out with the mean data of each character. The genetic diversity among the genotypes was computed by means of Mahalanobis (1928) D<sup>2</sup> statistic and the genotypes were grouped into clusters by following the Tochers's method.

**Table 1: The rice genotypes employed in the present study along with their pedigree**

S. No.	Designation	Cross combination/ Pedigree
1	MTU1075	MTU 2716/MTU 1010
2	MTU3626	IR 8/MTU 3
3	MTU 1064	PLA 1100/MTU 1010
4	MTU 7029	Vasista/Mahsuri
5	MTU 1061	PLA 1100/MTU 1010
6	MTU 4870	Sowbhagya/ARC6650
7	MTU 5249	MTU4569/ARC 6650
8	MTU 2716	Mashuri/Vijaya
9	MTU 2077	Sowbhagya/ARC 5984

10	MTU 1010	Krishnaveni/IR 64
11	MTU 5293	Sowbhagya/ARC 6650
12	BPT 2593	Mutant of BPT2270
13	BPT 2644	BPT 2270/NLR 145
14	BPT 2658	MTU 2077/AJAY/MTU 2077
15	BPT 2595	Mutant of BPT 2270
16	BPT 2741	Mutant OF BPT 2231
17	BPT 2571	CR 1009/NLR 33052
18	BPT 2660	BPT `768/NLR 145
19	BPT 2743	MTU 7029/NLR 34449
20	BPT 5204	GEB 24/TN 1//Mahsuri
21	BPT 2270	BPT 5204/CRM 1523
22	BPT 2231	BPT 4358/IR 64
23	BPT 2411	BPT 5204/BPT 4358
24	BPT 1768	BPT 3301/Mashuri Mutant
25	BPT 2295	BPT 1768/NLR 33641
26	NLR 33892	Tikkana/MTU 4870
27	NLR 20084	NLR 33057/Simhapuri
28	RGL 1414	RGL 4166/ MTU 7029
29	RGL 2537	T-145x CR I014
30	BPT 2673	BPT 5204/RP 4677-16-6-1-12-1-2
31	BPT 3291	Sona/Mashuri
32	MTU 1001	MTU 5249/MTU 7014

## Results and Discussion

The analysis of variance showed that the mean sum of squares for the genotypes were highly significant for all the traits measured. Character wise percent contribution towards genetic divergence by all the 10 characters is presented in the Table 2. In D<sup>2</sup> analysis, filled grains per panicle (38.51%), ear bearing tillers per plant (16.73%) and days to 50% flowering (10.89%) contributed maximum for the divergence. The observed results find support from studies conducted by Beevi and Venkatesan (2015), Islam

*et al.* (2004) and Kandamoorthy and Govindarasu (2005) who reported maximum contribution of filled grains/panicle, ear bearing tillers/plant and days to 50% flowering respectively.

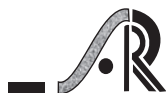
**Table 2: Contribution of different characters towards genetic divergence among 32 genotypes of rice (*Oryza sativa* L.)**

Source	Contribution %
Days to 50% flowering	10.89%
Plant height(cm)	7.06%
Ear bearing tillers per plant	16.73%
Panicle length(cm)	0.40%
Filled grains per panicle	38.51%
Test weight(g)	5.85%
Grain yield per plant(g)	9.48%
Grain length(mm)	5.85%
Grain breadth (mm)	4.84%
L/B ratio	0.40%

In the present study, 32 genotypes were distributed into 9 clusters at random with maximum number of genotypes in cluster I (12genotypes) from different locations (Table 3). Cluster IV was the second largest with 9 genotypes. The clusters II and IX are having three genotypes each. The clusters III, V, VI, VII and VIII were solitary clusters with nil intra-cluster D<sup>2</sup> values. The distribution of genotypes indicated that geographical diversity based on agro-climatic conditions and genetic diversity was not related and there are forces other than the geographical separation which are responsible for diversity such as natural and artificial selection, exchange of genetic material, genetic drift and environmental variation. The results were in accordance with the findings of Kandamoorthy and Govindarasu, (2005), Ravindrababu *et al.* (2006), Ramesh *et al.* (2007), Sharma *et al.* (2008) and Dushyantha (2008).

