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Assessment of genetic divergence in rice (*Oryza sativa* L.) germplasm using D^2 analysis

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Abstract

The present investigation was conducted with 41 genotypes of Rice during *Kharif 2023* in randomized block design (RBD) with three replications. The 41 rice genotypes were characterized based on 13 quantitative traits viz, days to 50 per cent flowering, days to maturity, flag leaf length, flag leaf width, the total number of effective tillers per plant, plant height (cm), panicle length (cm), the number of spikelets per panicle, biological yield, grain yield per plant, test weight, harvest index, using Mahalanobis D^2 statistics. D^2 analysis distributed the 41 genotypes into six clusters, of which cluster I was the largest with 36 genotypes. Lowest inter cluster distance was between cluster I and cluster IV which was 60.58, and highest inter cluster distance was between the cluster IV and cluster VI which was 247.17,Therefore genotypes present in these clusters should be used for the future hybridization program.

Introduction

Rice (*Oryza sativa*) belongs to the genus *Oryza* of Poaceae family (Gramineae), originating from South East Asia, grown extensively in humid tropical and sub-tropical regions of the world. Rice is a rainfed *kharif* season crop which is sown in the months of June – July in India. Rice is a staple food for over half of the world's population, particularly in Asia where this cereal grainis a fundamental part of the diet. Asia is known to be rice bowl of the world, as more than 90% of the world's rice is grown and consumed here. India is remarkably rich in rice diversity, including cultivars, landraces, wild and weedy relatives (DRR, Hyderabad)

Aarthi *et al*., (2019). Rice is a rich source of biology and for improving crop varieties that can tackle the modern agricultural challenges carbohydrates for energy, is also low in fat and protein content. While some fortified varieties may contain added vitamins and minerals, the refining process removes branand germ reducing its fibre content. The genetic variability among rice germplasm offers a wide scope for crop improvement by providing a pool of traits for adapting the crop to the diverse and changing environments. These improvements can also be focused towards nutritional quality, such as increasing essential vitamins and minerals. Examples include the development of Golden Rice, rich in beta-carotene and high iron and zinc rice varieties. Investigating the genetic diversity among rice groups provides a key to understand rice biology in new ways. This diversity is crucial for understanding rice. As in view of the above information, an experiment was carried out with 41 rice genotypes with the divergence among them using Mahalanobis D^2 analysis

Materials and Methods

The experiment was carried out during *Kharif*, 2023 with 41 rice genotypes in a Randomized Block Design (RBD) with three replications. The experiment was conducted in *kharif* 2023 at the field experimentation Centre of Department of Genetics and Plant Breeding, SHUATS Prayagraj. A single plot consisted of three rows of 3.7 meters each, with 20 cm row to row and 15 cm plant to plant spacing. Net area was 44.4 m². Data was recorded on 13 quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, the total number of effective tillers per plant, plant height (cm), panicle length (cm), flag leaflength, flag leaf width, the number of spikelets per panicle, biological yield, the number of grains per panicle, grain yield per plant (g), test weight(g), harvest index. Observations were recorded from ten randomly selected competitive plants of each genotype in each replication for selected traits.

Statistical Analysis

The mean values of all characters were compiled from the genotypes in all three replications and genetic divergence was estimated by Mahalanobis D^2 statistics (1952) was used for analysis of forty-onerice genotypes for all 13 characters. Tocher's method, by Rao (1952) was used for grouping genotypes into various clusters. Further, the ranking was done for each character based on their contribution towards divergence. Genetic divergence: Mahalanobis statistics was used for the quantitative assessment of genetic divergence for all the thirteen characters. It is essential for increasing crop productivity through breeding. Selection of diverse parents in breeding programme helps in isolation of superior genotypes. 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 a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population.

Results and Discussion

Analysis of variance showed significant difference among the genotypes for all the traits. This indicates that there was an ample scope for selection of best genotypes from the present cultivation. Fig 1. shows Genetic parameters for 13 quantitative characters of 41 genotypes in rice. Character contribution towards divergence is given in Table 1. Table 2. Shows Analysis of Variance for 13 different quantitative characters in rice. Genetic parameters for 13 quantitative characters of 41

