

## ASSESSMENT OF GENETIC DIFFERENCES AMONG NEWLY DEVELOPED ELITE RICE CULTURES OF MARUTERU

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**Abstract:** The nature and magnitude of genetic divergence were estimated in 93 elite rice cultures developed at RARS, Maruteru using Mahalanobis  $D^2$  statistics by considering eight yield and yield contributing traits. Mahalanobis  $D^2$  analysis revealed considerable amount of genetic diversity in the material studied. Based on the genetic distance the genotypes were grouped into 10 clusters. Cluster I was the largest with 40 genotypes followed by Cluster III with 17, Cluster II with 16, Cluster IV with 12 and Cluster IX & X with 2. Clusters V, VI, VII and VIII are monogenic. Cluster VI had highest mean values for test weight, panicle length; Cluster VIII had highest mean values for ear bearing tillers, number of grains per panicle; Cluster I had highest mean values for grain yield, while Cluster X recorded higher values for plant height at maturity. Traits like days to 50% flowering and plant height at maturity contributed maximum towards genetic divergence.

**Key words:** Genetic divergence, elite rice lines, Mahalanobis  $D^2$  analysis, Clustering.

**Introduction:** In India, rice is being cultivated in more than 42 m ha and is the major food crop for more than 70% of the population (Manohara and Singh, 2013). Rice accounts for between 35-60% of the caloric intake of three billion Asians. Andhra Pradesh Rice Research Institute, Maruteru, West Godavari, Andhra Pradesh is a premier rice research institute in India from where globally popular rice varieties were developed. In this Institute, varietal development is a continuous process and till to day 47 new varieties were released along with India's first two hybrids. In the varietal development programme many of the elite rice lines have been developed from several cross combinations by using pedigree method of breeding. Knowledge about genetic diversity and genetic relationships in the breeding material could be an invaluable aid in crop improvement strategies. Genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population. Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature. Several workers have emphasized the importance of genetic divergence and Mahalanobis  $D^2$  statistics for estimating genetic divergence. Hence the present study was aimed to know the nature and magnitude of genetic diversity among 93 rice cultures developed at Maruteru by using Mahalanobis  $D^2$  statistics.

**Materials And Methods:** Ninety three elite rice lines developed at APRRI & RARS, Maruteru were used for study. The experiment was conducted at APRRI & RARS, Maruteru during *Rabi* 2012-13 in randomized block design with two replications. Twenty eight days old seedlings were transplanted at the rate of one seedling per hill in 6.8 m<sup>2</sup> plots adopting spacing of 15

cm between rows 15cm between plants. All cultural operations and management practices were employed as and when necessary to rise healthy crop. Observations were recorded on days to 50% flowering, plant height at maturity (cm), ear bearing tillers/m<sup>2</sup>, number of grains/panicle, test weight (grams), panicle length (cm), spikelet fertility (%) and grain yield (g/m<sup>2</sup>). The data collected was subjected to Mahalanobis  $D^2$  statistic to assess genetic divergence among 93 genotypes following Mahalanobis (1936) generalized distance ( $D^2$ ) analysis as given by Rao (1952).

**Results And Discussion:** The analysis of variance revealed that the all rice lines studied differed significantly for all the characters studied indicating the presence of notable genetic variability among them. This implied that it would be judicious to classify the population on the basis of degree of divergence. On the basis of degree of divergence, 93 rice lines were grouped into 10 clusters. Distribution pattern indicated that cluster I had maximum number (40) of genotypes followed Cluster III with 17, Cluster II with 16, Cluster IV with 12, Cluster IX & X with 2 genotypes. and clusters V, VI, VII and VIII had only one genotype (table 1).

Cluster I was more divergent with cluster IX and less with cluster V (18.36). Cluster II had maximum divergence with cluster X (142.18) and closer to cluster VIII (24.32). Cluster III was divergent with Cluster IX (219.03) and less with Cluster VII (33.30). Cluster IV was nearer to Cluster VIII (44.84) and away from cluster X (129.54) (table 2). Clusters I, III, V, VI, VII and VIII had shown more diversity with cluster IX indicating that genotypes in cluster IX are genetically more divergent than others. Cluster II, IV and IX had showed maximum divergence with cluster X (142.180, 129.543 and 284.356 respectively).