**Table 3: Distribution of 32 genotypes into different clusters**

S. No.	Cluster No	No of genotypes	Name of the genotype
1	1	12	BPT 2743, BPT 2295, BPT 2593, BPT 2595, BPT 2270, BPT 2660, BPT 2571, MTU 4870, BPT 5204, BPT 2673, MTU 1061, MTU 2716.
2	2	3	BPT 2658, NLR 20084, NLR 33892
3	3	1	BPT 2644
4	4	9	MTU1075, MTU 1064, MTU 2077, MTU 5293, MTU 7029, BPT 3291, BPT 5204, BPT 2411, RGL 1414
5	5	1	BPT 1768
6	6	1	MTU 5249
7	7	1	RGL 2537
8	8	1	MTU3626
9	9	3	MTU 1010, BPT 2741, MTU 1001



The magnitude of intra cluster distance measures the extent of genetic diversity between the genotypes of same cluster which the inter cluster distance measures the extent of genetic diversity between two clusters. The maximum intra cluster distance value was observed in cluster IV followed by cluster IX and cluster I (Table 4). The high intra cluster distance in cluster IV indicates the presence of wide genetic diversity among the genotypes viz., MTU1075, MTU 1064, MTU 2077, MTU 5293, MTU 7029, BPT 3291, BPT 5204, BPT 2411 and RGL 1414 grouped in this cluster. Inter-cluster distances between nine clusters ranged from 89.84 (between cluster I and III) to 1404.24 (between cluster V and IX). The maximum inter cluster  $D^2$  values were observed between clusters V and IX followed by clusters V and VII. Based on these studies crosses may be made between genotypes of clusters IX (MTU 1010, BPT 2741, MTU 1001) and V (BPT 1768) followed by clusters VII (RGL 2537) and cluster V (BPT 1768) to obtain new desirable recombinants in rice. Cluster distances showed wide range among the genotypes studied, which indicated the presence of variation among the genotypes studied. For a successful breeding programme, selection of genetically diverse parents is an important pre-requisite to get better and desirable recombinants. Similar results were reported by Deepa *et al.*, (2005), Sobita *et al.*, (2006), Sandhya *et al.*, (2007), Ramesh *et al.*, (2007) and Parimalan *et al.*, (2008). Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of diverse clusters will express high heterosis and give more useful segregants. Maximum mean value for grain yield/plant was manifested by the genotypes grouped in cluster II (25.73) followed by cluster VI (23.70), cluster III (22.80) and cluster IX (21.76) (Table 5). Genotypes in

cluster VII recorded lowest mean for plant height (77.10), panicle length (16.03), filled grains per panicle (73.70) and grain yield per plant (10.90g). Along with grain yield, cluster II also manifested maximum mean for filled grains per panicle (158.45) and panicle length (23.53) and desirable mean value for test weight (21.77) which contributed to high grain yield. The lowest mean value for plant height (77.1) was recorded by cluster VII while the lowest mean for days to 50% flowering was observed in cluster IX (93.33) which can be utilized in hybridization programme for incorporation of earliness and dwarf plant stature into segregating population.

The genotype grouped in cluster VIII (MTU 3626) manifested maximum mean value for both grain length (6.5mm) and grain breadth (2.5 mm) which was also reflected by recording maximum mean for the test weight (27.23g). Among the nine clusters studied, the genotypes grouped in cluster III, V and I manifested desirable mean values for majority of characters studied viz., filled grains per panicle, panicle length, test weight, semi-dwarf plant stature and medium slender grain type. Hence the genotypes grouped in these clusters may also be utilized for transferring these traits into further segregating generations. Cluster IX recorded moderate mean values for filled grains per panicle, panicle length, grain yield per plant coupled with minimum mean for days to 50% flowering and maximum mean for ear bearing tillers per plant. Maximum inter cluster distance was recorded between clusters IX and V followed by cluster V and VII and II and VII. Hence the genotypes from these clusters may be utilized for hybridization programme to isolate desirable transgressive segregants. Based on these studies crosses may be made between genotypes of clusters IX (MTU 1010, BPT 2741, MTU 1001) and V (BPT 1768) followed by clusters VII (RGL 2537) and cluster V (BPT 1768) to obtain new desirable recombinants in rice.

**Table 4: Average intra-and inter-cluster  $D^2$  values among nine clusters in 32 rice (*Oryza sativa* L.) genotypes**

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	<b>55.1</b>	126.97	89.84	270.11	119.24	360.08	762.58	447.89	848.49
Cluster II		<b>31.22</b>	191.42	489.43	126.99	557.28	1175.16	641.64	1095.7
Cluster III			<b>0</b>	139.24	296.42	236.3	490.31	332.77	553.76
Cluster IV				<b>108.48</b>	582.83	143.66	245.26	192.01	376.09
Cluster V					<b>0</b>	721.14	1308.28	792.71	1404.24
Cluster VI						<b>0</b>	247.68	74.12	255.46
Cluster VII							<b>0</b>	338.96	286
Cluster VIII								<b>0</b>	211.65
Cluster IX									<b>96.59</b>

Diagonal bold values indicate intra cluster distances

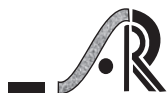
**Table 5: Mean values of nine clusters by Tocher's method for 32 genotypes of rice (*Oryza sativa* L.)**

