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Estimation of genetic variability, heritability and diversity for grain yield component characters in Rice (*Oryza sativa* L.)

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Abstract

The present study consists of 40 rice genotypes including one check variety were evaluated at Field Experimentation Centre of the Department of Genetics and Plant Breeding, to estimate genetic variability, heritability and diversity for 13 quantitative characters. The experiment was conducted by using Randomized Block Design with three replications during *Kharif*, 2021. MTU-1172 (71.287) to be high yielding followed by, MTU-1155 (67.334), SHIATS DHAN-6 (62.133) showed higher yield over the NDR359 (check). High to moderate estimates of GCV and PCV were recorded for Grain yield per hill followed by biological yield, harvest index, number of tillers/hill, test weight, number of spikelets/hill, number of panicles/hill, flag leaf width, flag leaf length and plant height. Divergence analysis following Mahalanobis (1936) D^2 analysis has revealed presence of substantial amount of genetic diversity among the genotypes. These 40 genotypes were grouped into 6 clusters by following Tocher's method as described by Rao (1952). Cluster I contain 35 genotypes, while the cluster II, III, IV, V, VI were Monogenotypic. The maximum inter cluster distance was observed between Cluster II and IV (188.41) and minimum between cluster I and II (152.00). Variance of cluster means revealed that Biological yield, Grain yield per hill, Number of spikelet's had a maximum contribution towards divergence in the present material. Thus, these genotypes present in these clusters provide a broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes for grain yield improvement in rice genotypes.

Keywords: Rice, GCV, PCV, variability, heritability, genetic divergence

Introduction

Rice (*Oryza sativa* L.), a member of the genus *Oryza* and family Gramineae, is one of the most important cereal food crops in the world (Poaceae). Only two species *Oryza sativa* and *Oryza glaberrima* are domesticated out of the 24 that make up the genus. *Oryza sativa* is a species with 12 basic chromosomes or 2n=24. Indica, Japonica, and Javanica are the three subspecies into which *Oryza sativa* cultivars can be separated. Indica rice cultivars can be grown in tropical and subtropical climates. Japonica cultivars are cultivated across the temperate zone, while Javanica varieties are mostly grown in select areas of Indonesia.

One of the main cereal crops, rice (*Oryza sativa* L.), provides the bulk of the world's population's carbohydrate needs. It provides 160 million economically disadvantaged people in rural areas with a means of surviving while also satisfying the caloric needs of 50% of the population (Santha *et al.*, 2016).

Perhaps the first grain was rice, which has been farmed for 10,000 years (Kovach *et al.*, 2007). In order to recognize the significance of rice, which is a staple food for 2.7 billion people worldwide, the International Year of Rice was founded in 2004. 9 percent of the world's arable land is occupied by it. Each year, rice provides 15% of the world's protein and 21% of the calories consumed by humans (IRRI, Rice Almanac, 4th Edition). 164.19 million hectares are currently used to grow rice, with an average yield of 4.25 tons per hectare and an annual production of roughly 513.02 million tons (USDA-2021). Asia, also referred to as the "rice bowl", produces and consumes more than 90% of the world's rice.

In India, rice is a staple food of 65% of the total population. It constitutes about 42% of the total food grain production and 45% of total cereal production. In India, rice is grown in 44.78 million ha, the production level is 115.65 million tons and the productivity is about 2.7 tons/ha during 2018-19 (NRRI-2019).

Genetic variability between the traits is essential for breeding and choosing the desired qualities. Heritability estimates that take genetic development into account are often better at foretelling the gain subject to selection. On the other hand, crop species need genetic variety to maintain high levels of output. The significance of knowledge on the level of genetic divergence in rice and its use for either choosing ideal parents or taking advantage of hybrid vigour. Finding varied genotypes to use in a hybridization programme to maintain variety is greatly aided by the analysis of the degree of divergence in a specific experimental material. It has been found that the Mahalanobis D^2 statistic is a useful tool for estimating genetic divergence within a population.

Materials and Methods

The experimental material for present investigation consists of forty genotypes including one check variety (NDR-359) obtained from Andhra Pradesh Rice Research Institute (APRRI) and Regional Agricultural Research Station (RARS), Maruteru and Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj Uttar Pradesh, was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj, U.P. during *Kharif* 2021-2022. The land was prepared by two harrowing followed by puddling. The experiment was conducted in Randomized Block Design (RBD) with three replications. The genotypes were sown on raised bed on 28th June, 2021 and transplanted om 21st July 2021 with Plant spacing between row to row and plant to plant is 20 cm × 15 cm.

