Assessmentof genetic diversity for grain yield in rice (*Oryza sativa* L.) genotypes under humid south eastern plain of Rajasthan

Abstract

Rice (*Oryza sativa* L.) is the most staple food source and grain for more than half of the world's population, therefore identify the best suitable genotypes for proper crossing is important to produce high yielding potential varieties with best cooking and biochemical quality characters. Diversity helps the plant breeder in selecting the best parents for breeding programmes.The genotypes were divided into1 to6 clusters grounded byMahalanobis's D^2 statistics. Cluster II comprise with the highest number of (8) genotypes from differentlyoriginated and cluster I compriseof 7 cultivars exhibit supreme grain yield whereas cluster VI consisted with the leastnumberof (1) genotypes. Maximum inter-cluster distance was recorded between cluster III and VI. Cluster I had the principle mean values for grain yield and Number of productive tillers per plant and Cluster VI had the head mean values for 1000-grain weight. These clusters of cultivars may serve as prospective donors for future hybridization programs to create high yielders if they possess the desired traits~~.~~

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Keywords: Cluster diagram, D^2 statistics, genetic diversity, Rice (*Oryza sativa* L.), grain yield,tochermethod.

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Introduction

For more than half of the world's population, rice (*Oryza sativa* L.) is the most significant food source (Violita2019). Ninety percent of the rice consumed globally is grown in Asia. India ranks first in area 45.77 million hectare and second in the production 124.37 million tonneswith a productivity of 2717 kg/ha. (Anonymous, 2020-21). Major Rice producing states are West Bengal, Andhra Pradesh,Utter Pradesh, Telangana,Chhattisgarh, Tamil Nadu,Punjab and Haryana. Rajasthan occupies an area of 0.199 million hectares with the production of 0.46 million tones and productivity of 2310 kg/ha. (Anonymous, 2018-2019). Kota (Hadoti) region (humid south eastern plain zone) occupies an area of 0.099 million hectare with a production of 0.35 million tones and productivity of 3530 kg/ha (Anonymous, 2018-2019). The usage of hybrid types should be considered for perspective considering the growing global population and the demand for increased rice productivity~~.~~(Tait and Barker 2011). Identification of cultivars that are appropriate for use in hybrid production programs is crucial in this respect since the cultivars that serve as the parents of hybrid varieties must also have high levels of farmer acceptance and high levels of specific combining ability for seed production~~.~~(Okada and Whitford2019). The main goals of rice breeding are to improve the primary and secondary yield components, yield stability, and grain quality, all of which are crucial for yield potential~~.~~(Heinemann *et al*. 2019). Determining the genetic diversity of plant species is crucial for breeding programs because it influences the choice of acceptable parents and the best possible use of heterosis~~.~~(Luo*et al*. 2019). Commonly used methods for assessing genetic diversity among parental genotypes include physical and physiological variances of significant economic and quantitative variables~~.~~(Ibraheem and El-Ghareeb2019). In addition, Evaluation of genetic diversity is crucial for identifying the available germplasm's source genes for specific features~~.~~(Roy and Panwar, 1993). Assessment of genetic diversity within and within groups or clusters is crucial for the right parent selection and a more effective search for heterosis~~.~~(Murty and Arunachalam, 1966). Rice requires suitable methods for breeding and introducing high-yielding quality cultivars because variety is the foundation of plant breeding and

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this plant has a vast genetic diversity and high adaptability range. This demands a solid grasp of its diversity and nature. Therefore, in order to maximize the use of genetic resources and ensure correct donor parent selection, this study was conducted to identify the genetic diversity in rice.

