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Genetic diversity studies for yield and quality traits in rice (*Oryza sativa* L.)

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Abstract
The experiment was conducted with Twenty-five rice genotypes during *Kharif* 2022 in a Randomized Block Design with three replications at Research and Educational farm, Department of Agriculture Botany, College of Agriculture, Dapoli to study the genetic divergence for yield and quality traits. Genetic divergence calculated by Mahalanobis's D^2 statistic grouped twenty-five rice genotypes into six clusters. Out of six clusters, cluster II was the largest (9 genotypes) followed by cluster III (5 genotypes), cluster IV (5 genotypes), cluster I (4 genotypes), while remaining two clusters had one genotype each. The high intra-cluster value was recorded in cluster IV followed by cluster II, cluster III, cluster I, thus indicating that the genotypes constituted in high intra-cluster value clusters might have different genetic constitution. The inter-cluster values were maximum in cluster V and VI followed by cluster III and VI, cluster I and V, cluster II and VI indicating significant difference between these clusters. Hence, the genotypes included in these clusters may be used in hybridization programmes.

Keywords: Genotype, hybridization, genetic divergence etc.

Introduction

Rice (*Oryza sativa* L.) serves as a main food source for more than half of the world's population, especially in Asia and Africa. More than 100 countries cultivate this crop, in which Asia contribute majority in area and production. The United Nation designated year 2004 as the 'International Year of Rice' with the theme "Rice is life" to highlight the significance of the rice crop as a source of food, for trade, and the tight ties between rice-based systems, many cultures and people worldwide, especially in developing countries.

In the year 2021 around the world, rice is grown over an area of 165.25 million hectares, with a total production of 787.29 million tonnes and yield of 4.76 t/ha (FAOSTAT, 2021). In India, rice is raised on an area of 46.00 million ha with an annual yield of 130.84 million tonnes and a productivity of 2.607 t/ha (Anonymous, 2023) [1]. Maharashtra covered rice crop over 14.65 lakh hectares of land with an annual production of 32.76 lakh tonnes and an average productivity of 2.180 t/ha, (Anonymous, 2023) [1]. Konkan region of Maharashtra is a significant rice-producing area with an area of about 3.69 lakh hectare producing yield of around 12.94 lakh tonnes and productivity of about 2.93 t/ha, (Anonymous, 2023) [1].

Any crop improvement program's success is affected by the genetic diversity of the genotypes. Estimating the genetic diversity in yield attributes is crucial for the policies that choose parents in crossing programmes. The plant breeders tend to assess genetic diversity from morphological characters because this is inexpensive, rapid, and simple to score. Genetic diversities effects on rice crop production, quality, and sustainability were examined in the project, along with the economic and social implications for farmers and other stakeholders. Overall, this study will add to our understanding of rice genetic diversity and provide insight into possibilities for rice breeding and crop improvement.

Materials and Methods

The field experiment was conducted at Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri, Maharashtra state during *Kharif* 2022. The experiment was laid out in Randomized Block Design (RBD) with three replications. The experimental material, 25 genotypes of rice was sown in the nursery on raised beds and seedlings were transplanted after 30 days of sowing with a spacing of 20 cm × 15 cm. From each genotypes per replication, five competitive plants were chosen at random

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excluding border row to record observations on 19 yield and quality traits *viz.,* Days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, number of total spikelets per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose (%), protein (%), carbohydrate (%), fat (%), iron (ppm), zinc (ppm) and calcium (ppm). The mean of five plants was subjected to statistical analysis. Genetic divergence was analyzed through Mahalanobis's D^2 statistical technique and clustering of genotypes was done by using Tocher's method as described by Rao (1952) [7]. Wilk's criterion was used to test the significance.

Results and discussion
Genetic divergence analysis and D^2 values calculated with Mahalanobis's D^2 statistics distribute twenty-five rice genotypes into 6 clusters (Table 1) and depicted in Fig 1. Among the 6 clusters, cluster II accommodated a greater number of genotypes (9 genotypes) followed by cluster III and cluster IV having same number of genotypes (5 genotypes each), cluster I (4 genotypes), cluster V and cluster VI (1 genotype each). Same results were earlier confirmed by Chandramohan *et al.,* (2016) [2] and Soundharya *et al.,* (2020) [8]. Chandramohan *et al.,* (2016) [2] grouped 44 rice genotypes into 11 clusters and Soundharya *et al.,* (2020) [8] grouped 20 genotypes into 4 cluster.

