

ASSESSMENT OF GENETIC DIVERSITY OF RICE (*Oryza sativa* L.) UNDER PRAYAGRAJ AGRO-CLIMATIC CONDITIONS

Abstract

The goal of the current study was to assess the genetic variability parameters and genetic diversity in 40 rice genotypes for 13 quantitative traits in the *Kharif*, 2022 Season at the field experimentation center, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Uttar Pradesh. Analysis of variance indicated highly significant differences among the genotypes for all the traits. Considerable variability existed among the genotypes for all the characters studied. It is concluded that among 40 genotypes of rice, Nellore Dhanyarasi showed early flowering (77 days), IR-64 had characters like early maturity (108 days), high grain yield per plant is seen in Shuats Dhan-6 (62.1 g), JHARA SEL showed high plant height (185 cm) and high biomass is seen in Shuats Dhan-6 (123.6 g), Swathi showed high panicle length (43.7 cm). Highest GCV and PCV were depicted for grain yield per plant, biological yield, harvest index and number of spikelets per panicle. The highest heritability was observed for Grain Yield per Plant followed by Harvest Index, Flag Leaf length, Biological Yield and Number of Spikelets per Panicle. The Genetic Advance in per cent of mean is high for grain yield per plant, biological yield, harvest index and number of Spikelets per Panicle. Based on D^2 values, 40 genotypes grouped into 7 clusters. Among 7 clusters, cluster I had a greater number of genotypes (26) followed by cluster II (8), III (2), IV, V, VI and VII (1) genotype each. Cluster VI and cluster III (365.72) followed by cluster VII and cluster V (363.6), were most diverse from each other and the genotypes included 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. The trait Grain yield per hill had maximum contribution towards to genetic divergence followed by biological yield, Harvest Index, Test Weight. Therefore, all these characters should be given due consideration during selection for crop improvement.

Keywords: Genetic Variability, Heritability, Genetic Advance, Diversity, Rice

Introduction

Rice (*Oryza sativa* L.) belongs to the genus *Oryza* of *Poaceae* family *Graminae* and is a true diploid with chromosome number $2n = 24$. Rice has been cultivated by mankind for more than 10,000 years. The cultivated varieties of *Oryza sativa* grouped into three sub species, *indica*, *japonica* and *javanica*. Where *indica* are grown through the tropical and sub-tropical region and *japonica* varieties are grown throughout the temperate zone and *javanica* are grown mainly in the part of Indonesia.

Rice important role in India economy being a staple food for two third of the overall population. The nutrient content of rice are 80% carbohydrates, 7-8% protein (The amino acid profile shows that it is rich in glutamic acid and Aspartic acid, highest quality cereal protein being

rich in lysine (3.8%), 3%, fiber, iron 1mg and zinc 0.5 mg (**Juliano et al. 1985**). Rice is a short-day autogamous crop.

Rice is a crop that self-pollinates and has short days. The crop needs a hot, humid climate with average temperatures between 2 and 37°C for the entirety of its life cycle. In India, rice is predominantly a Kharif crop and is widely grown in regions with abundant yearly precipitation. In areas with little rainfall, it is also grown under irrigation. In the eastern and southern parts of India, rice is a common ingredient in food.

The direct and indirect impacts of numerous independent variables on dependent variables are measured using path analysis. Selection becomes more successful when the cause-and-effect relationship is understood. The path coefficient, which measures the direct effect of a predictor variable on its response variable, is one component of path analysis; the indirect effect(s) of a predictor variable on the response variable through another predictor variable is the second component (**Dewey and Lu, 1959**). Path analysis has been used in plant breeding to help find features that can be used as selection criteria to boost crop output. (**Surek and Beser, 2003**).

Objectives

1. To estimate genetic variability, heritability and genetic advance for grain yield component characters of rice
2. To assess genetic diversity in different accessions of rice for different quantitative characters
3. To identify divergent parents for future hybridization programme

2. Materials and Methods

The present investigation was carried out at the Field Experimentation Center of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P. during *Kharif*, 2022. The university is situated on the left side of Allahabad Rewa National Highway, about 5km from Prayagraj city. All types of facilities necessary for cultivation of successful crop including field preparation inputs, irrigation facilities were provided from the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P.

