Assessment of Genetic Divergence in Rice (*Oryzasativa*L.) Germplasm using D^2 analysis

Original Research Article

ABSTRACT

The present investigation was conducted with 41 genotypes of Rice during Kharif 2023 under Randomized Block Design (RBD) with three replications.Data were recorded for thirteen quantitative characters to obtain estimates of variability, heritability, genetic advance and genetic divergence. Significant differences were observed among the genotypes for all the characters studied. This study concluded, the highest grain yield was observed in VASUMATHI 38.9 followed by DHAN-69 34.33based on mean performance at Prayagraj region. A higher magnitude of PCV as well as GCV coefficient of variation was noted for the 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. along with high genetic advance for number of spikelets per panicle (54.38), plant height (cm) (27.95), days to 50% flowering (22.93), and days to maturity (17.72). Biological yield (g) (15.33), harvest index (%) (11.06) and flag leaf length (cm) (10.05) D2 analysis distributed the 41 genotypes into six clusters.

The largest cluster was cluster I with 36 genotypes followed by cluster II, III, IV, V, VI with 1 genotype each. Highest contribution in manifestation of genetic divergence was exhibited by grain yield per plant (22.82) followed by biological yield (21.28) and test weight (12.56). Lowest intercluster distance was between cluster I and cluster IV which was (60.58). The intercluster distance was maximum between cluster IV and VI (247.17).Therefore, genotypes present in these clusters should be used for the future hybridization program.

Highlights

- Germplasms were grouped into 6 clusters.
- Cluster IV and VI were the most divergent clusters

Keywords: *Rice, genetic diversity, genetic advance, variability*

1. INTRODUCTION

Oryzasativa (2n=2x=24) is a diploid monocot flowering plant of the family Gramineae, which originated in Southeast Asia and is widely cultivated in the wet tropics and subtropics. It is a popular kharif crop in India sown during the months of June and July. Additionally, this grain is the main food source of over 50% of the population of this planet, especially Asia – where it is important in people nutrition.

This region accounts for more than 90% of rice produced and consumed globally, therefore Asia is the world's rice bowl states. Supported through FAO, USDA and individualcountries' agriculture departments, between 2023 and 2024, it was roughly estimated that 738 million metric tonnes would be the global production of rice, the quantity being metrics ton. Drawing data for the MOPN countries such as China and India are the highest producers while India alone consumes approximately 178 million metrics tons, highlighting the country's significant consumption rate of this vital crop.

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 activity removes bran and germ reducing its fibre content.Rice exhibits a wide range of morphological characteristics, including differences in grain size, shape, color and texture.

The genetic diversity among rice germplasms offers a large scope for crop improvement as it provides a pool of traits for adapting the crop to the varying and changingenvironments. These improvements can also befocused towards nutritional quality, such as increasing essential vitamins and minerals. The traditional breeding techniques as selection and crossbreeding still continue for the development of rice varieties.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.

Genetic diversity is important for find out genetic differences within a genotype. Diversity not only generates variability, but it also introduces new gene combinations ordifferent gene combinations. Mainly, understanding the extent and degree of genetic divergence aids in the preference of ideal parents for a breeding programme.

Genetic variability for quantitative traits is the basic component of breeding programme for broadening the gene pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable traits.The genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the germplasm.

Heritability measures the extent of phenotypic variation caused by the action of genes. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.Heritability and genetic advance are two complementary concepts.

As in view of the above information, an experiment was carried out in the field with 41 different rice genotypes for study the divergence among them using Mahalanobis D^2 analysis.

2. MATERIALS AND METHODS

The experiment was conducted during *Kharif,* 2023 with 41 rice genotypes. The experiment was done in aRandomizedblock design (RBD) with three replications to establish reproducibility and accuracy. The rice genotypes for this project were

provided by the Deparment of Genetics and Plant breeding, SHUATS. The study was carried out at the FieldExperimentation Centre of Department of Genetics and Plant Breeding, SHUATS Prayagraj. The 41 rice genotypes were initially grown in the nursery, where they were properly taken care of and well protected, to ensure proper germination and growth. Following this period, they were properly transplanted into the main field.

These practices can help in improving the capability of rice production, leading resources more effectively, and improving the sustainability of rice farming. A single plot consisted of three rows,each row of 3.7 meters each, with 20 cm row to row distance and 15 cm plant to plant distance to allow for optimal growth and development throughout the cropping season.

The total net areaof the experiment was 44.4 m^2 and the gross area was 117.9 m^2. Five competitive plants were randomly picked from each plot for recording data. Data was recorded on 13 quantitativetraits including, days to 50 %flowering, days to maturity, the total number of effective tillers per plant, plant height, panicle length, flag leaf length, flag leaf width, the number of spikelets per panicle, biological yield, the number of grains per panicle, grain yield per plant, test weight, harvest index.