Character / Cluster number	Days to 50% flowering	Plant height (cm)	Ear bearing tillers/plant	Panicle length (cm)	Filled grains per panicle	Test weight (g)	Grain yield per plant (g)	Grain length (mm)	Grain breadth (mm)	L/B ratio
Cluster I	115.54	97.91	9.23	22.00	143.25	18.10	19.46	5.63	2.03	2.74
Cluster II	<b>118.17</b>	<b>134.53</b>	8.45	<b>23.53</b>	<b>158.45</b>	21.77	<b>25.73</b>	5.54	<b>2.02</b>	2.68
Cluster III	111.00	113.00	11.65	22.19	137.90	15.53	22.80	5.65	2.05	2.75
Cluster IV	106.72	93.72	9.84	19.59	86.57	19.16	16.95	5.68	2.15	2.61
Cluster V	123.50	90.80	<b>7.45</b>	23.15	146.75	19.92	17.90	5.78	2.05	2.70
Cluster VI	103.00	87.95	9.90	16.66	115.50	21.27	23.70	5.50	2.35	<b>2.34</b>
Cluster VII	97.00	<b>77.10</b>	11.15	<b>16.03</b>	<b>73.70</b>	<b>16.45</b>	<b>10.90</b>	<b>5.10</b>	2.03	2.50
Cluster VIII	103.00	82.75	9.15	18.90	85.90	<b>27.23</b>	17.90	<b>6.50</b>	<b>2.50</b>	2.55
Cluster IX	<b>93.33</b>	96.50	<b>14.63</b>	21.42	122.00	22.85	21.76	6.35	2.14	<b>2.93</b>

Bold figures are indicated maximum and minimum mean values for each character.

**Table 6: Mean performance of 32 genotypes of rice (*Oryza sativa* L.) for yield components and quality parameters**

S. No.	GENOTYPES	DFE	PH (cm)	EBT/ P	PL(cm)	FGPP	TW(g)	GY/P (g)	GL(mm)	GB(mm)	L/B RATIO
1	MTU1075	108.50	101.95	8.55	22.48	100.90	20.76	21.60	6.35	2.20	2.85
2	MTU3626	103.00	82.75	9.15	18.90	85.90	<b>27.23</b>	17.90	6.50	<b>2.50</b>	2.55
3	MTU 1064	107.00	103.90	8.90	21.37	90.90	21.23	19.10	5.75	2.15	2.65
4	MTU 7029	112.00	90.95	10.55	18.58	60.00	17.62	15.60	5.58	2.19	2.54
5	MTU 1061	118.00	108.35	11.70	21.33	125.50	20.94	21.70	5.95	2.20	2.65
6	MTU 4870	117.00	102.90	9.55	19.77	137.00	18.8	20.60	5.75	2.30	2.45
7	MTU 5249	103.00	87.95	9.90	16.65	115.50	21.27	23.70	5.50	2.35	<b>2.34</b>
8	MTU 2716	110.00	90.90	6.85	20.36	127.65	20.31	16.10	5.80	2.10	2.75
9	MTU 2077	114.00	92.50	7.30	20.09	75.35	21.11	11.00	5.55	2.28	2.40
10	MTU 1010	<b>91.00</b>	91.30	14.60	21.22	129.00	24.55	19.75	<b>6.80</b>	2.03	<b>3.33</b>
11	MTU 5293	105.00	88.30	8.25	19.60	<b>55.90</b>	18.55	11.40	6.03	2.13	2.83
12	BPT 2593	117.00	102.20	8.50	23.57	161.95	16.63	19.00	5.75	2.00	2.80
13	BPT 2644	111.00	113.00	11.65	22.19	137.90	<b>15.53</b>	22.80	5.65	2.05	2.75
14	BPT 2658	120.00	128.00	10.35	23.72	156.95	23.03	<b>26.80</b>	5.58	1.95	2.75
15	BPT 2595	115.00	93.05	9.00	21.69	152.90	17.37	22.00	5.28	<b>1.85</b>	2.80
16	BPT 2741	92.00	86.65	14.95	23.80	132.50	19.99	25.60	5.75	2.13	2.65
17	BPT 2571	111.00	103.70	9.25	21.95	137.00	15.89	22.00	5.35	2.00	2.60
18	BPT 2660	112.00	101.30	10.85	22.02	<b>167.00</b>	15.86	23.50	5.59	1.98	2.75
19	BPT 2743	117.00	93.80	8.85	22.40	164.85	17.85	20.40	5.63	1.93	2.85
20	BPT 5204	105.00	88.50	11.20	16.90	105.00	15.81	14.65	5.10	1.85	2.70
21	BPT 2270	119.50	90.00	10.50	21.65	147.60	16.05	19.45	5.58	2.03	2.75
22	BPT 2231	115.50	95.15	8.90	22.52	104.65	20.70	19.90	5.66	2.00	2.83