The experimental material for present study is obtained from the Department of Genetics and Plant Breeding, SHUATS, Prayagraj (Allahabad). The details of experimental material are as follows:

Table 1 List shows the name of genotypes

S.NO	NAME OF GENOTYPES	S.NO	NAME OF GENOTYPES
1	AGNISAL	21	SWATHI
2	BOICHI	22	NELLORE MAHSURI
3	JHARA SEL	23	C.SEL-3
4	PULE	24	NELLURE SUGANDHA
5	LALBHUNA	25	BHARINI
6	JALDHAY APA-3	26	IR -64
7	KHAYAMDHAN	27	RDR-1140
8	TALMUNFAR	28	RNR-15459
9	BALAM	29	RNR-29325
10	LALMALA	30	RNR-15098
11	UBL-4	31	PUSHYAMI
12	LAGEDHAN	32	VARMA
13	KAUKA SEL	33	MTU-1280
14	BINNI	34	MTU-1212
15	SITAL KUCHI-6	35	MTU-1281
16	PAHARI BOICHI	36	SHUATSDHAN 2
17	CHAPKA CHAKLAO	37	SHUATS DHAN 3
18	NELLURE DHANYARASI	38	SHUATS DHAN 4
19	B.D.O.NAGRA	39	SHUATS DHAN 6
20	NELLORE SONA	40	NDR-359 (CHECK)

STATISTICAL ANALYSIS

- Analysis of variance (**Fisher, 1918**)
- Genetic Variability (**Burton, 1952**)
- Coefficient of variation (**Burton and De vane, 1953**)
- Genotypic coefficient of variation (**GCV**)
- Phenotypic coefficient of variation (**PCV**)
- Heritability broad sense (**Burton and Devane, 1953**)
- Genetic advance (**Johnson *et .al*, 1955**)
- D² analysis (**Mahalanobis, 1928**)

3 Results and Discussion

Analysis of variance

The analysis of variance for grain yield and its contributing traits has been presented in table-1. The mean squares due to genotypes were highly significant for all the characters indicating the presence of considerable amount of genetic variability in the material.

This study attempted to assess the mean values, range, coefficient of variation and critical difference of 40 rice genotypes for all 13 quantitative characters that are presented in which had revealed a range of variation for all the characters studied.

Grain Yield per Plant ranged from 8.1 to 62.1 g per plant, with a grand mean of 23.2 g. SHAUTS DHAN-6 (62.1 g) had the highest Grain Yield per Plant per plant, followed by SHAUTS DHAN-2 (51.5 g) and SHAUTS DHAN-3 (45.3 g). RNR-15459 (8.1 g) had the lowest minimum grain yield per plant, followed by C.SEL (10 g) and Lalmala (10.2 g).

Highest PCV were depicted for Grain yield per plant (53.4 %) followed by biological yield (41.3 %). Among the 13 quantitative characters, estimates of GCV were recorded highest for Grain yield per plant (52.2 %) followed by biological yield (39.8 %) and Harvest Index (29.8%). Moderate estimates of PCV were recorded for Number of Spikelets per panicle (27.9%), followed by number of tillers per hill (26.9%) and number of panicles per hill (25.9%). Low estimation of PCV were recorded for Days to maturity (8.7%) and Days to 50% flowering (12.2%).

Table 2: Analysis of Variance of thirteen traits in 40 promising rice lines for agronomic traits evaluated under field condition in *Kharif* 2022, at SHUATS, Prayagraj

Sr.No.	Trait	Mean sum of squares		
		Replications	Treatments	Error
	Degrees of freedom	2	39	78
1	Days to 50% flowering	10.008	540.83**	47.17
2	Days to maturity	5.70	478.20**	61.22
3	Plant height (cm)	113.967	1798.89**	121.96
4	Panicle length (cm)	10.398	54.43**	5.21
5	Flag leaf length	14.124	256.45**	6.08
6	Flag leaf width	0.01	0.13**	0.006
7	Number of tillers per hill	1.79	17.64**	0.79
8	Number of panicles per hill	1.86	15.15**	0.81
9	Number of Spikelets per panicle	863.349	10216.7**	376.34
10	Biological yield per plant (g)	125.58	1624.53**	41.79
11	Test weight (g)	8.933	69.24**	3.98
12	Harvest Index(%)	3.311	446.12**	8.40
13	Grain yield per plant(g)	17.22	445.81**	7.05