Material and Method

The present investigation was conducted atthe experimental field of Agricultural Research Station Ummedganj Kota the experimental materialwere evaluated in Randomized Block Design (RBD) comprised of25 rice genotypes (table 1)during kharif2019. The experiment was laid out with three replications. Theseedlings were transplantedwith spacingof 20 cm between rows and 15 cm between plants andobservations were recorded for ten traits *viz*.,days to 50% flowering (DF50%), days to maturity(DM), plant height (PL) (cm), number of productive tillers per plant (PTPP) , panicle length (PL) (cm), number of grains per panicle (GPP), 1000-grain weight (GW) (g), amylase per cent, protein per cent and grain yield per plant (GYPP) (g).The experimental plots were examined using the standard set of package of practices. Ten randomly chosen plants from each genotype were used to collect data. The indostat software application assessed all of the analyses for ten different morphological features of 25 rice genotypes. Based on an examination of the D^2 statistics using Mahalanobis (1936), the genotypes were categorized into clusters.

Table 1: 25 rice genotypes listwith their sources

Source	Genotypes names
A.R.S. KOTA	R.S.K.-1155-2-4-1
A.R.S. KOTA	R.S.K.-1155-3-3-1
A.R.S. KOTA	R.S.K.-1157-4-5-1
A.R.S. KOTA	R.S.K.-1157-6-3-1
A.R.S. KOTA	R.S.K.-1157-9-2-2
A.R.S. KOTA	R.S.K.-1161-1-1
A.R.S. KOTA	R.S.K.-1163-8-1
A.R.S. KOTA	R.S.K.-1165-4-2
A.R.S. KOTA	R.S.K.-1165-4-3
A.R.S. KOTA	R.N.S.K-1167-11-1
A.R.S. KOTA	R.N.S.K-1168-2-1
A.R.S. KOTA	R.S.K.-1164-1-1
A.R.S. KOTA	R.S.K.-1172-1-1
A.R.S. KOTA	R.S.K.-1221-1-1
A.R.S. KOTA	R.S.K.-1162-8-1
A.R.S. KOTA	R.S.K.-1164-6-1
A.R.S. KOTA	R.S.K.-1164-6-2
A.R.S. KOTA	R.S.K.-1165-3-1
A.R.S. KOTA	R.S.K.-1165-3-2
A.R.S. KOTA	R.N.S.K-1167-5-1
A.R.S. KOTA	R.S.K.-1155-6-1-2
A.R.S. KOTA	R.S.K.-1155-6-3-1
I.A.R.I NEW DELHI	P1121
I.A.R.I NEW DELHI	P2511
I.A.R.I NEW DELHI	P1460

Result and Discussion

Table 2 shows the outcome of the genotypes being divided into six clusters. The 25 rice genotypes were divided into six groups based on the D^2 values. Cluster VI has a single genotype. In each cluster, Cluster II had the most genotypes (8), followed by Cluster I with (7), Cluster III with (4), Cluster IV with (3), and Cluster V with (2). Six clusters' inter- and intra-cluster distances were displayed in Table 3. Cluster IV had an intra cluster distance of 0.00, while cluster VI's was 29.170. Cluster III (12.560), Cluster II (23.010), Cluster I (16.160), Cluster V (13.300), and Cluster IV (29.170) were the clusters with the smallest intra-cluster distances.Cluster III and cluster VI had the greatest inter-cluster distance (495.100), followed by cluster I and cluster III (391.900), cluster III and cluster V (369.880), cluster IV and cluster V (225.640), and cluster II and cluster III (211.670). Cluster I and VI (55.230) and cluster I and V (64.170) had the least intercluster distances, with cluster II and V having the largest (50.170). Since clusters VI only contain one genotype, the intra-cluster distance for these clusters was seen to be 0. The distance between clusters within cluster IV was the greatest, followed by clusters II, I, V, and III. Cluster III and V had the greatest inter-cluster distance, which was followed by cluster I and III and cluster III and V.The anticipated genetic diversity between two clusters is larger the farther apart they are from one another. Kulsum *et al*. (2013), Khare *et al*. (2015), Kumar *et al*. (2015), Umesh *et al*. (2016), Rukmini *et al*. (2020), and Sadia *et al*. (2020) all showed comparable results. For traits like grain yield per plant and the number of productive tillers per plant, genotypes in Cluster I showed higher mean values. Contrarily, clusters like IV showed grain yield per plant, protein content, amylose content percent, as well as ideal characteristics for early flowering and maturity. Cluster VI for plant height, panicle length, number~~o.~~ of grain per panicle number, and 1000-grain weight. Therefore, to carefully combine all the desired features, hybridization between the chosen genotypes from dissimilar clusters is required.

