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Genetic Divergence Analysis for Early Maturity, Yield and Yield Attributing Traits in Elite Rice (*Oryza sativa* L.) Germplasm

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ABSTRACT: Thirty-six genotypes of rice were imperiled to Mahalanobis's D^2 analysis to appraise the genetic diversity. All these entries were classified into five clusters with maximum intra cluster distance for cluster III (153.89). The maximum distance (intercluster) between cluster II and V (658.46 cm) followed by 632.32 cm (cluster II and IV), 577.58 cm (cluster III and V), 565.13 cm (cluster I and V) and 465.78 cm (cluster II and III). Least inter cluster distance was detected for cluster I and II (241.78 cm). Among the thirteen characters studied days to attain 50% flowering (21.9%), spikelets/panicle (17.43%), test weight (15.86%) and harvest index (15.00%) were the foremostsponsors towards divergence and accounted for about 70.19% of contribution towards total divergence.

Keywords: Rice, D^2 analysis, Genetic divergence, Inter and Intra cluster distance.

INTRODUCTION

Rice (*Oryza sativa* L.) is the foremostindispensable cereal cultivation crop in the world. Rice is also known as the "Grain of Life" because it being the staple food for more than 70% of our national population and source of livelihood for 120-150 million rural households and it is a backbone to the Indian agriculture (Singh *et al*., 2018). Uttar Pradesh is India's second largest rice producer, with 15.54 million tonnes (or 13.34 percent of total production) and 2.7 t/ha productivity (Agriculture statistics at a glance -2019, DAC&FW, GoI). Thus, it is understood that there is an extreme need for crop improvement.

In a crop advancement programme, it's critical to keep a pool of diverse and appealing donor parents on hand to help the breeder generate high-yielding rice varieties (Joshi *et al.*, 2013). Genetic diversity in crop plants is essential to sustain level of high productivity (Tripathi *et al.*, 2013). Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population (Ranjith *et al.*, 2018). It is the most important tool in the fingers of the plant breeder in choosing the dominantpaternities for hybridization programme. In light of foregoing, the current study aims to determine the genetic divergence for 35 elite rice lines (ABL) in terms of early maturity, yield, and quality attributes.

MATERIAL AND METHODS

The existingstudy was conducted at the Field Experimental Center of Department of Plant breeding, Naini Agricultural Institute, Shuats, Prayagraj, U.P. during *Kharif*-2020. The experimental material consists of 35 ABLs and one check varietylaid in Randomised Block Design (RBD) with three replications each.

Regular agronomic procedures were used to raise the crop. Days to attain fifty percent flowering, days to physiological maturity, and grain yield per plot were all recorded from all plants. Five plants were chosen at random from each genotype in each replication to record the yield and its causal features for the remaining characters.The genetic discrepancy among the genotypes was determined using multivariate analysis of Mahalanobis's D^2 (1936) and genotypes were classified into various clusters following Torcher's method (Rao, 1952).

RESULT AND DISCUSSION

The 36 accessions were clustered into five clusters based on their respectiveD^2 values (Table 1 and Fig. 1). Out of 5 clusters, cluster I is the major cluster encompassing 27 genotypes after that cluster II having 3 genotypes, cluster III having 4 genotypes, cluster IV and V each having 1 genotype and its group constellation pattern demonstrated the extension of significant amount of variability.

Table 1: Distribution of 36 rice genotypes into five cluster by Tocher's method.

Cluster number	Number of genotypes	Names of Genotypes
I	27	SHUATSDHANABL-06, SHUATSDHANABL-25, SHUATSDHANABL-21, SHUATSDHANABL-14, SHUATSDHANABL-23, SHUATSDHANABL-11, SHUATSDHANABL-24, SHUATSDHANABL-28, SHUATSDHANABL-17, SHUATSDHANABL-09, SHUATSDHANABL-03, SHUATSDHANABL-20, SHUATSDHANABL-05, SHUATSDHAN-7, SHIATSDHAN-2, SHUATSDHANABL-22, SHUATSDHANABL-26, SHIATSDHAN-5, SHUATSDHANABL-07, SHUATSDHAN-6, SHUATSDHANABL-12, SHUATSDHANABL-13, SHUATSDHANABL-04, SHUATSDHANABL-02, SHUATSDHANABL-01, SHIATSDHAN-3 and SHIATSDHAN-4.
II	3	SHUATSDHANABL-16, SHUATSDHANABL-19 and SHIATSDHAN-1
III	4	SHUATSDHANABL-08, SHUATSDHANABL-10, SHUATSDHANABL-27 and SHUATSDHANABL-18
IV	1	SHUATSDHANABL-15
V	1	NDR-359 (Check)