Observations were recorded from five randomly selected competitive plants of each genotype in each replication for selected traits. The focus of the study was on the genetic parameters such as heritability, variability, genetic advance and genetic diversityto provide insights of crop improvement.

3. STATISTICAL ANALYSIS

Mahalanobis D^2 takes into account both means and variances of the traits for having an extent of genetic divergence. The analysis of variance was worked out to testthe significance of F and t-tests. It was executed according to the strategy of RBD analysis for each character as for method prompted by Panse and Sukhatme (1967). The total variance and degree of freedom were partitioned into three components *viz*. replications, treatments and error.The mean values of all characters were compiled from the genotypes inall three replications and genetic divergence was estimated by Mahalanobis D^2 statistics was used for analysis of 41 rice genotypes for all 13 characters. Tocher's method, by Rao was implemented for classifying genotypes into clusters. There were six clusters which were formed after the analysis. Each cluster was having different genotypes according to their level of divergence in them. The Dendrogram shows the relationsbetween clusters at various points. For the 13 characters genetic parameters were also analysed. Further, the positioning was done for each character based on their commitment towards divergence. Sorting out of divergent parents in breeding programme helps in seperationof superior genotypes.

4. RESULTS AND DISCUSSION

Analysis of variance

Anovarevealednotable differences between the existing genotypes for all the traits. This indicates that there was a plenty of scope for selection ofbest genotypes from the present cultivation. The mean sum of squares due to the genotypes was significant for all the characters.Therefore, suggesting the existence of high genetic variability in the genotypes for all the traits. The presence of large amount of variability might be due to diverse source of genetic variability among the genotypes for all 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 analysis of variance for 13 quantitative characters in this study is presented in Table no.1. And the mean performance by the genotypes is given in the (table no.3).

GCV and PCV

According to Table 4, the estimates of GenotypicCoefficient of Variation and PhynotypicCoefficient of Variationwere consistent for all the traits, with PCV values beingnumerically higher than GCV values which indicated greater genotype and environment interaction. A huge quantity of variation in PCV was noticed for the variety to the maturity period in relation to the total tillers per plant. But a wide range of genotypic coefficient of variation (GCV) was observed for traits such as total number of tillers per plant and days to maturity.Higher values of GCV were recorded for total number of tillers per plant (21.20) while lower values were recorded for days to maturity (6.80). Other moderate estimates include biological yield per gram (16.68), grain yield per gram (16.13), number of spikelets per panicle (15.71), flag leaf length (cm) (14.72), flag leaf width (cm) (12.98),harvest index (percent) (12.85), plant height (cm) (12.10) and days to 50% flowering (11.58).

Whereas low GCV estimates were recorded for panicle length (9.16), test weight per gram (8.40) and days to maturity (6.80).Higher magnitude of

phenotypic coefficient of variation was recorded for Number of total tillers per plant (22.05), Moderate for grain yield per plant (g) (19.25), biological yield (g) (19.14), number of spikelets per panicle (17.15), flag leaf length (cm) (16.60), harvest index (%) (16.37), number of productive tillers per plant (16.33), flag leaf width (cm) (14.16), plant height (cm) (13.55), days to 50% flowering (12.78), panicle length (cm) (11.09), and test weight (g) (10.98). When observed lowest estimate of phenotypic coefficient of variation wasnoted for days to maturity (7.40).

Heritability

From Table4, broad sense heritability estimates for all thirteen characters except test weight were above 60%, with a range from 92.45% for total tillers to 61.55% for harvest index. High heritability estimates indicate that a significant portion of variation is due to genetic differences, and high heritability implies that the selection based on these traits is likely to be effective because the observed phenotypic variation closely reflects the underlying genetic variation This enhances the successful selection of desirable traits.

High estimates were found for traits as: days to maturity (84.49), flag leaf width (cm) (84.11), number of spikelets per panicle (83.88),number of productive tillers per plant (82.36), days to 50% flowering (82.14), plant height (cm) (79.78), flag leaf length (cm) (78.59), biological yield (g) (75.95), grain yield per plant (g) (70.27), panicle length (cm) (68.23), and harvest index (%) (61.55). And moderate estimate was for the test weight which is (47.70).

Figure4, illustrates the frequency distribution of broad - sense heritability estimates across thethirteen traits.

Genetic Advance

Table 4 outlines the genetic advance range between all the quantitative traits in the study which involves flag leaf width 0.31% and spikelets per panicle 54.38%. High genetic advances were noted for spikelets per panicle (54.38), plant height (cm) (27.95), when 50% flowering was observed (22.93), and the duration of maturity (17.72). Other traits such as biological yield (g) (15.33), harvest index (%) (11.06) and flag leaf length (cm) (10.05) recorded moderate genetic advance. The lowest genetic advances were observed for, grain yield per plant (g) (7.33), panicle length (cm) (3.87),total tillers per plant (3.51) test weight (g) (2.50), productive tillers per plant (2.16), flag leaf width (cm) (0.31).