23	BPT 2411	108.00	101.60	<b>15.35</b>	20.94	125.50	19.25	23.80	5.78	2.23	2.59
24	BPT 1768	<b>123.00</b>	90.80	7.45	23.15	146.75	19.91	17.90	5.78	2.05	2.70
25	BPT 2295	118.00	97.60	8.35	23.10	154.95	17.50	18.90	5.25	1.88	2.75
26	NLR 33892	117.00	<b>144.35</b>	8.20	<b>25.00</b>	127.85	21.77	26.60	5.51	2.15	2.55
27	NLR 20084	117.00	131.25	<b>6.80</b>	18.85	150.55	20.51	23.80	5.53	1.95	2.75
28	RGL 1414	100.00	96.25	10.40	19.51	83.95	19.32	17.30	5.28	2.08	2.50
29	RGL 2537	97.00	<b>77.10</b>	11.15	<b>16.03</b>	73.70	16.44	10.90	<b>5.10</b>	2.03	2.50
30	BPT 2673	116.00	96.00	8.50	23.63	137.90	19.31	<b>10.00</b>	5.95	2.05	2.85
31	BPT 3291	101.00	79.55	8.05	16.83	81.65	18.83	18.10	5.75	2.30	2.45
32	MTU1001	97.50	111.55	14.35	19.25	104.50	24.015	19.92	6.50	2.27	2.80
	<b>Mean</b>	<b>109.93</b>	<b>98.84</b>	<b>9.93</b>	<b>20.90</b>	<b>121.60</b>	<b>19.49</b>	<b>19.43</b>	<b>5.71</b>	<b>2.09</b>	<b>2.68</b>
	C.V.	1.43	5.16	10.68	9.01	9.52	6.88	10.77	2.67	4.34	4.62
	C.D. 5%	3.22	10.42	2.16	3.86	23.66	2.73	4.271	0.31	0.18	0.25

DFP- days to 50% flowering; PH - plant height ; EBT/P- ear bearing tillers per plant ; PL-panicle length ; FGPP- filled grains per panicle; TW-test weight; GY/P- grain yield per plant; GL- grain length; GB -grain breadth ; L/B ratio- grain length/grain breadth ratio

Note: Bold figures are maximum and minimum mean values for each character

## References

- Abodolereza A and Raionzer P. 2009. Food Outlook: *Global Market analysis*. 23-27.
- Beevi, AH and Venkatesan M. 2015. Genetic divergence studies in rice genotypes under saline condition. *International Journal of Current Advanced Research*. 4: 6-8.
- Deepa SP, Ibrahim SM, Vivekanandan P, Anbumalarmathi J and Sheeba A. 2005. Genetic divergence in rice (*Oryza sativa* L.). *Crop Research*. 30: 428-431.
- Dushyantha KBM. 2008. Genetic divergence in red rice. *Karnataka Journal of Agricultural Sciences*. 2: 346-348.
- Islam MR, Faruquei MAB, Bhuiyan MAR, Biswas PS and Salam MA. 2004. Genetic diversity in irrigated rice. *Pakistan Journal of Biological Sciences*. 7: 226-229.
- Kandamoorthy S and Govindarasu R. 2005. Genetic divergence in extra early rice (*Oryza sativa* L.) under two culture systems. *Indian Journal of Genetics and Plant Breeding*. 65: 43-44.
- Mahalanobis PC. 1928. A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal*. 25: 301-307.
- Murthy BR and Arunachalam V. 1966. The nature of divergence in relation to breeding system in some crop plants. *Indian Journal of Genetics and Plant Breeding*. 26: 188-198.
- Parimalan R, John Joel A and Vanniarajan C. 2008. Genotypes clustering in rice (*Oryza sativa* L.). *Crop Improvement*. 35:115-18.
- Ramesh C, Pradhan SK, Sanjay Singh, Bose LK and Singh ON. 2007. Multivariate analysis in upland rice genotypes. *World Journal of Agricultural Sciences*. 3(3): 295-300.
- Ravindrababu V, Sandhya K, Shobharani N and Ravi C. 2006. Genetic divergence analysis using quality traits in rice (*Oryza sativa* L.). *Oryza*. 43(4): 260-263.
- Sandhya KN, Ravindra BV, Ansari NA and Ravi C. 2007. Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.). *Crop Improvement*. 34(1):12-15.
- Sharma A, Gupta KR and Rakesh Kumar. 2008. Genetic divergence in basmati rice (*Oryza sativa* L.) under irrigated ecosystem. *Crop Improvement*. 35(1): 8-10.
- Sobita DL, Abhishek D, Manish K, Pandey and Kole CR. 2006. Depiction of genetic diversity in rice. *Crop Research* 32(3):459-461.
- Tripathi RP, Sharma P and Singh S. 2005. Tillage index: An approach to optimize tillage in rice-wheat system. *Soil Tillage Research*. 80: 125-137.