

Study of Genetic Diversity in Rice (*Oryza sativa* L.) Genotypes for Yield and Related Traits using D² Analysis in the South-Eastern Plain Zone of Rajasthan

Guddi Takar^{1*}, Manoj Kumar², Sandhya², D.L. Yadav², B.K. Patidar³,
Govind Tikiani¹ and Rajesh Naga¹

¹M.Sc. Research Scholar, Department of Genetics and Plant Breeding,
College of Agriculture Umedganj, Agriculture University, Kota (Rajasthan), India.

²Assistant Professor, Agricultural Research Station,
Umedganj, Agriculture University, Kota (Rajasthan), India.

³Associate Professor, Agricultural Research Station,
Umedganj, Agriculture University, Kota (Rajasthan), India.

(Corresponding author: Guddi Takar*)

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ABSTRACT: The present experiment was carried out with 25 genotypes including 4 checks in RBD design with three replications during *Kharif* 2023 to study the nature and extent of diversity present among genotypes. The observations were recorded for nine characters namely days to 50% flowering, days to maturity, plant height (cm), number of effective tillers/plant, number of panicle/m², number of grains/panicle, panicle length (cm), 1000-grain weight (g), grain yield/plant (g). Based on their level of divergence, 25 genotypes were classified into five distinct non-overlapping clusters using Tocher's method. Cluster II showed maximum intra-cluster distance values, followed by cluster I, while cluster III, IV and V reported zero intra-cluster distance, indicating that these clusters were monogenotypic in nature. The inter-cluster D² values was maximum between cluster III and IV, followed by cluster IV and V, cluster III and V, indicating that there was greater diversity present among these genotypes. Thus, in order to produce better and more desirable recombinants and increase rice grain production, hybridization programmes should employ the genotypes of these clusters.

Keywords: D² statistics, intra and inter-cluster, Diversity & Tocher's method.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop in the world and has been cultivated by mankind for more than 10,000 years. It originated in South East Asia. Rice genome is composed of 12 chromosomes (2n=24) and belongs to the family Gramineae (Poaceae). The genus *Oryza* consists of 24 species, of which 22 are wild and two are cultivated viz., *Oryza sativa* and *Oryza glaberrima*. The *sativa* rice germplasm of the world is commonly divided into three sub-species i.e., *Indica*, *Japonica* and *Javanica* (Vinoth *et al.*, 2016). Sub species *Indica* are cultivated in tropical and sub-tropical regions of the globe, subspecies *Japonica* are grown throughout the temperate zone and subspecies *Javanica* are grown mainly in parts of Indonesia (Priya *et al.*, 2017). All germplasm found in Asia, America and Europe belongs to the species *Oryza sativa*, while in West Africa it belongs to *Oryza glaberrima*. Rice is a short day autogamous crop and a staple food for about 2/3 of the entire population and plays an important role in the Indian economy (Kumar *et al.*, 2017). Rice is a short day crop and requires a hot and humid climate with an average temperature of 21 to 37°C throughout its life. Rice contains 80% carbohydrates, 7-8% protein, 3% fat and 3% dietary fibre and also contributes, nutritionally, significant amounts of vitamins like thiamine, riboflavin, niacin and zinc (Ray *et al.*, 2016).

In India, rice production during 2022-23 was 165.30 million tonnes in an area of 44.10 million hectares with a productivity of 3780 kg/ha (Anonymous, 2022-23). In Rajasthan, rice occupies an area of 0.23 million hectares with the production of 0.66 million tonnes and productivity of 2860 kg/ha (Anonymous, 2022-23). Genetic diversity determines the inherent potential of a cross for heterosis and the frequency of desirable recombinants in advanced generations. Mahalanobis (1936) D² statistics is a valuable tool used in quantifying the degree of divergence (Ramya and Senthilkumar 2008). It helps the breeder to estimate the genetic divergence in the population for use in plant breeding programmes. Cluster analysis is a statistical approach for converting numerous characteristics of objects into quantitative measures (similarity distance) and, as a result grouping them into clusters at relatively closer distances. By keeping all these considerations in mind, the present experiment was undertaken to study genetic diversity among 25 rice germplasms to identify diverse genotypes for future studies and further crop improvement.

