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

ABSTRACT

The present investigation was conducted with 41 genotypes of Rice during Kharif 2023 under Randomized Block Design (RBD) with three replications. The data was 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 that from the genotypes the highest grain yield was observed in (VASUMATHI) 38.9 followed by (DHAN-69) 34.33 on the basis of mean performance at Prayagraj region. 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

Rice (*Oryza sativa*) is a diploid which we put as (2n=2x=24), and a monocotyledonous angiosperm belongs to the genus Oryza of Poaceae family (Gramineae), beginning from South East Asia, developed broadly in humid tropical and sub-tropical locales of the world. Rice is a rain fed kharif season crop that is sown in the months of June – July in India. Rice is a staple meal for over half of the world's population, in particular in Asia where this cereal grain is anessential 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. As of the available data for the year 2023-24, on the basis of reports from the sources as FAO, USDA and all the national agriculture departments, the global estimate was around 738 million metric tons. Top two producing countries were China and India. India with approximate 178 million metric tons, which gives an idea about the consumption rate for rice in India.

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 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 diverse 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. 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 in a randomizedblock design (RBD) with three replications 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, 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 diversity.

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 in all 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 categorizing 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 partioning of superior genotypes.

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	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

4. RESULTS AND DISCUSSION

Analysis of variance

Anova revealednotable differences between the existing genotypes for all the traits. This indicates that there was an ample scope for selection of best 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 foregoing estimates of GCV and PCV are ideal in relation for all character types, but PCV will always have a larger numerical value than GCV. 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 (table no. 4), 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 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).
(Figure no.4), is the representation of a graph depicting frequency of the broad sense heritability in 13 characters.

Genetic Advance

Table no.4 outlines the genetic advance range between all the quantitative traits in the study which included 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 obtained 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).

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 in accordance 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 given in (Table no.4).

Cluster mean for different characters

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 mean value 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

In fig.no. 2. the dendrogramis showing the clustering of 41 genotypes by using Tocher 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 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).

(Table no.7) 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. In (Figure no.3), using cluster diagram thediagramatic representation of the intercluster 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

The percent contribution of thirteen characters towards total genetic divergence is listed in (Table 2). The selection and choice of parents substantially depends upon contribution of characters towards divergence. In the present investigation 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).

According toUsha Kumari and Rangasamy (1997)the characters days to maturity and panicle per hill were the main contributors to divergence and ought to serve as a foundation for selection for genotypes. To put it in another way, choosing these characters could be fruitful.

Sl. No.	Source	Contribution %
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	Number of 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 2. Percent contribution towards divergence

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.

