GENETIC DIVERGENCE IN MID EARLY GROUP GENOTYPES OF RICE (*Oryza sativa* L.)

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ABSTRACT: Sixty four mid early group genotypes of rice were studied for genetic diversity for yield and yield contributing characters. Cluster analysis revealed sixty four genotypes were grouped into 11 clusters. The pattern of distribution of genotypes into different clusters was at random. Plant height contributed maximum towards genetic divergence followed by days to 50% flowering. The maximum inter cluster distance observed for between 4 and 7 (182.08) followed by cluster 1 and 4 (169.94). The genotypes from these clusters can be utilized in hybridization programme for improvement of rice.

Key words: Rice, D^2 statistics, Genetic diversity, Cluster distance.

INTRODUCTION

Genetic diversity among the parents is a pre-requisite for any breeding programme. Study on genetic diversity helps and improves the chances of selecting better sergeants for various traits. Precise information on the nature and degree of genetic divergence would help for different breeding programmes to exhibit higher amount of heterotic expression in segregating generations. Therefore the present investigation was under taken to study the nature and magnitude of genetic divergence among 64 mid early group genotypes of rice to identify diversified genotypes.

MATERIALS AND METHODS

Sixty four mid early group rice genotypes (duration of 120-130 days) having different geographical origins were grown during *kharif*, 2011 at Regional Agricultural Research Station, Warangal in two replications in simple lattice design with a spacing of 20 X 15 cm. Cultural practices were followed to raise the crop as per the standard recommendations. Five randomly selected plants were used for recording observations on six characters viz., days to 50% flowering, effective tillers per plant, Plant height, panicle length, test weight and yield which is converted into kg per ha. The data were subjected to analysis of variance and multivariate analysis using statistics (Malanobis, 1928). Based on genetic distances (D^2 values), the genotypes were grouped into clusters of genetically closer related groups following the Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variability among mid early group rice genotypes for all the characters studied. Sixty four genotypes were grouped into 11 clusters based on D^2 values. Clustering of 64 genotypes into different clusters by Tocher's method are presented in table 1, Average intra (Bold values) and inter cluster D^2 values of 11 clusters for 64 genotypes in rice are presented in table 2, Cluster mean values for different characters presented in table 3 and Contribution of different traits towards genetic divergence in 64 genotypes of rice presented in table 4 respectively. The maximum inter cluster distance observed for between 4 and 7 (182.08) followed by cluster 1 and 4 (169.94). The genotypes from these clusters can be utilized in hybridization programme for improvement of rice. Cluster VII had maximum intra cluster distance followed by clusters V, I and III. Maximum genotypes (28) were grouped under cluster I followed by clusters III (13) and V (10). The clustering pattern of different genotypes from different geographical regions into different clusters was random. This suggests that geographical diversity does not necessarily relate to genetic diversity.

Cluster IV had highest value for plant height; Cluster X had highest value for effective tillers per plant and test weight, Cluster II characterized by highest yield. The selection and choice of parents depends on contribution of characters towards genetic divergence (Nayak *et a*l., 2004). In the present study plant height (Eswara Reddy *et al*.,, 2014), days to 50% flowering followed by test weight had maximum contribution towards genetic divergence. The maximum inter cluster distance observed for between IV and VII (182.08) followed by cluster I and IV (169.94) suggesting that the genotypes in these clusters could be fully utilized in crossing programmes to explore the wide range of heterosis for improvement of rice.

`Table 1. Clustering of 64 genotypes into different clusters by Tocher's method.