Table 1: Distribution of 25 genotypes into SIX different clusters

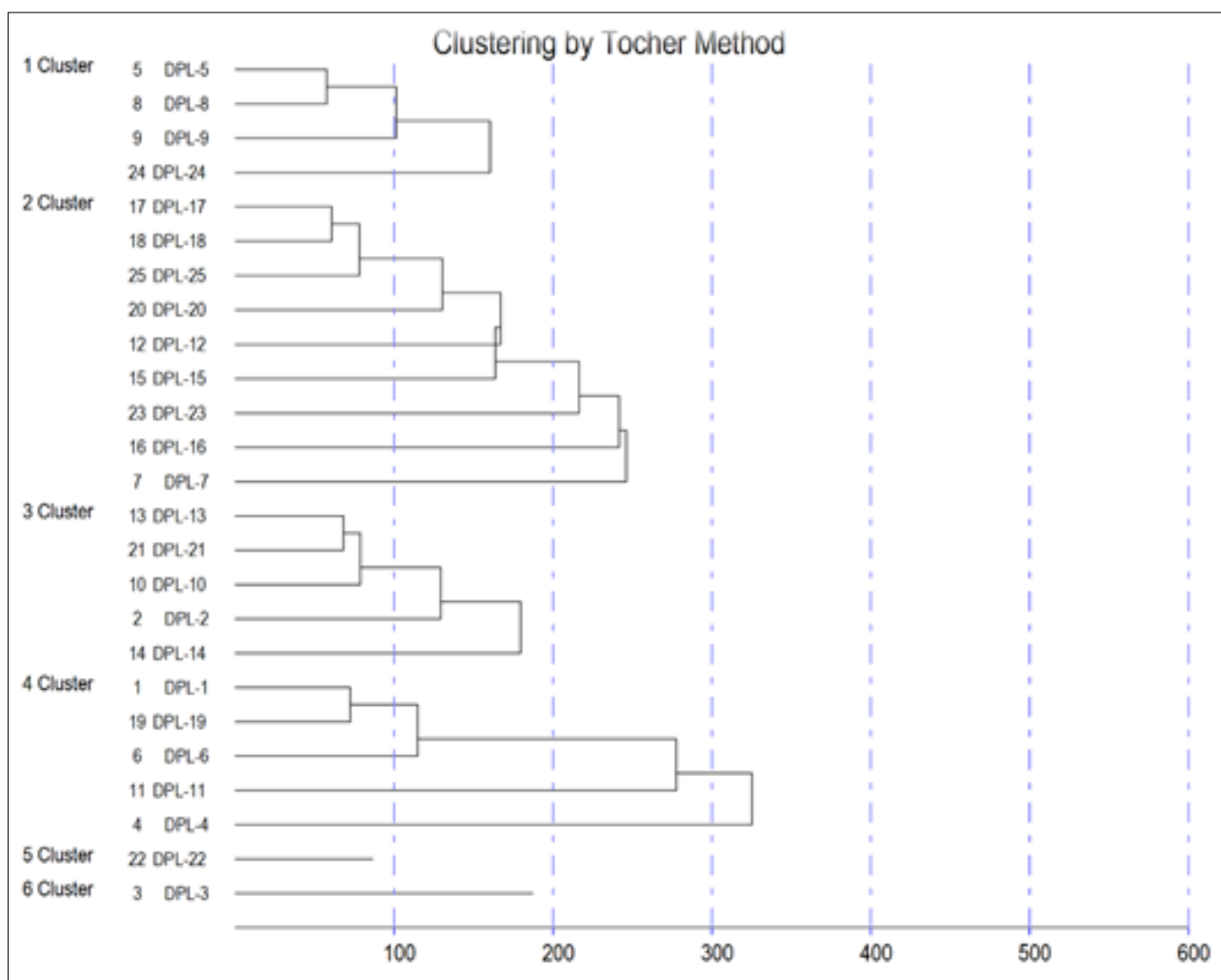| Cluster Group	No. of Genotypes	List of Genotypes
I	4	DPL-5, DPL-8, DPL-9 & DPL-24
II	9	DPL-17, DPL-18, DPL-25, DPL-20, DPL-12, DPL-15, DPL-23, DPL-16 & DPL-7
III	5	DPL-13, DPL-21, DPL-10, DPL-2 & DPL-14
IV	5	DPL-1, DPL-19, DPL-6, DPL-11 & DPL-4
V	1	DPL-22
VI	1	DPL-3

