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Clustering of Rice Genotypes - *A Multivariate Approach*

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ABSTRACT

An important step in plant breeding programs is identification of parents that are genetically distant from each other, to find crossing combinations with better prospects of hybrid vigor. The potential of identifying genetically distant parents depends on genetic diversity of population. 60 Rice genotypes from diverse origins have been employed to study genetic variation in order to identify the most effective components of grain yield. Using cluster analysis, the genotypes were grouped into 8 clusters of which clusters II was the largest cluster consisting of 21 genotypes while cluster III, IV, VII and VIII are the smallest clusters with only a single genotype each. The maximum intra cluster distance (D = 371.74) was found in cluster VI consisting of 8 genotypes NLR 33358, ADT 45, ADT 37, JGL 1118, IR 10F221, NLR 3367, IR 64197 and ADT 43. From the inter cluster D^2 values of eight clusters, it can be seen that the highest divergence occurred between cluster V and cluster VI (1651.37) While the minimum inter cluster distance was noticed between cluster IV and cluster VII (94.06). Out of 17 characters studied the maximum contribution (79.66 %) towards total divergence is by 5 characters only. They are days to maturity, test weight, flag leaf width, flag leaf length, Days to 50% flowering. These characters should be taken into consideration while selecting parents for hybridization.

Key words: *Genotypes, Genetic diversity, Cluster analysis, Mahalanobis D^2*

Rice **(***Oryza sativa* L.) is the most important cereal food crop in the world providing food to over 75 % of Asian population and more than three billion of world population which represents 50 to 80 % of their daily calorie intake (Khush, 2005) and 55% of the protein intake in their average daily diet and aptly describes the slogan "Rice is life". Next to China, India is the second largest producer and consumer of rice. For meeting the dietary requirements of increasing population, genetic improvement of rice with higher yield, good grain quality, resistance to biotic and abiotic stresses is the most logical and promising approach. Genetic improvement mainly depends upon inclusion of genetically diverse parents having wider variability for different yield and quality characters in hybridization program. The more diverse the parents, the higher are the chances of obtaining more amounts of heterotic expression in F_1 and superior recombinants in the segregating generations. A lack of diversity in germplasm limits long-term progress in plant breeding. The level of genetic diversity that characterizes commercially important crops is a matter of considerable concern, as it is generally agreed that access to genetic diversity has been and remains important in maintaining and increasing agricultural productivity (Ahmadikhah, 2006). Therefore, the genetic diversity is the basis of plant breeding. Plant breeders use the present diversity in plant populations and varieties to develop new varieties or to transmit the desirable traits into undesirable varieties (De et al., 1992). Significant emphasis is being paid to comprehensive analysis of genetic diversity in numerous field crops for long-term success of breeding program and maximum exploitation of the genetic resources (Belaj *et al.,* 2002).

MATERIAL AND METHODS

A secondary data which is relevant to the study was collected from Agricultural Research Station(ARS), Nellore, Andhra Pradesh, at which experiment was carried out on 60 rice genotypes and the data was collected on yield and yield attributes viz., 50 % flowering, days to maturity, Plant height, Panicle length, flag leaf length, flag leaf width, flag leaf area, productive tillers, filled grains/panicle, ill filled grains/panicle, SCMR (SPAD Chlorophyll meter reading), plant yield, Test weight, Grain length, Grain width, grain l/b ratio and Harvest index, during early *kharif*, 2016.

The present investigation aimed to assess the nature and magnitude of genetic divergence present in the 60 rice genotypes and to select suitable diverse genotypes as parents for further utilization in grain yield improvement programs. Genetic diversity analysis was done following D^2 statistics proposed by Mahalanobis (1936). The varieties were classified into a number of clusters by Toucher's method as described by Rao (1952). Statistical analysis for the above characters were done by using INDOSTAT software.

RESULTS AND DISCUSSION

ANOVA showed that the studied genotypes had significantly differences in all traits. The between-group variation tended to exceed the within-group variation. Therefore, subsequent analyses were conducted. The genotypes were grouped into 8 clusters