****indicates significance at 1% level of significance**

Table 3: Genetic parameters of grain yield and yield components of 40 promising rice lines for agronomic traits evaluated underfield condition in Kharif 2022, at SHUATS, Prayagraj

SR.NO	Trait	GCV (%)	PCV (%)	h ² (Broad sense) (%)	GA (5%)	GA% (5%)
1	Days to 50% flowering	12.2	13.8	77.7	23.3	22.1
2	Days to maturity	8.7	10.5	69.4	20.2	15.0
3	Plant height (cm)	16.1	17.7	82.1	44.1	30.0
4	Panicle length (cm)	15.1	17.4	75.9	7.3	27.2
5	Flag leaf length	22.1	22.9	93.2	18.2	44.0
6	Flag leaf width	16.9	18.0	88.2	0.4	32.8
7	Number of tillers per hill	26.9	28.7	87.6	4.6	51.9
8	Number of panicles per hill	25.9	28.0	85.5	4.2	49.3
9	Spikelets per panicle	27.9	29.4	89.7	111.7	54.4
10	Biological yield per plant (g)	39.8	41.3	92.7	45.5	78.9
11	Test weight (g)	22.7	24.7	84.5	8.8	43.1
12	Harvest Index	29.8	30.7	94.6	24.2	59.7
13	Grain yield per plant	52.2	53.4	95.4	24.3	104.9

GCV: Genotypic Coefficient of Variation, **PCV:** Phenotypic Coefficient of Variation, **h²:** Heritability, **GA:** Genetic Advance, **GA% of Mean:** Genetic Advance at percent of mean