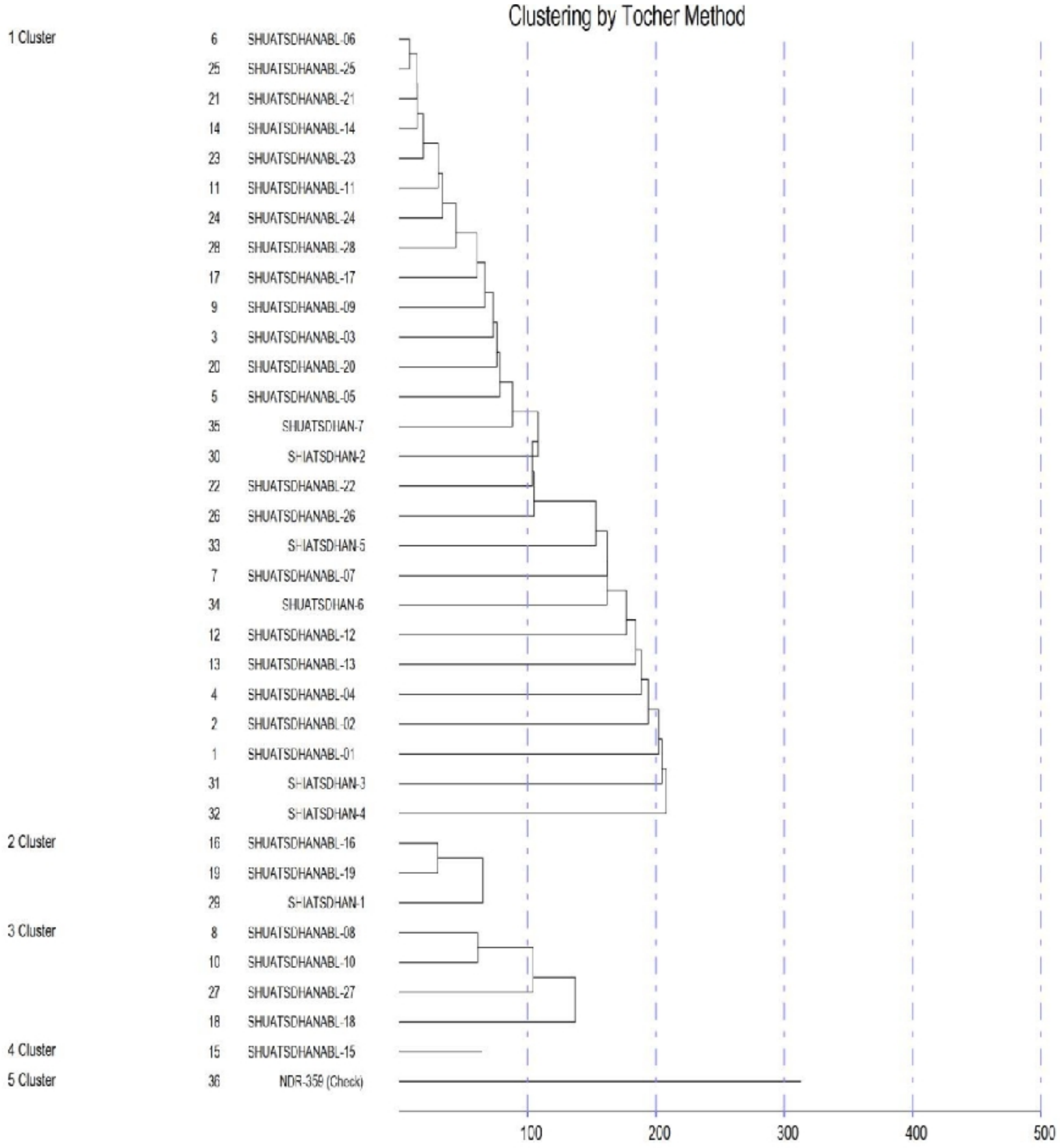

Fig. 1. Dendrogram showing clustering pattern of 36 rice genotypes during *Kharif*- 2020 using Tocher's method.

