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## Genetic divergence analysis in rice (*Oryza sativa* L.) under lowland condition

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### Abstract

Genetic diversity is one of the most basic prerequisites in any crop improvement programme. It acts as a reservoir for identifying superior genes influencing quantitative traits of the crops and use of rice genetic resources. Genetic divergence study was carried out at research farm of Dr. Rajendra Prasad Central Agricultural University Pusa, Samastipur, with 24 diverse lowland rice genotypes. Which were shown in R.B.D. design and were analysed for genetic divergence with the help of Mahalanobis's  $D^2$  statistics. The 24 rice genotypes were grouped into eight clusters. Cluster II was found to be largest comprising of 13 genotypes followed by cluster III having 3 genotypes, cluster I and cluster VIII having 2 genotypes each and cluster IV, cluster V, Cluster VI and cluster VII having 1 genotype each. The highest intra cluster distance was observed in cluster VIII (5.75) followed by Cluster II (5.70). Maximum inter cluster distance (18.03) was observed between cluster I and Cluster VII followed by inter cluster distance (14.57) between cluster I and cluster VI. The pattern of distribution of genotypes from different geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. Per cent contribution of all ten characters towards total genetic divergence was found maximum for plant height followed by days to flowering, grain filling rate. It was observed that plant height ranked 1st maximum times followed by days to flowering, grain filling rate, 1000 grain weight. The genotype in cluster I and cluster VII due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized in future for heterosis breeding programme for getting high yielding recombinants.

**Keywords:** Genetic divergence, yield attributes, multivariate analysis

### Introduction

Rice (*Oryza sativa* L.) is one of the most important food crops of the world particularly Asian countries where it is the staple food. The estimated world rice production for the year 2019-20 is 496.67 million metric tons (USDA, 2020) [1]. In India, low-land rice area is about 14.4 million hectares, which accounts 32.4 per cent of the total area under rice crop in the country. It Production is highly variable. It is usually transplanted in levelled, bunded fields that retain surface water but the depth and duration of the soil varies greatly from year-to-year within a growing season. Depending upon the depth of water it can further classified to shallow water (<50cm), semi deep water (50-100cm) and deep water (>100cm). The water supply is variable, and both drought and flooding may occur in the same season. Rain fed low land rice system is also classified as favourable drought prone, submergence prone and drought and submergence prone. Soil fertility is low and problem soils are common in this ecosystem. Most of the farmers are resource poor.

It is produced in wide range of locations and under different ecosystem and climatic conditions. As it grows in variable climatic condition and having such an extended geographical distribution throughout the world and it is the crop with maximum germplasm diversity. As the consequence of great geographical distribution and extending its boundaries to various climatic conditions it faces several forms of a biotic stresses occurring in those environment and flooding being of those. The yield potential of rice is also less than the average yield of rice in lowland ecosystem. However, the crops suffer due to lack of potential and adaptable variety for this situation. Therefore, study of the diversity of rice in lowland flooded area is of prime importance for the development of new varieties, to sustain the rice production in lowland rice. Genetic divergence among the genotypes play an important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004) [5] and it also helps in the development of superior recombinants (Manonmani and Khan, 2003b) [3]. Genetic diversity analysis is done with help of  $D^2$  statistics developed by P.C. Mahalanobis.

Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence.

### Materials and Method

The present research work was conducted at Rice research farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during kharif 2006. The experimental materials comprised of 24 genotypes including check selected genetically diverse true breeding genotypes for lowland rice obtained from different geographical regions and abroad of India through AICRP on rice. The details pedigree and source of rice genotypes were presented in table-1. The experimental materials were sown in nursery beds in 13<sup>th</sup> June 2006 and transplanting was done on 17<sup>th</sup> July 2006. The experiment was laid out in the Randomized Block Design with three replications under lowland conditions. Each genotype was grown in plot size of 2.0m x 3.0m with 15 cm x 10cm spacing and seedlings were sown with two to three seedlings per hill within the rows. The water depth in the field varied from 20cm-40cm during crop growth period. The recommended packages of practices were followed during the crop growth period in respect of irrigation, weeding, transplanting and fertilization. Replication wise data on the basis of five randomly taken competitive plants for ten characters were recorded for the following traits *viz.*, Days to 50% flowering, Days to maturity, Plant height (cm), Tillers per square meter, Panicle length (cm), Spikelet fertility (%), Grain filling period (days), Grain filling rate (kg/days), 1000-grain weight(g), Grain yield (q/ha). The data recorded for all the characters were subjected to analysis of various parameters of genetic diversity. The  $D^2$  values were calculated by using the formula of Mahalanobis (1936) [4].  $D^2$  statics as suggested by Tocher (Rao 1952) [6] was used for clustering pattern of various genotypes, cluster mean, intra and inter-cluster distances formation.