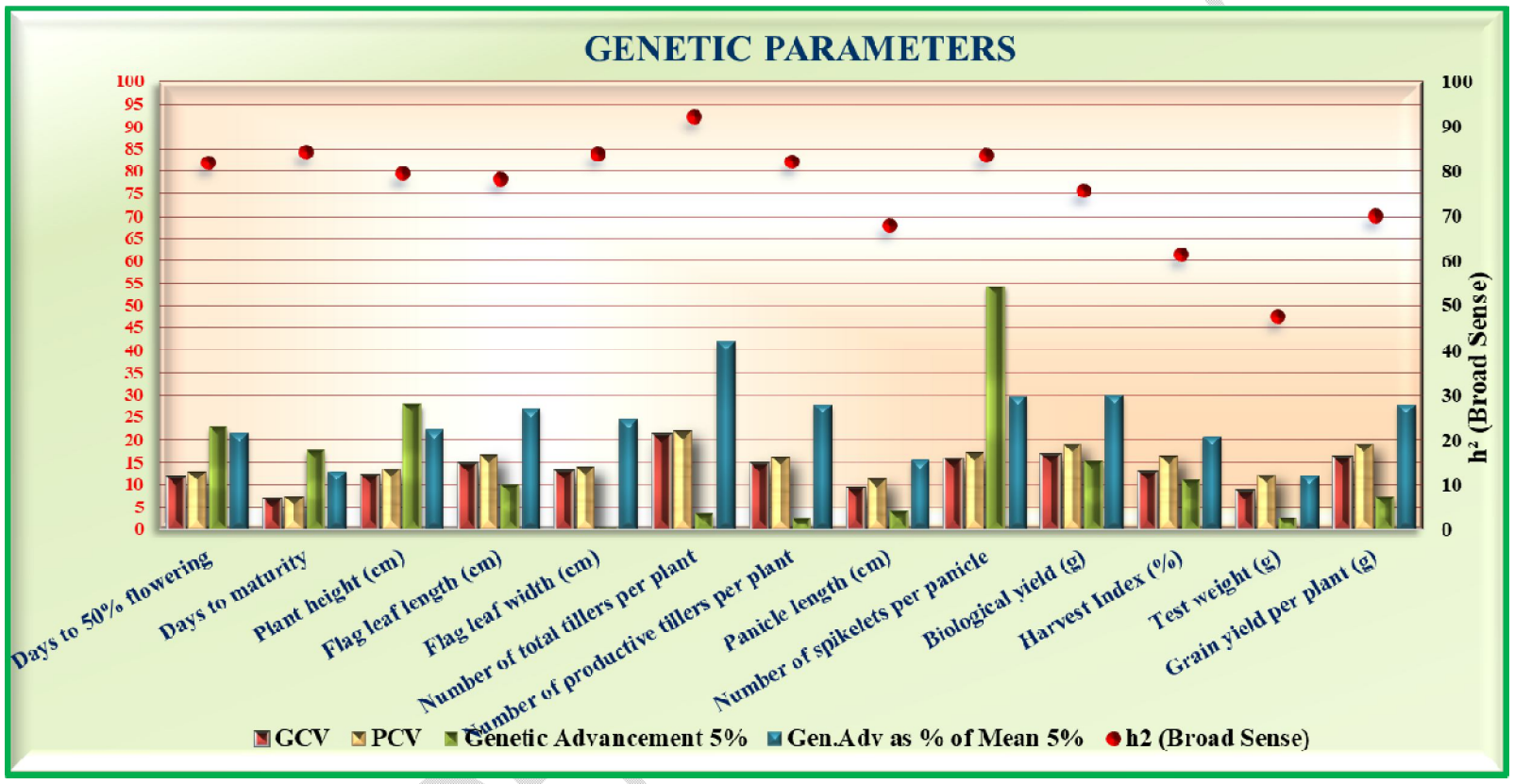


Fig. 1.Diagram showing the genetic parameters GCV, PCV, heritability, genetic advance and genetic advance as % of mean 5%

