



Assessment of Genetic Diversity for Yield Components and Quality Parameters in Rice (*Oryza sativa*.L.)

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ABSTRACT

Genetic divergence using Mahalanobis D^2 statistic was worked out in 70 genotypes of rice. The genotypes were grouped into five clusters using Tocher's method. Cluster I had the largest number of genotypes while the remaining clusters possessed single genotype only. Greater genetic divergence was found between cluster III and cluster V followed by cluster IV and cluster V and cluster III and cluster V, thus suggesting that the genotypes of these clusters may be exploited to explore the fullest range of variability for the character (s) and to realize good recombinant lines.

Key words : Genetic diversity, Yield.

Rice is the unique grain that is nearly entirely used as human food, unlike other cereals, which are also used extensively as feed (Swaminathan, 1999). Therefore, evaluation of rice germplasm is an important step for the fulfillment of human demand and options. Quality of rice may be considered from the view point of size, shape and appearance of grain, milling quality and cooking properties (Dela Cruz and Khush, 2000). Knowledge on genetic divergence of the germplasm lines is of immense important for the breeders in hybridization programme whereas, the diversity among the parents is of utmost importance, as the crosses between the parents with maximum genetic divergence would more likely yield desirable recombinants in the segregating generations. D^2 statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes. An attempt was made in the present investigation to study the genetic divergence, variability and association of various yield components and quality parameters on grain yield in seventy germplasm lines of rice.

MATERIAL AND METHODS

Seventy genotypes collected from various research stations were evaluated in a randomized block design with two replications during kharif 2010 at Rice Research Unit, Bapatla. Each

genotype was raised in two rows of five metre length with a spacing of 20x15cm between and within the rows, respectively. Observations were recorded on five randomly selected plants from each replication for 6 yield components *viz.*, days to 50% flowering, plant height, ear bearing tillers, panicle length, test weight and grain yield/plant. The quality parameters *viz.*, head rice recovery, kernel length, kernel breadth, L/B ratio, kernel length after cooking, elongation ratio, water uptake, volume expansion ratio and amylose content were estimated replication wise on plot basis as per the standard procedures delineated by Murthy and Govindaswamy (1967), Juliano (1971) and Little *et al* (1958). The mean values were utilized for the analysis of genetic divergence using Mahalanobis D^2 statistics. Tocher's method was employed for grouping the genotypes into different clusters as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the existence of genetic variability. Based on the relative magnitude of D^2 values, all the genotypes were grouped into five clusters (Table 1). Majority of the genotypes were grouped in cluster I while the rest were mono genotypic clusters. The pattern of distribution of

Table 1. Distribution of rice genotypes in different clusters.

S.No.	Cluster No	Name of the genotypes
1	1	BPT 5204, MTU1010, JGL-3844, NLR 34449, MTU 1081, MTU 1075, JGL 13595, MTU 1001, MTU 1031, MTU 1032, MTU 1038, MTU 5182, MTU 5249, MTU 5293, MTU 3626, MTU 4870, MTU 1061, MTU 1064, MTU 1071, MTU 1078, MTU 1098, MTU 2077, MTU 2067, MTU 2716, MTU 7029, BPT 3291, BPT 1768, BPT 2231, BPT 1235, BPT 2295, JGL 1798, JGL 384, JGL 3855, WGL 48684, Kavya, WGL44645, RNR 880, RNR 23064, RNR 2465, M7, Co 10754, Tellahamsa, IR 64, Betagamlet, BM 71, NLR 145, NLR 3041, NLR 3042, RGL 22600, RGL 2537, RGL 2538, ADT 43, PR 103, PR 106, RDR 73905, PLA 1100, TN1, Mahsuri, IR64, IR8, NLR 28523, NLR 33892, JGL11727, PLA 838, Jaya, RNR 883
2	2	CSR4
3	3	Somasila
4	4	CRMR1523
5	5	Chittimutyalu

genotypes indicated that majority of genotypes under study had narrow genetic diversity among them. The similarity in the base population from which they had been evolved might be the cause of genetic uniformity. However, the unidirectional selection potential for one particular trait or a group of linked traits in several places may produce similar phenotypes which can be aggregated into one cluster irrespective of their geographic origin. Likewise, it is also true that selection produce genetically diverse genotypes of same pedigree. This indicates that the pedigree record may not necessarily be an indicator of genetic divergence. This is in conformity with the earlier findings of Bhadru *et al.* (2012).