### Results and Discussion

The analysis of variance revealed significant differences among 24 diverse genotypes for all the ten characters studied. The genotypes were grouped into eight clusters on the basis of relative magnitude of  $D^2$  value present in table-2 The cluster II included maximum 13 number of genotypes, Cluster III having 3 genotypes, cluster I and cluster VIII having 2 genotypes each and Cluster IV, cluster V, cluster VI and cluster VII comprised of 1 genotype each. Several genotypes of different geographical origins were grouped in the same cluster II. In contrast genotypes originated from the same source were scattered in different clusters, suggesting no relationship between geographical origin and genetic divergence of the genotypes. This tendency of genotypes occurring in clusters cutting across the geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity in lowland rice. Similarly, the genotypes from the same geographical area falling into different clusters may be due to selection and

genetic drift under diverse environmental condition with same geographical area. The same observation were found by Singh U.K. *et al.* (1999) [8], Shivani *et al.* (2018) [7], Kumari P. *et al.* (2018) [2], Guru T. *et al.* (2017) [1] and also suggested that geographical diversity may not always be a useful index of genetic diversity in rice.

The intra cluster distance (table 3) ranged from 0.00 (cluster IV, cluster V, cluster VI and cluster VII) to 5.75 (cluster VIII). The highest intra cluster distance was observed in cluster VIII (5.75) followed by cluster II (5.70), cluster III (5.36). The inter-cluster divergence varied from 5.07 to 18.03. The maximum inter cluster distance was recorded between cluster I and cluster VII (18.03) followed by cluster I and cluster VI (14.57). The minimum inter cluster distance was recorded between cluster IV and cluster V (5.07) indicating that the above information, some lines were genetically very closed to each other and rest possessed marked difference between them. Hence inference could be drawn that present set of test material possess substantial quantity of genetic diversity among them. Similar divergence estimation based on  $D^2$  distance was observed by Shivani *et al.*, (2018) [7], and Kumari *et al.* (2018) [2].

The relative contribution of different characters to the total divergence was assessed by rank total and average  $D^2$  as presented in table 4. Among different characters, the order of contribution to the total genetic divergence were high for plant height (30.07%) moderate for days to 50% flowering (25%) and low (0.36 to 23.55) for rest of the character.

The mean value of the cluster for all the traits under study which is presented in table-5 and it is clear from the observation that the maximum mean value of the genotypes for the characters *i.e.* tillers per square meter (252.50), spikelet fertility (81.50) and grain yield (51.39) were found in cluster I, and their respective minimum values (178.00) were observed in cluster VI, (51.33), 19.45 in cluster VII the highest mean value of the genotypes for, grain filling rate (149.05) was found in cluster II with the respective lowest mean 72.00 in cluster IV. The highest mean value of the genotypes for the character panicle length (26.0) was found in cluster III with the respective minimum value 19.00 in cluster V. The all cluster had shown maximum cluster mean except cluster IV and V. Cluster VI showed higher cluster mean for the characters days to 50% flowering (140.33), grain filling period (34.00) with their respective lowest mean 116.89 and 28.11 in cluster III. Cluster VII exhibited higher cluster mean for the character plant height (148.33) and 1000 grain weight (24.00) along with their respective lowest mean value 87.33 and 16.00 in cluster I. Character having maximum value in cluster VIII was found in days to maturity with its respective minimum cluster mean 150.67 for cluster III. It is clear from the observation that the mean performance of the genotypes in different clusters in respect of various traits that cluster I had the highest value for three characters namely number of tillers per square meter, spikelet fertility and grain yield.

**Table 1:** Details of rice genotypes

Sl. No.	Genotypes	Source
1	OR 2147-3	OUAT, Orissa
2	OR 1898-2-35	OUAT, Orissa
3	NDR 9930070	NDUAT, Masodha, U.P.
4	NDR9830131	NDUAT, Masodha, U.P.

5	NDR9830123	NDUAT, Masodha, U.P.
6	TTB 297-8-9	RARS, Titabar, Assam
7	TTB 302-1-2	RARS, Titabar, Assam
8	TTB 303-1-2	RARS, Titabar, Assam
9	TTB 297-18-2	RARS, Titabar, Assam
10	TTB 297-18-9	RARS, Titabar, Assam
11	TTB 297-8-12	RARS, Titabar, Assam
12	TTB 298-1-9	RARS, Titabar, Assam
13	CN 1233-18-6-1	RRS, Chinsurah, W.B.
14	CN 1163-6-13	RRS, Chinsurah, W.B.
15	CN 1232-17-5-21-1	RRS, Chinsurah, W.B.
16	RAU 619-108-5	RAU, Pusa, Bihar
17	RAU 678-82-4	RAU, Pusa, Bihar
18	RAU 729-12-81	RAU, Pusa, Bihar
19	CR 874-23	CRRI, Cuttack, Orissa
20	Savitri	CRRI, Cuttack, Orissa
21	Sabita	West Bengal
22	Swarna	APRRS, Cuttack, Orissa
23	Swarna (Sub-1)	IRRI, Philippines
24	Satyam	RAU, Pusa, Bihar

