

Genetic divergence studies in rice genotypes

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ABSTRACT

Genetic divergence was assessed among 40 rice genotypes using Mahalanobis's D^2 analysis. The 40 rice genotypes were grouped into five clusters. Cluster I was found to be the largest comprising of 25 genotypes followed by cluster III having 8 genotypes and cluster V included 5 genotypes. Cluster II and IV had single genotype each. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters viz. leaf area at 90 DAS, Number of grains panicle⁻¹ and days to 50% flowering contributed maximum towards genetic divergence among the genotypes.

Keywords: rice, yield components, physiological character, quality characters

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. The nature and magnitude of genetic divergence would help the plant breeder in choosing right choice of parents for crossing programme in order to obtain higher amount of heterotic expression in F_1 s and broad spectrum of variability in subsequent segregating generations (Vivekanandan and Subramanian, 1993). The present investigation was undertaken for estimating genetic divergence of selected genotypes as it permits precise comparison among all possible pairs of genotypes in any given group before effecting actual crosses.

MATERIALS AND METHODS

The experimental material consisted of 40 diverse rice genotypes and were grown in a randomised block design with three replications at the wetland farm of S.V. Agricultural College, Tirupati during dry season 2007-08. Twenty one days old seedlings were transplanted with a spacing of 20 cm x 15 cm and each genotype was grown in three rows of 3m length. Appropriate management and cultural practices were followed to raise a good crop. Observations on 23 important yield components, quality and physiological characters were recorded based on five randomly selected plants in each genotype in each replication. The genetic diversity between the genotypes was worked out using

Mahalanobis's D^2 (1936) statistics and grouping of genotypes into clusters was done using Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters. All the 40 rice genotypes were grouped into 5 clusters (Table 1). Cluster I was the largest among all the clusters which included 25 genotypes followed by cluster III comprised of 8 genotypes and cluster IV with 5 genotypes. Cluster II and IV had single genotype each. The clustering pattern showed that genotypes collected from the same geographic origin were found to be distributed in different clusters. Similar findings of non-correspondence of genetic divergence with geographic diversity were reported earlier in rice by Vivekanandan and Subramanian (1993), Rahaman *et al.* (1997) and Shanmugasundaram *et al.* (2000). Murthy and Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances.

The intra-cluster average D^2 values ranged from 0.00-22.66 (Table 2). The highest intra-cluster distance (22.66) was observed in the cluster V, indicating wide genetic variation among the genotypes included in the cluster. It is reported that genotypes would produce

Table 1. Clustering pattern of 40 rice genotypes

Cluster No.	Number of genotypes	Name of the genotypes
I	25	NLR 33654, BPT 1235, Salivahana, MTU 1006, Dular, IET 8585, BPT 5204, NLR 145, NLR 33356, MTU 1010, NLR 33358, NLR 33636, NLR 34449, NLR 33057, NLR 30491, Vasundhara, MTU 1071, NDLR 8, N 22, JGL 1798, NLR 33671, Sasyashree, Mahsuri, ARC 10550, NLR34242
II	1	MTU 9993
III	8	TKM-6, NLR 34303, ADT 43, JGL 384, ARC 6605, CRMR 1523, TN-1, Heera
IV	1	ADT 37
V	5	MTU 4870, MTU 1001, Suduhonerwala, MO-1, PTB 33

more desirable breeding materials for achieving maximum genetic advance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines (Rahman *et al.*, 1997). Therefore, genotypes from cluster V should be given emphasis while selection of parents for hybridization programme since most of the elite breeding cultivars were included in this cluster.

The highest inter-cluster distance was observed between the cluster IV and V (4037.33) indicating high divergence of genotypes included in these two clusters. The lowest inter-cluster distance was observed between the cluster II and III (286.22) indicating that genotypes included in them were closely related (Table 2). According to Rahaman *et al.*, (1997), crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. Thus, selection of genotypes from these clusters for a crossing programme will produce desirable transgressive segregants.

Table 2. Inter-cluster and Intra-cluster (diagonal) average of D² and D values (parenthesis) of 40 rice genotypes (Tocher's method)

Cluster Number	I	II	III	IV	V
I	371.71 (19.28)	661.51 (25.72)	786.36 (28.06)	576.48 (24.01)	2974.61 (54.54)
II		0.00 (0.00)	286.62 (16.93)	1296.72 (36.01)	1438.68 (37.93)
III			480.04 (21.91)	1354.97 (36.81)	1809.65 (42.54)
IV				0.00 (0.00)	4037.33 (63.54)
V					513.47 (22.66)