Table 1. Clustering pattern of 60 Genotypes

Cluster No.	No. of genotypes	Name of genotype (S)
I	16	NLR 33359, IR 11C214, IR 11C202, IR 11C221, IR 11C219, NLR 3414, MTU 1010, IR 10C172, NLR 3242, NLR 3413, IR 11C186, NLR 3407, NLR 3411, HH25-DT20-DT2-DT1, NLR 4002, NLR 3296
II	21	NLR 3251, LR 3369, NLR 3302, NLR 3353, NLR 3366, NLR 3415, NLR 3354, NLR 34449, NLR 3417, NLR 3410, NLR 3346, MDT 6, NLR 3217, NLR 34242, NLR 40065, NLR 30491, NLR 33671, NLR 3412, WHITE PONNI, NLR 3408, NLR 3042
III	1	IR 64
IV	1	IR 11C228
V	11	NLR 40058, JGL 1798, NLR 3350, NLR 34303, MDT 10, NLR 40024, IR 62, IR 109A235, BG 367-2, NLR 3241, NLR 33057
VI	8	NLR 33358, ADT 45, ADT 37, JGL 1118, IR 10F221, NLR 3367, IR 64197, ADT 43
VII	1	IR 11C208
VIII	1	TN 1

Table 2. Average intra and inter-cluster distances (D^2 values) among eight clusters of 60 rice genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	96.88	166.04	169.85	135.10	469.09	645.09	233.98	667.81
II	166.04	111.58	321.74	271.79	546.60	571.31	446.76	596.93
III	169.85	321.74	0.00	279.38	221.02	1155.84	250.83	635.57
IV	135.10	271.79	279.38	0.00	650.01	569.48	94.06	806.02
V	469.09	546.60	221.02	650.01	209.92	1651.37	556.47	625.24
VI	645.09	571.31	1155.84	569.48	1651.37	371.74	934.58	1491.99
VII	233.98	446.76	250.83	94.06	556.47	934.58	0.00	933.07
VIII	667.81	596.93	635.57	806.02	625.24	1491.99	933.07	0.00

Note: Diagonal values are intra-cluster distances. Off-diagonal values are inter-cluster distances

Table 4. Contribution of different characters towards genetic divergence

S.No.	Source	Contribution %	Times Ranked 1st
1	Days to 50% Flowering	6.10	108
2	Days to Maturity	35.99	637
3	Plant Height cm	1.69	30
4	Panicle Length cm	2.66	47
5	Flag Leaf Length cm	6.72	119
6	Flag Leaf Width cm	10.68	189
7	Flag Leaf Area cm:	0.51	9
8	Producctive Tillers/ Plant	0.4	7
9	Filled Grains/ Panicle	0.28	5
10	Ill Filled Grains/ Panicle	1.58	28
11	SCMR	1.19	21
12	Plant Yield	5.42	96
13	Test Weight	20.17	357
14	Grain Length	1.19	21
15	Grain Width	3.56	63
16	Grain L/B Ratio	0.06	1
17	harvest Index	1.81	32

Table 3. Mean values of eight clusters

ıster lo.	Days to 50 % Flowering	Days to Maturity	Plant Height cm	Panicle Length cm	Flag Leaf Length cm	Flag Leaf width cm	Flag Leaf Area cm	Productive Tillers/Plant	Filled Grains per Panicle	Ill Filled Grains/ Panicle	SCMR	Plant Yield	Test Weight	Grain Length	Grain Width	Grain L/B ratio	Harvest Index
I	94.13	122.25	103.64	23.43	25.75	1.43	27.78	6.34	100.07	21.77	36.93	12.96	20.82	8.83	2.28	3.88	51.49
II	94.29	122.38	97.16	22.25	28.84	1.52	32.97	6.58	114.30	23.50	35.45	12.76	17.10	7.91	2.25	3.51	47.27
II	98.00	127.00	103.45	22.60	24.30	1.43	25.97	7.72	69.02	16.87	37.48	12.51	22.64	9.94	2.32	4.30	57.45
V	92.50	120.50	118.95	26.45	27.11	1.29	26.25	7.36	84.77	30.46	33.02	13.03	21.30	8.87	2.51	3.55	42.43
V	102.64	131.64	104.11	23.11	29.34	1.54	33.89	6.02	114.01	22.93	36.39	13.33	20.08	8.51	2.33	3.65	49.19
VI	85.81	112.81	93.58	22.29	30.18	1.42	32.29	6.17	108.03	20.36	37.10	12.42	18.94	7.89	2.50	3.17	52.06
VII	94.50	121.50	133.25	24.25	29.69	1.28	28.51	5.50	92.56	32.80	35.18	11.22	21.75	8.79	2.53	3.47	39.98
III	89.00	138.00	97.90	25.25	33.02	1.53	37.77	4.86	147.53	30.60	38.12	12.61	17.15	7.29	2.46	2.90	46.97

based on D^2 value (Table 1, Fig1). Out of eight clusters obtained, cluster II was the largest with 21 genotype, followed by cluster I (16 genotypes), cluster V (11 genotypes), cluster VI (8 genotypes) while cluster III, IV, VII and VIII are the smallest clusters with only a single genotype each. The grouping of genotypes from same source into different clusters as observed in present study may be because of free exchange of breeding material among different regions. Singh *et al.* (2012).

