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Research Article

Estimating genetic divergence in rice (*Oryza sativa* L.) using D^2 analysis

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Abstract

Rice is the staple food across Asia, where around half of the world's poorest people live and hence that necessitates breeding for high yielding genotypes. Genetic diversity present in the germplasm is pre-requisite for crop improvement as it helps in the development of superior recombinants. Knowledge about genetic diversity between the genotype can be utilized for the selection of diverse parents in hybridization programmes. In this study, using Mahalanobis D^2 statistics twenty four advanced genotypes were grouped into five different clusters based on their level of divergence. The Cluster III displayed the maximum intra-cluster distance with six genotypes followed by cluster II with ten genotypes. The cluster II and IV exhibited the maximum inter-cluster distance. Among the traits, days to 50% flowering contributed the highest towards total divergence.

Key words

Rice, Genetic diversity, D^2 statistics.

INTRODUCTION

The first step before initiating any breeding programme is the assessment of diversity among the set of genotypes. The success of plant breeding programme depends on the development of high yielding, input responsive, better quality and disease and insect resistant varieties. This in turn depends on the selection of suitable plants to be utilized in breeding programme. Genetic diversity present in the germplasm is pre-requisite for crop improvement as it helps in the development of superior recombinants. Knowledge about genetic diversity between the genotype can be utilized for the selection of diverse parents in hybridization to exploit the heterosis. Mahalanobis D^2 statistics assist in grouping the genotypes into different clusters based on their divergence level. This analysis takes into account the contribution of each character towards the total divergence. So, that provides the idea about the total genetic divergence among the genotypes with the estimates of Inter-cluster and Intra-cluster distance. Hybridization involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulting probably due to the complementary interaction of divergent genes in parents (Ovung et al., 2012). Therefore, helps to pick up appropriate genotypes for utilization in the hybridization programme.

MATERIALS AND METHODS

The present investigation was conducted during the *Kharif* season 2016-2017 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi using twenty four rice genotypes which were received from IRRI Networking Project, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (**Table 1.**). The experiment was laid out in randomized block design (RBD) with three replications. Twenty five days old seedlings were transplanted in main research plot. Each plot consisted of five rows of 1.5 m length with spacing 15 × 20 cm. The crop was maintained as per the standard agronomic practices. The field observations were recorded for 19 quantitative traits including Days to 50% Flowering, Days to Maturity, Plant Height (cm), Hulling %, Milling %, Kernel Length (mm), Kernel Breadth (mm), L/B Ratio, Panicle Length (cm), Tillers/ Plant, Effective Tillers/ Plant, Spikelet/ Panicle, Fertile Grain/ Panicle, Spikelet Fertility (%), Sterile Spikelet/ Panicle, 1000 Grain Weight(g), Grain Weight/Panicle(g), Grain Yield/ Plant(g) and Grain Yield/ Plot(g). Analysis of variance is used for testing whether there is significant difference among the treatments or not by following the procedure of randomized block design (RBD) analysis (Panse and Sukhatme, 1967). The genetic divergence was estimated based on Mahalanobis' generalized distance as described by Rao (1952). The genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952).

Table 1. List of Genotypes studied with their sources.

Sl no.	Genotypes	Source of genotypes
1	IR 92522-47-2-1-4	IRRI
2	IR 92522-45-3-1-4	IRRI
3	IR 91648-B-85-B-1-1	IRRI
4	IR 91648-B-215-B-2-1	IRRI
5	IR 91648-B-58-B-7-3	IRRI
6	IR 96321-315-402-B-1	IRRI
7	IR 96321-327-300-B-1-1	IRRI
8	IR 94391-587-1-2-B	IRRI
9	IR 85604-19-2-3-2-2	IRRI
10	IR 82475-110-2-2-1-2	IRRI
11	IR 96248-16-3-3-1-B	IRRI
12	IR 96248-16-3-3-2-B	IRRI
13	IR 97477-110-3-1-B	IRRI
14	IR92978-192-1-2 (R-306)	IRRI
15	IR91953-141-2-1-2 (R-119)	IRRI
16	IR92937-178-2-2 (R-155)	IRRI
17	MTU1010	APRRI, Maruteru, AP
18	Swarna Sub1	IRRI
19	Swarna	APRRI, Maruteru, AP
20	Lalat	OUAT, Orissa
21	R-RHZ-7	IGKV, Raipur
22	CGZR-1	IGKV, Raipur
23	IR64	IRRI
24	Sambha Mahsuri	APRRI, Maruteru, AP

