

Genetic Divergence among Advanced Breeding Lines of Medium Duration Rice (*Oryza Sativa L.*)

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Abstract: An investigation was carried out with the 51 genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. 13 yield traits were recorded on the genotypes raised in the randomized block design with three replications. The 51 genotypes were grouped into eight clusters based on Euclidean cluster analysis with cluster IV, VII, VIII containing the maximum of 9 genotypes. Maximum intra-cluster distance was observed in cluster II indicating greater genetic divergence between the genotypes belong to this cluster. Test weight, Flag leaf width and plant height contributed 52.94 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters V and VIII followed by IV and VIII indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Keywords: Genetic divergence, Hybridization, Inter-cluster distance, Intra-cluster distance.

1. Introduction

Rice (*oryza sativa L.*) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). It is based on multivariate analysis and grouped into various clusters as given by Spark (1973). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 51 rice genotypes and to identify the diverse genotypes for future breeding programme.

2. Materials and Methods

Fifty one diverse genotypes of rice from different geographical origin were transplanted in the randomized block design with three replications, at the Experimental Farm of the Department of the Genetics and Plant breeding, Sam Higginbottom Institute of Agriculture technology and Sciences, Allahabad, during Kharif 2012. In each replication, single seedling was transplanted per hill with 20*15 cm spacing. The observations were recorded on five randomly taken plants from each plot for days to 50 per cent flowering, plant height, number of tillers per hill, number of panicles per hill, panicle length, number of spikelets per panicle, flag leaf length, flag leaf width, test weight, days to maturity, biological yield per hill, harvest index and grain yield per hill. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters by applying tocher clustering method (Spark, 1973). Intra and inter-cluster distances and

mean performance of the clusters for the characters were also computed.

3. Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters indicating existence of variability among the genotypes for the characters studied. Based on the relative magnitude of D^2 values, 51 genotypes were grouped into 8 clusters (Table 1). The clusters IV, VII and VIII were the biggest consisting of 9 genotypes followed by 8 in cluster III, 7 in cluster VI, 5 in cluster II, 3 in cluster I and 1 in cluster V. the clustering pattern of genotypes revealed that there was no parallelism between clustering pattern and geographical distribution of genotypes.

Table 1: Grouping of 51 rice genotypes into different clusters.

Cluster Number	Number of Genotypes	Genotypes Included
I	3	KMP 149, TM 07275, NP-6226
II	5	CN 1740-5-3-3-2-MLD.9, KAGR 426, JGL 18065, IR 64(NC), NDR 370133
III	8	PA 6201 (HC), NDR 9479 (IR 70174-14-SRN-4-UBN-2-B-1-2-2), IR 64(NC), CRK 27, UPRI 2009-9, OR 2404-RKP-4, OR 2324-25-1, R 1582-814-1-258-1
IV	9	CN 1744-21-5-1-MLD 10, KAGR 559-1, HKR 07-147, HKR 08-62, R 1576-1700-1-560-1, UPR 3528-12-1-12, JKRH-2066 (Hybrid), KPH-385 (Hybrid), CRR 624-207-B-1-B
V	1	NDR-359
VI	7	ORJ-7, SVH-026 (Hybrid), Parvathi (Hybrid), UPR 3425-11-1-1, UPR 3413-8-2-1, CR 2644-2-6-4-3-2, NK 6303 (Hybrid)
VII	9	Lalat, TRC 2008-6, RP 5213-69-13-3-

		4-1-2-B, HRI-176 (Hybrid), 26 P 29 (Hybrid), CR 2706 (IR 84895-B-CRA-171-32-1-2-1), NVSR-178, ORS-325, R 1528-1058-1-110-1
VIII	9	GK 5016 (Hybrid), CN 1446-5-8-17-1-MLD-4, IR 78091-6-2-3-1-1, NP-124-8, R 1535-1382-1-1667-1, CR 264-26-1-2-2, Lalat (RC), PA 6201 (Hybrid Check), KPH-371 (Hybrid)

clusters (Table 2). The clusters III, IV, VI, VII and VIII (0.00) consisted of only one genotype hence; they lack intra-cluster distance (0.00). The relative divergence of each cluster from other cluster (inter-cluster distance) indicated greater divergence between cluster V and VIII (80.36), followed by cluster IV and VIII (63.16). The minimum inter-cluster distance was recorded between cluster I and VIII (43.48). The selection of divergent genotypes from above cluster would produce a broad spectrum of variability for yield traits, which may enable further selection and genetic improvement.

