



# **Genetic Divergence Analysis for Yield and Quality Traits in Rice (*Oryza sativa* L.) Germplasm under Irrigated Conditions**

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

The present investigation was carried out to conduct genetic divergence analysis for yield and quality traits in rice (*Oryza sativa* L.) germplasm under irrigated conditions. The experiment was conducted at crop research farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj. The experiment was performed with 40 rice genotypes with 13 quantitative characters and 8 qualitative characters. Analysis of variance revealed that all the genotypes showing significant at 1% level of significance for all the characters. According to mean table Shiats dhan-7, Shiats dhan-2 show greater mean in grain yield per plant. Genetic parameters show PCV greater than GCV in all the characters, the traits Grain yield per plant and biological yield exhibits greater in both GCV and PCV. Heritability showing high range of estimates in all the characters as Days to maturity, Days to 50% flowering exhibit greater among all the characters. Number of spikelets per panicle, biological

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yield shows highest among the characters in Genetic advance. According to D<sup>2</sup> analysis, the total genotypes are divided into five clusters, Cluster II showing greater in Intra cluster distance, Cluster V and Cluster I combination showing greater in Inter cluster distances. The Cluster IV showing highest among the clusters in the mean of Grain yield per plant. According to percentage contribution Grain yield per plant showing highest among the characters. Quality analysis had done on 35 genotypes, based upon quality characters Hulling percentage showing genotype Ajaya greater and genotype MTU-2032 shows greater in Kernel elongation ratio.

**Keywords:** Rice; genetic divergence; D<sup>2</sup> analysis; clusters analysis.

## 1. INTRODUCTION

Rice (*Oryza sativa* L.), chromosome number 2n=24, belongs to family Poaceae. *Oryza Sativa*, in the Indian subcontinent more than a quarter of the cultivated land is given to rice. It is a very essential part of the daily meal in the southern and eastern parts of India it is believed, is associated with wet, humid climate, though it is not a tropical plant [1-4].

Rice is the most significant food crop in terms of human nutrition and caloric intake, accounting for more than one-fifth of all calories consumed globally. Per 100-gram serving, white rice contains 68% water, 28% carbs, 3% protein, a minimal amount of fat, B vitamins (Thiamine), iron, niacin, vitamin B6, pantothenic acid, and manganese [5-9]. Milling byproducts such as bran and rice polish (finely powdered bran and starch resulting from polishing) are occasionally utilized as livestock feed.

Oil is extracted from bran for both food and industrial use. Broken rice is used in brewing, distilling, and starch production. Feed, cattle bedding, roof thatching, carpets, clothing, packing material, and broom straws are all made from straw [10,11].

“Rice-based farming systems are the most productive agroecosystems in Asia and produce the majority of food for most of the people” (Bijay-Singh et al. 2008). “Therefore, regional food security depends upon maintaining the productivity of rice and the crops that are grown in rotation with it” (Dixon et al. 2001). Fukai and Ouk (2012), “in a comprehensive review of rice production in the Mekong region of Asia, concluded that productivity (yield) was primarily driven by water and nutrient supply which, to some extent, was mediated through soil type and position of the paddy in the toposequence”.

Genetic diversity studies are important in academics because they aid in the assessment

and comprehension of species diversity and genetic composition [12-14]. They are used to establish genetic links between individuals, to discover and conserve optimal parental genotypes, and to aid in systematic agricultural growth (Tomar et al. 2021). Cross combinations combining divergent parents offer the possibility of bringing together gene constellations of various types, as well as promising segregant derivatives that come from the complimentary interaction of divergent genes in parents.

“Genetic divergence is an efficient parameter in selection of parent for hybridization programme. Information about degree of genetic divergence and nature would help plant breeders in choosing the appropriate parent for the breeding programme” (Vivekananda and Subramanian, 1993). The degree of divergence in germplasm is provided by D<sup>2</sup> analysis which was developed by Mahalanobis [15] This analysis gives information about inter and intra cluster distance that provide information of diversity at cluster level and crossing between germplasm of diverse cluster may give heterotic progeny Keeping this in view, the present study was focused to assess the genetic diversity 40 promising rice genotypes using Mahalanobis D<sup>2</sup> statistics.