Table 2. Analysis of variance (ANOVA) for 19 quantitative traits in twenty four rice genotypes

Source of variation	df	Mean sum of squares									
		Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Hulling %	Milling %	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio	Panicle Length (cm)	Tillers/ Plant
Replicate	2	0.0972	0.3472	3.2349	1.2294	4.5395	0.0554	0.0036	0.0482	1.5792	0.1667
Treatments	23	460.25**	461.24**	156.38**	13.71*	40.12**	2.00**	0.07**	1.12**	15.73**	5.26**
Error	46	0.7349	1.1443	10.1274	6.7736	16.8970	0.0432	0.0075	0.0393	1.3109	1.5403

Source of variation	df	Mean sum of squares								
		Effective Tillers/ Plant	Spikelet/ Panicle	Fertile Grain/ Panicle	Spikelet Fertility (%)	Sterile Spikelet/ Panicle	1000 Grain Weight(g)	Grain Weight/ Panicle (g)	Grain Yield/ Plant(g)	Grain Yield/ Plot(g)
Replicate	2	0.1992	29.3285	122.3610	57.6237	197.2847	1.0043	0.1911	0.8104	7455.8184
Treatments	23	3.94**	5488.86**	3162.44**	160.89**	1033.22**	31.96**	0.80**	13.78**	437824.12**
Error	46	1.0976	181.5182	288.7524	31.9141	76.3154	0.5566	0.0972	3.5692	8312.4023