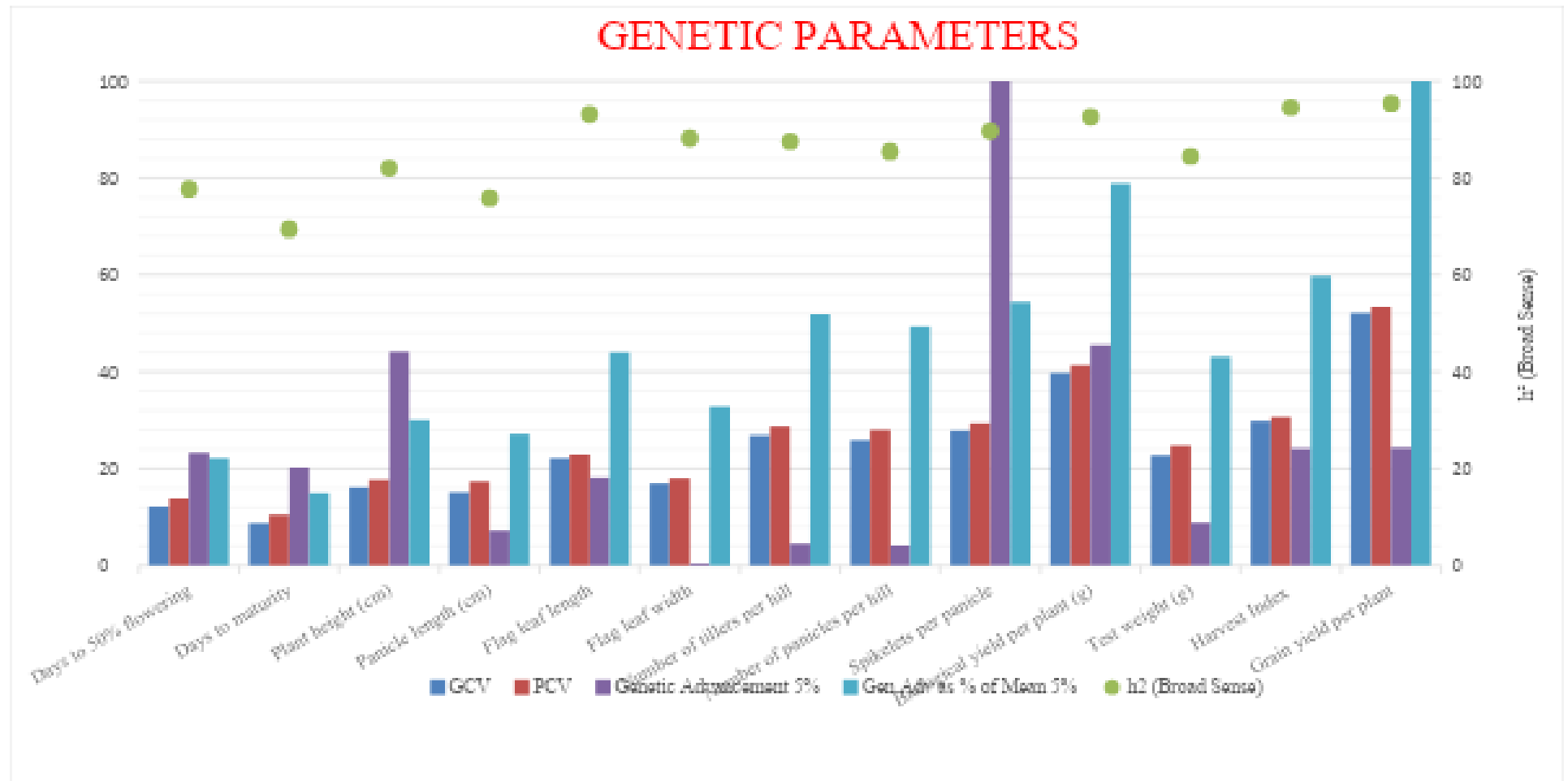


Fig.1 Bar diagram depicting GCV, PCV, heritability and genetic advance for 13 quantitative characters of rice.

Heritability

The traits with high heritability estimates showed that variation in these traits predominantly governed by heritable factors, whereas both genetics and environment played equivalent roles in the expression of traits with moderately high heritability indicated that the expression of the trait was mostly influenced by environment rather than genetic. Traits with high heritability estimates in broad sense can be utilized for genetic improvement as they are least influenced by the environmental effects and thus having a potential for large genetic determination.

The estimates of heritability from present investigation are presented in (Table 3). In the present study, heritability (broad sense) ranged from 95.4% to 69.4%. The highest heritability (above 60% is seen in all parameters) was observed for Grain Yield Per Plant (95.4 %) Harvest Index (94.6 %), Flag Leaf Length (93.2 %), Biological yield (92.7 %).

Genetic advance

In the present study a perusal of genetic advance (Table 3) showed that it was high for Number of spikelets per Panicle (111.7) followed by biological yield (45.5), Plant Height (44.1) and Grain Yield Per Plant (24.3). Genetic advance showed that it was low for Flag leaf width (0.4), Number of panicles per hill (4.2), Number of tillers per hill (4.6). Genetic advance as percent mean

Heritability does not alone does not provide any indication of the amount of genetic improvement that would result from the selection of individual genotypes. Thus, to arrive at more reliable conclusion high heritability should be accompanied by high genetic advance (**Johnson *et al.* 1955**). Thus, knowledge of heritability and genetic advance of the character indicate the scope for the improvement through selection. In the present investigation, high genetic gain was recorded for Grain Yield Per Plant (104.9 %), Biological yield (78.9 %), Harvest Index (59.7 %), Number of spikelets per panicle (54.4 %), Number of tillers per hill (51.9 %), Number of panicles per hill (49.3 %), Flag leaf length (44 %), Test Weight (43.1%), Flag leaf width (32.8 %), Plant height (30 %), Panicle Length (27.2 %), Days to 50% flowering (22.1 %) and Days to maturity (12 %).

Cluster Group	No. of Genotypes	List of Genotypes
Cluster-I	26	Khayamdham, Talmunfar, Lalmala, Balam, Ubl-4, Kaukasel, Lagedhan, Plue, Lalbhuna, Jaldhay Apa-3, Mtu-1212, Boichi, Chapka Chaklao, Pahari Boichi, Varma, Nellore Dhanyarasi, Pushyami, Nellore Sona, RNR-15098, Nellore Mahsuri, Bharini, Binni, C. Sel-3, Jhara Sel, RNR-29325 & RNR-15459
Cluster-II	8	Ir-64, Rdr-1140, Shauts Dhan-3, Shauts Dhan-2, Mtu-1280, Shauts Dhan-6, Shauts Dhan-4 & Mtu-1281
Cluster-III	2	Swathi, Nellore Sugandha
Cluster-IV	1	B.D.O. NAGRA
Cluster-V	1	Agnisal
Cluster-VI	1	Sital Kuchi-6
Cluster-VII	1	NDR-359 (Check)