### 1.1 Objectives

1. To assess the genetic diversity of 40 genotypes for yield and quality attributing characters
2. The evaluate rice genotypes for yield and yield attributing traits
3. To identify divergent parents for future hybridization programme

## 2. MATERIALS AND METHODS

The experiment was conducted at Crop research farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and sciences in *Kharif*, 2022. The

experimentation site is situated 98m above sea level at 25.57°N latitude and 81.56°N longitude. This area's Subtropical Climate has extremely hot and cold seasons. Temperatures might drop as low as 1-2 degrees Celsius in December and January, especially during the winter season. The temperature might reach 46 to 48 degrees Celsius during Summer.

The experiment was conducted with 40 genotypes (Table 1) of rice in randomized block design with three replications with row-to-row spacing 30cm and plant to plant 15cm. In each replication 5 randomly selected plants were evaluated and recorded on following 13 quantitative characters viz Days to 50% flowering, Days to maturity, Plant height, Flag leaf length, Flag leaf width, Number of tillers per hill, Number of panicles per hill, Panicle length, Number of spikelets per panicle, biological yield, Harvest Index, Test weight and Grain yield per plant and Quality characters viz Hulling percentage, Kernal length before cooking, Kernal breadth before cooking, Kernal length after cooking, Kernal breadth after cooking, Kernal length/breadth ratio before and after cooking, Kernal elongation ratio.

Analysis of Variance (ANOVA) to compare the rice genotypes for yield, and yield attributes were determined using the F-test in R software. The approaches estimated the phenotypic and genotypic variance components and coefficients of phenotypic and genotypic variation to compare trait variation, suggested by Lush (1940) and Chaudhary and Prasad (1968). Genotypic variation coefficient (GVC), phenotypic variation coefficient (PVC), heritability in a broad sense (h<sup>2</sup>b), genetic advance (GA), genetic advance as percentage of means (GAM). The Traits measures were calculated following formulae (Johnson HW, 1955).

$$\text{Genotypic variance } (\sigma^2 g) = (\text{MSg} - \text{MSe})/r$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + (\sigma^2 e)/r$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{x} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{x} \times 100$$

$$\text{Heritability } (h^2b) = (\sigma^2 g / \sigma^2 p) \times 100$$

$$\text{Genetic Advance (GA)} = k \times (\sigma_p) \times (h^2b)$$

$$\text{Genetic advance as percentage of Mean (GAM)} = (\text{GA}/X) \times 100$$

Where,

MSg = Mean sum of genotypes

MSe = Mean sum of error

r = number of replications

σ<sup>2</sup>e = environmental variance

x = grand mean

k = intensity of selection at 5%

The Software called R-Studio and SPSS was used to perform the analysis mentioned above.

### 3. RESULTS AND DISCUSSION

The analysis of variance revealed that for all 13 quantitative traits shows highly significant among all the genotypes for all the characters at 1% level. The presence of genetic variances in the experimental material suggests the importance of genetic variety in identifying the optimal genetic make-up, allowing for more selection scope. The analysis of variance for different characters are presented in Table 2.

The mean sum of squares due to genotypes shows significant differences to all the characters. This indicates that there is a presence of sustainable variability among

**Table 1. List of genotypes were used in the research**

RNR-1446		MTU-1032		WGL-44		JARAVA	
2	JGL-24423	12	MTU-1271	22	BPT-01	32	KRISHNA HAMSA
3	NLR	13	MTU-1064	23	MTU-1262	33	SAMPADA
4	DURGA PADDY	14	DRRH-2	24	BPT-02	34	AJAYA
5	KNM-118	15	NLR-145	25	INDRANI	35	JARAVA
6	MTU-1311	16	NLR-40054	26	SIDHA SANNALU	36	SHIATS DHAN-2
7	MTU-1121	17	NLR-4001	27	SIGNET-5455	37	SHIATS DHAN-3
8	MTU-2032	18	TRIGUNA	28	ANKUR POOJA	38	SHIATS DHAN-6
9	MTU-1010	19	KSRV-140	29	WGL-1119	39	SHIATS DHAN-7
10	IR-64	20	HMT	30	KAVERI	40	NDR-359 (Check)