*Significant at $p<0.05$; **Significant at $p<0.01$

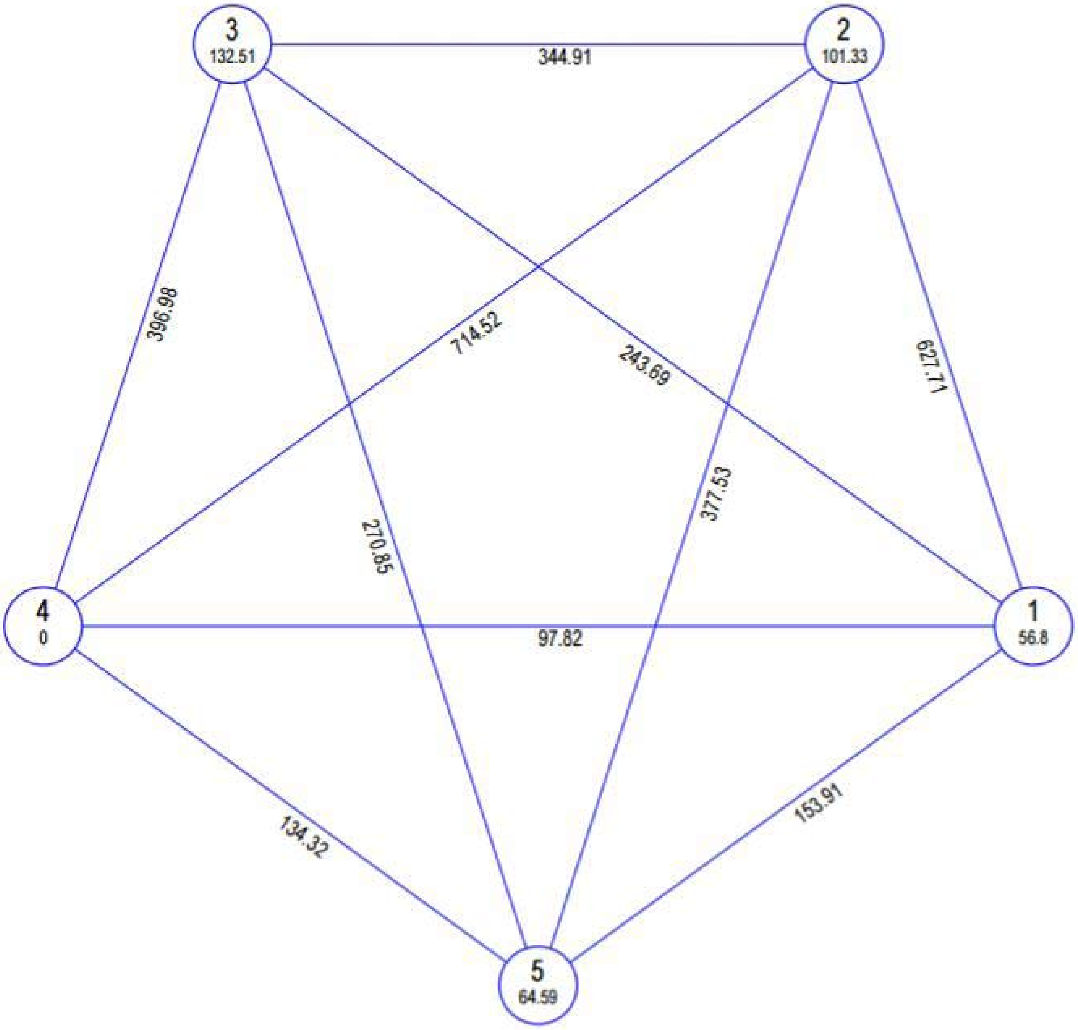

Fig 1. Average Intra and Inter-cluster distances among nine clusters (by Tocher method).

RESULTS AND DISCUSSION

It is noticeable from the analysis of variance that genotypes differed significantly for all the nineteen characters studied, which is presented in **table 2.** This specified that there is significant variability for grain yield and yield components traits studied.

In the present study, D^2 analysis revealed the presence of considerable diversity in the set of 24 rice genotypes. Based on their level of divergence, the genotypes formed five different clusters (**Table 3.**). The intra-cluster distance for cluster IV was observed to be zero since that contain only one genotype. Cluster III displayed the maximum intra-cluster distance with six genotypes followed by cluster II with ten genotypes. The genotypes with close relationship fall in the same cluster and the genotypes which show relatively more divergence were contained in the different clusters. Therefore, it could be probable that genotypes gathered together in one cluster were less divergent than those which are positioned in different clusters. The cluster II and IV exhibited the maximum inter-cluster distance followed by cluster I and II signifying that the hybridization between the genotypes fall in diverse clusters would yield desirable segregates with the accumulation of favorable genes in the segregating generations (**Fig 1.**). The greater the distance between two clusters, higher is the expected genetic advance between them. Therefore, clustering pattern provide the proper picture about the diversity among the genotypes and useful in selecting diverse parents for hybridization program. However, while selecting parents for hybridization programmes their yield potential should not be overlooked (Singh *et al.*1987).

A study of cluster means revealed the presence of considerable differences in the mean values of different characters (**Table 4**). The distribution of highest and lowest mean values for different characters in distinct cluster indicated the traits contributing to the total divergence. In this regard, days to 50% flowering contribute highest towards divergence followed by grain yield per plot, spikelet per panicle and grain yield per plant (**Table 5**). These results were in agreement with the findings of Bose and

Table 3. Grouping of twenty four rice genotypes into five clusters (by Tocher method)

