



Genetic Diversity Analysis for Yield Parameters in Rice (*Oryza sativa*. L) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. Author BS designed the study, performed the field work, statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Author BS managed in work planning and preparation of the manuscript. Authors RR, FS, YS and PJN managed the literature searches. Author MV managed the supervision of the present research work and corrected the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was conducted during *Kharif*, 2019 at Regional Sugarcane and Rice Research Station, Rudrur, Nizamabad. Twenty rice genotypes were studied to assess genetic diversity analysis for days to fifty percent flowering, plant height (cm), ear bearing tillers per m², panicle length (cm), number of filled grains per panicle, test weight (g) and plot yield (kg/ha). Based on the analysis, the genotypes were grouped into four clusters. The maximum number of genotypes (14 genotypes) was grouped in cluster I. Cluster II and III consists of three and two genotypes respectively. Remaining cluster was represented by a single genotype. Maximum inter cluster

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distance was observed between I and II (27.46) followed by between cluster I and IV (23.19) and between cluster II and IV (20.43) indicating wider genetic diversity between genotypes. Hence these lines may be utilized in a further breeding programme for the exploitation of hybrid vigour. Among the seven traits studied, the number of filled grains per panicle contributed maximum divergence (42.68%) followed by days to 50% flowering (32.04%), grain yield per plot (12.01%) and ear bearing tillers per m² (8.12%). Hence these altogether contribute more than ninety per cent towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Keywords: Genetic diversity; rice; yield parameters; genotypes.

1. INTRODUCTION

Globally rice is cultivated in an area of 161.1 million hectares with a production of 495.87 million metric tonnes [1]. In India, rice is cultivated in an area of 42.94 million hectares producing 112.9 million tonnes with an average productivity of 2585 kg ha⁻¹ [2].

In Telangana, rice is cultivated in 1.719 million hectares with a production of 5.825 million tonnes and an average productivity of 3387 kg ha⁻¹ [2]. To increase the productivity of country, there is a need to develop high yielding varieties.

The extensive phenotypic and genotypic variation within the *Oryza sativa* makes these varieties a powerful tool to study rice genetic diversity. Hence, to study the nature and magnitude of genetic divergence and characters contributing to it should be based on sound scientific procedures such as D² analysis to measure the genetic divergence among the test entries and their grouping into different clusters. Therefore, in addition to studies on mean performance, the evaluation of material for genetic divergence and variability and also association among various yield and quality would be more useful to the plant breeders. Parents identified, on divergence for any breeding program would be more promising [3]. Grouping or classification of genotypes based on a suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on a multivariate scale, Mahalanobis D² – statistic has proved to be a powerful technique [4].

2. MATERIALS AND METHODS

The present experiment was conducted during *Kharif*, 2019 at Regional Sugarcane and Rice Research Station Farm, Rudrur, Nizamabad. The materials comprised of 20 rice genotypes. The experimental material was planted in a randomized block design with three replications. Twenty-six days old seedlings were transplanted

at 20 cm apart between the rows and 15 cm between the plants. All the recommended agronomic practices and plant protection measures were taken up to raise a healthy crop. Data was collected from ten randomly selected plants from each plot and the observations viz., days to fifty per cent flowering, plant height, panicle length, number of productive tillers per m², number of filled grains per panicle, 1000 grain weight and grain yield per plot and were included in the study. The mean of five plants was subjected to statistical analysis. Wilk's criterion was used to test the significance of difference in the mean values for all the ten characters. Genetic diversity was studied following [5] D² statistics and clustering of genotypes was done on the basis of D² values according to Tocher's method as described by Rao [6]. Statistical analysis was done by INDOSTAT program.

3. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied, indicating the existence of variability among the genotype. Based on D² analysis, twenty genotypes were grouped into four clusters (Table 1). Cluster I was the largest comprising of fourteen genotypes followed by clusters II with three genotypes, cluster III with two genotypes, cluster IV was monogenetic cluster, suggesting the existence of a high degree of heterogeneity among the genotypes. The pattern of distribution of genotypes within different clusters was random and independent of geographical origin or region of adaptation [7].

The intra and inter cluster distance is presented in Table 2. Inter-cluster distance was higher than intra-cluster distance, indicating wider genetic diversity among the genotypes. The maximum inter-cluster distance was observed between cluster I and II (27.46) followed by between cluster I and IV (23.19) and between cluster II and IV (20.43). The greater the distance between two clusters, the wider the genetic diversity

among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high desirable segregants. The minimum inter-cluster distance was found between cluster III and IV (13.75). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties may not give desirable segregants.

The maximum intra-cluster distance was observed in cluster II (8.52) followed by cluster I (8.07) and cluster III (8.02). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through inter-varietal hybridization [8].

The cluster means for each of seven characters are presented in Table.3. It can be seen from the data that considerable differences existed for all the characters under study. The data indicated that the cluster means for days to 50 per cent flowering was highest in cluster VI (106.00) and the lowest in cluster I (82.38). Plant height was exhibited highest and lowest means in cluster I (122.03 cm) and IV (109.40 cm), respectively. Cluster III recorded highest mean for panicle length (26.08 cm), while lowest in cluster II (23.99 cm). Cluster III recorded the highest number of ear bearing tillers per m² (399.17) and the lowest recorded in cluster I (329.98). The number of filled grains per panicle was highest in cluster II (319.81) and lowest in cluster I (145.32). Cluster I showed highest test weight (25.44 g) while in cluster II it was low (15.26). Highest grain yield per plot was recorded in cluster II (9058 kg/ha) and lowest in cluster IV (7577.38 kg/ha). None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster II, and III recorded desirable mean value for maximum number of productive

traits thereby hybridization between genotypes of different clusters (cluster II and III) is necessary for the development of desirable genotypes.