In each replication and in each plot, selection of five plants is done randomly and tagged except the border plants to minimize border effects. All the 13 characters studied and recorded on five randomly selected plants except days to flowering and days to maturity. grain weight of the grains was recorded with the help of physical balance.

The software called “R-Language” was used to perform the analysis mentioned above.

Results and Discussion

Analysis of variance for quantitative characters of rice (*Oryza sativa* L.)

Analysis of variance for different characters is presented in Table 1. The mean squares due to genotypes showed highly significant differences (α=0.01) for all characters indicating the presence of substantial amount of genetic variability among the rice genotypes. It indicated that there is an ample scope for selection of promising lines from the present gene pool for yield and its component characters. The presence of large amount variability might be due to diverse source of material taken as well as environmental influence affecting the phenotypes. Replications were non-significant for all the characters indicating good homogeneity among replications.

Among 40 genotypes, genotype MTU-1172 (71.287gm), MTU-1155 (67.334gm), SHIATS DHAN-6 (62.133gm), MTU-1224 (54.85gm), SHIATS DHAN-2 (51.467gm) were found to be superior in grain yield.

In the present study phenotypic coefficient of variation were higher than genotypic coefficient variation indicating that these characters are influenced by the environment for all the characters. Classified variability as low if coefficient of variation (<10%), moderate (10-20%) and high (>20%). High PCV and GCV were observed for the grain yield per hill (35.618), biological yield (30.927), harvest index (26.051), number of tillers/hill (23.941), test weight (22.591), number of spikelet’s (21.254), number of panicles/hill (20.109). moderate PCV and GCV were observed for the flag leaf length (16.747), flag leaf width (15.162), days to 50% flowering (13.466), plant height (10.308). Low PCV and GCV were observed for the panicle length (9.772), days to maturity (7.439).

Heritability

Johnson *et al.* (1955) Classified heritability as low (<30%), medium (30-60%), and high (>60%). The following traits having the higher heritability days 50% flowering (95.075), biological yield (94.048), grain yield per hill (93.654), test weight (92.934), days to maturity (91.662), number of tillers/hill (90.479), number of spikelets per panicle (90.163), number of panicles/hill (88.853), harvest index (83.291), flag leaf width (81.907), flag leaf length (81.322), plant height (60.019). A moderate heritability observed for panicle length (38.896).

Genetic Advance as percent mean

The estimation of genetic advance as percent mean is classified as low (<10%), moderate (10 to 20%) and high (>20%) proposed by Johnson *et al*., 1955. High GAM was observed for grain yield per hill (68.717), biological yield (59.919), harvest index (44.698), number of tillers (44.623), test weight (43.249), number of spikelet’s (39.477), number of panicles/hill (36.806), flag leaf length (28.054), days 50% flowering (26.373), flag leaf width (25.583). Except panicle length (7.83) the following characters shows moderate gam for days to maturity (14.047), plant height (12.745).

Mahalanobis D^2 analysis

The data collected on 13 yield and yield contributing characters for 39+1(check) genotypes of rice were subjected to genetic divergence by using Mahalanobis D^2 statistic. The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity. The distribution of 39+1 (check) genotypes into six clusters was by Tocher method at a random with maximum number of genotypes (Thirty-five) for Cluster I and minimum (one) in Cluster II, III, IV, V. The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation.

Intra and Inter cluster average divergence (D^2)

Highest intra cluster distance was observed for cluster I (75.97). In the present study, the highest inter cluster distance (188.41) was found between cluster II and IV followed by cluster III and IV with a distance of 184.42, cluster III and V with a distance of 184.28, cluster I and VI with a distance of 174.94, cluster I and III with a distance of 162.57, cluster I and II with a distance of 152.00. Suggesting that selection of two parents from more divergent parents in hybridization programme to produce the better yield traits from the diverse parents and also more of combining ability each other.

Cluster mean values for quantitative characters of rice genotypes

Mean performance of a cluster is the mean of overall values of individual correlated variables of all genotypes included in that cluster. Highest cluster mean for grain yield per hill was recorded in cluster V (33.30) followed by cluster I (33.85), cluster IV (54.85), cluster VI (62.13), cluster III (67.33) and cluster II (71.29).

Contribution of individual characters towards total divergence

The present study, maximum contribution towards total divergence was exhibited by biological yield (24.36), grain yield per hill (22.18), number of spikelets (12.36), harvest index (10.26), number of panicles per hill (8.46), test weight (5.64), number tillers (5.00), flag leaf width (3.59), flag leaf length (3.08), days to 50% flowering (2.69), days to maturity (2.00) and minimum contribution by panicle length (0.26) and plant height (0.13). While selecting parents in hybridization programme genotypes having the more divergence between grain yield per hill have fruitful improvement traits in progenies in selection procedures.