Clusters	Genotypes	Number
I	IR 96321-315-402-B-1, IR 96321-327-300-B-1-1, Swarna, IR 97477-110-3-1-B , IR 91648-B-85-B-1-1	05
II	MTU1010, IR64, IR 94391-587-1-2-B, IR 85604-19-2-3-2-2, IR 92522-47-2-1-4, IR 92522-45-3-1-4, CGZR-1, IR 96248-16-3-3-2-B, IR 96248-16-3-3-1-B, IR 82475-110-2-2-1-2	10
III	IR 91648-B-215-B-2-1, Swarna Sub 1, Lalat, IR92978-192-1-2 (R-306), IR92937-178-2-2 (R-155), IR91953-141-2-1-2 (R-119)	06
IV	Sambha mahsuri	01
V	IR 91648-B-58-B-7-3 R-RHZ-7	02

Table 4. Mean values of different characters of 24 rice genotypes grouped in five clusters.

	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Hulling %	Milling %	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio	Panicle Length (cm)	Tillers/ Plant
Cluster I	121.733	147.667	95.854	76.207	71.707	5.611	2.087	2.703	23.902	10.022
Cluster II	95.167	120.967	98.411	76.137	67.790	7.023	1.855	3.828	25.560	11.100
Cluster III	112.278	138.778	103.037	77.218	72.154	6.587	2.017	3.274	26.241	10.944
ClusterIV	122.000	146.667	89.289	76.300	73.410	5.227	1.803	2.903	21.589	14.222
Cluster V	112.333	138.000	104.100	77.975	69.223	5.827	1.767	3.313	27.059	10.000

	Effective Tillers/ Plant	Spikelet/ Panicle	Fertile Grain/ Panicle	Spikelet Fertility (%)	Sterile Spikelet/ Panicle	1000 Grain Weight(g)	Grain Weight/ Panicle (g)	Grain Yield/ Plant(g)	Grain Yield/ Plot(g)
Cluster I	8.200	212.446	155.267	73.196	57.178	20.007	2.931	21.112	3481.716
Cluster II	9.133	135.432	108.967	80.371	26.467	25.113	2.663	20.217	3327.650
Cluster III	9.519	165.741	135.852	82.166	29.833	24.472	3.094	24.081	4041.028
ClusterIV	11.222	212.000	143.113	67.333	68.889	15.800	2.080	19.927	3252.667
Cluster V	7.833	225.388	192.945	85.938	32.444	18.817	3.585	19.740	3220.375

Table 5. Percentage contribution of each character towards total genetic divergence in 24 genotypes

	Source	Contribution %
1	Days to 50% Flowering	64.49
2	Days to Maturity	0.98
3	Plant Height (cm)	1.09
4	Hulling %	1.09
5	Milling %	0.01
6	Kernel Length (mm)	0.36
7	Kernel Breadth (mm)	0.01
8	L/B Ratio	0.01
9	Panicle Length (cm)	1.09
10	Tillers/ Plant	0.01
11	Effective Tillers/ Plant	0.01
12	Spikelet/ Panicle	7.25
13	Fertile Grain/ Panicle	1.09
14	Spikelet Fertility (%)	0.01
15	Sterile Spikelet/ Panicle	0.01
16	1000 Grain Weight(g)	0.01
17	Grain Weight/ Panicle (g)	0.01
18	Grain Yield/ Plant(g)	3.99
19	Grain Yield/ Plot(g)	18.48

Pradhan (2006); Banumathy *et al.* (2010); Sabesan *et al.* (2010); Ovung *et al.* (2012), Kumar *et al.* (2014) and Dey *et al.* (2020) who have also studied divergence in rice using 35, 53, 26, 70, 29 and 29 genotypes respectively.

In the present group of rice genotypes considered, based on the information attained from D^2 analysis, genotypes belonging to the most divergent clusters *viz*., cluster II and IV with proper mean values and with desirable traits can be utilized for hybridization programme to accumulate favorable alleles and desirable traits into single background and hence effective in developing improved cultivars.

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