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Genetic Diversity Studies on Quality Characters in Long Duration Genotypes of Rice (*Oryza Sativa L.*)

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ABSTRACT

Thirty four long duration genotypes were evaluated for physico-chemical and cooking characters to study the diversity pattern among the genotypes. The genotypes were grouped into seven clusters. Maximum ten genotypes were grouped in clusters I and III followed by six in cluster IV. The clusters V, VI and VII are represented by single genotype indicating high degree of heterogeneity among the genotypes. The maximum inter cluster distance was observed between clusters II and VII followed by clusters IV and VII and maximum intra cluster distance was observed in cluster IV followed by cluster III, II and I respectively. Percentage of contribution towards total divergence is highest in protein percentage (50.80) followed by alkali digestion value (32.44), amylose content (6.60), kernel length after cooking (6.42), water uptake (0.89), hulling percentage (0.36), kernel length (0.0) and milling percentage (0.0).

Key words : Genetic divergence, Quality characters, Rice.

Rice (*Oryza sativa* L.) is the staple food of India and occupies 44.6 million ha. But due to regular flood, cyclone and drought, the production is very low. In order to meet the food requirement of the increasing population, development of high yielding varieties is essential. Breeders mostly focus on high yield. The consumers prefer quality rice. Hence breeders should give due importance to the quality traits in their breeding programme besides yield.

Genetic divergence is an efficient tool for an efficient choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Because cross between genetically divergent parents are likely to produce high heterotic effects. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekananda and Subramaniam, 1993). Keeping this in view 34 genotypes are analyzed for quality characters to study the clustering pattern so as to be utilized in the hybridization programme.

MATERIAL AND METHODS

The material comprised of 34 long 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

The analysis of variance showed significant differences among the genotypes for 9 quality characters and indicated very high variability. Based on D values, 34 genotypes of rice were grouped into 7 clusters (Table 1). Maximum 10 genotypes were grouped in clusters I and III. Cluster IV is the second largest with 6 genotypes and cluster II (5 genotypes).The clusters V, VI and VII are

Table 1. Clustering pattern of 34 long duration genotypes of rice by Tocher's method

Cluster No.	No. of genotypes	Genotypes
I	10	NLR 20136, BPT 2411, BPT 2449, BPT 2481,RDR 34, BPT 2425, BPT 2455, BPT 2450, NLR 20146, BPT 2475
II	5	BPT 2478, BPT 2495, BPT 2441, BPT 1768,BPT 2482
III	10	BPT 2412, BPT 2480, BPT 2466, MTU 1064, NLR 20131, MTU 7029, MTU II 236-12-1-1, RGL 7001, BPT 2479, MTU 1956-18-2-3-1
IV	6	MTU II 231-8-1-1-1, MTU 1769 16-2-5-1, BPT 2045, BPT 2445, BPT 2409, MTU II 225-9-1-1
V	1	MTU 1770-24-3-1-1-1
VI	1	BPT 3291
VII	1	RGL 7002

Table 2. Average intra- and inter cluster D^2 values among 7 clusters in 34 long duration genotypes of rice.

1	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster
I Cluster	**141.504**	556.761	379.956	369.752	430.651	624.084	675.080
II Cluster		**199.680**	666.081	473.952	1162.646	317.162	1530.228
III Cluster			**255.247**	829.681	392.416	542.358	512.218
IV Cluster				**259.704**	1037.210	814.115	1505.682
V Cluster					**0.000**	845.185	565.470
VI Cluster						**0.000**	1333.018
VII Cluster							**0.000**

Bold and diagonal values indicate intra cluster distances.

represented by single genotypes respectively indicating high degree of heterogeneity. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related. This suggests that there are forces other than geographical separation such as natural or artificial selection, exchange of breeding material, genetic drift and environmental variation. The results were in accordance with the findings of (Kandamoorthy and Govindarasu, 2005, Ravindrababu *et al*., 2006, Ramesh Chandra *et al*., 2007, Arun Sharma *et al.,* 2008 and Dushyantha Kumar, 2008).