Table 4 Grouping of 40 Rice genotypes in to different clusters

Clusters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster -V	Cluster -VI	Cluster -VII
Cluster-I	63.67	120.80	108.49	117.92	130.94	176.48	160.36
Cluster-II		105.07	136.13	186.38	167.26	254.63	199.62
Cluster-III			15.84	254.19	202.34	365.72	192.72
Cluster-IV				0.00	211.40	42.05	123.10
Cluster-V					0.00	246.31	363.60
Cluster-VI						0.00	221.70
Cluster-VII							0.00

Table -5: Grouping of 40 genotypes onto different clusters

Fig. 2 Inter and intracluster distance of 40 genotypes of rice

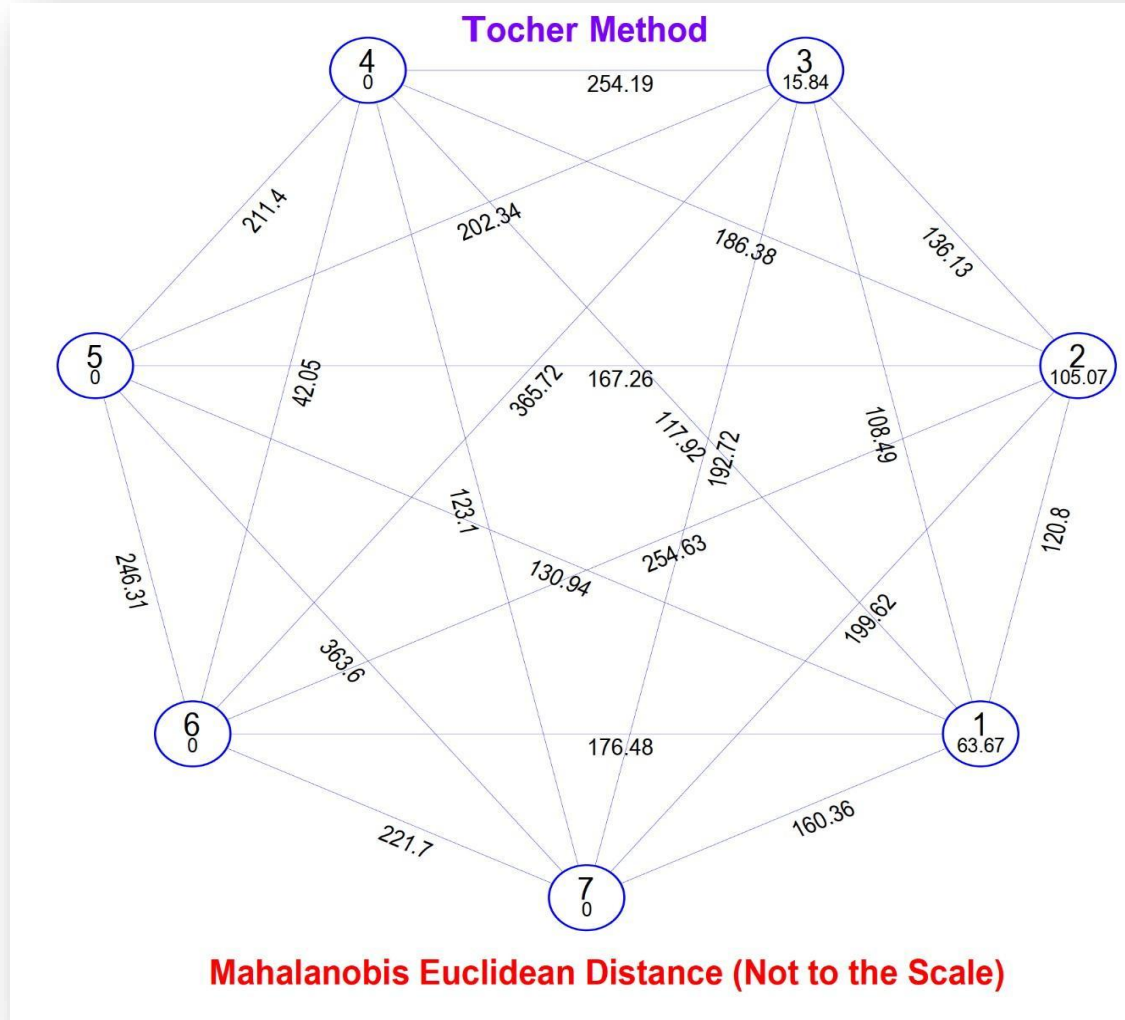


Table 6 Cluster Mean of 13 biometrical traits of 40 rice genotype

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster -V	Cluster -VI	Cluster -VII
DF50	108.9	98.54	82.83	115.33	107.33	118.67	105.00
DM	138.55	125.92	117.00	142.33	141.63	145.33	131.00
PH	151.94	134.91	113.84	163.28	177.68	159.59	125.00
PL	25.50	27.89	39.03	24.30	29.80	24.43	27.97
FLL	40.59	41.69	24.24	55.25	45.13	78.59	35.81
FLW	1.17	1.34	1.17	0.88	1.00	0.97	1.83
NTH	7.89	10.96	8.40	9.33	7.94	9.80	15.60
NPH	7.64	10.50	8.40	7.73	7.40	9.00	14.00
NSPP	196.59	234.94	228.90	191.73	204.93	167.80	210.60
BYH	50.49	78.85	35.43	60.53	114.00	68.80	51.50
TW	19.67	23.40	26.00	13.73	15.34	17.36	23.10
HI	36.93	52.40	52.85	33.42	32.57	25.75	44.00
GYH	17.96	40.68	18.67	20.13	37.14	17.80	22.66

DF50: Days to 50% flowering, **DM:** Days to maturity, **FLL:** Flag leaf length (cm), **FLW:** Flag leaf width (cm), **PH:** Plant height (cm), **NTH:** Number of tillers per Hill, **NPH:** Number of Panicles per Hill, **PL:** Panicle length (cm), **NSPP:** Number of Spikelets per Panicle, **BY:** Biological Yield (g), **HI:** Harvest index (%), **TW:** Test weight (g), **GYPP:** Grain Yield per Plant (g)

Inter and intra cluster distance