MATERIAL AND METHODS

The experiment was carried out with twenty-five of rice along with 4 checks in Randomized Block Design (RBD) with three replications at Agricultural Research Station, Umedganj, Kota, Rajasthan, during *Kharif*

2023. The plot size for each genotype was 5m × 1.2 m with a spacing of 20 cm × 10 cm. The observations were recorded on five randomly selected plants per plot for nine characters *viz.*, plant height (cm), number of effective tillers/plant, number of panicle/m², number of grains/panicle, panicle length (cm), 1000-grain weight (g), grain yield/plant (g), whereas, the observations for days to 50% flowering and days to maturity were recorded on a whole plot basis. Using Mahalanobis D²

statistics, the data on different characters were subjected to an analysis of genetic divergence. The genotypes were then grouped into different intra-cluster and inter-cluster groups using Tocher's method, as described by Rao (1952). It calculates the relative contributions of each character to the overall divergence and quantifies the variation in intra- and inter-cluster distance.

Table 1: List of twenty five rice genotypes used in the study.

Sr. No.	Name of the genotypes	Source
1.	IET-29142	IIRR, Hyderabad
2.	IET-28954	IIRR, Hyderabad
3.	PR-124	PAU, Ludhiana
4.	IET-28950	IIRR, Hyderabad
5.	IET-28959	IIRR, Hyderabad
6.	IET-31004	IIRR, Hyderabad
7.	BPT-5204 (C)	IIRR, Hyderabad
8.	IET-31011	IIRR, Hyderabad
9.	IR-64(C)	IRRI, Philippines
10.	DRR Dhan-45	IIRR, Hyderabad
11.	DRR Dhan-48 (C)	IIRR, Hyderabad
12.	IET-31035	IIRR, Hyderabad
13.	Chittimuthyalu	IIRR, Hyderabad
14.	DRR Dhan-49	IIRR, Hyderabad
15.	HKR-126	HAU, Haryana
16.	HKR-128	HAU, Haryana
17.	PR-129	PAU, Ludhiana
18.	PR-130	PAU, Ludhiana
19.	HKR-46	HAU, Haryana
20.	HKR-47	HAU, Haryana
21.	PR-106	PAU, Ludhiana
22.	PR-131	PAU, Ludhiana
23.	PR-113	PAU, Ludhiana
24.	Govind	IIRR, Hyderabad
25.	Jaya (C)	NRRI, Cuttack

RESULTS AND DISCUSSION

The 25 genotypes were grouped into five clusters based on the Tocher's method, indicating the average D² values of intra and inter-cluster distance and the nearest and farthest cluster from each other based on D² Values that are presented in the Table 3. Among five clusters, cluster I was the biggest with 19 genotypes *viz.*, PR-113, JAYA, IET-31011, IET-28950, DRR Dhan-45, IET-31004, IET-31035, HKR-128, HKR-46, HKR-126, PR-130, PR-129, PR-106, IR-64, IET-28954, IET-28959, PR-124, PR-131 and Govind; cluster II contained 3 genotypes *i.e.*, Chittimuthyalu, DRR Dhan-49 and DRR Dhan-48 while, rest of the clusters contained a single genotype only. Cluster III (HKR-47), cluster IV (IET-29142) and cluster V (BPT-5204) were found to be monogenotypic. The intra-cluster distance ranged from 0.00 (cluster III, IV, V) to 51.5 (cluster II). Cluster II showed maximum intra-cluster distance values (51.5) followed by cluster I (38.14). While cluster III, IV and V reported zero intra-cluster distance, indicating these clusters were monogenotypic in nature. Higher intra-cluster distance displayed that there was greater diversity present among the genotypes assigned to those respective clusters and minimum intra-cluster distance, indicating that genotypes present in cluster were closely related to each other. Similarly,

the Inter-cluster distances varied from 82.23 to 249.98. The inter-cluster D² values was maximum between cluster III and IV(249.98), followed by cluster IV and V (217.18), cluster III and V (201.7), cluster II and III (190.79), cluster I and V(167.55), cluster II and cluster IV (127.21), cluster I and II (114.55), cluster II and cluster V (91.84), cluster I and cluster III (87.13) and cluster I and cluster IV (82.23). Wider genetic diversity among genotypes is indicated by a greater inter-cluster distance between two clusters. Thus, a high heterotic combination would arise from hybridization between genotypes having the maximum inter-cluster distance. The mean values of nine characters for five clusters are presented in Table 3. The cluster IV with genotype IET-29142 was found earliest for days to 50% flowering and days to maturity, while cluster III (HKR-47) had higher cluster mean for plant height (cm), number of effective tillers/plant, number of panicle/m², number of grains/panicle, panicle length (cm), 1000-grain weight (g) and grain yield/plant (g). Thus, in order to produce better and more desirable recombinants from hybridization programmes, a breeder must carefully integrate all the desired traits of diverse genotypes with high cluster mean values. Similar results were earlier reported by Rathan *et al.* (2020); Chhodavadiya *et al.* (2023).