**Table 2. Analysis of variance (ANOVA) among 40 rice genotypes of 13 quantitative traits**

Sl.No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	39	78
1	Days to 50% flowering	5.137	218.817**	3.106
2	Days to maturity	4.684	282.894**	3.128
3	Plant height (cm)	111.142	464.06**	44.497
4	Flag leaf length (cm)	3.411	81.401**	9.063
5	Flag leaf width	0.035	0.08**	0.012
6	Number of tillers per hill	1.271	11.358**	0.581
7	Number of panicles per hill	1.308	11.249**	0.656
8	Panicle length (cm)	2.484	17.116**	1.521
9	Number of spikelets per panicle	415.312	9950.761**	439.358
10	Biological yield (g)	1.015	1231.134**	22.435
11	Harvest Index (%)	38.724	183.005**	19.414
12	Test weight (g)	6.204	50.245**	3.834
13	Grain yield per plant (g)	9.932	322.234**	4.975

\*\* Significant at 1 percent level of significance

the genotypes. The performance of the genotypes with respect to these characters were statistically different that suggesting scope for improvement. The genotypes Shiats Dhan-7 (62.13), Shiats Dhan-2 (51.46), Shiats Dhan-3 (45.33), MTU-1271 (41.73), RNR-1446 (41.46).

The variability estimates such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense ( $h^2$ ), genetic advance (GA), genetic advance as percent of mean (GAM) for thirteen quantitative characters. For all the characters PCV shows greater than GCV indicating that the variation occurred due to environment [16]. Grain yield per plant shows greater among all the characters in both GCV and PCV followed by biological yield, number of spikelets per panicle, number of panicles per hill and Test weight.

In every character, heritability is showing high range of estimates. These characters reveal no evidence of low and moderate estimates of heritability. The high heritability values indicates that they were less influenced by the environment. This effective selection of feature based on phenotypic expression utilizing a simple selection approach.

In heritability high range is showing by the characters (Table 3), Days to maturity (96.75), Days to 50% flowering (95.89), Grain yield per plant (95.50), Biological yield (94.75) and Number of spikelets per panicle (87.82). Genetic advance is showing values range between 0.25 to 108.75. The genetic advance showing greater in Number of spikelets per panicle (108.70),

followed by biological yield (40.244), Plant height (21.21) and Grain yield per plant (20.70).

Genetic advance as percentage of mean shows greater in grain yield per plant (75.89), followed by biological yield (70.14), Number of spikelets per panicle (56.74), Number of panicles per hill (36.093) and Number of tillers per hill (34.75). All of the qualities tested had a high heritability as well as a high percentage mean advance, indicating that the characters are primarily influenced by additive gene action. As more additive genes accumulate, leading to greater improvement, simple selection of these qualities based on phenotypic expression would be beneficial.

The experiment was conducted with 40 genotypes, based on cluster analysis the genotypes are divided into five clusters (Table 4, Fig 1). In the five clusters Cluster I has 34 genotypes which has greater number among the 5 clusters. Cluster II contains 3 genotypes and remaining clusters contains single genotypes.

According to Inter and Intra cluster analysis values among five clusters, intra cluster values ranged from 0 to 84.64 and inter cluster average  $D^2$  values ranges from 138.85 to 607.86 (Table 5, Fig 2). Intra cluster analysis reveals Cluster II (86.84) shows greater and next Cluster I (67.27). According Inter cluster analysis Cluster V and Cluster I (607.86) and next Cluster V and Cluster IV (584.4). By the cluster analysis we should consider the divergent parents easily. This divergence analysis provides vast scope in breeding programme for the selection of parents for future crosses for better crop improvement.

**Table 3. Genotypic parameters of 13 quantitative traits in rice genotypes**

Sl.No.	Characters	GCV	PCV	h2 (Broad Sense)	Genetic Advancement 5%	Gen.Adv as % of Mean 5%
1	Days to 50% flowering	8.736	8.922	95.859	17.102	17.619
2	Days to maturity	7.511	7.636	96.754	19.568	15.22
3	Plant height (cm)	9.745	11.188	75.863	21.219	17.484
4	Flag leaf length (cm)	14.345	16.826	72.682	8.624	25.193
5	Flag leaf width	12.455	15.412	65.311	0.25	20.735
6	Number of tillers per hill	18.183	19.599	86.076	3.622	34.752
7	Number of panicles per hill	19.079	20.775	84.335	3.555	36.093
8	Panicle length (cm)	9.087	10.331	77.37	4.131	16.465
9	Number of spikelets per panicle	29.394	31.364	87.829	108.704	56.746
10	Biological yield (g)	34.987	35.948	94.725	40.244	70.147
11	Harvest Index (%)	15.213	17.716	73.745	13.063	26.913
12	Test weight (g)	18.477	20.641	80.139	7.253	34.075
13	Grain yield per plant (g)	37.699	38.576	95.507	20.703	75.896

