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Genetic analysis for yield and its contributing traits in advanced breeding lines of rice (*Oryza sativa* L.)

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Abstract

A field experiment was conducted at Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, during 2024. To evaluate 61 rice genotypes including four checks *viz.*, Swarna, NDR 8002, Pooja and Chhattisgarh Dhan 1919. For analysis of genetic variability and divergence among the rice genotypes. Analysis of variance revealed highly significant differences among the lines, indicating substantial genetic variability. Genetic parameter evaluation showed higher PCV values than GCV, indicating the influence of environmental factors on the expression of the traits. High heritability, along with a higher genetic advance as a percentage of the mean, were recorded for quantitative characters *viz.*, Number of total grains per panicle, test weight, biological yield per plant, number of unfilled grains per panicle and harvest index, indicating the predominance of additive gene action. Genetic diversity analysis grouped into 5 clusters. The highest number of genotypes appeared in Cluster I, which contain 19 genotypes followed by Cluster IV, which contain 15 genotypes followed by Cluster V, which contain 12 genotypes followed by Cluster III, which contain 9 genotypes followed by Cluster II, which contain 6 genotypes. This study signifies the importance of genetic variability and divergence. The diverse lines can be utilized further rice improvement programme.

Keywords: Rice, GCV, PCV, heritability, genetic advance and genetic divergence

1. Introduction

Rice (*Oryza sativa* L.) (2n =24) is one of the most cultivated grain crop in India as well as in Asian countries and is a staple diet of major parts of India. India is an important center for rice cultivation and consumption and stands second position in production after China. The major rice production states in India are West Bengal, Chhattisgarh, Tamil Nadu, Haryana and Kerala of India and consumption also. Rice is known as the "Grain of Life' because it provides food for more than one-third of the world's population. Furthermore, the United Nations has designated 2004 as the "International Year of Rice" to recognize the importance of rice in man life. Rice is endowed with a wealth of genetic diversity (Akshay *et al.*, 2022) [2].

FAO (Food and Agriculture Organization) expects world rice production to reach a record 543 million tons (milled basis) in 2024-25. China and India are the world's largest rice producers and consumers. China consumed almost 145 million metric tons of milled rice in 2024, making it the world's leading rice consumers. India is ranked second with 121 million metric tons of rice consumption in the same period. This increase in rice production is driven by good crops in India and favorable weather conditions in Cambodia and Myanmar. (Anonymous, 2025) [3].

For effective genetic improvement knowledge on the magnitude and nature of the genetic variation governing the inheritance of quantitative characters like yield and its contributing traits is very important. Therefore, achievement on plant breeding activities depends on the presence of genetic variability in desired traits and selection ability of plant breeder (Adhikari *et al.*, 2018) [1].

Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone. In addition, relationship between yield and yield attributing traits are prime important for direct and indirect selection of traits to which contributes to yield (Chaudhary *et al*., 2023) [6].

Genetic diversity is essential for crop improvement programs as it aids in analyzing and monitoring genetic relationships in accessions, identifying diverse parental combinations to create segregating progenies with high genetic variability, and obtaining potential recombination for further selection and introgression of desirable genes (Pachauri *et al*., 2023) [21].

2. Material and Methods

The experimental material consists of 57 Genotypes of rice along with 4 checks *viz*. Swarna, Chhattisgarh Dhan-1919, NDR-8002 and Pooja. The experiment was laid out in puddled field condition by following Randomized Complete Block Design. The experimental area was divided into 2 replications each consisting of 57 treatments including 4 checks.