The average intra and inter cluster D^2 values are presented in (Table 2, Fig 2). Intra cluster D^2 values ranged from 0.00 (Clusters III, IV, VII and VIII) to 371.74 (Cluster VI) followed by cluster V (209.92); cluster II (111.58); cluster I (96.88). The highest intra cluster distance (371.74) in cluster VI indicates wide genetic variation among the genotypes belonging to these clusters. The III, IV, VII and VIII clusters consisted of only one genotype each hence they lacked intra-cluster distance (0.00).

The inter cluster D^2 was maximum between clusters V and VI (1651.37) indicating that genotypes in V were far diverse from those of VI. Choosing of genotypes belonging to distant clusters was expected to execute maximum heterosis in crossing and to be used in hybridization program for obtaining a wide spectrum of variation among the segregants. The least distance was observed between cluster IV and VII (94.06) which indicated genotypes included in them were closely related (Table 2).

The cluster wise mean values for 17 characters were presented in Table 3. These are helpful to assess the superiority of clusters during the improvement of characters through hybridization programme. The cluster mean values showed a wide range of variation for majority of the characters undertaken in the present study. The diversity was also supported by the appreciable amount of variation among the cluster means for different characters. It is observed that cluster III as well as cluster VIII had recorded highest mean values for most of the characters. Cluster III exhibited highest mean values for number of productive tillers per plant, test weight, grain length, grain L/B ratio and harvest index and cluster VIII exhibited highest mean values for days to maturity, flag leaf length, flag leaf area, number of filled grains per panicle and SCMR, hence selection of this genotype for direct use may be beneficial. Whereas cluster V had highest mean values for Days to 50% flowering, flag leaf width and grain yield per plant. Cluster VII had highest mean values for plant height, ill filled grains per panicle and grain width. Cluster IV exhibited highest mean value for Panicle length. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