**Table 4. Distribution of clusters of 40 rice genotypes**

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	34	MTU-1010, IR-64, DURGA PADDY, NLR, JGL-24423, MTU-1311, MTU-1032, KNM-118, KSRV-140, KRISHNA HAMSA, WGL-44, NDLR, MTU-2032, MTU-1064, MTU-1121, NLR-40054, HMT, TRIGUNA, DRRH-2, SAMPADA, BPT-01, BPT-02, MTU-1262, INDRANI, RNR-1446, MTU-1271, NLR-4001, NLR-145, SHUATS DHAN-3, WGL-1119, JARAVA, SHUATS DHAN-6, SIDHA SANNALU & SHUATS DHAN-2
2 Cluster	3	SIGNET-5455, ANKUR POOJA & NDR-359 (Check)
3 Cluster	1	AJAYA
4 Cluster	1	SHUATS DHAN-7
5 Cluster	1	KAVERI

**Table 5. Cluster distances of 40 genotypes of rice**

	Cluster Distances				
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	67.27	185.92	138.85	183.98	607.86
Cluster 2		84.64	207.24	239.34	209.8
Cluster 3			0	374.99	584.4
Cluster 4				0	579.55
Cluster 5					0

Based on the cluster means (Table 6) for days to 50% flowering varied from 80 (cluster III) to 97.7 (cluster I), Days to maturity ranged from 107 (cluster V) to 130.55 (cluster I), Plant height range from 116 (cluster III) to 138.59 (cluster IV). For grain yield per plant, cluster mean values Cluster IV (62.13), Cluster V (33.80) showing greater in grain yield per plant.

According to percentage contribution Table 7, Grain yield per plant (18.5), Biological yield

(11.23), Harvest index (10.5) and test weight (9.87). Based on the percentage contribution, we should easily consider in the selection of parents for the future hybridization and better crop improvement.

From mean performance of quality characters on 35 rice genotypes (Table 8), the Hulling percentage showing range from 56 to 78 % with the grand mean of 68.31 %. The genotype Ajaya (78) showing greater in hulling percentage.

Kernel length before cooking showing range from 5 to 8 with the grand mean of 6.40, the genotype Krishna hamsa (8) showing greater. Kernel breadth before cooking showing range from 1 to 2.3 with the grand mean of 1.86, shows the highest genotype in Jarava (2.28), Kernel length / Breadth Ratio Before cooking showing range from 3 to 4.2 with the grand mean of 3.48 and

Kernel length / Breadth Ratio After cooking showing range from 3 to 3.9 with the grand mean of 3.17 both showing the highest in HMT genotype. Kernel Elongation Ratio showing range from 1 to 1.5 with the grand mean of 1.22, the genotype KNM-118 (1.45) showing greater among all genotypes.