Table 1: List of experimental materials used in the current study

S. No.	Genotypes	S. No.	Genotypes
1	R2882-KH-23-LST-C53-83-1	31	R2840-KH23-LST-C1-11-1
2	R2848-KH-23-LST-C9-70-1	32	R2843-KH-23-LST-C4-29-1
3	R2885-KH-23-LST-C56-92-1	33	R2872-KH-23-LST-C42-8-1
4	R2893-KH-23-LST-C64-40-1	34	R2853-KH-23-LST-17-31-1
5	R2846-KH-23-LST-C7-80-1	35	R2864-KH-23-LST-C33-25-1
6	R2853-KH-23-LST-17-26-1	36	R2864-KH-23-LST-C33-10-1
7	R2893-KH-23-LST-C64-80-1	37	R2851-KH-23-LST-C14-95-1
8	R2851-KH-23-LST-C14-80-1	38	R2865-KH-23-LST-C34-40-1
9	R2840-KH23-LST-C1-4-1	39	R2856-KH-23-LST-C20-14-1
10	R2849-KH23-LST-C1-52-1	40	R2845-KH-23-LST-C6-60-1
11	R2871-KH-23-LST-C41-60-1	41	R2844-KH-23-LST-C5-4-1
12	R2856-KH-23-LST-C20-82-1	42	R2854-KH-23-LST-C18-6-1
13	R2853-KH-23-LST-17-37-1	43	R2848-KH-23-LST-C9-45-1
14	R2841-KH23-LST-C3-21-1	44	R2856-KH-23-LST-C20-35-1
15	R2856-KH-23-LST-C20-31-1	45	R2844-KH-23-LST-C5-57-1
16	R2869-KH-23-LST-C38-48-1	46	R2853-KH-23-LST-C17-54-1
17	R2869-KH-23-LST-C38-31-1	47	R2880-KH-23-LST-C51-4-1
18	R2853-KH-23-LST-17-39-1	48	R2892-KH-23-LST-C63-50-1
19	R2856-KH-23-LST-C20-20-1	49	R2853-KH-23-LST-C17-70-1
20	R2856-KH-23-LST-C20-27-1	50	R2843-KH-23-LST-C4-22-1
21	R2871-KH-23-LST-C41-63-1	51	R2846-KH-23-LST-C7-1-1
22	R2853-KH-23-LST-17-33-1	52	R2848-KH-23-LST-C9-86-1
23	R2865-KH-23-LST-C34-50-1	53	R2869-KH-23-LST-C38-79-1
24	R2876-KH-23-LST-C47-80-1	54	R2845-KH-23-LST-C6-20-1
25	R2882-KH-23-LST-C53-55-1	55	R2869-KH-23-LST-C38-1-1
26	R2853-KH-23-LST-17-20-1	56	R2856-KH-23-LST-C20-32-1
27	R2851-KH-23-LST-C14-96-1	57	R2864-KH-23-LST-C33-45-1
28	R2882-KH-23-LST-C53-78-1	58	Swarna
29	R2852-KH-23-LST-C16-80-1	59	NDR 8002
30	R2893-KH-23-LST-C64-79-1	60	Pooja
		61	Chhattisgarh Dhan 1919

On the 27th of June 2024, seeds of all genotypes were sown in nursery beds at IGKV, Raipur and 20 to 25 days old seedlings were transplanted to the main field on the 10th of August, 2024. Twenty-one day old seedlings were manually transplanted in single rows, with each hill containing one seedling. The spacing was maintained at 20 cm between rows and 15 cm between plants. To ensure a uniform plant population, gaps were filled within a week. Days to 50 % flowering, height of the plant (cm), number of effective tillers per plant, panicle length (cm), number of filled spikelets per panicle, total number of spikelets per panicle, percentage of spikelet fertility (%), 1000 grain weight (g), harvest index (%) and grain yield per plant (g) were recorded.

The statistical analysis was performed using OPSTAT software for analysis of variance, genetic parameters and XLSTAT software for genetic diversity**.**

2.1 Analysis of Variance

As per standard statistical procedure, analysis of variance was calculated for each of the characters separately using a randomized block design (Panse and Sukhatme, 1978) [22]. The significance was tested by referring to the values of ‘F’ table.

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of i^{th} genotype and j^{th} replication

μ=general mean

g_i = effect of i^{th} genotype

r_j= effect of j^{th} replication

e_{ij}= random error associated with i^{th} genotype and j^{th} replication

The significance test was carried out by referring to F table values. The calculated value of 'F' was compared with table value of 'F' at 5% and 1% level of probability against error degree of freedom, Le (r-1) (t-1).

2.2 Assessment of variability

2.2.1 Mean

The mean is calculated by the following formula:

$$\bar{X} = \sum \frac{Xi}{n}$$

Where,

$\sum$ Xi= Sum of all observation of i^{th} character, N = No. of observations

2.2.2 Range

The range of distribution was showed by the limit of the smallest and the largest value of observations.

Range = Highest value – Lowest value

2.2.3. Phenotypic coefficient of variation (PCV %)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

PCV (%) = Phenotypic coefficient of variation,

σ_p^2 = Phenotypic variance

$\bar{X}$= Mean of the character

2.2.4 Genotypic coefficient of variation (GCV %)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

GCV (%) = Genotypic coefficient of variation, σ_g^2= Genotypic variance

$\bar{X}$= Mean of the character

The genotypic and phenotypic coefficients of variation were categorized as per the method suggested by Sivasubramanian and Madhavamenon (1973) [29]:

- 0-10% = Low
- 10-20% = Moderate
- >20% = High

2.2.5 Heritability % (broad sense)

Heritability in terms of broad sense ($h^2{}_{bs}$) was evaluated by using formula. It expressed as %

$$(h^2{}_{bs}) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2= Genotypic variance,

σ_p^2= