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Assessment of Genetic Diversity for Grain Yield and its Attributes among Diverse Genotypes of Rice (*Oryza sativa* L.)

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Abstract

A field experiment was conducted at Crop Research Centre, Chirodi, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut UP during kharif season of 2013. The material taken for this study consisted of 30 rice genotypes from different rice eco-geographical regions of India. All the genotypes were grown in randomized block design with three replications. 30 genotypes were grouped into six clusters (Table 2). The cluster II was the biggest consisting of 08 genotypes followed by 06 in each cluster I and III, 5 in cluster V, 4 in clusters IV, and cluster number VI had single genotype. intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster V (315.822) and lowest intra cluster distance was recorded for cluster VI (0.000). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. Genotypes constituting Cluster V exhibited excellence in early maturity, shortest plant height and highest effective tillers per plant are expected to exhibit high heterosis and are also likely to produce new combinations with desired traits.

Key words : Rice, genetic diversity

Introduction

Rice (*Oryza sativa* L.) is the prime food crop of the world for more than half of the global populations. India is the second largest producer and consumer of rice next to China. As the population is increasing alarmingly, it is projected that the demand of rice in 2025 A.D. would be 140mt as against the production of about 131.9 mt. Hence, in order to meet the food requirement of growing population and indispensable demand, development of high yielding varieties or improvement through genetic manipulation is the only way. The success of any breeding programme depends on the selection of parents for hybridization and the parents involved should be divergent. The information about the nature and magnitude of genetic divergence existing in the available material of a particular crop is essential for selection of diverse parents, which upon hybridization may provide a greater possibility of obtaining desirable segregates in segregating generations (Vivekananda and Subramanian, 1993) . Genetic divergence is an efficient tool for the selection of parents and its importance for recombination breeding in self pollinated crop such as rice to recover desirable segregates has also been repeatedly emphasized (Sarawgi, A.K. and Rita Binse. 2007). In the present study, an attempt was made to assess the genetic divergence using Mahalanobis D^2 statistics and different clustering procedures, based on yield and its attributes among rice genotypes to develop high yielding varieties.

Materials and Methods

A field experiment was conducted during *kharif* season of 2013 at Crop Research Centre, Chirodi, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut UP. The material taken for this study consisted of 30 rice genotypes from different rice eco-geographical regions of India. All the genotypes were grown in randomized block design with three replications. The seedlings were transplanted to main field by transplanting single seedling per hill in 5 rows plots of 5 meter length following 20cm spacing between rows and 15cm within the row. Recommended agronomic practices and need based plant protection measures were taken up. Observations were recorded on eleven quantitative characters *viz.,* Days to 50% flowering, Days to maturity, Plant height (cm), Flag leaf area (cm^2), Panicle length (cm),

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Effective tillers per plant, Spikelet's per panicle, 1000-grain weight (g), Biological yield per plant (g), Grain yield per plant (g) and Harvest index (%). Genetic diversity analysis was done following the D2 statistics proposed by Mahalanobis (1936).

Results and Discussion

The analysis of variance revealed significant differences among the all genotypes for all the characters indicating existence of variability among the genotypes for the characters studied (Table 1). Based on the relative magnitude of D^2 values, 30 genotypes were grouped into six clusters (Table 2). The cluster II was the biggest consisting of 08 genotypes followed by 06 in each cluster I and III, 5 in cluster V, 4 in clusters IV, and cluster number VI had single genotype. The clustering pattern of genotypes revealed that there was no parallelism between clustering pattern and geographical distribution of genotypes. Similar results were observed by Chandra *et al.,* (2007), Vennila *et. al.,* (2011), Allam, *et al.,* (2015) and Ghosh, and Sharma (2012). Data present in Table 3 revealed that the intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster V (315.822) and lowest intra cluster distance was recorded for cluster VI (0.000). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances. The diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding rice varieties.

The relative divergence of each cluster from other cluster (inter-cluster distance) indicated greater divergence between cluster VI and III (6162.283) followed by cluster I and III (5031.37). The minimum inter cluster distance was recorded between cluster VI and I (173.02). The clearly indicates that the genotypes included in this clusters are having broad spectrum of genetic diversity and could very well be used in hybridization program of rice for improving grain yield.