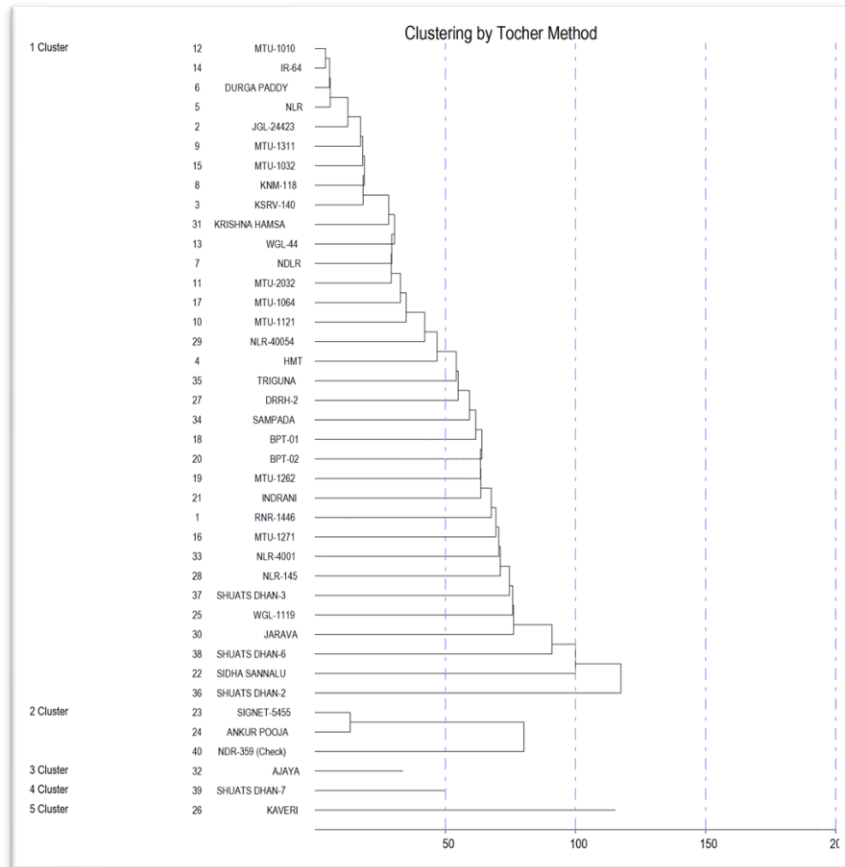


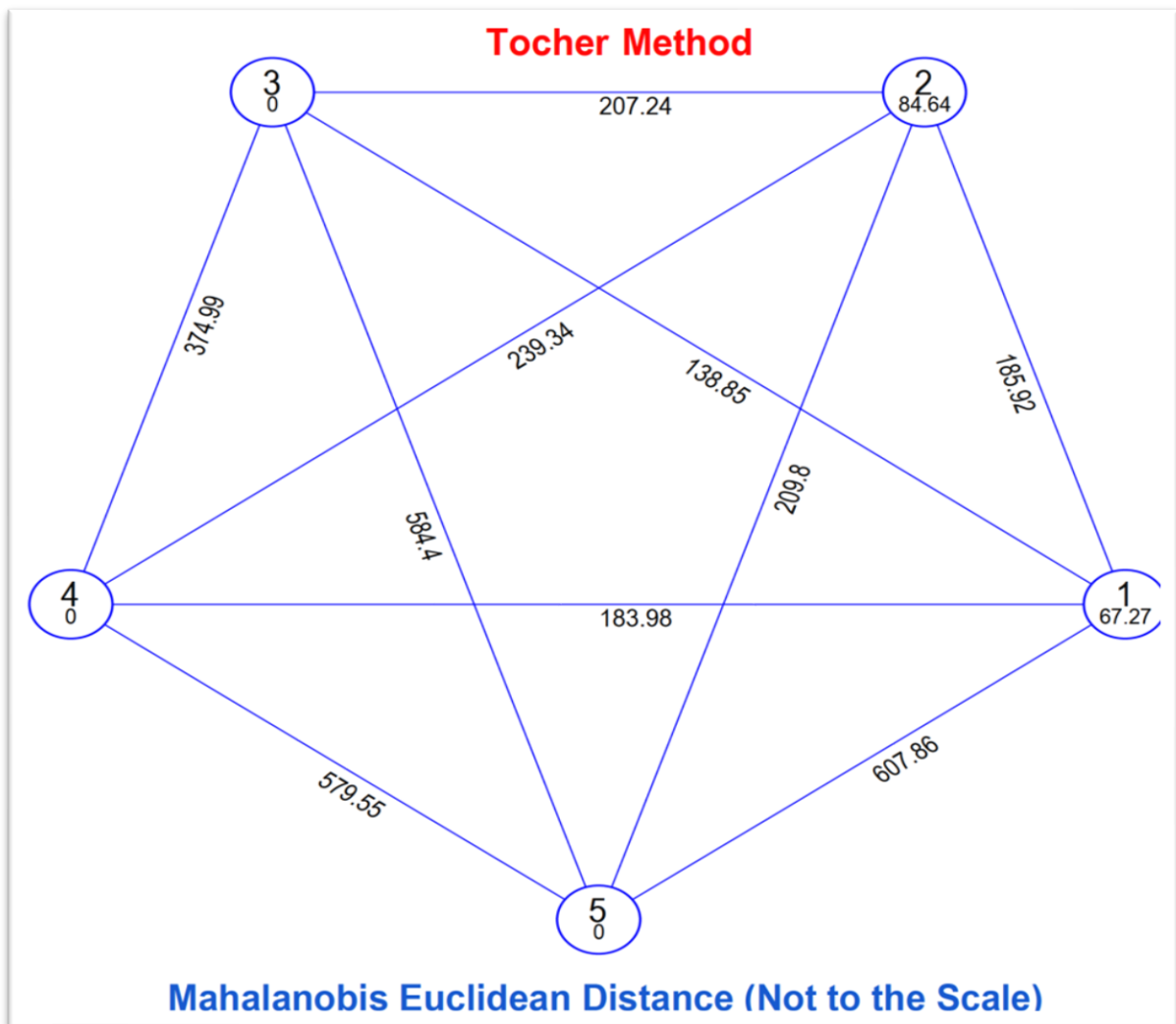
Fig. 1. Dendrogram showing distribution of clusters of 40 rice genotypes