Cluster means (table 3) revealed that days to 50% flowering had highest mean value in cluster X (107.5 days) and lowest cluster I ( 84.714 days) indicating that the genotypes in these cluster belong to long and early duration groups respectively. Cluster VI had taller genotypes which was denoted by highest mean for plant height at maturity (124.45cm) where as genotypes in clusters I, II and VII are semi dwarf types (~90cm). Clusters II, IV, IX and X recorded more ear bearing tillers (>400 per m<sup>2</sup>) while cluster I had lowest tillers of 309.271 per m<sup>2</sup>. Highest test weight was recorded in cluster V (25.65 grams) indicating that the genotype 2203-13-2-2-4 is bold grain type. The genotypes in clusters II, VII and X are slender grain types which was indicated by their lower mean values (16.9, 16.25, 16.96 respectively) which is consumer preferred grain type. Highest mean values for panicle length was observed in cluster VI (24.9cm), spikelet fertility in cluster VI (79.24%). The highest grain yield was recorded in cluster IV (6615.024kg/ha) followed by cluster VI (6310.25kg/ha). The highest grain yield in MTU 2199-43-1 may be due to high number of grains per panicle,

while long panicle and more spikelet fertility are the key traits for high grain yield in cluster VI. The cluster means clearly reflected the genetic distances among the genotypes studied.

Regarding contribution towards genetic divergence, the trait days to 50% flowering contributed maximum (44.34%) followed by plant height at maturity (26.32%), ear bearing tillers/m<sup>2</sup> (7.36%) and grain yield (6.73%) (table 4). Earlier workers also reported similar results for one or more traits (Manohara and Singh., 2013; Chamundeswari *et al.*, 2012; Chanbeni *et al.*, 2012; Hosan *et al.*, 2010; Sabesan *et al.*, 2009). The characters test weight (5.14%), panicle length (4.23%), spikelet fertility (4.04%), number of grains/panicle (1.82%) contributed less to genetic divergence in the material studied.

From the present study it is concluded that though several rice lines had developed at same research institute all of them had shown considerable diversity for yield and yield components indicating that the material under study has good potential either to use as parents in crossing programme or to use as cultivars.

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**Table 1: Distribution of elite rice lines into clusters**

S. No	Cluster number	No. of rice lines	Designation of rice lines
1	I	40	MTU II 365-42-1-1-1, MTU II 365-68-1-1-1, MTU II 356-17 -1-1, PS 8-7-1-1, MTU II 365-15-1-1-1, MTU II 369-96-1-1, MTU II 365-75-1-1, MTU II 356-8-2-1-1, MTU II 371-44-1-1, MTU II 365-79-1-1-1, MTU II 365-30-1-1-1, PS 2-11-1-1, MTU II 369-67-2-1, MTU II 365-94-1-1-1, RM 9-28-1-1, MTU II 369-93-1-1-1, MTU II 338-32-1-1, 2117-21-1, MTU II 365-57-1-1-1, MTU II 367-46-1-1, RM 39-13-1-1, 2046-1-2-1-1-1, RM 33-13-1-1, 2133-5-2-1-1, MTU2199-47-1, MTU 2203-15-3-2, MTU II 356-8-1-1, MTU II 365-14-1-1, PS 2-21-1-1, MTU II 338-15-1-1-1, MTU 2199-52-1, 2203-2-1-2-3, MTU II 365-34-1-1, MTU 2199-53-1, MTU 2203-15-1-2, MTU 2199-46-1, MTU 2204-5-2-1, MTU 2204-5-3-2, 2161-8-1-4-1-1, 2091-6-3-1-2
2	II	16	RM 39-56-1-1, RM 39-55-1-1, RM 39-52-1-1, 2204-2-1-2-5, 2204-2-1-2-4, 2204-8-1-1-2, 2203-11-1-1-1, PS 2-21-1-2, MTU 2161-8-1-4, 2203-15-3-1-1, MTU 2105-32-1-3-1, MTU 2113-3-1-1-5, MTU 2204-6-1-2, MTU II 338-25-1-1-1, MTU II 383-32-1-1-1, MTU II 367-81-1-1
3	III	17	MTU 157-43-2-2-1, MTU 157-43-2-2-2, MTU 157-43-2-2-2-3, MTU 2204-20-1-1, MTU 1010, MTU 2024-23-3-1, MTU 2199-88-1, MTU 2204-21-1-1, IM 7 (IR 06 M143), MTU 1081, IM 6 (UPR 3413-18-2-1), 2204-8-1-2-1, MTU 2204-5-1-1, MTU 2199-65-1, IME 7 (IR 65482-7-216-1-2-B), MTU 2199-44-1, MTU 2203-7-1-2
4	IV	12	MTU II 369-7-2-14, MTU II 369-33-1-1, 2133-11-2-1, RM 2-55-1-1, MTU II 367-41-2-1, RM 2-60-2-1, RM 5-42-2-1, 2203-19-1-2-1, MTU II 369-84-1-1-1, MTU 2201-18-1, MTU 2201-19-1, MTU 2199-41-1
5	V	1	2203-13-2-2-4
6	VI	1	MTU 2199-43-1
7	VII	1	RM 2-44-1-1
8	VIII	1	2166-3-2-1-2-1
9	IX	2	MTU II 338-38-1-2, RM 7-53-1-1
10	X	2	MTU 2199-178-1, MTU 2199-73-1