High genetic advance indicates that a trait will respond well to selection leading to significant improvement in the future generations. Also it shows that there is proportion of the phenotypic variation is due to the additive genetic variation.

Low genetic advances implies that the trait will not show considerable improvement through selection. And as for the selection of this traits, it will only result in minor improvements through generations.

Genetic Advance as Percent of Mean

High genetic advance as percent of mean were observed for number of total tillers per plant (41.99), biological yield (g) (29.94), number of spikelets per panicle (29.64), grain yield per plant (g) (27.86), number of productive tillers per plant (27.72), flag leaf length (cm) (26.88), flag leaf width (cm) (24.53), plant height (cm) (22.26), days to 50% flowering (21.62), harvest index (%) (20.76) and panicle length (cm) (15.59), which is equivalent with results of Kumar *et al.* (2020)and Naveen *et al.*, (2022), Santhoshini*et al.*, (2023)and Moderate estimates were observed in days to maturity (12.88) and test weight (g) (11.95) as specified in (Table no.4).

Cluster mean for different characters

The cluster means serves as a source for identifying how typical a point is which is in the cluster. It helps determining the compactness and separation of clusters .Considerable distinctness in cluster mean values were observable for all the characters.

Cluster I

Cluster I showed highest mean value for Number of spikelets per panicle (180.24) and lowest mean value for Flag leaf width (1.25cm).

Cluster II

Cluster II showed highest mean value for Number of spikelets per panicle (208.27) and lowest mean value for Flag leaf width (1.53cm).

Cluster III Cluster III showed highest mean value for Plant height (164.67cm) and lowest meanvalue for Flag leaf width 1.00cm).

Cluster IV

Cluster IV showed highest mean value for Number of spikelets per panicle (190.40) and lowest mean value for Flag leaf width (0.93cm). A comparison of the mean value of thirteen characters of different clusters has been presented in (Table 6).

Cluster V

Cluster V showed highest mean value for Number of spikelets per panicle (299.13) and lowest mean value for Flag leaf width (1.23cm).

Cluster VI

Cluster VI showed highest mean value for Number of spikelets per panicle (210.60) and lowest mean value for Flag leaf width (1.83cm). High mean value genotypes can be used as parents in upcoming breeding programmes or directly for adaptation.

Cluster composition and distances

Cluster composition is the grouping of similar data points based on their charaters. In fig.2.the dendrogramillustrates theclustering of 41 genotypes by usingTocher method for grouping genotypes.Cluster I had maximum number of genotypes that is 36 and cluster II, III, IV, V, VI were having a single genotype each as given in (table no.5).

The Mahalanobis D^2 measures the distance between a point and the mean of a distribution considering the variance and covariance of the data. It is useful for clustering. The intracluster distance ranged from 0.00 to 38.45. The maximum intracluster distance was recorded for cluster I (38.45) while the minimum intracluster distance was recorded for cluster II, III, IV, V and VI (0.00).

As per Table7, the intercluster distance is maximum between cluster IV and VI (247.17) followed by cluster V and cluster VI (244.18), cluster II and cluster VI (226.38) and cluster III and cluster VI (220.43), I cluster and VI cluster (198.42) and III cluster and V cluster (134.92) suggesting that the genotypes present in the clusters may be used as parents for hybridization programme to develop desirable types.

The lowest intercluster distance that exists between the genetic cluster I and cluster IV, implies that they are nearly related to each other. The biggest intercluster distance lies between the cluster IV and cluster VI, which indicates that the genotypes in these clusters are more distinct from and well-isolated from each other.Figure3, using cluster diagram the diagramatic representation oftheintercluster and intracluster distances between the six clusters is shown.To realize much variability and high heterotic effect recommended that parents should be selected from the clusters having wider intercluster distance.

Percent contribution towards divergence

Percent contribution towards divergence is used to measure the degree to which different factors or components contributeto the overall divergence in a data set or system. It provides the ranking of the characters based on their importance in defining the clusters which can be used in further analysis. This helps in identifying which traits are more influential in causing the divergence. The percent contribution of thirteen characters towards total genetic divergence is listed in Table 2. The selection and choice of parents basicallydepends upon involvement of characters towards divergence. In the present study the highest contribution in manifestation of genetic divergence was displayed by grain yield per plant (g) (20.24) followed by number of total tillers plant (19.76) and number of spikelets per plant (14.51). To put it in another way, choosing these characters could be fruitful. Focusing on the characters with higher percent contributions can enhance the accuracy and interpretability of the clustering results.