The genotypes of cluster II had recorded the highest grain yield plant⁻¹ while the genotypes of cluster V recorded the lowest grain yield (Table 3a and 3b). Further, the genotypes of cluster II also recorded the longest panicle length, high 1000-grain weight, more dry matter plant⁻¹ at 60 DAS, high leaf area at 60 DAS, leaf area index at 60 DAS and 90 DAS, high CGR, lengthy kernels and highest kernel elongation ratio. The genotypes of cluster III had more number of productive tillers plant⁻¹ and were earlier to flower. Cluster IV included the genotypes having the highest number of grains panicle⁻¹, high NAR value at 60-90 DAS, kernel L/B ratio and harvest index. Relatively taller genotypes were included in cluster V and also they had high leaf area at 90 DAS and dry matter plant⁻¹ at 90 DAS. The promising genotypes with high mean values for above traits from divergent clusters are selected as parents for hybridization programme to develop high yielding rice varieties.

Among all the characters, leaf area at 90 DAS contributed the maximum towards genetic divergence (59.10%) followed by number of grains panicle⁻¹ (15.13%) and days to 50% flowering (6.92%). The maximum contribution of days to 50% flowering and number of grains panicle⁻¹ to genetic divergence in rice were reported earlier by Gahalain (2006) which corroborated the results of the present study.

The greater the distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the clusters having maximum inter-cluster distance can be selected to yield superior segregates (Mishra *et al.*, 2003; Chaturvedi and Maurya, 2005). In the present study, genotypes from cluster IV, V and I can be selected for crossing programme to get desirable transgressive segregants.

Table 3a. Cluster means and percent contribution of twenty three characters for divergence in 40 genotypes of rice

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers plant ⁻¹	Panicle length (cm)	1000-Grain Weight (g)	No. of Grains panicle ⁻¹	Grain yield plant ⁻¹ (g)	LA at 60 DAS (cm ²)	LA at 90 DAS (cm ²)	SCMR before panicle initiation	SCMR after panicle initiation
I	95.80	129.04	98.02	1178	22.62	21.07	142.76	28.72	413.63	556.23	40.47	35.38
II	95.67	128.67	105.65	12.73	24.24	27.6	125.53	35.37	599.85	788.12	43.87	39.63
III	84.00	120.04	105.75	13.00	23.22	21.06	123.31	26.33	590.18	762.52	41.12	36.33
IV	87.33	114.00	89.03	10.20	20.79	16.19	199.93	26.93	423.53	460.52	38.93	40.57
V	101.00	134.20	120.40	9.54	23.52	24.69	133.32	25.36	421.11	1130.51	39.56	33.55
C.V(%)	6.92	0.77	2.82	0.00	0.00	0.26	15.13	0.00	6.41	59.10	0.00	0.00

LA – Leaf Area, DAS – Days After Sowing, SCMR - SPAD Chlorophyll Meter Reading

Table 3b. Cluster means and percent contribution of twenty three characters for divergence in 40 genotypes of rice

Cluster No.	DMP at 60 DAS (g)	DMP at 90 DAS (g)	LAI at 60 DAS	LAI at 90 DAS	CGR at 60-90 DAS (g m ⁻² day ⁻¹)	NAR at 60-90 DAS (gdm ⁻² day ⁻¹)	Harvest index (%)	Kernel Length (mm)	Kernel breadth (mm)	Kernel L/B Ratio	Kernel Elongation Ratio
I	6.94	21.67	1.99	2.81	22.6	0.04	48.54	6.05	2.19	2.77	1.45
II	10.45	34.08	2.83	3.48	34.6	0.05	50.86	6.29	2.34	2.70	1.36
III	8.15	25.08	2.64	3.07	24.71	0.04	45.64	5.63	2.29	2.44	1.50
IV	9.78	25.51	2.09	2.43	26.61	0.06	51.46	5.19	2.48	2.02	1.39
V	7.85	35.66	1.87	2.80	42.4	0.06	45.20	5.78	2.48	2.35	1.46
C.V. (%)	0.00	0.77	0.00	1.03	0.26	0.64	0.77	0.51	4.10	0.51	0.00

DMP – Dry Matter Plant⁻¹, LAI – Leaf Area Index, CGR – Crop Growth Rate, NAR – Net Assimilation Rate

The genotypes from cluster V i.e. PTB 33, MTU 4870 having desired characters like leaf area at 60 DAS and 90 DAS, dry matter plant⁻¹ and crop growth rate; NLR 33654 from cluster I having high value for grain yield and dwarf plant type and Heera from cluster III having earliest days to 50% flowering and CRMR 1523 having high values for panicle length and 1000 grain weight can be selected as ultimate parents for inclusion in the hybridization programme. Thus, the crosses resulting from these divergent parents are expected to throw wide spectrum of variability for yield and its component characters in the segregating generations.

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