Inter and intra cluster distances are furnished in Table 5. The intra cluster values ranged from 0 to 105.07. The maximum intra cluster distance was observed in cluster II (105.07). The minimum intra cluster distance for cluster IV, V, VI and VII exhibited zero. The inter cluster distance differ from 42.05 (between IV and VI) to 365.72 (between III and VI). Other inter cluster distance were between these values. The highest inter cluster distance observed between cluster VI and cluster III (365.72) followed by cluster VII and cluster V (363.6), cluster VI and cluster II (254.63), cluster IV and cluster III (254.19) and cluster VI and cluster V (246.31). The minimum intercluster distance observed between cluster VI and IV (42.05), cluster III and cluster I (108.49), and cluster IV and cluster I (117.92).

Cluster means

The results of cluster mean were furnished in Table-6. **Days to 50% flowering**

Cluster mean of days to 50% flowering ranged from 82.83 (cluster III) to 118.67 (cluster VI).

Days to maturity

Cluster mean of Days to maturity varied from 117 (cluster III) to 145.33 (cluster VI). The clusters viz., cluster I (138.55), cluster V (141.67), cluster IV (142.33) and cluster VI (145.33) had significant and higher than grand cluster mean (134.54).

Plant height

Cluster mean of plant height varied from 113.84 (cluster III) to 177.68 (cluster V). The clusters viz., cluster I (151.94), cluster VI (159.59), cluster IV (163.28), cluster V (177.68) had significant and higher than grand cluster mean (146.61).

Flag leaf length

Cluster mean of Flag leaf length (cm) varied from 24.24 (cluster III) to 78.59 (cluster VI). The clusters viz., cluster IV (55.25) had significant and higher than grand cluster mean (45.9).

Flag leaf width

Cluster mean of Flag leaf width (cm) varied from 0.88 (cluster IV) to 1.83 (cluster VII). The clusters viz., cluster III (1.34) had significant and higher than grand cluster mean (1.19).

Number of tillers per hill

Cluster mean of Number of tillers per hill varied from 7.89 (cluster I) to 15.6 (cluster VII). The clusters viz., cluster II (10.96) had significant and higher than grand cluster mean (9.99).

Number of panicles per hill

Cluster mean of Number of panicles per hill varied from 7.4 (cluster V) to 14.0 (cluster VII). The clusters *viz.*, cluster II (10.5) had significant and higher than grand cluster mean (9.24).

