Genetic Divergence in Medium Duration Genotypes of Rice (*Oryza Sativa L.*)

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ABSTRACT

Genetic divergence study of 19 medium duration genotypes of rice for 20 characters led to their grouping into five clusters. Protein percentage (43.27) showed maximum contribution towards genetic divergence followed by alkali digestion value (27.49), amylose content (9.94), grain length (5.26), grain width (5.26), water uptake (2.92), kernel breadth (1.17), test weight (1.17), days to 50% flowering (1.17), filled grains per panicle (0.58), kernel length after cooking (0.58), panicle length (0.58) and tillers per plant (0.58). The maximum inter cluster D^2 values was observed between cluster II and III followed cluster II and V and cluster I and II.

Key words : Cluster analysis, Genetic divergence, Mehalanobis D^2 analysis, Rice.

Rice (*Oryza sativa* L.) offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative characters. Assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding programme. Genetic variability is the prerequisite for making the progress in crop improvement. As, such, inclusion of genetically divergent parents in the breeding programmes is essential to create new variability in any crop. In the present investigation, an attempt was made to classify and to know the genetic diversity for certain yield and quality traits for use in hybridization programme to improve yield.

MATERIAL AND METHODS

The material comprised of 19 medium duration rice genotypes collected from Rice Research Unit (RRU), Bapatla and Directorate of Rice Research, Hyderabad. The experiment was conducted at Agricultural College Farm, Bapatla, during *kharif* 2010. Thirty days old seedlings were transplanted in the main field. The main field was laid out in a randomized block design with three replications. Each experimental unit consisted of 10 m^2 and the spacing adopted was 20 cm between rows and 15 cm between plants. The recommended package of practices was followed for raising a healthy crop. Single plant observations were recorded on ten plants selected at random per variety per replication and their means were used for statistical analysis. However, observations on test weight, days to 50% flowering and grain yield per plant were recorded on plot basis. The analysis of genetic divergence using Mahalanobis D^2 analysis was done as described by Rao (1952) and grouping of genotypes into different clusters was carried out by using cluster analysis

RESULTS AND DISCUSSION

Out of the 5 clusters obtained by grouping 19 medium duration genotypes based on relative magnitude of D^2 values, cluster I was the largest one with 8 genotypes . Clusters II, III, IV and V had 6, 3, 1 and 1 genotypes respectively (Table 1). The clustering pattern indicated existence of significant amount of variability, which was in conformity with the findings of Kandamoorty and Govindarasu, (2005), Ravindrababu *et al.,* (2006) and Ramesh Chandra *et al.,* (2007).

Maximum intra-cluster distance (Table 2) of 423.816 observed in cluster II followed by 403.327 for cluster III, 285.886 for cluster I, while it was zero for clusters IV and V. Thus, selection of genotypes based on high per se and other desirable traits from cluster I which had maximum number of 8 genotypes might be fruitful to generate the breeding material. The maximum inter cluster D values was observed between cluster II and III followed by cluster I and II. Based on these studies crosses may be made between genotypes of clusters II (RDR 23,

Table 1. Clustering pattern of 19 medium duration genotypes of rice (*Oryza sativa* L.) by Tocher's method.

Cluster No.	No. of genotypes	Genotypes
I	8	WGL 482, MTU 1001, RNR 2472, WGL 404, JGL 16259,MTU 1769-1-1, NLR 3093, MTU 1075
II	6	RDR 23, JGL 17204, WGL 401, NLR 3084, WGL II 218-5-1, RNR 2378
III	3	RDR 40, JGL 15230, JGL 11727
IV	1	MTU PLA 99-1-3-1-2
V	1	NLR 3090

Table 2. Average intra- and inter cluster D^2 values among 5 clusters in 19 medium duration genotypes of rice (*Oryza sativa* L.).

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster
I Cluster	**285.886**	691.918	496.246	518.391	554.427
II Cluster		**423.816**	1024.68	601.633	902.211
III Cluster			**403.327**	666.803	677.984
IV Cluster				**0.000**	518.246
V Cluster					**0.000**

Bold and diagonal values indicate intra cluster distances

JGL 17204, WGL 401, NLR 3084, WGL II 218-5-1 and RNR 2378) and cluster V (NLR 3090) to obtain new desirable recombinants in rice. Hence, hybridization between genotypes selected from these two clusters (II and V) results in expression of hybrid vigour in higher magnitudes and production of large number of desirable recombinants for both yield and quality. Hybridization between genetically distant genotypes to generate promising breeding material was suggested by earlier workers Deepa Sankar *et al.,* (2005), Sobita Devi *et al.,* (2006) and Sandhya Kishore *et al.,* (2007).