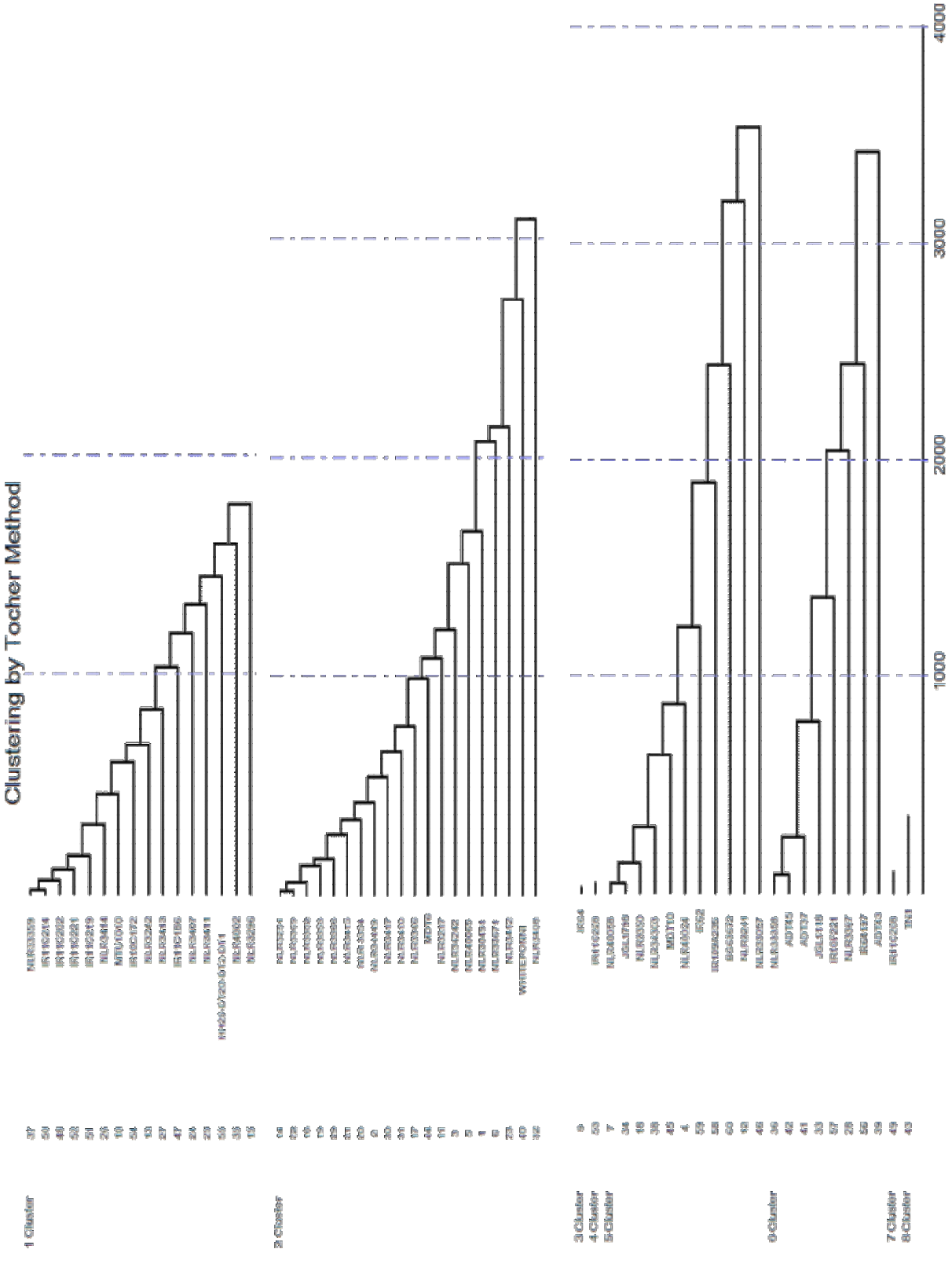

Fig 1a. Dendrogram showing relationship among 60 Ricegenotypes in eight clusters based on Mahalanobis' D^2 values

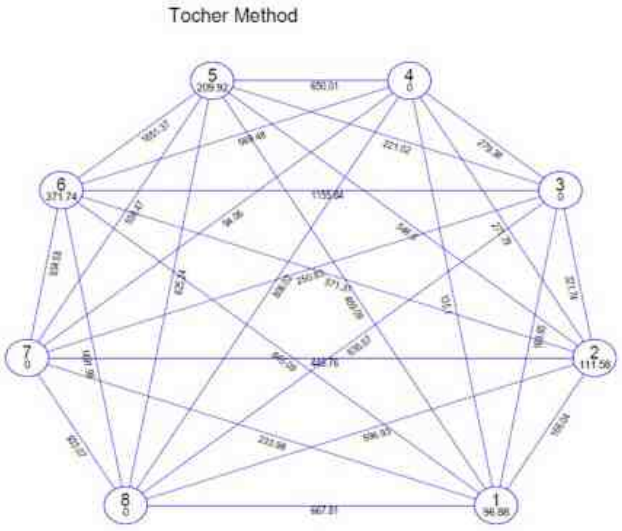

Fig 1b. Intra and inter-cluster distance of 60 Ricegenotypes in eight clusters based on Tocher's method

Contribution of different quality characters to total divergence is presented in Table 4. The trait days to maturity (35.99) showed maximum contribution towards genetic divergence followed by test weight (20.17), flag leaf width (10.68), flag leaf length (6.72), Days to 50% flowering (6.10), grain yield per plant (5.42), grain width (3.56), Panicle length (2.66), harvest index (1.81), plant height (1.69), ill filled grains per panicle (1.58), SCMR (1.19), grain length (1.19), flag leaf area (0.51), number productive tillers per plant (0.40), number of filled grains per panicle (0.28) and grain L/B ratio (0.06).

Out of 17 characters studied the maximum contribution (79.66 %) towards total divergence is by 5 characters only. They are days to maturity, test weight, flag leaf width, flag leaf length, Days to 50% flowering. These characters should be taken into consideration while selecting parents for hybridization. On the other hand low contributing characters towards total genetic diversity were grain L/B ratio, productive tiller per plant, number of filled grains per panicle and flag leaf area.

CONCLUSION

It is well known that crosses between divergent parents usually produce greater heterotic effect than between closely related ones. Considering the importance of genetic divergence, the present study indicated that parental lines selected from Cluster V (NLR 40058, JGL 1798, NLR 3350, NLR 34303, MDT 10, NLR 40024, IR 62, IR 109A235, BG 63672, NLR 3241 and NLR 33057) and Cluster VI (NLR 33358, ADT 45, ADT 37, JGL 1118, IR 10F221, NLR 3367, IR 64197 and ADT 43) followed by Cluster VI (NLR 33358, ADT 45, ADT 37, JGL 1118, IR 10F221, NLR 3367, IR 64197 and ADT 43) and Cluster VIII (TN 1) could be used in crossing programmes to achieve desired segregants.

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