Table 2: Grouping of 25 genotypes of rice into 5 clusters (by Tocher's method).

Cluster No.	No. of Genotypes	List of Genotypes
1	19	PR-113, JAYA, IET-31011, IET-28950, DRR Dhan-45, IET-31004, IET-31035, HKR-128, HKR-46, HKR-126, PR-130, PR-129, PR-106, IR-64, IET-28954, IET-28959, PR-124, PR-131 and GOVIND
2	3	Chittimuthyalu, DRR Dhan-49 and DRR Dhan-48
3	1	HKR-47
4	1	IET-29142
5	1	BPT-5204

Table 3: Average intra and inter-cluster distance based on corresponding D² values.

Clusters	1	2	3	4	5
1	38.14	114.55	87.13	82.23	167.55
2		51.5	190.79	127.21	91.84
3			0	249.98	201.7
4				0	217.18
5					0

Table 4: Mean values of different characters for 25 genotypes of rice grouped in different clusters.

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of effective tillers/plant	Number of panicles/m ²	Number of grains/panicle	Panicle length (cm)	1000-grain weight (g)	Grain yield/plant (g)
1	87.44	124.53	101.82	13.02	273.75	183.79	24.65	26.18	33.53
2	100	133.89	101.06	12.44	247.44	124.44	22.41	21.66	23.15
3	94.67	132	112.6	14.33	345.67	213	28.39	29.74	47.87
4	81	116	98.17	11.33	250	131.67	24.07	21.37	19.63
5	105	138	79.33	10.67	293.33	203.33	18.78	13.87	21.68

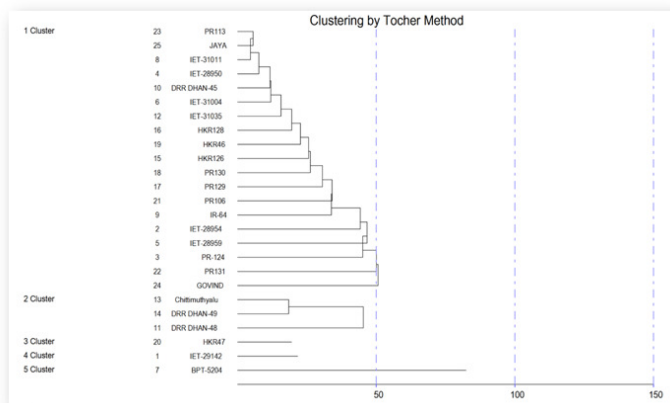


Fig. 1. Graphical representation of clustering by Tocher's method.

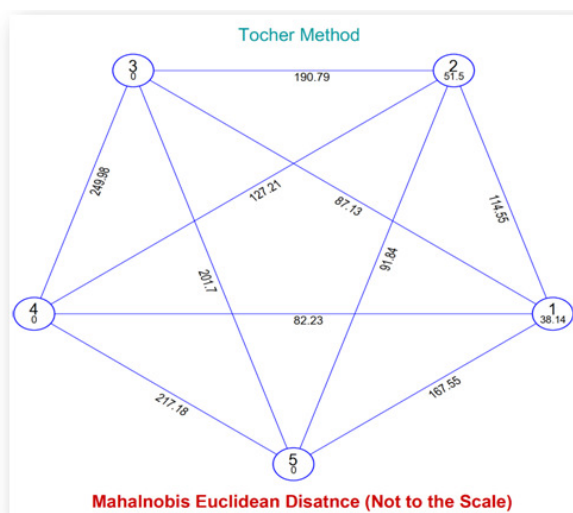


Fig. 2. Diagrammatic representation of intra and inter-cluster distance.

CONCLUSIONS

From the current study, it can be suggested that genotypes from cluster IV should be selected for developing early maturity varieties of rice while genotypes from cluster III should be selected for selection as parents in hybridization programmes for improving grain yield in rice. Maximum intra-cluster distance displayed by cluster II followed by cluster I, indicating that there was greater diversity present among these genotypes. Highest inter cluster distance was observed between cluster III and IV and cluster IV and V, which indicates wider genetic diversity among genotypes. Thus, the genotypes of these clusters should be employed in hybridization programmes to produce better and more acceptable recombinants in order to increase rice grain yield.

FUTURE SCOPE

Based on D² data, the current study aids in the identification of diverse genotypes which is pre-request for any successful breeding programmes for enhancing yield and its contributing attributes.

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Conflict of interest. None.

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