Table no.2. Percent contribution towards divergence

Sl no.	Source	Contributio %
1	Days to 50% flowering	1.1
2	Days to maturity	2.32
3	Plant height	1.1
4	Flag leaf length (cm)	6.83
5	Flag leaf width	10
6	Number of total tillers plant	19.76
7	Numberof productive tillers	3.41
8	Panicle length	5.24
9	Number of spikelets per panicle	14.51
10	Biological yield	6.34
11	Harvest Index	0.98
12	Test weight	8.17
13	Grain yield per plant	20.24

Table 1.Shows Analysis of Variance for 13 different quantitative characters in rice.

Sr. No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	**2**	**40**	**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% level of significance
**Significant at 1% level of significance

Table 3. Mean performance of 41 rice genotypes for 13 characters during Kharif-2023

Sl. No.	Genotypes	DFF	DM	PH	FLL	FLW	NTTP	NPTP	PL	NSPP	BY	HI	TW	GY
1	MTU-1035	123.00	146.33	102.17	36.70	1.57	9.03	8.93	25.87	161.93	50.93	53.17	22.40	26.53
2	KANUKASEL	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
3	LALBHUNA	112.00	146.00	151.97	30.07	1.07	9.73	9.13	24.37	165.60	61.60	55.67	22.13	33.10
4	NAGARJUNA	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
5	IR-64	83.33	117.00	111.73	32.07	1.20	9.23	8.27	26.87	236.30	61.20	44.77	23.73	27.20
6	KSRV-140	117.33	155.00	102.03	31.93	1.23	8.83	8.20	22.37	184.10	56.80	49.00	20.30	27.33
7	SHALIVAHANA	120.00	156.00	142.97	45.10	1.23	8.53	8.47	28.57	214.00	50.70	57.97	17.47	28.73
8	MTU-1064	119.33	146.00	142.50	42.03	1.13	6.33	6.33	24.50	143.10	37.50	55.20	21.60	19.77
9	MTU-1280	114.00	140.00	144.47	41.57	1.20	6.43	6.47	28.93	158.67	56.70	38.40	24.13	21.53
10	MTU-1190-VERMA	116.67	145.00	131.00	32.97	1.17	8.20	8.20	24.10	179.00	66.07	34.30	23.73	22.27
11	MTU-1212	115.67	148.00	130.43	37.43	1.17	7.47	7.07	27.00	162.30	57.47	52.73	24.20	29.93
12	MTU-2032	128.00	140.00	130.30	41.03	1.03	8.80	8.47	20.83	165.10	35.40	58.97	20.27	19.30
13	MTU-1075 PUSHYAMI	127.00	155.00	122.40	29.97	1.13	6.23	6.00	22.13	173.73	41.67	63.27	22.40	24.67
14	MTU-1271	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
15	MTU-1311	117.33	133.00	122.33	28.03	1.17	5.60	5.60	23.40	156.00	31.80	59.17	21.33	17.87
16	MTU-1121	117.67	155.00	118.97	32.40	1.17	6.20	6.20	22.17	200.93	52.53	55.23	22.70	28.70
17	MTU-1281	119.33	148.00	120.67	29.60	1.20	7.00	6.63	24.77	172.73	40.40	58.53	21.33	22.47
18	UBL-4	120.67	149.00	128.93	27.77	1.27	6.00	5.83	24.83	175.33	49.33	57.73	21.33	25.40
19	DHAN-52	93.00	128.00	133.93	43.57	1.40	6.13	5.47	25.23	150.33	31.33	64.50	21.37	19.60
20	BINA DHAN-17	92.00	126.00	122.40	48.43	1.17	5.50	5.53	30.13	145.00	31.03	58.40	21.60	17.90
21	INDRANI	96.00	130.00	116.50	43.43	1.23	7.20	6.73	27.53	179.27	57.73	46.80	20.27	26.13