Table 6. Cluster means of different characters in rice

Traits	Cluster Means: Tocher Method				
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Days to 50% flowering	97.70	97.67	80.00	92.00	96.00
Days to maturity	130.55	120.67	114.00	121.00	107.00
Plant height (cm)	120.48	125.80	116.00	138.59	126.13
Flag leaf length (cm)	33.99	34.40	34.00	41.91	34.62
Flag leaf width	1.18	1.49	1.00	1.45	1.35
Number of tillers per hill	10.16	12.20	8.73	15.07	11.27
Number of panicles per hill	9.71	11.00	7.13	13.60	10.27
Panicle length (cm)	24.86	27.72	21.45	26.23	27.61
Number of spikelets per panicle	192.63	188.77	74.67	284.27	187.73
Biological yield (g)	56.88	51.61	22.67	123.60	59.73
Harvest Index (%)	47.47	52.22	64.81	50.41	55.87
Test weight (g)	21.05	22.59	19.67	19.33	29.17
Grain yield per plant (g)	26.50	27.07	13.07	62.13	33.80

**Table 7. Percentation contribution towards divergence of 13 quantitative characters**

SL.NO.	Source	Contribution %	Times ranked 1st
1	Days to 50% flowering	5.98	46
2	Days to maturity	4.98	38
3	Plant height (cm)	3.89	30
4	Flag leaf length (cm)	3.60	28
5	Flag leaf width	3.65	28
6	Number of tillers per hill	7.50	58
7	Number of panicles per hill	5.76	44
8	Panicle length (cm)	5.55	43
9	Number of spikelets per panicle	8.99	69
10	Biological yield (g)	11.23	86
11	Harvest Index (%)	10.50	81
12	Test weight (g)	9.87	76
13	Grain yield per plant (g)	18.50	142