Conclusion

Among 40 genotypes MTU-1172 (71.28) and MTU-1155 (67.33) genotypes were found to be superior for grain yield per hill over the check (NDR-359). High to moderate estimates of GCV, PCV, High heritability coupled with high genetic advance as percent mean in the present genotypes was recorded for grain yield/hill, biological yield, harvest index, number of tillers/hill, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of the characters. Cluster II and IV (188.41), cluster III and IV (184.42) had high inter cluster distances, were most diverse from each other and the genotypes present in these clusters provide a broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes for grain yield improvement in rice genotypes.

Table 1: Analysis of Variance for 13 quantitative characters of 30 rice genotypes during *kharif-2021*

Sr. No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	39	78
1.	Days to fifty percent flowering	31.42	617.03**	10.47
2.	Plant height	32.86	380.51**	69.13
3.	Flag leaf length	2.40	107.53**	7.64
4.	Flag leaf width	0.005	0.103**	0.007
5.	Number of tillers	0.27	18.50**	0.62
6.	Number of panicles/hill	0.11	11.71**	0.47
7.	Panicle length	4.70	11.83**	4.06
8.	Number of spikelets	295.17	6812.12**	239.04
9	Days to maturity	2.02	293.90**	8.64
10.	Biological yield	37.78	1695.82**	35.03
11.	Harvest index	62.98	412.22**	25.83
12.	Test weight	0.84	55.28**	1.36
13.	Grain yield per hill	18.85	494.75**	10.92

*and **indicate Significant at 5% and 1% level of significance.

Table 2: Estimation of variability and genetic parameters for 13 quantitative characters in rice germplasm for *kharif* 2021

Traits	GCV	PCV	h^2 (Broad Sense)	Genetic Advancement	Gen. Adv as % of Mean
Days to fifty percent flowering	13.13	13.46	95.07	28.56	26.37
Plant height	7.98	10.30	60.01	16.25	12.74
Flag leaf length	15.10	16.74	81.32	10.71	28.05
Flag leaf width	13.72	15.16	81.90	0.33	25.58
Number of tillers	22.77	23.94	90.47	4.78	44.62
Number of panicles/hill	18.95	20.10	88.85	3.76	36.80
Panicle length	6.09	9.77	38.89	2.06	7.83
Number of spikelets	20.18	21.25	90.16	91.56	39.47
Days to maturity	7.12	7.43	91.66	19.23	14.04
Biological yield	29.99	30.92	94.04	47.00	59.91
Harvest index	23.77	26.05	83.29	21.33	44.69
Test weight	21.77	22.59	92.93	8.41	43.24
Grain yield per hill	34.46	35.61	93.65	25.31	68.71

h^2 =Heritability, GCV= Genotypic Coefficient of Variation, PCV=Phenotypic Coefficient of Variation

Table 3: Grouping of fifty rice genotypes based on D^2 values

Cluster Group	No. of genotype	List of genotypes
1 Cluster	35	MTU-2032, MTU-1061, PLA-1100, MTU-1064, MTU-1171, MTU-1238, MTU-1311, BPT-02, MTU-5293, MTU-2077, MTU-1032, MTU-1282, MTU-1262, BPT-01, MTU-1271, MTU-1121, SHIATS DHAN 4, MTU-1001, MTU-1239, BPT-5204, SHIATS DHAN 1, MTU-7029, MTU-1156, MTU-1153, SHIATS DHAN-3, MTU-1223, MTU-3626, JGL-24423, SHIATS DHAN-7, NLR-34449, MTU-1010, MTU-1210, SHIATS DHAN-5, SHIATS DHAN-2, RNR-1 5048.
2 Cluster	1	MTU-1172
3 Cluster	1	MTU-1155
4 Cluster	1	MTU-1224
5 Cluster	1	NDR-359 (CHECK)
6 Cluster	1	SHIATS DHAN-6