Cluster III (153.89) had the greatest intra cluster distance, followed by cluster I (151.31), cluster II (75.4), and cluster IV and V (0.00) (Table 2 and Fig. 2), demonstrating that there is discrepancy among germplasm lines within these clusters.This helps in bringing together diverse gene combinations, promising hybrid derivatives probably due to complementary interaction of divergent genes in parents.

The inter cluster distance ranged from 241.78 cm (cluster I and II) to 658.46 cm (cluster II and V) respectively. The highest distance (intercluster) was marked between cluster II and V (658.46 cm) from the (Table 2 and Fig. 2) followed by 632.32 cm (cluster II and IV), 577.58 cm (cluster III and V), 565.13 cm (cluster I and V) and 465.78 cm (cluster II and III). Shortest distance (intercluster) was marked for cluster I and II (241.78 cm) (Table 2). The selection of contrary genotypes from the above clusters would result in a varied range of yield variability, allowing for further selection and genetic improvement.Almost identical results were reported by Satish *et al.*, (2017), Maumitha *et al.*, (2019) and Supriya *et al.*, (2017).

Table 2: Estimates of average intra (diagonal) and inter cluster average distances for different quantitative characters in rice.

	1 Cluster	**2 Cluster**	**3 Cluster**	**4 Cluster**	**5 Cluster**
1 Cluster	**151.31**	241.78	286.74	280.04	565.13
2 Cluster		**75.4**	465.78	632.32	658.46
3 Cluster			**153.89**	436.71	577.58
4 Cluster				**0**	441.39
5 Cluster					**0**

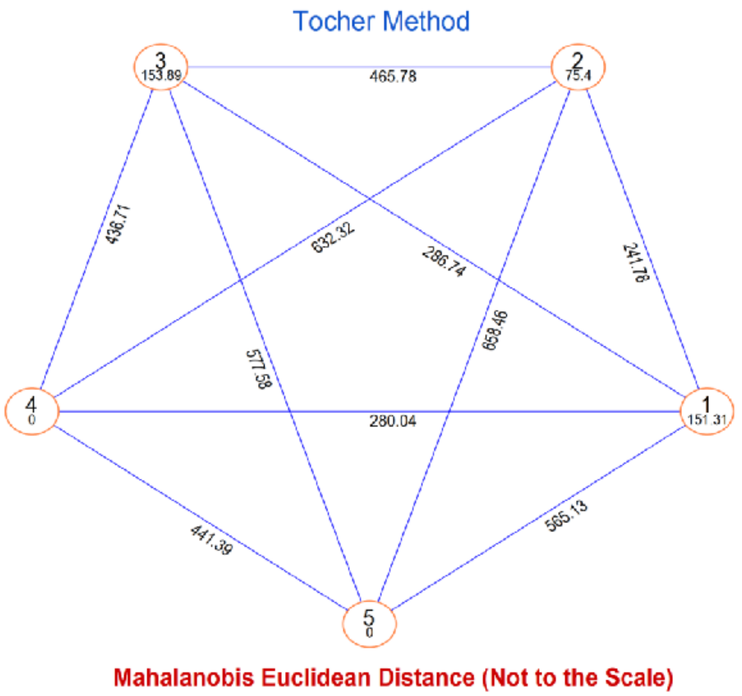

Fig. 2. Cluster diagram showing relative position of clusters and the inter and intra cluster distances within them (distances are not the scale).

Table 3 shows the cluster means of thirteen characters across five clusters under submergence conditions. There were no genotypes with all of the desirable qualities that could be directly selected in any of the clusters.Cluster V (NDR-359) (Check) had showed utmost mean values for tillers/hill, length of the panicle, flag leaf length, flag leaf width and biological yield/hill followed by cluster IV (SHUATSDHANABL-15) had exhibitedmaximum mean values for panicle/hill, harvestindex, test weight and grain yield/hill. Cluster III (SHUATSDHANABL-08, SHUATSDHANABL-10, SHUATSDHANABL-27 and SHUATSDHANABL-18) had maximum mean values for days to attain 50% flowering, plant height and days to attain maturity. In future breeding programmes, genotypes selected from these clusters with maximun mean values would bechosen directly as parents. While conducting genetic diversity studies in deep water rice genotypes. Bose and Pradhan (2005) and Sridhar *et al.*, (2016) revealed similar findings.