Cluster means showed appreciable differences for all the fifteen characters studied (Table 2). Highest mean values for ear bearing tillers (10.59), head rice recovery (60.09) and grain yield/plant (18.23) was recorded in cluster I while maximum panicle length was observed in cluster V. The lowest value for days to 50% flowering (69.0) and plant height (82.0) was observed in cluster III which can be utilized as parents for incorporating earliness and dwarf plant stature. Maximum head rice recovery was recorded in cluster I (60.09) followed by cluster III (59.85). Genotypes possessing longer kernel length (above 6.0mm) were present in three clusters *viz.*, cluster IV followed by III and II. Maximum kernel length was recorded in cluster IV while minimum kernel

length was observed in cluster V. Genotypes in cluster V possessed minimum kernel breadth while the cluster IV recorded maximum kernel breadth. Among the seventy genotypes studied, long slender grain types were grouped in cluster III, where as cluster II and IV possess long bold grain types. All medium slender grain types were observed in cluster I, while cluster V possessed short bold grain types. Maximum kernel length after cooking and elongation ratio were observed in cluster III while the mean value for water uptake ranged from 90.0 (cluster II) to 255.0 (cluster IV). Maximum grain yield per plant was observed in cluster I followed by cluster III and II.

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared in first rank and its respective percent of contribution towards genetic divergence was presented in table 3. Percentage contribution of each character is calculated on the basis of occurrence of these ranks. With 34.29 per cent contribution days to 50% flowering and with 24.43 per cent contribution test weight followed by grain yield (15.82%) were the major force of discrimination among the genotypes tested for the characters studied. The observed results find support from studies conducted by Nibedita *et al* (2010), Karthikeyan (2002) and Senapati and Sarkar

Table 2. Cluster means of genotypes for various yield components and quality parameters in 70 genotypes of rice.

Cluster	DFE	PH	EBT	PL	TW	HRR	KL	KB	L/B	KLAC	ER	WU	VER	AC	GY
I	107.51	95.72	10.59	22.80	19.52	60.09	5.61	1.99	2.85	8.89	1.62	200.23	4.20	24.09	18.23
II	94.5	125.50	9.99	22.75	25.20	52.40	6.26	2.25	2.80	8.70	1.40	90.0	3.40	25.05	11.06
III	69.0	82.0	6.75	22.05	22.75	59.85	6.55	2.06	3.19	11.30	1.82	187.50	4.80	23.17	15.70
IV	126.5	108.0	8.16	23.55	32.29	50.70	6.73	2.66	2.54	9.14	1.35	255.00	4.25	25.95	8.96
V	101.0	148.50	6.05	24.40	10.98	51.05	3.72	1.87	1.99	5.65	1.53	200.00	4.28	22.40	10.85

(2005) who reported maximum contribution of days to 50% flowering, test weight and grain yield per plant, respectively for genetic divergence in rice.

The magnitude of intra-cluster distance measures the extent of genetic diversity between the genotypes of same cluster while the inter-cluster distance measures the genetic distance between two clusters. The intra cluster distance was maximum in cluster I (323.83) (Table 4). The maximum inter cluster distance of 2255.24 was observed between cluster III and cluster V followed by cluster IV and cluster V (1818.08) and cluster III and cluster V (1606.57).

Considering the importance of genetic distance, relative contribution of characters towards total divergence and yield potential of genotypes, the present investigation suggests that parental lines selected from cluster V (Chittimutyalu) for slender grains, Cluster I (BPT 2270, BPT 2231, NLR 145, MTU 1061 and MTU 1064) for grain yield per plant and cluster III (Somasila) for earliness and dwarf plant stature could be used in the hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations.

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Table 3. Contribution of different characters towards genetic divergence in 70 genotypes of rice.

Character	Times ranked first	Percent contribution towards divergence
Days to 50% flowering	828	34.29
Plant height	304	12.59
Ear bearing tillers	2	0.08
Panicle length	2	0.08
Test weight	590	24.43
Head Rice Recovery	17	0.70
Kernel length	101	4.18
Kernel breadth	29	1.20
Length/breadth ratio	3	0.12
Kernel length after cooking	51	2.11
Elongation ratio	2	0.08
Water uptake	85	3.52
Volume expansion ratio	14	0.58
Amylose content	5	0.21
Grain yield/plant	382	15.82

Table 4. Average intra and inter cluster distances among five clusters of rice in 70 genotypes.

Cluster	I	II	III	IV	V
I	323.83	815.42	847.75	872.81	1376.21
II		0.00	889.47	715.88	786.26
III			0.00	1606.57	2255.24
IV				0.00	1818.08
V					0.00

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