**Table 2:** Distribution of twenty four entries of lowland rice in different cluster

Cluster	No. of entries	Name of the entries
I	2	Swarna, Swarna (Sub. – 1)
II	13	NDR 9830123, Local check. TTB 297-18-2, TTB 297-18-12, TTB 302-1-2, OR 2147-35, OR 1898-2-35, NDR 9930070, NDR 9830131, TTB 298-1-9, TTB 297-8-9, TTB 303-1-2, TTB 297-18-9
III	3	RAU 649-108-5, RAU 678-82-4, RAU 729-12-81
IV	1	Sabita
V	1	CR 874-23
VI	1	CN 1232-17-5-21-1
VII	1	CN 1233-18-6-1
VIII	2	CN 1162-6-13, Savitri

**Table 3:** Intra-inter cluster distance

	Group I	Group II	Group III	Group IV	Group V	Group VI	Group VII	Group VIII
Group I	1.00	9.63	8.40	12.72	10.40	14.57	18.03	10.78
Group II		5.70	8.60	7.09	7.38	8.45	11.40	9.47
Group III			5.36	8.91	7.20	12.14	13.69	11.28
Group IV				0.00	5.04	5.20	6.43	9.04
Group V					0.00	7.84	9.32	8.57
Group VI						0.00	5.36	8.16
Group VII							0.00	11.57
Group VIII								5.75

**Table 4:** Per cent contribution of ten characters towards divergence in rainfed lowland rice

## III. Intra and inter cluster distance

Characters	No. of times appearing first in ranking	Per cent contribution towards genetic divergence
1. Days to 50% flowering	69	25.00
2. Days to maturity	2	0.72
3. Plant height	83	30.07
4. Tillers per sq. meter	01	0.36
5. Panicle length	2	0.72
6. Spikelet fertility	24	8.70
7. Grain filling period	1	0.36
8. Grain filling rate	65	23.55
9. 1000-grain weight	27	9.78
10. Grain yield	2	0.72

**Table 5:** Cluster mean for different characters of lowland rice.

Cluster/Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50% flowering	117.00	128.00	116.89*	131.00	125.00	140.33**	140.00	138.67
Days to maturity	155.00	159.08	150.67*	173.33	159.67	174.00	174.33	174.50**
Plant height	87.33*	124.03	110.63	140.67	120.00	135.67	148.33**	95.67
Tillers per sq. meter	252.50**	241.54	168.67	207.00	189.00	178.00*	190.33	205.00

Panicle length	21.50	23.28	26.00**	21.00	19.00*	21.67	23.00	20.67
Spikelet fertility	81.50**	75.90	74.67	69.33	62.33	63.67	51.33*	67.33
Grain filling period	29.00	30.90	28.11*	32.00	26.00	34.00**	60.33	32.50
Grain filling rate	126.50	149.05**	106.78	72.00*	102.67	78.67	60.33	107.33
1000-grain weight	16.00*	18.05	21.11	23.00	19.00	18.00	24.00**	20.17
Grain yield	51.39**	45.18	30.00	23.33	26.67	26.67	19.45*	35.28

\* Lowest mean value\*\* Highest mean value

## Conclusion

The observation on ten traits of the twenty four genotypes were use to obtain D<sup>2</sup> values which grouped these genotypes into eight clusters. The pattern of distribution of genotypes from different geographical regions into different clusters was random. The clustering pattern revealed that geographical isolation in not the only factor causing genetic diversity in lowland rice. The geographical diversity may not be always being useful index of genetic diversity in lowland rice. The highest inter-cluster distance were observed between cluster I and cluster VII, revealed that the genotypes belongs to these clusters were more divergent and used as a good parents in future breeding programme. In general inter cluster distance were higher in magnitude than the intra cluster distance. The mean performance of genotypes in different cluster in respect of various traits revealed that cluster I had the highest value for three characters namely number of tillers per square meter, spikelet fertility and grain yield. Those observations suggested that crossing of genotypes from cluster II and cluster IV, V, VI, and cluster VII showing high cluster distance and good mean performance may help in obtaining early maturing, dwarf and high yielding genotypes, such combination may be useful in identifying dwarf and high yielding variety for lowland rice.

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