When selecting on clusters for further selection and making choice of parents for hybridization, the traits that contribute the most to the divergence should be given more weight.Out of thirteen characters studied, the supreme contribution towards divergence (Table 4) was made by D50% F (21.9%), spikelets/panicle (17.43%), test weight (15.86%) and harvest index (15.00%) which accounted for about 70.19% of total divergence. As a result, these characteristics should be prioritized when selecting parents for hybridization programmes.The results were in conformism with Ramanjaneyulu *et al.*, (2014) and Devi *et al.*, (2015) for 1000 grain weight, Srinivas *et al.*, (2015) for days to fifty percent flowering and number of filled grains per panicle.

Table 4 and Fig. 3 shows the number of times each of the thirteen characters appeared in first rank, as well as their percentage contribution to genetic divergence.The findings revealed that the contribution of days to attain 50% flowering (21.9%) by 138 times ranking first subsequently number of spikelets per panicle (17.43%), test weight (15.86%), harvest index (15.00%) and plant height (0.32%) by taking twice ranking first, grain yield per (9.00%) by one time.

Table 3: Cluster Means for 13 quantitative traits in 36 rice genotypes for *Kharif*- 2020.

Characters	Days to 50% Flowering	Plant Height (cm)	Tillers/ hill	Panicles/ hill	Panicle Length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Spikelets/ panicle	Days to Maturity	Biological yield /hill (g)	Harvest index (%)	Test weight (g)	Grain yield per hill (g)
Cluster 1	91.44	118.57	9.28	8.91	25.47	33.5	1.28	159.69	121.47	37.09	50.69	23.22	18.79
Cluster 2	90.89	116.56	8.44	8.25	24.89	32.11	1.21	242.22	120.89	38.68	51.35	17.87	19.79
Cluster 3	103.5	119.17	9.03	8.8	23.75	34.83	1.55	144.83	133.5	43.47	48.3	20.36	21.09
Cluster 4	85.33	125	10.07	9.8	25.67	35	1.62	103	115.33	43.97	54.28	31.4	23.88
Cluster 5	98	104.67	20.22	17	34.55	43.33	1.99	223	130	48.97	46.38	30.11	22.62

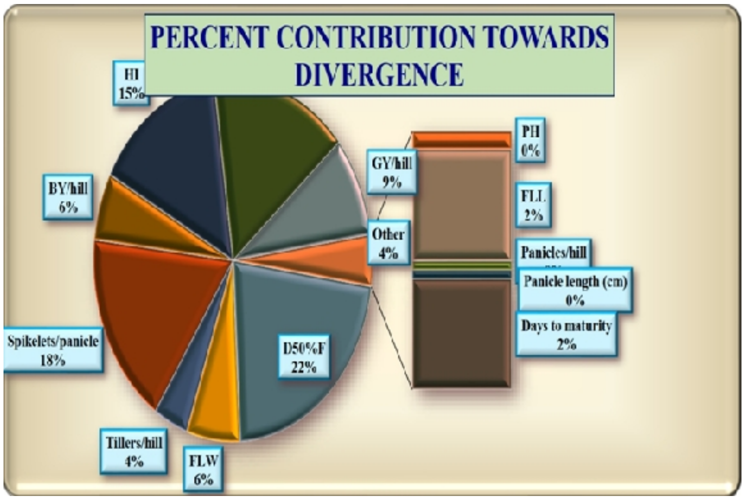

Fig. 3. Percent contribution towards divergence.

Table 4: Percent contribution of different quantitative characters to genetic diversity.

Sr. No.	Source	Contribution %	Times ranked 1st
1	D50%F	21.9	138
2	Plant height	0.32	2
3	Tillers/hill	4	0
4	Panicles/hill	0.16	0
5	Panicle length	0.16	0
6	Flag leaf length	2	0
7	Flag leaf width	6.19	0
8	Spikelet's/panicle	17.43	2
9	Days to maturity	1.98	0
10	Biological yield/hill	6	0
11	Harvest index	15	2
12	Test weight	15.86	2
13	GY/hill	9	1

CONCLUSION

Cluster analysis revealed that there was a lot of variation between germplasm lines in different clusters for different characteristics in the studied population. Recombination breeding between germplasm lines belonging to Cluster III, which has the shortest intra-cluster distance, can increase yield potential.Because the longest inter-cluster distance was seen between cluster II and V, cluster II and IV, cluster III and V, cluster I and IV, and cluster III and V, taking into consideration crosses involving genotypes from these clusters would promote extensive and desirable recombination in segregating generations.

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