The maximum intra-cluster distance (Table 2) was observed in cluster II (9.23) followed by cluster V (7.91) indicating limited genetic diversity among genotypes representing these

Table 2: Intra (Diagonal) and Inter Cluster (offdiagonal) distance (D^2) in rice germplasm

Clusters	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster	VIII Cluster
I	*5.41	10.91	18.26	16.17	22.37	17.57	27.99	43.48
II		*9.23	13.24	15.10	27.48	23.85	21.72	48.07
III			*0.00	23.79	34.93	29.23	27.77	50.03
IV				*0.00	13.02	27.33	22.35	63.16
V					*7.91	38.01	23.90	80.36
VI						*0.00	39.19	55.91
VII							*0.00	59.40
VIII								*0.00

The average cluster wise mean values for different characters were presented in Table 3 used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster V showed early flowering, flag leaf length, number of tillers per hill, number of panicles per hill, number of spikelets per panicle, biological yield, test weight, harvest index and seed

yield per plant. Cluster II recorded shortest plant stature. Cluster VI exhibited highest panicle length. Among the 13 characters studied, test weight contributed maximum of 27.37 per cent, followed by flag leaf width (12.94 per cent), plant height (12.63 per cent), and number of panicles per hill (10.20 per cent) towards genetic diversity (Table 4).

Table 3: Cluster mean values of 8 clusters for 13 quantitative characters in rice and their contribution towards Genetic divergence

Clusters	Days to 50% Flowering	Plant Height (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	No of Tillers/Hill	No of Panicles/Hill	Panicle Length (cm)	No of Spikelets/Panicle	Biological Yield/Hill (gm)	Days to Maturity	Test Weight (gm)	Harvest Index (%)	Economic Yield/Hill
1 Cluster	96.84	129.69	35.07	1.96	22.81	21.91	31.63	255.80	100.19	122.84	24.78	39.77	53.51
2 Cluster	96.23	125.58	32.47	1.99	19.95	18.81	30.84	243.00	100.31	117.93	25.37	47.18	53.52
3 Cluster	97.66	119.90	32.46	1.73	16.33	15.33	23.66	239.80	97.33	113.66	23.99	45.30	47.66
4 Cluster	97.66	128.40	30.06	2.60	22.60	22.26	32.00	262.20	106.66	114.33	21.04	53.63	46.66
5 Cluster	96.88	133.52	35.54	3.13	20.68	20.46	30.66	247.84	101.44	114.88	21.66	42.20	44.88
6 Cluster	95.00	131.53	37.26	1.80	18.26	17.73	31.66	249.66	100.00	161.33	22.19	48.46	50.66
7 Cluster	97.00	130.86	38.53	2.86	17.53	17.13	29.00	223.33	103.66	120.00	23.44	53.66	64.33
8 Cluster	95.33	135.16	50.01	1.59	41.40	36.76	23.66	309.16	123.66	133.20	29.16	50.88	66.64

Table 4: Relative contribution (%) of individual trait to the divergence among 51 rice genotypes

S. No	Characters	No. of times ranked first	Contribution (%)
1	Days to 50% Flowering	45	3.53
2	Plant height	161	12.63
3	Flag leaf length	40	3.14
4	Flag leaf width	165	12.94
5	Number of tiller/hill	46	3.61
6	Number of panicles/hill	2	0.16
7	Panicle length	119	9.33
8	Days to maturity	15	1.18
9	Number of spikelets / panicle	25	1.96
10	Biological yield	72	5.65
11	Harvest index	130	10.20
12	Test weight	349	27.37
13	Seed yield / plant	106	8.31

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