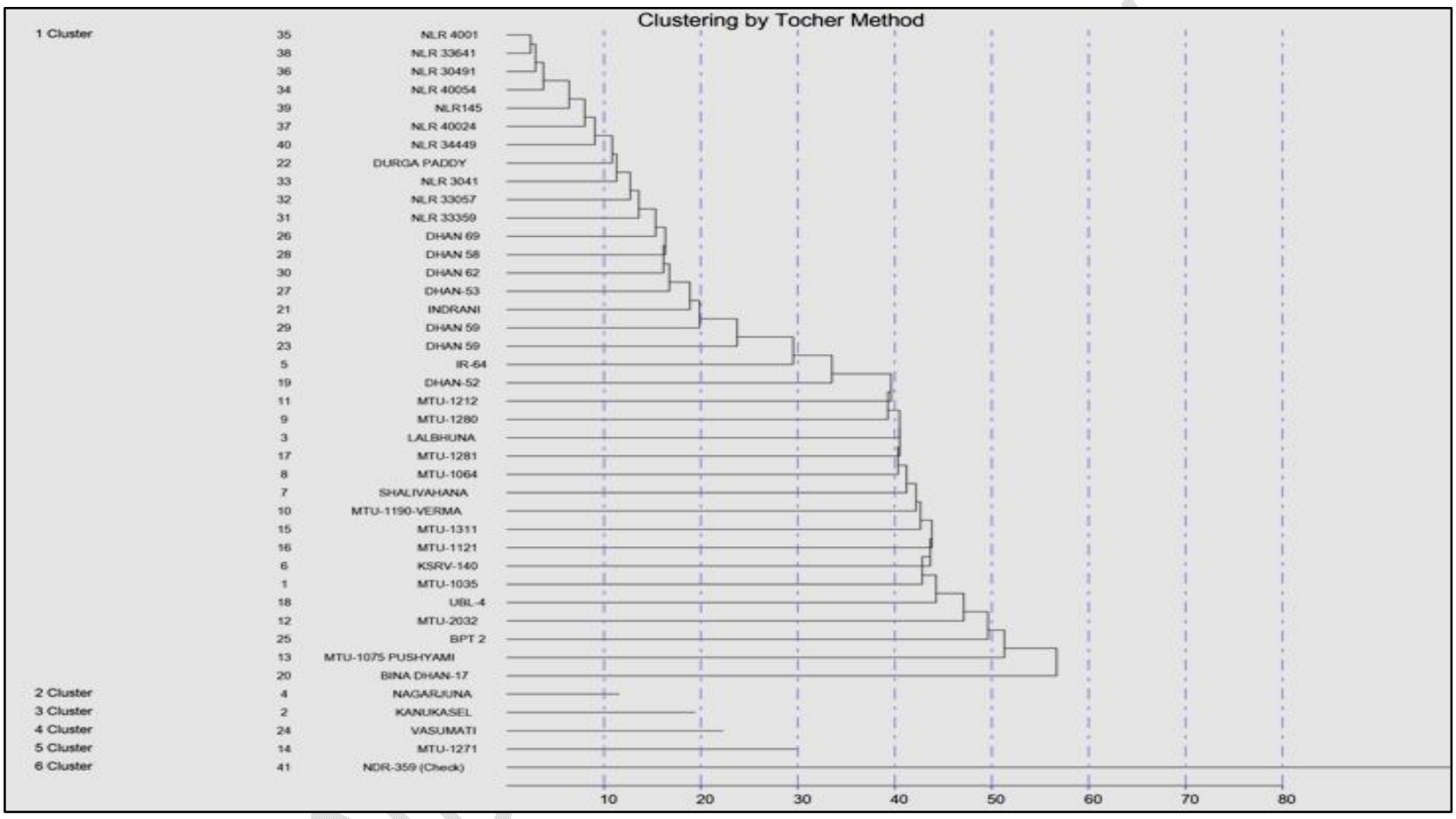


Fig. 2. Dendrogram showing the clustering of 41 genotypes by Tocher method

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

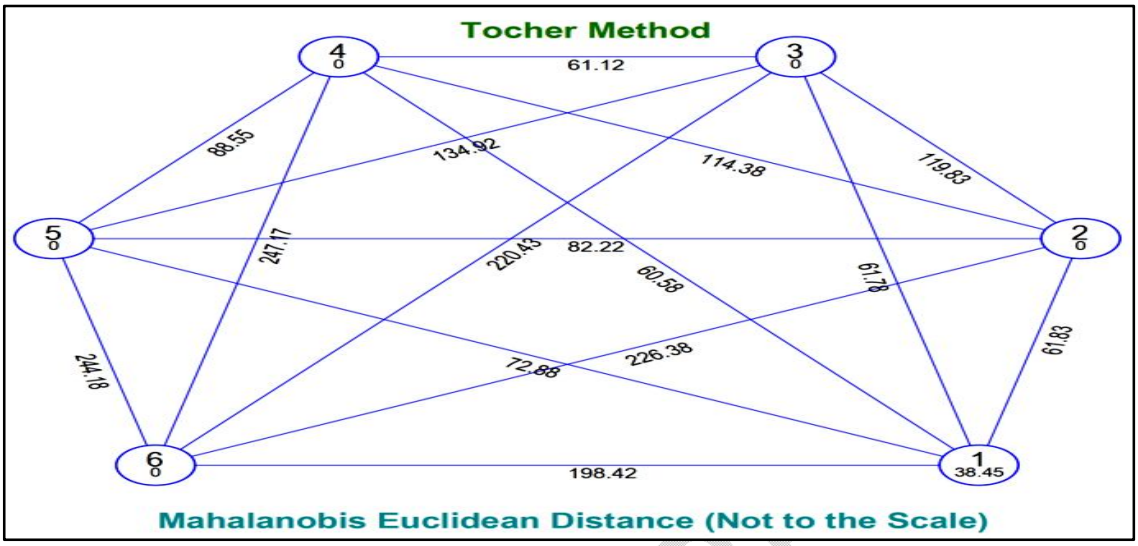
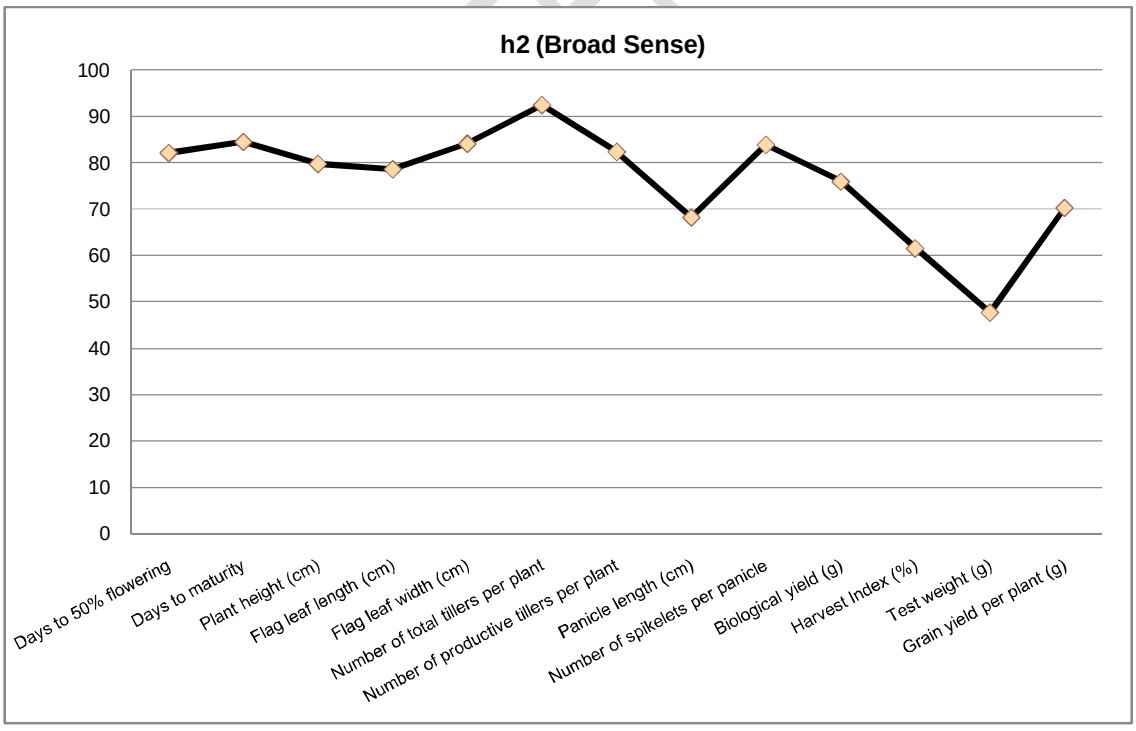


Fig. 4. Graph depicting frequency for broad sense heritability for 13 characters



There is a need to start 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 short time (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 was found that changed cultivars genotypes VASUMATI, DHAN 69 were the best in terms of grain yield based on mean performance at Prayagraj region. The higher magnitude of PCV and GCV coefficient of variation was recorded for number of total tillers per plant.Heritability and expected geneticadvance in percent of the mean values for the number of total tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, plant height, days to maturity, and days to 50% flowering were observed in the present investigation.

The number of total tillers per plant showed the highest genetic advance as a percentage of the mean, followed by biological yield, the number of spikelets per panicle, grain yield per plant, the number of productive tillers per plant, and flag leaf length. While moderate genetic advance as a percent of mean was observed in, Panicle length, Days to maturity, Test weight.

The largest cluster was cluster I followed by cluster II, III, IV, V, VI. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by grain yield per plant followed by number of total tillers plant and number of spikelets per plant. The intercluster distance was maximum between cluster IV and VI.Therefore, genotypespresent 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.

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