22	DURGA PADDY	102.00	139.00	135.67	42.50	1.33	8.77	8.47	26.93	187.80	55.93	47.50	18.33	26.23
23	DHAN 59	100.00	135.00	161.63	33.93	1.17	8.00	7.53	25.50	184.10	56.80	49.00	21.87	27.33
24	VASUMATI	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
25	BPT 2	121.00	136.00	102.93	32.20	1.07	10.00	8.93	18.27	140.77	50.00	59.83	21.37	29.27
26	DHAN 69	98.00	135.00	119.47	44.20	1.20	9.43	8.73	23.63	177.67	58.13	59.93	22.13	34.33
27	DHAN-53	100.00	137.00	112.93	33.47	1.27	10.40	9.33	23.53	168.40	52.93	54.87	20.27	28.80
28	DHAN 58	103.00	135.00	122.17	31.43	1.27	9.97	9.07	23.90	182.23	55.87	49.83	18.33	27.03
29	DHAN 59	98.00	130.00	140.73	35.13	1.40	6.60	6.33	24.87	184.10	56.80	49.00	20.27	27.33
30	DHAN 62	97.00	136.00	111.50	33.57	1.20	9.60	9.13	24.00	171.37	43.00	61.20	21.33	26.37
31	NLR 33359	93.00	128.00	125.90	39.33	1.20	7.13	7.07	25.90	204.10	57.67	45.23	19.93	25.67
32	NLR 33057	95.33	130.00	121.67	38.30	1.17	7.93	7.40	27.70	186.97	45.70	49.83	18.73	22.33
33	NLR 3041	93.67	128.00	111.50	40.60	1.30	9.83	8.93	24.47	165.33	49.27	49.77	16.73	24.23
34	NLR 40054	93.67	130.00	128.90	35.47	1.33	8.63	8.20	24.13	215.87	50.67	52.20	20.80	25.63
35	NLR 4001	93.00	128.00	125.27	36.43	1.37	7.93	7.70	22.83	197.27	45.87	62.40	19.47	28.17
36	NLR 30491	88.33	125.00	124.07	35.73	1.40	9.10	8.47	22.67	198.40	52.40	52.57	18.40	27.20
37	NLR 40024	99.00	132.00	114.60	38.43	1.30	9.40	8.93	22.30	196.27	52.33	63.80	18.40	32.37
38	NLR 33641	93.00	128.00	128.03	34.70	1.47	7.63	7.60	23.03	193.93	48.20	54.03	18.40	26.13
39	NLR145	95.33	130.00	120.57	40.77	1.53	8.93	8.33	23.53	209.13	57.07	58.67	20.00	32.73
40	NLR 34449	99.00	132.00	118.73	44.33	1.40	9.13	8.87	24.03	201.40	46.90	47.27	17.23	22.00
41	NDR-359 (Check)	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

Mean	106.07	137.57	125.54	37.40	1.26	8.36	7.80	24.83	183.47	51.19	53.26	20.95
CV	5.40	2.91	6.09	7.68	5.64	6.06	6.86	6.25	6.89	9.38	10.15	8.80
SEm	3.31	2.31	4.42	1.66	0.04	0.29	0.31	0.90	7.30	2.77	3.12	1.06
CD at 5%	9.31	6.51	12.43	4.67	0.12	0.82	0.87	2.52	20.53	7.81	8.79	2.99
CD at 1%	12.34	8.64	16.48	6.19	0.15	1.09	1.15	3.34	27.22	10.35	11.65	3.97
Minimum	83.33	117.00	85.07	27.77	0.93	5.50	5.47	18.27	125.47	31.03	34.30	16.73
Maximum	128.00	156.00	164.67	51.93	1.83	15.60	9.33	30.13	299.13	66.07	66.07	24.80
Replication	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Treatment	S	S	S	S	S	S	S	S	S	S	S	S

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

Table 4. Estimates of the Genetic parameters for 13 quantitative characters in Rice

Sl. No.	Genetic Parameters	GCV	PCV	H^2 (Broad Sense)	Genetic Advance 5%	Genetic Advance as % of Mean 5%
1	Days to 50% flowering	11.58	12.78	82.138	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	79.779	27.95	22.26
4	Flag leaf length (cm)	14.72	16.60	78.594	10.05	26.88
5	Flag leaf width (cm)	12.98	14.16	84.109	0.31	24.53
6	Number of total tillers per plant	21.20	22.05	92.451	3.51	41.99
7	Number of productive tillers per plant	14.82	16.33	82.364	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	83.881	54.38	29.64
10	Biological yield (g)	16.68	19.14	75.954	15.33	29.94
11	Harvest Index (%)	12.85	16.37	61.551	11.06	20.76
12	Test weight (g)	8.40	12.17	47.7	2.50	11.95
13	Grain yield per plant (g)	16.13	19.25	70.27	7.33	27.86

GCV - Genotypic Coefficient of Variation, PCV- Phenotypic Coefficient of Variation, h^2 – Heritability.