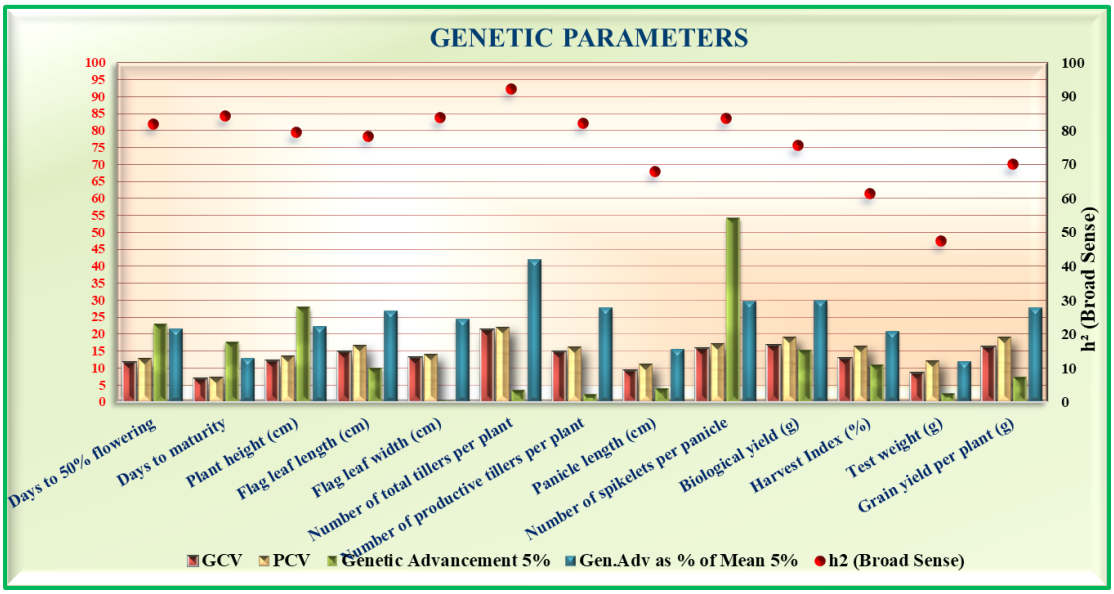

Fig. 1. Genetic parameters for 13 quantitative characters of 41 genotypes in rice.

genotypes in rice are presented in Table 3. The mean sum of squares due to the genotypes were significant for all the characters, suggesting the existence of high genetic variability among the genotypes for all the traits. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. Using the pivotal condensation method, the mean values of genotypes were transformed into standardized uncorrelated mean values.

The relative contribution of different characters included in the study towards diversity is presented in Table 1. Grain yield contributed (20.24%), followed by number of total tillers per plant (19.76%), number of spikelets per panicle (14.51%), flag leaf width (10 %) and test weight (8.17%). Flag leaf length (6.63%), biological yield (6.34%), panicle length (5.24%), number of productive tillers per plant (3.41%), days to maturity (2.32%), days to 50% flowering (1.1%), plant height (1.1%), and harvest index (0.98%). Similar results were obtained by Beevi and Venkatesan (2015), Raghavendra *et al*., (2018) and Devi *et al*., (2019). In general, estimates of PCV were higher than their corresponding GCV how ever good correspondence was observed between GCV and PCV for all characters. Both higher magnitude of PCV and GCV coefficient of variation was recorded for number of total tillers per plant (22.05) and (21.20). Whereas the lowest PCV and GCV coefficient of variation was recorded for Days to maturity (7.40 and 6.80). High estimates of heritability (above 60%) in broad sense were recorded for all the thirteen characters under study, which ranged from 92.45% (number of total tillers per plant) to 61.55 (harvest index (%). High heritability was observed for all traits viz.; number of total tillers per plant (92.45), days to maturity (84.49), number of spikelets per panicle (83.88), days to 50% flowering (82.14), plant height (cm) (79.78), flag leaf length (cm) (78.59), flag leaf width (cm) (84.11), number of productive tillers per plant

Table 1. Relative contribution of 13 characters

Source	Contribution %	Times ranked 1st
Days to 50% flowering	1.1	9
Days to maturity	2.32	19
Plant height (cm)	1.1	9
Flag leaf length (cm)	6.83	56
Flag leaf width (cm)	10	82
Number of total tillers plant	19.76	162
Number of productive tillers	3.41	28
Panicle length (cm)	5.24	43
Number of spikelets per plant	14.51	119
Biological yield (g)	6.34	52
Harvest Index (%)	0.98	8
Test weight (g)	8.17	67
Grain yield (g)	20.24	166

ANOVA Summary

Table 2. Shows Analysis of Variance for 13 different quantitative characters in rice.