Table 4 displays the cluster means of various quantitative features for various clusters. Cluster III had the days to 50 per cent flowering ~~-~~(79.080), followed by Cluster IV (86.220), and Cluster II (97.380), while Cluster V had the greatest value for days to 50% flowering (102.670), followed by Cluster VI (101.000), and Cluster I (98.860). Cluster III (113.000 days) and Cluster IV (121.780 days) showed early maturity, while Cluster V (137.830 days) and Cluster VI (137.330 days) showed late maturity. The cluster V is followed in plant height by the cluster V, both measuring 116.330 cm. For cluster III, the smallest plant height (99.330 cm) was noted.Cluster I (10.000) had the most productive tillers per plant, followed by Cluster IV (9.000) and Cluster V (8.500). While cluster III had the fewest productive tillers per plant (6.420) and cluster II had the most (6.920). Cluster III has the shortest panicle length (25.470) and is followed by cluster II (27.570) while cluster VI has the longest panicle length (28.770), followed by cluster I (28.530). Cluster V had the most grains per panicle (189.670), followed by cluster VI (178.000), and cluster II (172.710), while cluster III had the fewest grains per panicle (134.500).Cluster VI had the highest 1000-grain weight (g), followed by cluster I (28.200) and cluster IV (27.540), while cluster III had the lowest 1000-grain weight (22.520). Cluster I had the highest grain yield per plant (g) value, followed by clusters IV (15.610) and V (14.900), while cluster VI had the lowest output per plant (9.470 g). Cluster IV had the highest protein level (9.170), whereas cluster V had the lowest protein value (7.160). Cluster IV was predicted to have the highest amylose percentage (26.710), followed by cluster III (23.950) and cluster V (23.000). For traits like GYPP and the PTPP, genotypes in Cluster I showed higher mean values. The mean values for GYPP, protein Per cent, and amylose per cent were all higher in clusters like IV, which were also more favorable for early blooming and maturity. Cluster VI for PH, PL, GPP and weight per 1000 grains. Therefore, to carefully combine all the desired features, hybridization between the chosen genotypes from dissimilar clusters is required.

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Table 2: dividing the 25 rice genotypes into 6 clusters (using Tocher's approach)

Cluster No.	**Name of genotypes**	**Number of genotype**
i	R.S.K.-1155-2-4-1, R.S.K.-1155-3-3-1, R.S.K.-1157-4-5-1, R.S.K.-1157-6-3-1, R.S.K.-1157-9-2-2, R.S.K.-1155-6-1-2, R.S.K.-1155-6-3-1	7
ii	R.S.K.-1164-1-1, R.S.K.-1172-1-1, R.S.K.-1221-1-1, R.S.K.-1162-8-1, R.S.K.-1164-6-1, R.S.K.-1164-6-2, R.S.K.-1163-8-1,P1460	8
iii	R.S.K.-1165-4-2, R.S.K.-1165-4-3, R.S.K.-1165-3-1, R.S.K.-1165-3-2	4
iv	R.N.S.K.-1167-11-1, R.N.S.K.-1168-2-1,R.N.S.K.-1167-5-1	3
v	P1121, P2511	2
vi	R.S.K.-1161-1-1	1

Table 3: Based on the matching D^2 values, the average intra- and inter-cluster distance

Clusters	**i**	**ii**	**iii**	**iv**	**v**	**vi**
i	**16.160**	94.620	391.900	145.980	64.170	55.230
ii		**23.010**	211.670	133.360	50.170	130.440
iii			**12.560**	149.750	369.880	495.100
iv				**29.170**	225.640	210.400
v					**13.300**	109.740
vi						**0.000**

Table 4: Mean values of various attributes for 25 rice genotypes arranged in several clusters