Fig 1: Clustering by tocher method

Intra and Inter cluster distances were given in Table 2 and depicted in Fig 2. The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes. The maximum intra-cluster D^2 value was observed for cluster IV (315.33) followed by cluster II (230.42), cluster III (171.85), cluster I (167.05), whereas both cluster V and cluster VI observed zero intra-cluster D^2 values. The high intra cluster values in cluster IV indicated the presence of wide genetic diversity among the genotypes. Devi *et al.,* (2019) [3] reported similar findings.
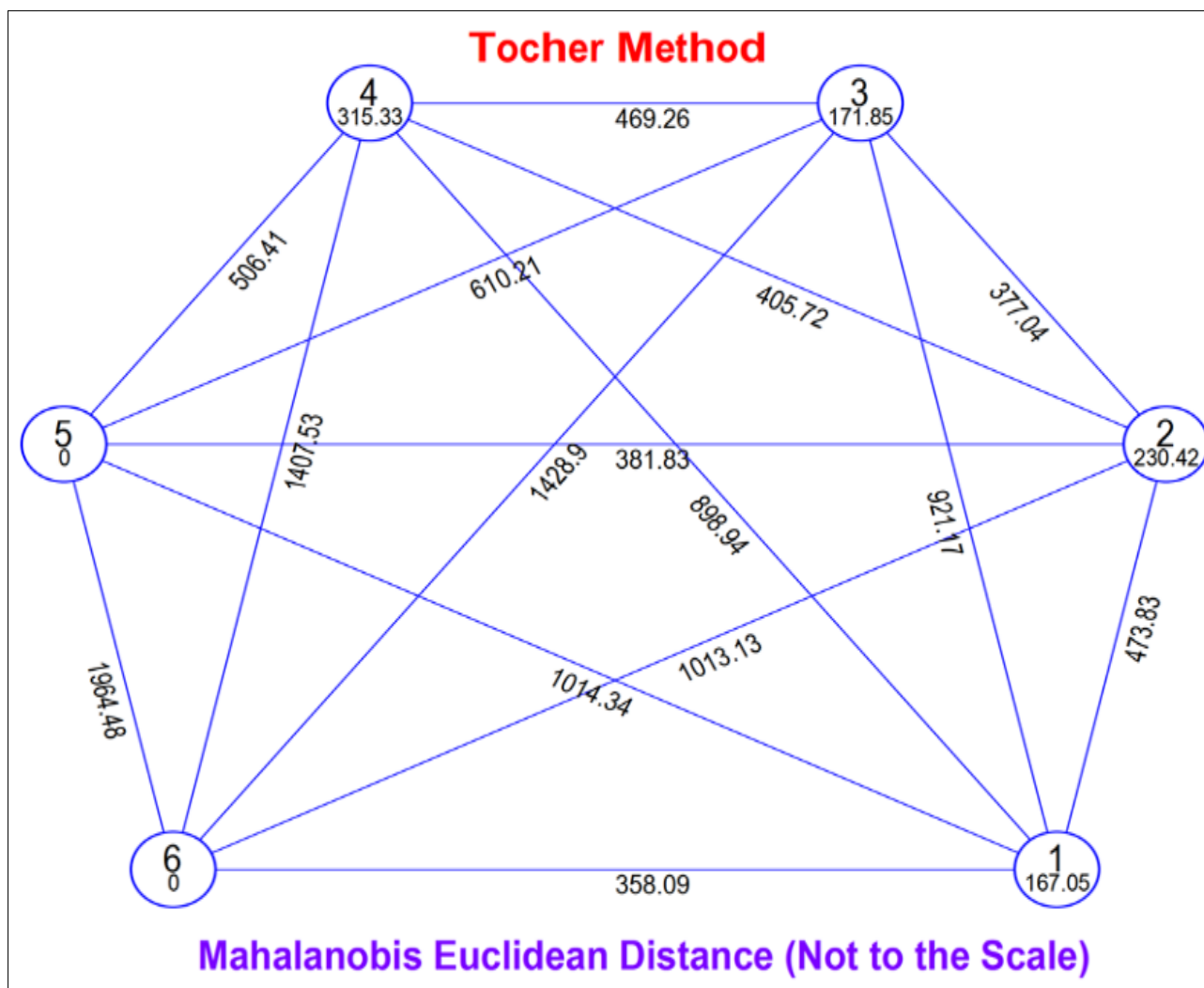
Fig 2: Cluster Diagram (Tocher Method)

Table 2: Average intra and inter cluster values in six clusters (D^2) in rice

	I	II	III	IV	V	VI
I	167.05	473.83	921.17	898.94	1014.34	358.09
II		230.42	377.04	405.72	381.83	1013.13
III			171.85	469.26	610.21	1428.90
IV				315.33	506.41	1407.53
V					0.00	1964.48
VI						0.00

The maximum inter-cluster D^2 value was observed between cluster V and cluster VI (1964.48), then between cluster III and cluster VI (1428.90), cluster IV and cluster VI (1407.53), cluster I and cluster V (1014.34) and cluster II and cluster VI (1013.13), whereas minimum inter-cluster D^2 values was recorded between cluster I and cluster VI (358.09) then between cluster II and cluster III (377.04), cluster II and cluster V (381.83), cluster II and cluster IV (405.72) and cluster III and cluster IV (469.26). Umesh *et al.,* (2016) [10] recorded similar results and support the current findings.