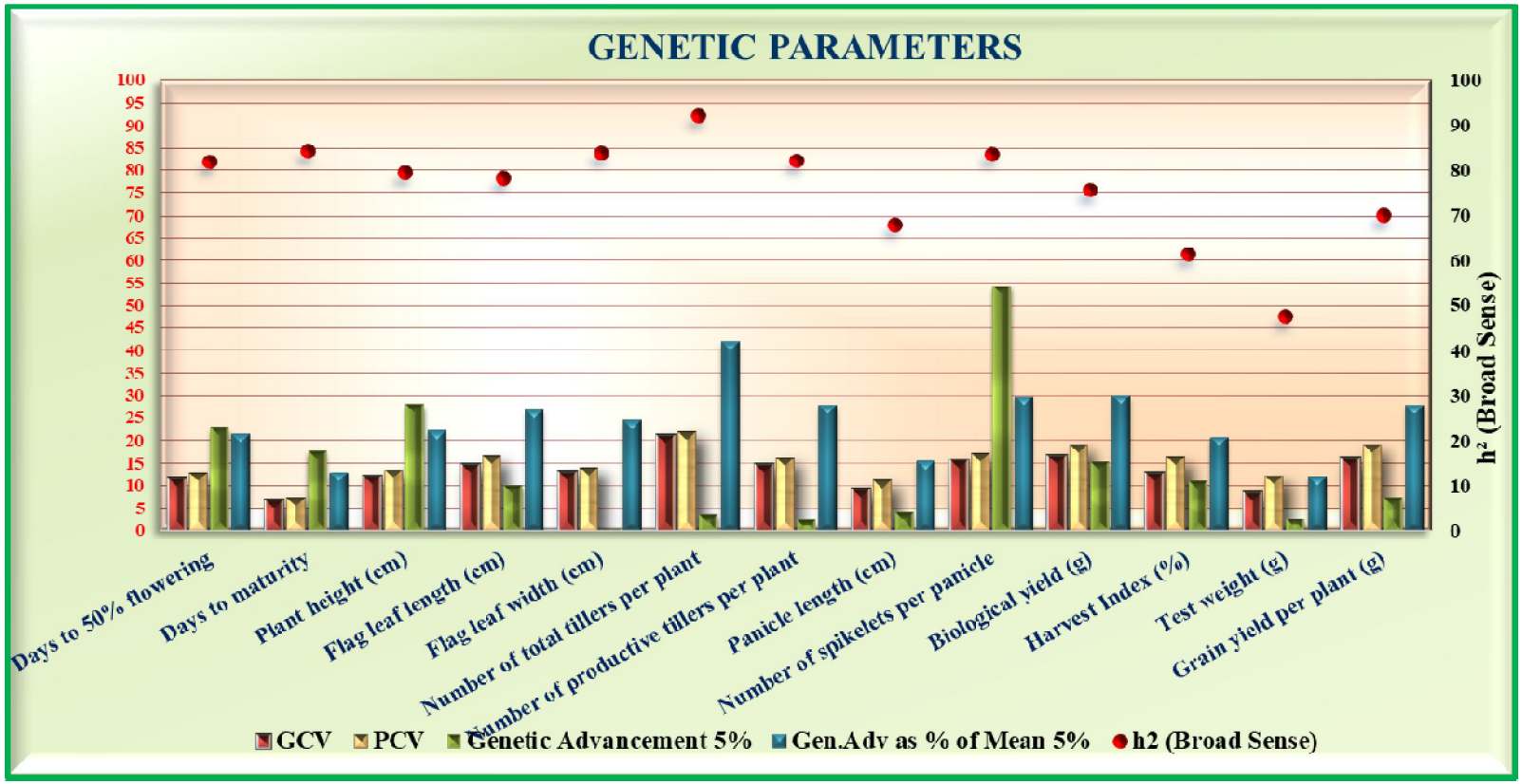


Fig. 1.Diagram showing the genetic parameters GCV, PCV, heritability, genetic advance and genetic advance as % of mean 5%