The intra and inter cluster D^2 values (Table 2) revealed that inter cluster D^2 values were greater than intra-cluster D^2 values. The maximum inter-cluster D^2 values was observed between clusters II and VII (1530.228) followed by clusters IV and VII (1505.682). Based on these studies crosses may be made between genotypes of cluster II (BPT 2478, BPT 2495, BPT 2441, BPT 1768 and BPT 2482) and VII (RGL 7002) followed by cluster IV(MTU II

Table 3. Mean values of seven clusters by Tocher's method for 34 long duration genotypes of rice.

	Kernel length (mm)	Kernel breadth (mm)	KLAC (mm)	Water uptake (ml)	Alkali digestion value	Amylose Content	Protein %	Hulling %	Milling %
I Cluster	5.683	1.967	9.152	282.500	1.817	24.463	6.615	78.021	68.442
II Cluster	5.252	2.043	9.227	277.333	5.893	24.586	5.663	78.469	68.919
III Cluster	**5.734**	1.895	10.007	289.833	4.197	23.907	8.056	78.060	68.109
IV Cluster	5.457	1.931	9.973	281.944	1.894	24.474	**4.876**	79.084	69.444
V Cluster	5.257	**1.807**	**12.050**	**303.333**	1.833	22.687	8.383	**77.737**	68.657
VI Cluster	5.573	**2.057**	8.920	**245.000**	**6.633**	**21.647**	6.640	**79.313**	**66.397**
VII Cluster	**4.880**	1.903	**7.740**	301.667	**1.500**	**25.237**	**9.737**	78.320	**69.480**

Bold and diagonal values indicate intra cluster distances.

Table 4. Contribution of different characters towards genetic divergence in 34 long duration genotypes of rice.

Source	Times Ranked 1st	Contribution %
Kernel length (mm)	0	0.00
Kernel breadth (mm)	1	0.18
Kernel length after cooking (mm)	36	6.42
Water uptake (ml)	5	0.89
Alkali digestion value	182	32.44
Amylose content	37	6.60
Protein percentage	285	50.80
Hulling percentage	2	0.36
Milling percentage	0	0.00

231-8-1-1-1,MTU 1769 16-2-5-1,BPT 2045, BPT 2445,BPT 2409 and MTU II225-9-1-1) and cluster VII (RGL 7002) to obtain new desirable recombinants in rice. Maximum intra-cluster D^2 value was observed in cluster IV followed by cluster III, cluster II and cluster I. The high intra- cluster distance in cluster IV indicates the presence of wide genetic diversity among the genotypes *viz.*, MTU II 231-8-1-1-1, MTU 1769 16-2-5-1, BPT 2045, BPT 2445, BPT 2409 and MTU II 225-9-1-1. For a successful breeding programme selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. Similar results were reported by (Deepa Sankar *et al*., 2005, Sobita Devi *et al*., 2006, Sandhya Kishore *et al*., 2007, Ramesh Chandra *et al*., 2007 and Parimalan *et al*., 2008).

The cluster mean values for 9 characters are presented in Table 3. kernel length had a range of 4.880 for cluster VII to 5.734 for cluster III; kernel breadth had a range of 1.807 for cluster V to 2.057 for cluster VI; kernel length after cooking had a range of 7.740 for cluster VII to 12.050 for cluster V; water uptake varied from 245.00 for cluster VI to 303.333 for cluster V; alkali digestion value ranged from 1.500 for cluster VII to 6.633 for cluster VI; amylose content varied from 21.647 for cluster VI to 25.237 for cluster VII; protein percentage ranged from 4.876 for cluster IV to 9.737 for cluster VII; hulling percentage ranged from 77.737 for cluster V to 79.313 for cluster VI and milling percentage varied from 66.39 for cluster VI to 69.48 for cluster VII. The clusters V, VI and VII had high mean values for these 9 quality characters.

Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

The per cent contribution towards genetic divergence by all the 20 characters is presented in Table 4. The trait protein percentage (50.80) showed maximum contribution towards genetic divergence followed by alkali digestion value (32.44), amylose content (6.60), kernel length after cooking (6.42), water uptake (0.89), hulling percentage (0.36), kernel breadth (0.18), kernel length (0.0) and milling percentage (0.0). Hence protein percentage, alkali digestion value, amylose content and kernel length after cooking contributed 96.26 percent towards total divergence. Therefore hence these characters should be given importance during hybridization and selection of segregating populations.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated from the study that hybridization between the genotypes of clusters II and VII will be beneficial. The genotypes of these clusters may be used as parents selected for future breeding programme.

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