Sr. No.	Source	Mean Sum of Squares (MSS)		
	Degrees of freedom	Replication 2	Treatment 40	Error 80
1	Days to 50% flowering	8.8370	485.47**	32.812
2	Days to maturity	3.5450	278.687**	16.07
3	Plant height	63.7910	750.69**	58.482
4	Flag leaf length	21.8310	99.173**	8.254
5	Flag leaf width	0.0010	0.085**	0.005
6	Number of total tillers per plant	0.7320	9.679**	0.256
7	Number of productive tillers per plant	0.8120	4.297**	0.286
8	Panicle length	4.3580	17.934**	2.41
9	Number of spikelets per panicle	238.8680	2652.363**	159.672
10	Biological yield	51.7680	241.736**	23.075
11	Harvest Index	52.5840	169.662**	29.239
12	Test weight	2.6640	12.69**	3.397
13	Grain yield per plant	8.6840	61.589**	7.611

* Significant at 5 percent level of significance
** Significant at 1 percent level of significance

(82.36), biological yield (g) (75.95), grain yield per plant (g) (70.27), panicle length (cm) (68.23), and harvest index (%) (61.55). High genetic advance was observed for days to 50% flowering(22.93), plant height (cm) (27.95) and number of spikelets per panicle (54.38), (17.72), flag leaf length (cm) (10.05), biological yield (g) (15.33) and harvest index (%) (11.06).

Clustermean for different characters

Cluster I showed highest mean value for Number of spikelets per plant (180.24) and low-

Table 3. Genetic parameters for 13 quantitative characters of 41 genotypes in rice.

Sr. No.	Characters	GCV	PCV	h^2 (Broad Sense) %	Genetic Advance (5%)	Gen. Adv as % Mean of 5%
1	Days to 50% flowering	11.58	12.78	82.14	22.93	21.62
2	Days to maturity	6.80	7.40	84.49	17.72	12.88
3	Plant height (cm)	12.10	13.55	79.78	27.95	22.26
4	Flag leaf length (cm)	14.72	16.60	78.59	10.05	26.88
5	Flag leaf width (cm)	12.98	14.16	84.11	0.31	24.53
6	Number of total tillers per plant	21.20	22.05	92.45	3.51	41.99
7	Number of productive tillers per plant	14.82	16.33	82.36	2.16	27.72
8	Panicle length (cm)	9.16	11.09	68.23	3.87	15.59
9	Number of spikelets per panicle	15.71	17.15	83.88	54.38	29.64
10	Biological yield (g)	16.68	19.14	75.95	15.33	29.94
11	Harvest Index (%)	12.85	16.37	61.55	11.06	20.76
12	Test weight (g)	8.40	12.17	47.70	2.50	11.95
13	Grain yield (g)	16.13	19.25	70.27	7.33	27.86

Table 4. Cluster composition of 41 rice genotypes

Cluster	Number of genotypes	Name of the genotypes
I	36	NLR4001, NLR 33641, NLR 30491, NLR 40054, NLR145, NLR40024, NLR 34449, DURGA PADDY, NLR3041, NLR33057, NLR33359, DHAN 69, DHAN 58, DHAN 62, DHAN- 53, INDRANI, DHAN 59, DHAN 59, IR-64, DHAN-52, MTU-1212, MTU-1280, LALBHUNA, MTU- 1281, MTU-1064, SHALIVAHANA, MTU-1190-VERMA, MTU-1311, MTU-1121, KSRV- 140, MTU-1035, UBL-4, MTU-2032, BPT 2, BINA DHAN-17 and MTU-1075 PUSHYAMI
II	1	NAGARJUNA
III	1	KANUKASEL
IV	1	VASUMATI
V	1	MTU-1271
VI	1	NDR-359 (Check)

Table 4. Cluster Means: Tocher Method

	DF50 %	DM	PH	FLL (cm)	FLW (cm)	NTP	NPT	PL	NSPP	BY (g)	HI (%)	TW (g)	GY (g)
Cluster 1	105.41	137.13	125.05	36.80	1.25	8.08	7.68	24.58	180.24	50.16	53.63	20.68	25.88
Cluster 2	126.00	148.00	85.07	38.67	1.53	8.20	8.07	23.30	208.27	53.13	58.30	20.00	30.47
Cluster 3	123.00	148.00	164.67	36.60	1.00	9.47	9.27	24.83	125.47	64.83	37.60	23.73	24.17
Cluster 4	105.67	138.00	149.43	51.93	0.93	9.33	8.53	29.37	190.40	59.53	66.07	22.93	38.90
Cluster 5	94.00	138.00	121.03	45.93	1.23	9.27	9.20	27.57	299.13	64.13	46.90	24.80	30.13
Cluster 6	105.33	131.00	125.00	35.83	1.83	15.60	8.17	27.97	210.60	51.50	44.00	23.10	22.67

DF-Days to flowering, DM-Days to maturity, PH- Plant height, FLL-Flag leaf length, FLW- Flag leaf width, NTP-No. of Total tillers, NPT-Number of productive tillers, PL- Panicle length, NSPP-No. of spikelets per panicle, BY-Biological yield, HI- Harvest index, TW- Test weight, GY- Grain yield

est mean value for Flag leaf width (1.25cm). Cluster II showed highest mean value for Number of spikelets per plant (208.27) and lowest mean value for Flag leaf width (1.53cm). Cluster III showed highest mean value for Plant height (164.67cm) and lowest mean value for Flag leaf width 1.00cm). Cluster IV showed highest mean value for Number of spikelets per plant (190.40) and lowest mean value for Flag leaf width (0.93cm). Cluster V showed highest mean value for Number of spikelets per plant (299.13) and lowest mean value for Flag leaf width (1.23 cm). Cluster VI showed highest mean value for Number of spikelets per plant (210.60) and lowest mean value for Flag leaf width (1.83cm). The genotypes with high mean values may be directly used for adaptation or may be used as parents in future breeding programme.