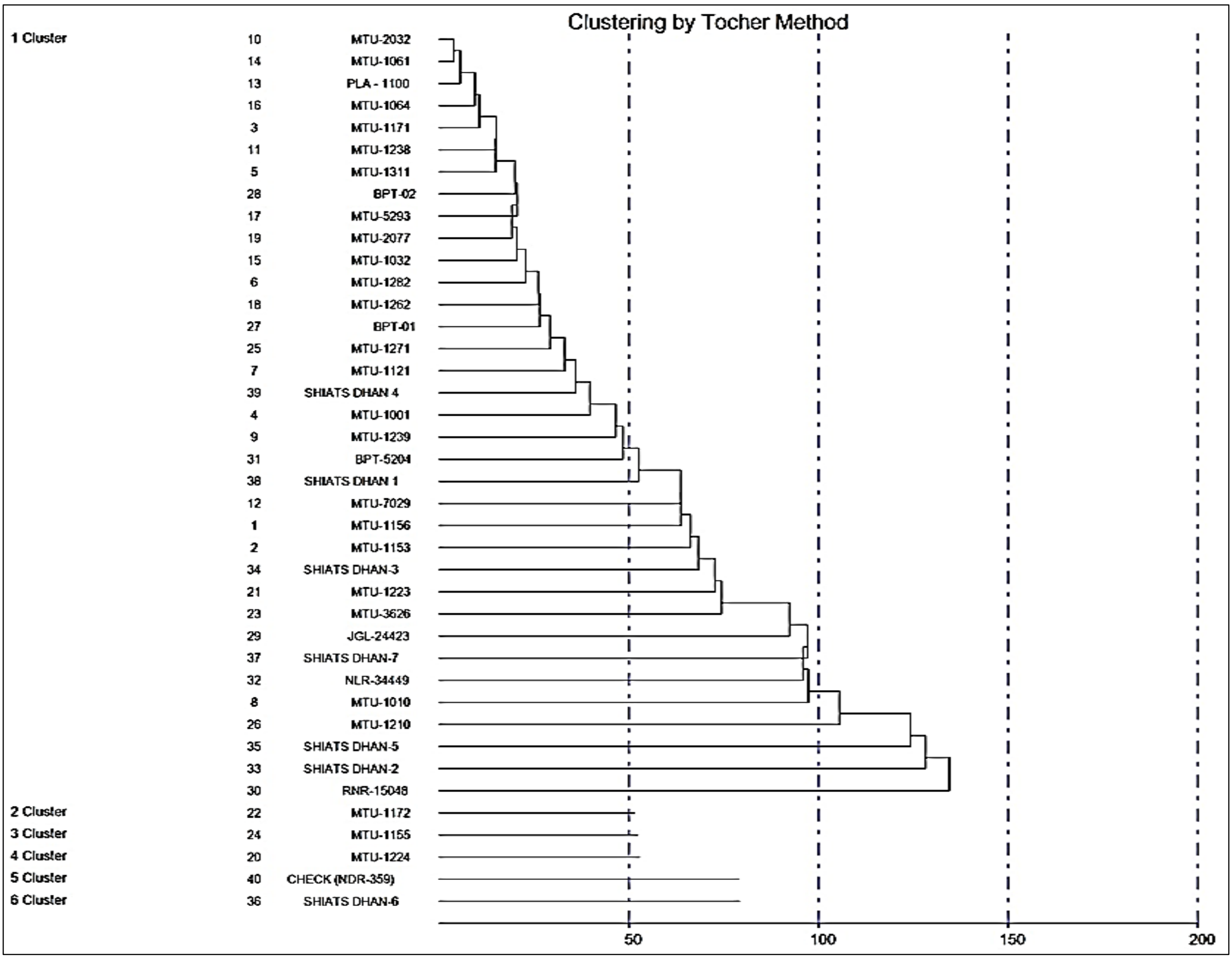

Fig 1: Dendrogram depicting clustering of rice genotypes into 6 clusters

Table 4: Average intra and inter cluster distance (D^2) values for six clusters in Fourty Rice genotypes

Cluster Distances						
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster 1	75.97	152.00	162.57	143.17	145.89	174.94
Cluster 2		0.00	98.10	188.41	180.26	151.57
Cluster 3			0.00	184.42	184.28	90.00
Cluster 4				0.00	79.63	99.60
Cluster 5					0.00	115.52
Cluster 6						0.00

Table 5: Mean values of the eight clusters for eleven characters in fifty rice genotypes