Characters	**DF50%**	**DM**	**PH (cm.)**	**PTPP**	**PL (cm.)**	**GPP**	**1000-GW (g)**	**Amylose (%)**	**Protein (%)**	**GYPP (g)**
i	98.860	134.620	112.480	10.000	28.530	169.950	28.200	23.420	8.150	17.970
ii	97.380	132.330	107.380	6.920	27.570	170.710	23.860	23.480	8.000	11.030
iii	79.080	113.000	99.330	6.420	25.470	134.500	22.520	23.950	7.580	10.810
iv	86.220	121.780	102.780	9.000	27.810	151.890	27.540	26.710	9.170	15.610
v	102.670	137.830	116.330	8.500	27.730	189.670	24.430	23.000	7.160	14.900
vi	101.000	137.330	116.000	5.670	28.770	178.000	30.330	23.830	8.370	9.470

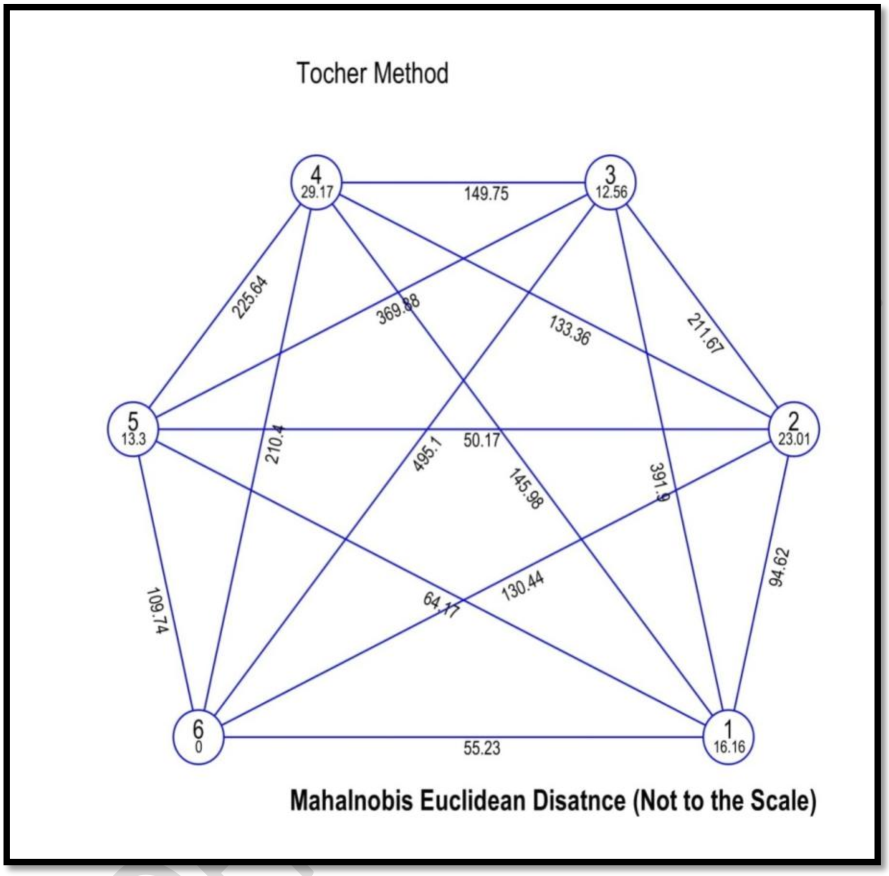

Fig 1:Cluster placement with relation to average intra and inter distance.

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Conclusion

The variety of the parents is crucial for a successful breeding program because crosses between parents with the highest genetic divergence are more likely to result in progenies with desired recombinants. However, depending on knowledge of the genetic variety and variability existing in the available germplasm, it is preferable to choose acceptable genetically divergent parents~~.~~(Singh and Chaudhary 1977). The genetic variety of many traits taken as a whole is frequently reflected in the variation between different genotypes within a species. The D^2 statistic, which Mahalanobis introduced in 1936, is one of the most effective methods for quantifying genetic diversity.This method assesses the generating forces at the intra and intercluster levels, assisting in the choice of genetically diverse parents for use in hybridization.The D^2 statistic quantifies the level of diversification and establishes the proportionate contribution of each character to the overall degree of divergence.

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