The crossing between the entries belonging to cluster pairs having large inter cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in rice. Magnitude of heterosis for yield and its components were found to be higher in crosses between parents with intermediate divergence than the extreme one [9] and [10]. The selection on diverse parents for hybridization programme should be made after considering the inter-cluster distances and mean performance of genotypes for different characters. The lines belonging to diverse clusters and showing high mean performance in a desirable direction for different traits may be chosen as a parent.

The contribution of each trait to total divergence is presented in Table 4. The number of times that each of the seven characters appeared in the first rank and its respective per cent contribution towards genetic divergence. The results showed that the contribution of the number of filled grains per panicle was highest towards genetic divergence (42.68%) by taking 322 times ranking first, followed by days to 50% flowering (32.04 %) by 204 times, grain yield per plot (kg/ha) (12.01 %) by 85 times, ear bearing tillers per m² (8.21%) by 51 times. The minimum percentage of contribution was observed in test weight (4.16%) taking 24 times, followed by panicle length (0.9%) by eight times. The traits viz., number of filled grains per panicle, days to 50% flowering, and grain yield per plot, ear bearing tillers per m² contributed more than ninety per cent towards total divergence. The results were in conformity with [11,12,13]. Hence, these characters should be given importance during hybridization and selection in the segregating population under water stress condition.

Table 1. Clustering pattern among twenty rice genotypes

Cluster no.	No. of genotypes	Names of the genotypes
I	14	RDR-1935 (3), RDR-1929 (16), RDR-1933 (7), RDR-1931 (6), RDR- 1925 (13), RDR-1928(10), RDR-1921(4), RDR-1934(5), RDR-1920(9), RDR 1926(12), RDR-1614(1), RDR-1615(2), RDR-1930(17) and MTU-1010(18)
II	3	RDR-1927(11), RDR-1923(15) and RDR-1924(8)
III	2	RDR-1922 (14) and JGL-3844(20)
IV	1	JGL-3855 (19)

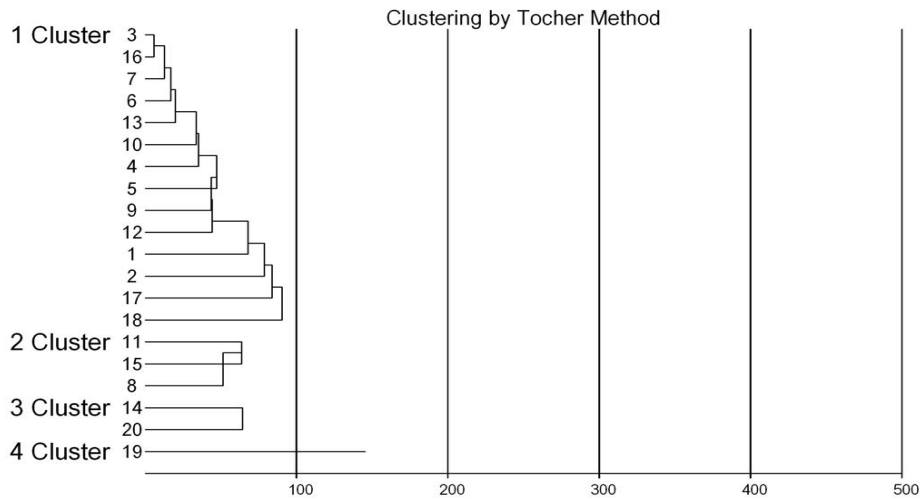


Fig. 1. Clustering by tocher method

Table 2. Intra (diagonal) and Inter cluster average of D² values of twenty rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	8.07	27.46	16.62	23.19
Cluster II		8.52	18.33	20.43
Cluster III			8.02	13.75
Cluster IV				0.00

Table 3. Cluster means of different yield characters in twenty rice genotypes

Cluster no.	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Ear bearing tillers per m ²	Number of filled grains per panicle	Test weight (1000 grain) (g)	Grain yield per plot (7m ²) (kg/ha)
Cluster I	82.38	122.0	24.14	329.98	145.32	25.44	7924.50
Cluster II	90.44	119.0	23.99	364.89	319.81	15.26	9058.53
Cluster III	92.50	112.0	26.08	399.17	215.67	22.29	8697.92
Cluster IV	106.00	109.4	24.97	337.00	215.27	17.73	7577.38

Table 4. Relative contribution of different traits towards total genetic divergence in rice

S. no.	Character	No. of times ranked first	Contribution (%)
1	Days to 50% flowering	204	32.04%
2	Plant height (cm)	0	0.00%
3	Panicle length (cm)	8	0.9%
4	Ear bearing tillers per m ²	51	8.21%
5	Number of filled grains per panicle	322	42.68%
6	Test weight (1000 grains)	24	4.16%
7	Grain yield per plot (kg/ha)	85	12.01%

4. CONCLUSION

Intra cluster D² values ranged from zero (cluster IV) to 8.52 (cluster II). Maximum intra cluster distance was observed in cluster II (8.52) indicating that some amount of genetic divergence still existed among the genotypes.

Advantage could be made use for further improvement through recombination breeding.

Based on the inter cluster distances, selection of genotypes from cluster II (RDR-1927, RDR-1923 and RDR-1924), Cluster IV (JGL-3855) and Cluster III (RDR-1922 and JGL-3844) would be

highly useful for generating desirable segregating populations.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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