Cluster Means: Tocher Method												
	Days to percent flowering	**Plant height**	**Flag leaf length**	**Flag leaf width**	**Number of tillers**	**Number of panicles hill**	**Panicle length**	**Number of spikelets**	**Days to maturity**	**Biological yield**	**Harvest index**	**Test weight**	**Grain yield per hill**
Cluster 1	108.29	127.02	38.08	1.29	10.12	9.79	26.40	231.52	137.46	75.28	45.69	19.29	33.85
Cluster 2	123.00	145.96	52.91	1.18	13.93	13.13	27.06	191.87	150.00	98.97	72.05	25.00	71.29
Cluster 3	112.00	145.64	36.93	1.58	12.00	12.00	28.11	227.80	140.00	161.80	41.62	25.00	67.33
Cluster 4	110.00	102.06	28.09	0.97	13.93	13.27	22.60	259.80	123.00	67.20	81.61	13.50	54.85
Cluster 5	104.67	125.00	35.81	1.80	19.60	14.00	27.97	210.60	131.00	51.50	64.66	23.10	33.30
Cluster 6	92.00	138.59	41.91	1.46	15.07	13.60	26.23	284.27	121.33	123.60	50.33	17.00	62.13

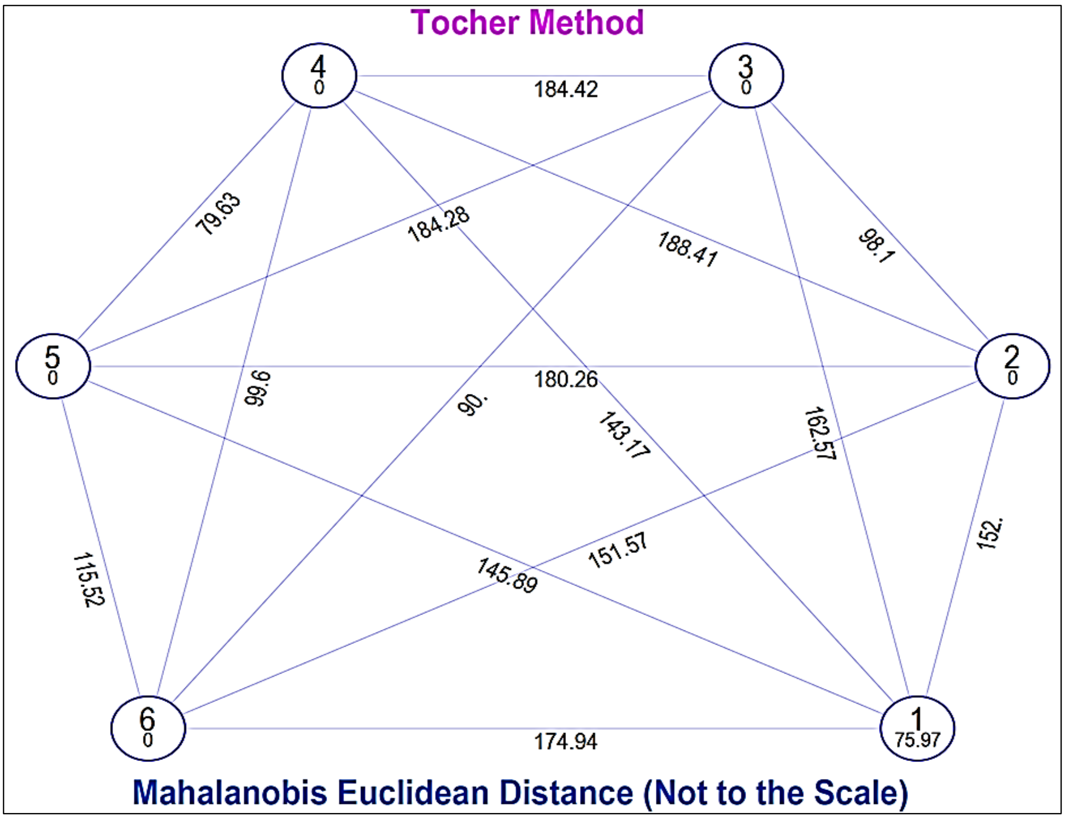

Fig 2: Cluster diagram depicting intra and inter-cluster distances. (The figure is not exactly to the scale)

Table 6: Per cent contribution towards divergence of eleven different characters of Rice genotypes

Sl. No.	Source	Contribution %	Times ranked 1st
1.	Days to fifty percent flowering	2.69	21
2.	Plant height	0.13	1
3.	Flag leaf length	3.08	24
4.	Flag leaf width	3.59	28
5.	Number of tillers	5.00	39
6.	Number of panicles/hill	8.46	66
7.	Panicle length	0.26	2
8.	Number of spikelets	12.36	112
9.	Days to maturity	2.00	15.38
10.	Biological yield	24.36	190
11.	Harvest index	10.26	80
12.	Test weight	5.64	44
13.	Grain yield per hill	22.18	173

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