A wide range of variation was registered in the cluster means for most of the characters studied (Table 3). Higher genetic differences were observed in case of plant height, days to 50 % flowering, filled grains per panicle, water uptake, hulling and milling percentage. The genotypes included in the cluster III exhibited average performance for most of the characters and has high mean values for plant height, tillers per plant, ear bearing tillers per plant, panicle length, days to 50 % flowering, grain width, flag leaf length, test weight and kernel breadth. Cluster IV contained genotypes (MTU PLA 99-1-3-1-2) of higher filled grains per panicle, grain length, grain yield per plant, kernel length, water uptake, alkali digestion value, amylose content, hulling percentage and milling percentage. The genotype NLR 3090 of cluster V had highest kernel length after cooking and protein percentage. Parents having many desirable traits might be considered as good parents to create further variability for the traits under studies.

Consideration of relative contribution of individual traits to the genetic divergence revealed that protein percentage (43.27) showed maximum contribution towards genetic divergence followed by alkali digestion value (27.49), amylose content (9.94), grain length, (5.26), grain width (5.26), water uptake (2.92), kernel breadth (1.17), test weight (1.17), days to 50 % flowering (1.17), filled grains per panicle (0.58), kernel length after cooking (0.58), panicle length (0.58) and tillers per plant (0.58).

Table 3. Mean values of five clusters by Tocher's method for 19 medium duration genotypes of rice (*Oryza sativa* L.).

	Plant height (cm)	Total tillers / Plant	EBT/ Plant	Panicle length (cm)	Days to 50% flowering	Filled grains/ Panicle	Grain length (mm)	Grain width (mm)	Flag leaf length (cm)	Test weight (g)
I Cluster	88.754	14.867	9.842	22.271	100.542	221.221	7.988	2.952	25.438	20.340
II Cluster	99.039	16.800	11.661	23.156	102.500	202.533	8.241	2.690	29.839	20.618
III Cluster	**114.400**	**17.744**	**14.000**	**24.911**	**105.111**	227.133	7.643	**3.030**	**33.044**	**20.733**
IV Cluster	**82.633**	**10.767**	**8.240**	**20.733**	**97.000**	**285.233**	**8.320**	2.103	27.633	19.413
V Cluster	107.033	11.033	9.840	22.767	100.333	**181.467**	**7.243**	2.103	24.100	**17.527**

	Grain yield/ plant (g)	Kernel length (mm)	Kernel breadth (mm)	KLAC (mm)	Water uptake (ml)	Alkali digestion value	Amylose Content	Protein %	Hulling %	Milling %
I Cluster	24.700	5.795	**1.983**	10.070	270.208	1.667	24.069	6.761	77.820	68.318
II Cluster	23.678	5.913	2.165	10.066	278.333	4.439	24.409	**5.292**	76.726	67.481
III Cluster	30.211	**5.792**	**2.231**	9.823	277.778	2.456	**22.413**	8.519	77.663	**66.558**
IV Cluster	**32.333**	**5.950**	2.100	**9.587**	**285.000**	**4.767**	**26.203**	8.020	**86.953**	**73.830**
V Cluster	**21.067**	5.927	2.153	**10.673**	**265.000**	**1.267**	25.913	**8.853**	77.187	68.387

Bold values are minimum and maximum values

Table 4. Contribution of different characters towards genetic divergence in 19 medium duration genotypes of rice (*Oryza sativa* L.).

	Source	Times Ranked 1st	Contribution %
1	Plant height (cm)	0	0.00
2	Total number of tillers per plant	1	0.58
3	Ear bearing tillers per plant	0	0.00
4	Panicle length (cm)	1	0.58
5	Days to 50% flowering	2	1.17
6	Filled grains per panicle	1	0.58
7	Grain length (mm)	9	5.26
8	Grain width (mm)	9	5.26
9	Flag leaf length (cm)	0	0.00
10	Test weight (g)	2	1.17
11	Grain yield per plant (g)	0	0.00
12	Kernel length (mm)	0	0.00
13	Kernel breadth (mm)	2	1.17
14	Kernel length after cooking (mm)	1	0.58
15	Water uptake (ml)	5	2.92
16	Alkali digestion value	47	27.49
17	Amylose content	17	9.94
18	Protein percentage	74	43.27
19	Hulling percentage	0	0.00
20	Milling percentage	0	0.00

Crossing among divergent parents having desirable traits is most likely to produce better hybrids and desirable recombinants. The greater distance between the clusters (II, III and V) indicates higher genetic diversity between them.

Based on the inter-cluster distance and high per se for other desirable attributes associated, the parents as indicate in the discussion are expected to give promising segregants for grain yield and quality in segregating generations.

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