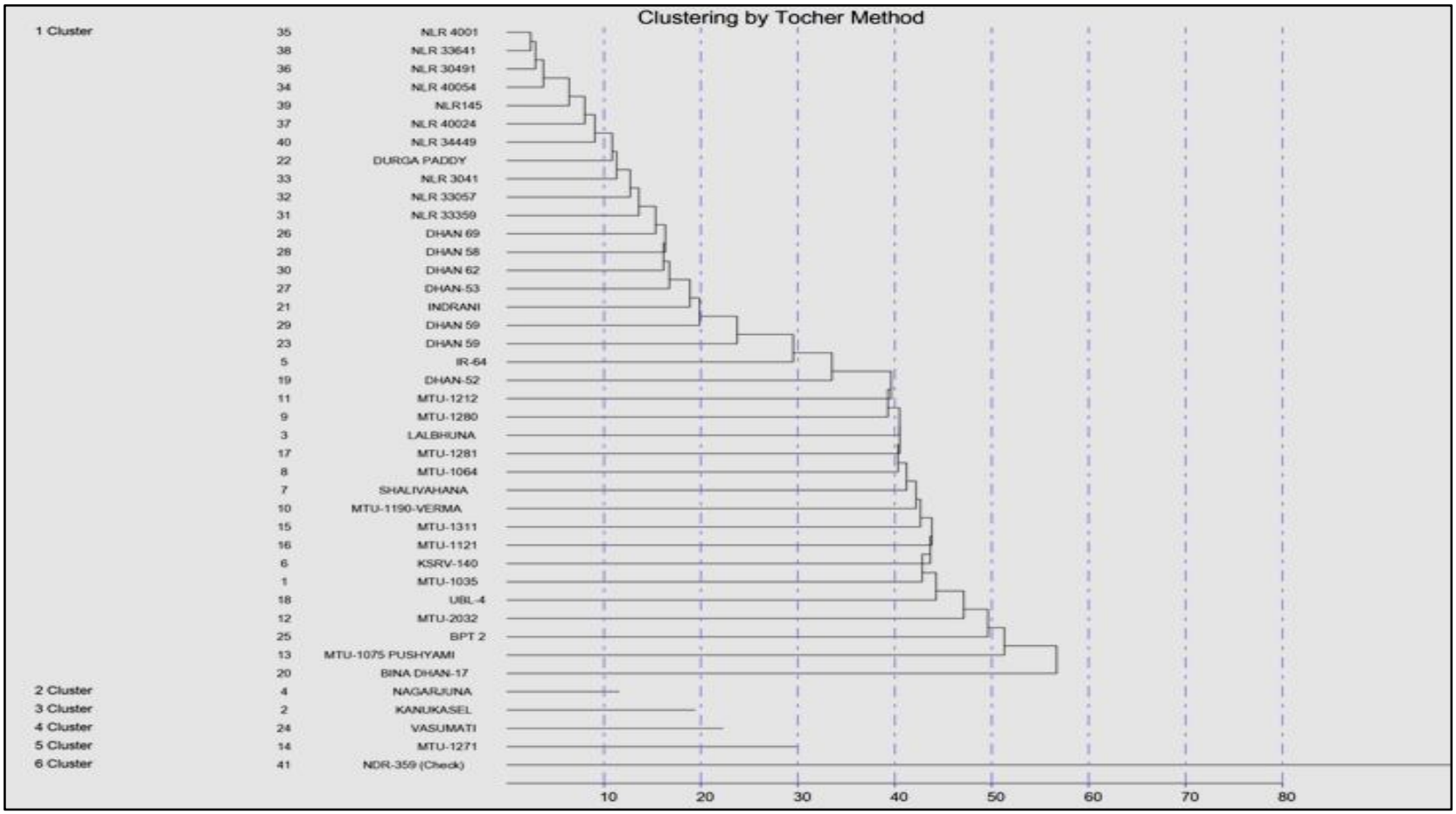


Fig. 2. Dendrogram showing the clustering of 41 genotypes by Tocher method

Table 5. Cluster composition of 41 rice genotypes

Cluster	No. 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 6. Cluster means for six clusters and 13 quantitative characters

Cluster means : Tocher method													
	DFF	**DM**	**PH**	**FLL**	**FLW**	**NTTP**	**NPTP**	**PL**	**NSPP**	**BY**	**HI**	**TW**	**GY**
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 7. Inter-cluster and Intra-cluster distance (diagonal) D^2 values of 41 rice

	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

Fig. 3. Representation of cluster distances between the six clusters using cluster diagram