Cluster No.	Number of genotypes	Name of the genotypes
I	28	KMP194, CRR648-B-838-1-B, PAU3832-44-6-4-5, KJT20-3-35-1-17, PAU3832-78-4-1-4, R 1527-947-1-78-1, CN1744-21-5-1-MLD12, JGL 18065, IR-64, CR2933-12-3-2-1, KAGR426, R1576-1700-1-560-1, R1582-814-1-258-1, KMP-128, NDR 9479, AAIR203, HKR 07-147, RNR 6368, UPRI 2009-9, MTU-1010, RNSK1093-3, CN1740-5-3-3-2-MLD9, SYE-4-32-11-25-41, SKL-3-22-19-31-55-11, NP-6226, KAGR559-1, CB07 702, CRK 27
II	1	CB 08-534
III	13	RP5213-69-13-3-4-1-2-B, OR2324-25-1, CR2642-30, TRC2008-6, CR2642-51, OR2404-RKP-4, NDR2106, CR 2932-37-4-2-1, HKR08-62, CR2931-18-3-1-2, ORJ-7, RP5207-Bio-BK49-77-3-1, UPR 3443-7-2-1
IV	2	CN 1780-4, CN 1777-8
V	10	UPR3528-12-1-1, KJT15-1-36-5-23-16, TRC2008-7, MTU 1121, CB 07 537, WGL-23985, TM07275, KMP149, CB 08 524, JRW 605
VI	1	RP5212-56-12-9-3-2-1-1
VII	4	KAGR 424, CRR 649-IR77298-14-1-2-1, NWGR6072, CRR648-B-673-1-B
VIII	1	RP5207-Bio-BK39-164-2-1
IX	2	RPHR 5123-10-3-7-27-6-1-6-1, RPHR 5123-10-3-7-27-6-1-6-2
X	1	UPR 3528-12-1-1
XI	1	TRC 2008-9

Table 2. Average intra (Bold values) and inter cluster D^2 values of 11 clusters for 64 genotypes in rice.

Cluster	1 Cluster	2 Cluster	3 Cluster	4Cluster	5 Cluster	6 Cluster	7 Cluster	8Cluster	9 Cluster	10Cluster	11 Cluster
1 Cluster	**14.05**	21.52	33.35	169.94	26.05	24.11	30.00	64.02	61.95	67.98	66.98
2 Cluster		**0.000**	26.77	134.28	20.31	13.22	39.27	25.82	52.03	57.37	44.18
3 Cluster			**12.29**	75.65	39.29	24.71	43.92	32.97	40.04	58.56	43.99
4Cluster				**2.81**	152.72	131.75	182.08	68.75	105.91	129.94	81.25
5 Cluster					**16.76**	44.87	57.27	55.04	85.59	44.40	39.27
6 Cluster						**0.000**	26.84	34.09	31.08	87.72	71.20
7 Cluster							**35.96**	86.23	39.43	86.34	94.85
8Cluster								**0.000**	30.48	94.51	44.68
9 Cluster									**7.92**	149.68	98.97
10Cluster										**0.000**	17.91
11 Cluster											**0.000**

Table 3. Cluster mean values for different characters in mid early group rice genotypes.

	Days to 50% flowering	Effective tillers/plant	Plant height (cm)	Panicle length (cm)	Test weight (g)	Yield (kg/ha)
1 Cluster	92.02	10.41	111.53	23.69	20.70	4663
2 Cluster	94.50	11.00	120.00	25.35	15.00	6535
3 Cluster	97.42	10.38	131.98	27.50	19.00	5011
4 Cluster	111.00	9.00	160.70	27.23	21.98	4633
5 Cluster	100.80	11.35	103.75	22.81	18.02	5106
6 Cluster	87.00	8.50	133.50	26.50	19.56	5071
7 Cluster	87.38	10.63	122.53	27.57	24.53	5179
8 Cluster	98.50	10.50	142.50	23.17	13.70	4522
9 Cluster	88.00	10.50	152.55	22.81	20.41	5229
10 Cluster	111.00	12.00	104.80	25.35	25.11	4637
11 Cluster	111.00	11.00	118.70	22.90	23.86	4582

Table 4. Contribution of different traits towards genetic divergence in 64 genotypes of rice.

S.No	Character	Times ranked 1st
1	Days to 50% flowering	533
2	Effective tillers/plant	20
3	Plant height (cm)	806
4	Panicle length (cm)	140
5	Test weight (g)	196
6	Yield	184

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