The cluster mean values for 19 traits are given in Table 3 and indicated a wide range of mean values between the traits. Percent contribution of various characters towards genetic divergence is also given in Table 3. The experimental finding displays that the contribution of grain yield per plant (15.77%) was highest towards genetic divergence followed by straw yield per plant (12.32%), harvest index (8.5%) test weight (8.22%), number of total spikelets per panicle (7.88%), number of filled grains per panicle (7.43%), days to fifty percent flowering (4.34%), protein content (4.32%), panicle length (3.88%), days to maturity (3.76%), number of productive tillers per plant (3.76%) respectively to the genetic divergence. These findings were supported by Toshimenla *et al.*, (2015) and recorded maximum contribution of grain yield per plant towards genetic divergence. Chandramohan *et al.,* (2016) [2] recorded higher contribution of days to 50% flowering and 1000 grain weight towards total divergence. Soundharya *et al.*, (2020) [8] reported higher contribution by number of filled grains per panicle followed by days to fifty percent flowering.

The lowest contribution towards genetic divergence from the character Ca content (1.33%), followed by Zn content (1.67%), amylose content (2.33%), carbohydrate content (2.54%), plant height (2.65%), spikelet fertility (2.65%), Fe content (3.21%), fat content (3.44%) respectively to the genetic divergence.

Table 3: Cluster mean performance and contribution towards divergence of nineteen characters in rice genotypes

Sr. No.	Characters	Clusters						Contribution%
		I	II	III	IV	V	VI	
1.	Days to fifty percent flowering	114.08	98.04	81.53	92.20	94.33	122.67	4.34
2.	Days to maturity	145.42	127.85	110.73	123.73	124.00	150.00	3.76
3.	Number of productive tillers per plant	6.62	6.70	7.93	6.76	5.67	7.20	3.76
4.	Panicle length (cm)	24.30	23.68	21.36	25.15	23.33	22.20	3.88
5.	Plant height (cm)	141.97	119.76	93.72	108.29	87.37	160.2	2.65
6.	Grain yield per plant (g)	14.02	15.02	12.85	20.28	18.15	12.45	15.77
7.	Straw yield per plant (g)	25.12	22.06	20.80	26.52	24.88	24.53	12.32
8.	Harvest Index (%)	35.86	40.39	38.39	42.96	42.20	33.64	8.5
9.	Test weight (g)	20.75	24.76	21.10	23.02	33.09	14.31	8.22
10.	Number of filled grains per panicle	99.05	112.62	81.19	155.54	128.99	82.53	7.43
11.	Number of total spikelets per panicle	134.61	151.46	103.54	191.06	165.00	113.02	7.88
12.	Spikelet fertility (%)	74.22	74.68	78.44	81.42	78.18	73.02	2.65
13.	Protein (%)	5.66	5.85	6.54	7.36	4.37	8.68	4.32
14.	Amylose (%)	19.18	19.06	20.83	20.66	20.38	20.89	2.33
15.	Carbohydrate (%)	80.29	81.16	82.12	80.17	82.52	79.68	2.54
16.	Fat (%)	15.01	15.91	15.91	15.77	17.28	16.04	3.44
17.	Fe (ppm)	16.12	15.62	17.13	16.38	15.30	16.87	3.21
18.	Zn (ppm)	12.22	11.41	12.05	10.08	9.90	7.32	1.67
19.	Ca (ppm)	90.39	90.70	91.65	82.25	56.28	56.71	1.33

Conclusion

The current study revealed that the genotypes included in cluster V and VI are most diverse to each other due to maximum inter-cluster value. Therefore, genotype included in these clusters *viz*., DPL-22 and DPL-3 have a broad-spectrum variability in segregating generations and may be used for hybridization programme. Among nineteen characters studied, grain yield per plant recorded highest contribution towards genetic divergence followed by straw yield per plant, harvest index and test weight. Hence, these characters may be taken into account during selection of genotypes for further crop improvement programmes.

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