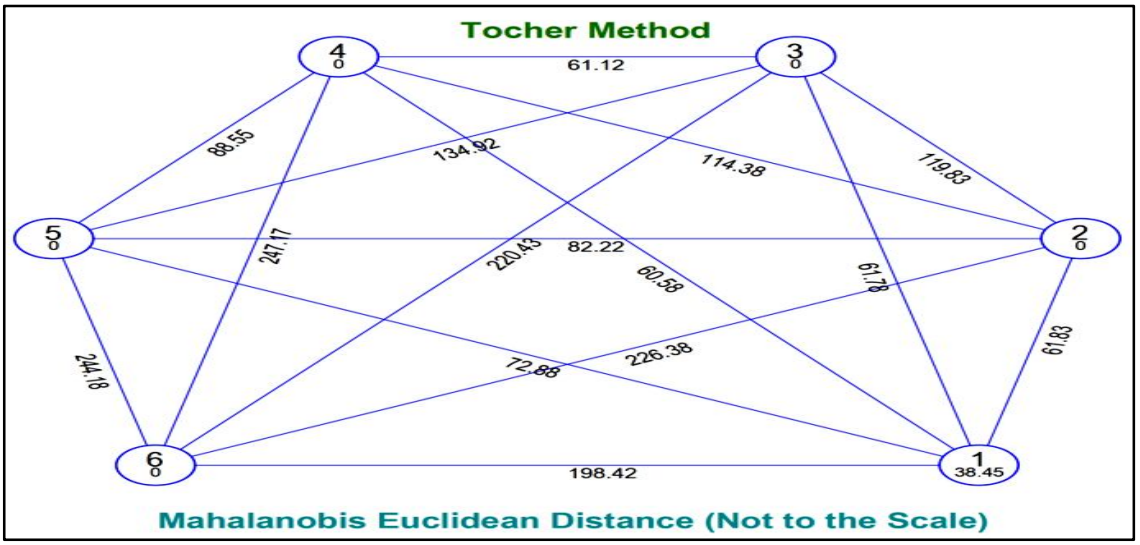
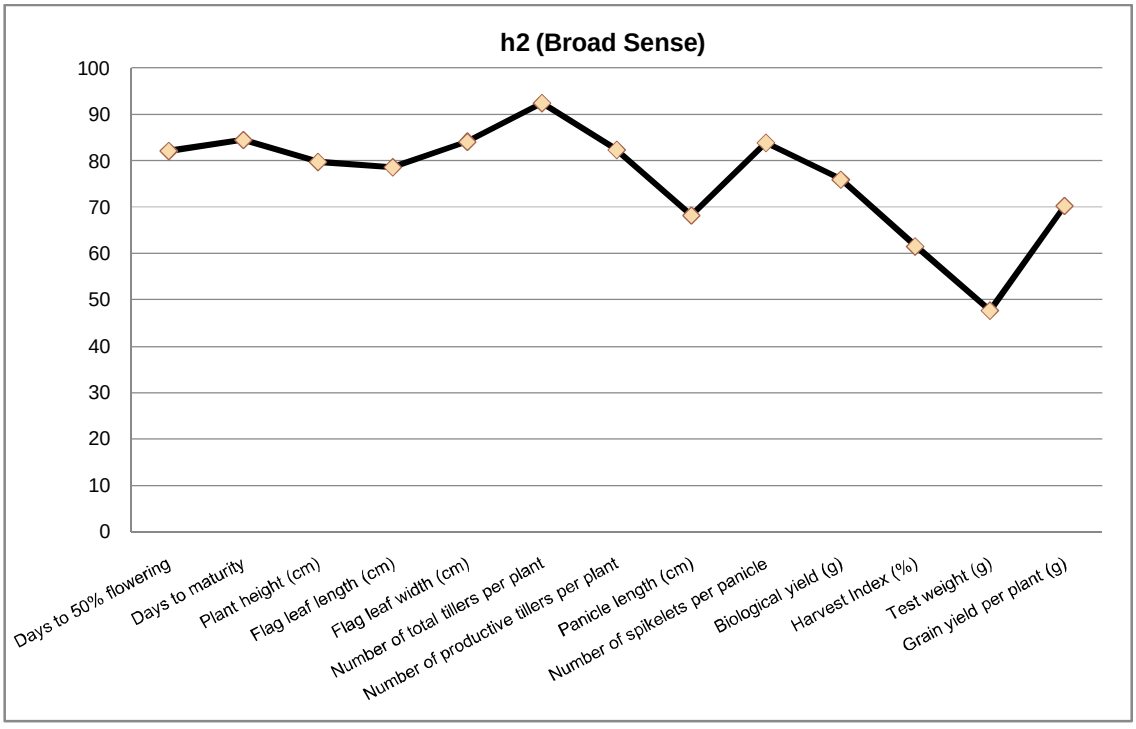


Fig. 4. Graph depicting frequency for broad sense heritability for 13 characters



There is a need to initiate a crossing program between the genotypes from the most distant clusters. The greater the distance between the clusters, also the greater the genetic variability of the genotypes found in these clusters. However, while estimating genetic diversity of the parents to be used in hybridization programme, it has been noticed that parents with wide genetic diversity and high yielding potential are likely to produce better segregants in a shorterperiod (Roy and Panwar, 1993).

On the basis of D^2 values, the 41 genotypes were grouped into six clusters using Tocher method (Singh and Choudhary, 1977).

CONCLUSION

In this study, it wasfound that the changed cultivars genotypes VASUMATI and DHAN 69 were the best in terms of grain yield based on mean performance at Prayagraj region.

The highest coefficients of variation, both in terms of PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation), were recorded for the number of total tillers per plant.The higher magnitude of PCV and GCV coefficient of variation was recorded for number of total tillers per plant. Estimates of PCV were higher than their corresponding GCV however 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).Estimates of genotypic coefficient of variation and phynotypic coefficient of variationwere consistent for all the traits, with PCV values being numerically higher than GCV values which indicated greater genotype and environment interaction.

The present investigation registered 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. Number of total tillers per plant showed highest genetic advance (41.99) as percentage of mean, followed by, biological yield (g) (29.94), Number of spikelets per panicle (29.64), Grain yield per plant (g) (27.86), Number of productive tillers per plant (27.72), Flag leaf length (cm) (26.88). While moderate genetic advance as a percent of mean was observed in, Panicle length (cm) (15.59), Days to maturity (12.88), Test weight (g) (11.95). Having high heritabillity means that it has a significant portion of variation which is due to genetic differences, and high heritability implies that the selection based on these traits is likely to be effective.

The largest cluster was cluster was clsuer I with 36 genotypes followed by cluster II, III, IV, V, VI, with one genotype each. The maximum inter cluster distance was between cluster IV and VI (247.17). In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by grain yield per plant (g) (20.24) followed by number of total tillers plant (19.76) and number of spikelets per plant (14.51).

The more the intercluster distance is, the more they are distinctly related. Therefore, genotypes present in the clusters having maximum intercluster distance 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. Further testing of these genotypes is required to confirm the consistency of results.

DISCLAIMER (ARTIFICIALINTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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