**Fig. 2. Cluster diagram showing inter and intra clusters distances**

**Table 8. Mean performance of quality characters on 35 rice genotypes**

Genotypes	HP (%)	KLB (mm)	KBB (mm)	KL/B RBC	KL/B RAC	KLAC (mm)	KBAC (mm)	KER
RNR-1446	68	6.82	1.79	3.83	2.74	7.76	2.83	1.14
JGL-24423	70	6.67	2.2	3.04	2.75	8.2	2.99	1.23
NLR	68	6.32	2.12	2.99	2.81	7.6	2.72	1.20
DURGA PADDY	66	6.58	2.16	3.05	2.85	7.76	2.73	1.18
KNM-118	72	5.3	1.61	3.32	3.13	7.69	2.47	1.45
MTU-1311	70	5.97	1.87	3.21	2.81	7.79	2.77	1.31
MTU-1121	72	5.86	1.88	3.13	2.87	7.7	2.69	1.31
MTU-2032	62	5.21	1.41	3.71	3.33	7.44	2.24	1.43
MTU-1010	72	6.63	2.05	3.24	3.06	8.17	2.68	1.24
IR-64	69	6.19	1.68	3.73	3.30	8.19	2.51	1.33
MTU-1032	68	5.47	2.02	2.71	2.80	7.48	2.68	1.37
MTU-1271	56	5.66	1.63	3.47	3.45	7.35	2.13	1.30
MTU-1064	60	5.77	1.99	2.93	3.00	6.98	2.33	1.21
DRRH-2	66	7.27	2.05	3.55	3.53	8.38	2.39	1.15
NLR-145	76	7.04	1.89	3.76	3.21	7.79	2.46	1.11
NLR-40054	75	6.62	1.66	4.01	3.08	7.88	2.57	1.19
NLR-4001	74	6.037	1.74	3.48	2.99	7.06	2.39	1.17
TRIGUNA	65	6.31	1.66	3.83	3.35	7.72	2.32	1.23
KSRV-140	70	7.01	1.79	3.93	3.82	8.05	2.11	1.15
HMT	68	7.31	1.74	4.22	3.93	8.2	2.09	1.12
NDLR	70	6.33	2.05	3.10	3.08	7.41	2.41	1.17
WGL-44	65	7.29	1.78	4.10	3.22	8.74	2.72	1.20
BPT-01	68	5.96	1.59	3.77	3.09	6.88	2.23	1.15
MTU-1262	70	5.71	1.64	3.51	3.38	7.5	2.23	1.31
BPT-02	68	5.73	1.89	3.04	2.84	7.18	2.53	1.25
INDRANI	65	6.29	1.99	3.17	3.08	7.99	2.6	1.27
SIDHA SANNALU	65	5.9	1.74	3.40	3.23	7.13	2.22	1.21
SIGNET-5455	68	6.44	1.79	3.61	3.45	7.78	2.26	1.21
ANKUR POOJA	69	6.04	1.92	3.16	2.92	7.72	2.65	1.28
WGL-1119	68	7.03	1.94	3.63	3.00	8.08	2.71	1.15
KAVERI	68	5.61	1.66	3.39	3.12	6.8	2.19	1.21
JARAVA	67	7.93	2.28	3.49	3.21	8.81	2.75	1.11
KRISHNA HAMSA	70	8	2.09	3.87	3.79	8.53	2.27	1.07
SAMPADA	65	7.15	1.87	3.84	3.38	7.93	2.35	1.11
AJAYA	78	6.5	1.88	3.46	3.30	7.42	2.26	1.14
Mean	68.31	6.40	1.86	3.48	3.17	7.75	2.47	1.22
Minimum	56	5	1	3	3	7	2	1
Maximum	78.0	8.0	2.3	4.2	3.9	8.8	3.0	1.5

HP(%) : Hulling percentage, KLB(mm) : Kernel length before cooking, KBB(mm) : Kernel breadth before cooking, KL/B RBC : Kernel length/breadth Ratio before cooking, KL/B RAC : Kernel length/breadth ratio after cooking, KLAC(mm) : Kernel length aftercooking, KBAC(mm) : Kernel breadth after cooking, KER : Kernel elongation ratio

#### 4. CONCLUSION

From the present investigation it is concluded that on the basis of mean performance among 40 genotypes of rice SHIATS DHAN-7 was found to be superior in grain yield per plant followed by SHIATS DHAN-2. Analysis of Variance for

thirteen quantitative traits revealed that the mean sum of squares due to genotypes showed high significant differences for all the characters at 1% level of significance in rice germplasm. High phenotypic and genotypic coefficient of variation were recorded for Grain yield per plant. High Heritability coupled with high genetic advance as



percent mean was recorded for characters like Days to maturity followed by Days to 50% flowering indicating that these characters are less influenced by environmental effects and selection on the basis of phenotypic performance of genotypes would be more efficient in further improvement of these traits. Based on D2 Statistics, 40 genotypes were grouped into five clusters, cluster I was largest consisting of 34 genotypes. The highest inter cluster distance was found between cluster V & cluster I (607.86) followed by cluster III and cluster V (584.4). The divergent genotypes from clusters I, III, IV, are Ajaya, SHIATS DHAN-2, SHIATS DHAN-7 and Kaveri. Hence, these genotypes can be used as parents for further hybridization to develop new cultivars with broad genetic base.

### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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