**Table 2: Inter and Intra cluster D<sup>2</sup> values**

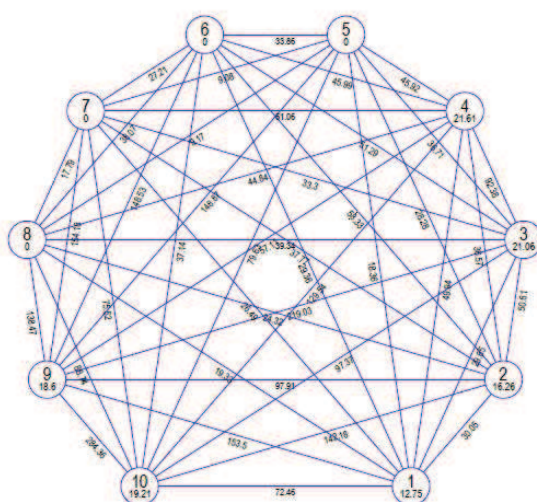
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	<b>12.755</b>	30.051	29.854	49.935	18.358	29.361	26.492	19.327	153.503	72.462
Cluster II		<b>16.262</b>	50.612	36.569	28.276	58.332	37.773	24.323	97.915	142.180
Cluster III			<b>21.062</b>	92.383	36.710	51.293	33.297	39.335	219.034	97.366
Cluster IV				<b>21.607</b>	45.924	45.985	51.059	44.839	57.106	129.543
Cluster V					<b>0.000</b>	33.856	9.084	9.173	148.873	79.630
Cluster VI						<b>0.000</b>	27.211	38.074	148.528	37.140
Cluster VII							<b>0.000</b>	17.786	154.181	75.519
Cluster VIII								<b>0.000</b>	138.467	88.740
Cluster IX									<b>18.599</b>	284.356
Cluster X										<b>19.212</b>

**Table 3: Cluster means for the characters studied**

Character/ Cluster	Days to 50% flowering	Plant height at maturity (cm)	Ear bearing tillers/ m <sup>2</sup>	Number of grains/ panicle	Test weight (grams)	Panicle length (cm)	Spikelet fertility (%)	Grain yield (kg/ha)
Cluster I	84.714	90.350	309.271	216.071	21.643	21.286	74.016	6017.929
Cluster II	88.292	91.200	409.933	291.375	16.900	21.333	65.773	6146.500
Cluster III	88.567	100.027	366.667	288.867	17.453	21.513	57.940	5705.500
Cluster IV	91.190	101.919	410.876	303.143	18.169	21.531	67.230	6615.024
Cluster V	86.438	102.663	334.950	197.563	25.650	23.113	67.731	6232.125
Cluster VI	86.500	124.450	387.200	277.250	21.950	24.900	79.240	6310.250
Cluster VII	95.625	91.950	382.067	278.250	16.250	19.650	64.595	5373.792
Cluster VIII	96.750	107.175	313.500	263.875	20.388	23.588	66.711	4923.000
Cluster IX	100.000	104.114	415.486	240.929	19.150	21.036	51.006	5848.571
Cluster X	107.500	96.940	406.560	272.600	16.960	22.340	53.141	4573.400

**Table 4: Contribution of yield and yield components towards genetic divergence**

S.No	Source	Times Ranked 1st	Contribution (%)
1	Days to 50% flowering	1897	44.34
2	Plant height at maturity (cm)	1126	26.32
3	Ear bearing tillers/ m <sup>2</sup>	315	7.36
4	Number of grains/ panicle	78	1.82
5	Test weight (grams)	220	5.14
6	Panicle length (cm)	181	4.23
7	Spikelet fertility (%)	173	4.04
8	Grain yield (kg/ha)	288	6.73



**Fig: Cluster Diagram (Mahalanobis Euclidian distance)**

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