Panicle length

Cluster mean of Panicle length varied from 24.30 (cluster IV) to 39.03 (cluster III). The clusters *viz.*, cluster V (29.8) had significant and higher than grand cluster mean (28.42).

Biological yield

Cluster mean of biological yield varied from 35.43 (cluster III) to 114 (cluster V). The clusters *viz.*, cluster VI (68.8) and cluster II (78.85) had significant and higher than grand cluster mean (65.66).

Harvest index

Cluster mean of harvest index varied from 25.75 (cluster VI) to 52.85 (cluster III). The clusters *viz.*, cluster VII (44) and cluster II (52.4) had significant and higher than grand cluster mean (39.70).

Number of spikelets per panicle

Cluster mean of Number of spikelets per panicle varied from 167.8 (cluster VI) to 234.94 (cluster II). The clusters *viz.*, cluster VII (210.6) and cluster III (228.9) had significant and higher than grand cluster mean (205.07)

Test weight

Cluster mean of Test weight (g) varied from 13.73 (cluster IV) to 26 (cluster III). The clusters *viz.*, cluster VII (23.10) and cluster II (23.4) had significant and higher than grand cluster mean (19.8).

Grain yield per hill

Cluster mean of grain yield per hill varied from 17.8 (cluster VI) to 40.68 (cluster II). The clusters *viz.*, cluster V (37.14) had significant and higher than grand cluster mean (25.01).

Contribution towards divergence

The per cent contribution of 13 biometrical traits of 40 rice genotypes towards genetic divergence was estimated and given in Table-7 and Figure 4. The trait Grain yield per hill (17.3%) had maximum contribution towards to genetic divergence followed by biological yield (14.2), Harvest Index (13%), Test Weight (12.6%), Number of spikelets per panicle (8.96%), Number of panicles per hill (8.67%), Flag leaf length (6.54%), Flag leaf width (5.54%), Number of tillers per hill (5.36%), Plant height (2.5%), Days to 50% flowering (2.0%), Days to maturity (1.79%), Panicle length (1.54%)

Table. 7 Per cent contribution of 13 biometrical traits of 40 rice genotypes towards genetic divergence

SL.NO.	Source	Contribution %	Times ranked 1st
1	Days to 50% flowering	2.00	16.00
2	Days to maturity	1.79	14.00
3	Plant height (cm)	2.50	19.00
4	Panicle length (cm)	1.54	12.00
5	Flag leaf length(cm)	6.54	51.00
6	Flag leaf width(cm)	5.54	43.00
7	Number of tillers per hill	5.36	42.00
8	Number of panicles per hill	8.67	68.00
9	Number of Spikelets per panicle	8.96	70.00
10	Biological yield per plant (g)	14.20	111.00
11	Test weight (g)	12.60	98.00
12	Harvest Index(%)	13.00	101.00
13	Grain yield per plant(g)	17.30	135.00

4.CONCLUSION

Considerable variability existed in the genotypes for all the characters studied. These were the genotypes with high mean values in desirable direction i.e., From the present investigation it is concluded that among 40 genotypes of rice, Nellore Dhanyarasi showed early flowering (77 days), IR-64 had characters like early maturity (108 days), High Grain Yield per Plant is seen in Shuats Dhan-6 (62.1 g), JHARA SEL showed high plant height (185 cm) and high Biomass is seen in Shuats Dhan-6 (123.6 g), Swathi showed high Panicle Length (43.7 cm). Highest GCV and PCV were depicted for Grain Yield per Plant, Biological Yield, Harvest Index and Number of Spikelets per Panicle. The highest heritability was observed for Grain Yield per Plant followed by Harvest Index, Flag Leaf length, Biological Yield and Number of Spikelets per Panicle. The Genetic Advance (GA) in per cent of mean is high for Grain Yield per Plant, Biological Yield, Harvest Index and Number of Spikelets per Panicle. Based on D^2 values 40 genotypes grouped into 7 clusters. Among 6 clusters, cluster I had a greater number of genotypes (26) followed by cluster II (8), III (2), IV, V, VI and VII (1) genotype each. Cluster VI and cluster III (365.72) followed by cluster VII and cluster V (363.6), 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. The trait Grain yield per hill had maximum contribution towards to genetic divergence followed by biological yield, Harvest Index and Test Weight. Therefore, all these characters should be given due consideration during selection for crop improvement.

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