The average cluster wise mean values for different characters are presented in Table 4 which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture (Babu *et al.* 2003). Cluster I characterized by early flowering, desirable spikelet's per panicle, thousand grain weight and harvest index. Cluster VI showed superior panicle length, highest yield per plant and desirable flag leaf area. Thus the genetically diverse genotypes of cluster VI (VLD 62) and Cluster I *i.e.* Pusa 2511, Pusa Basmati 1, Pusa 1121, Pusa Basmati 2, CSR 30 and MAUB 13 could be crossed to get desirable segregates with higher yield for developing superior variety of rice. Genotypes constituting Cluster V exhibited excellence in early maturity, shortest plant height and highest effective tillers per plant are expected to exhibit high heterosis and are also likely to produce new combinations with desired traits.

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Table 1: Analysis of variance (ANOVA) for eleven characters in rice (*Oryza sativa* L.)

Source of Variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf area (cm^2)	Panicle length (cm)	Effective tillers/ plant	Spikelet's/ plant	1000- grain weight (g)	Biological yield/ plant (g)	Harvest index (%)	Grain yield/ plant (g)
Replications	2	1.900	1.733	33.385	0.25	1.596	9.141	256.97	0.000	2.28	2.50	7.49
Treatments	29	134.76**	52.62**	1742.76**	90.02**	35.27**	38.704**	6666.07**	37.52**	3343.41**	71.50**	88.13**
Error	58	1.71	1.45	13.91	2.01	2.618	4.80	131.82	0.008	149.92	3.43	9.36

*,** Significant at 1 % and 5 % level probability, respectively.

Table 2: Distribution of Thirty genotypes of Rice (*Oryza sativa* L.)

Clusters Number	No. of genotypes	Genotypes
I	6	Pusa 2511, Pusa Basmati-1, Pusa-1121, Pusa Basmati 2,CSR 30, MAUB13
II	8	MAUB 1, Vallabh Basmati 21, NDR 359, Pant Dhan-12, VLD- 30177, PR-106, VLD- 81, Vallabh Bangni,
III	6	Vallabh Basmati- 24, Nagina-22, TETEP, VLD 86, VLD 85, VLD 61
V	4	PR- 113, CSR 27, PR- 114, CSR- 10
V	5	Pusa 1401, Govind, Basmati 370, Vallabh Basmati-22, Pant Sugandh 15
VI	1	VLD- 62

Table 3: Estimation of average Inter and Intra cluster (D^2 values) distance in rice (*Oryza sativa* L.)

Cluster	I	II	III	IV	V	VI
I	**96.063**	1117.181	5031.374	372.771	2892.287	173.026
II		**111.286**	1593.327	340.425	594.644	1676.463
III			**196.430**	3048.271	564.644	6162.283
IV				**82.015**	1456.010	678.675
V					**315.822**	3778.000
VI						**0.000**

Bold values = intra cluster distance.

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Table 4: Cluster means values for eleven characters in rice (*Oryza Sativa* L.)

S. No.	Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf area (cm^2)	Panicle length (cm)	Effective tillers/plant	Spikelet's/ panicle	1000- grain weight (g)	Biological yield/ plant (g)	Harvest index (%)	Grain yield/ plant (g)
1.	I	94.167	125.167	112.633	91.63	25.517	15.583	183.567	26.751	106.283	26.640	28.367
2.	II	101.524	125.952	124.581	89.66	24.743	16.533	148.895	20.000	132.486	18.596	24.724
3.	III	98.600	126.400	116.493	90.46	27.120	14.733	171.773	23.599	162.000	20.235	32.520
4.	IV	101.944	128.944	100.011	98.88	25.033	14.978	125.556	25.500	133.489	21.231	27.978
5.	V	99.667	122.333	88.244	80.66	24.244	22.422	115.711	20.668	98.556	26.311	23.778
6.	VI	109.400	128.400	134.387	99.33	27.840	16.693	160.187	18.000	176.840	16.382	28.693