Cluster distances and composition

Cluster means of all the characters is presented in Table 6. The intra cluster distance ranged from 0.00 to 38.45. The maximum intra cluster distance was recorded for cluster I (38.45) while the minimum intra cluster distance was recorded for cluster II, III, IV, V and VI (0.00). The inter cluster distance was maximum between cluster III and VI (247.17) followed by cluster V and VI (244.18), cluster II and VI (226.38) and cluster III and VI (220.43), I and VI (198.42) and III and V (134.92) suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to develop desirable type. To realize much variability and high heterotic effect recommended that parents should be selected from two clusters having wider inter cluster distance. Similar explanation was given by, Ranjith *et al.*, (2018), Amegan *et al*., (2020) and Sudeepthi *et al.*, (2020).

The lowest inter cluster distance is between the cluster I and cluster IV which is 60.58, which shows that they are closely related to each other. The highest inter cluster distance is between the cluster IV and cluster VI which is 247.17, which displays that the genotypes present in these clusters have more distinct and are well-separated from each other. Acrossing programme should be initiated between the genotypes belonging to more divergent clusters. The greater the distance between to clusters, the wider the genetic diversity between their genotypes. However, while considering genetic diversity among the parents to be included in hybridization programme, parents with high yielding potential and wide genetic diversity likely to yield superior segregants within a short period (Roy and Panwar, 1993). Based on D^2 values, forty-one genotypes were grouped into six clusters using Tocher method (Singh and Choudhary, 1977). Clusters with their genotypes are presented in Table 4. Cluster I had thirty-six genotypes, whereas Cluster II, III, IV, V, and VI had single genotype in each. Inter-cluster and In-

Table 5. Inter-cluster and Intra-cluster(diagonal) D^2 values of 41 rice genotypes

	DF50 %	DM	PH	FLL (cm)	FLW (cm)	NTP	NPT	PL	NSPP	BY (g)	HI (%)	TW (g)	GY (g)
Cluster 1	105.41	137.13	125.05	36.80	1.25	8.08	7.68	24.58	180.24	50.16	53.63	20.68	25.88
Cluster 2	126.00	148.00	85.07	38.67	1.53	8.20	8.07	23.30	208.27	53.13	58.30	20.00	30.47
Cluster 3	123.00	148.00	164.67	36.60	1.00	9.47	9.27	24.83	125.47	64.83	37.60	23.73	24.17
Cluster 4	105.67	138.00	149.43	51.93	0.93	9.33	8.53	29.37	190.40	59.53	66.07	22.93	38.90
Cluster 5	94.00	138.00	121.03	45.93	1.23	9.27	9.20	27.57	299.13	64.13	46.90	24.80	30.13
Cluster 6	105.33	131.00	125.00	35.83	1.83	15.60	8.17	27.97	210.60	51.50	44.00	23.10	22.67

Table 6. Cluster Means: Tocher Method

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	38.45	61.83	61.78	60.58	72.88	198.42
Cluster 2		0	119.83	114.38	82.22	226.38
Cluster 3			0	61.12	134.92	220.43
Cluster 4				0	88.55	247.17
Cluster 5					0	244.18
Cluster 6						0

tra-cluster (diagonal) D^2 values of 41 rice genotypes are given in Table 5.

Conclusion

This study concluded that the higher magnitude of PCV and GCV coefficient of variation was recorded for number of total tillers per plant. High heritability along with high genetic advance as percent of mean for number of total tillers per plant, number of productive tillers per plant, panicle length (cm), number of spikelets per panicle, plant height (cm), days to maturity and days to 50% flowering. The lowest distance was between cluster I and cluster IV which was 60.58, indicating that they are closely related to each other. The highest inter cluster distance was between cluster IV and cluster VI which to genetic diversity in 41 genotypes was 247.17, which suggests that the genotypes present in these clusters have more distinct and are well-separated from each other. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability in segregating generations and may be used as parents for future hybridization program to develop desirable type. And all the genotypes performed well and gave more values for respective characters as compared to the check variety.

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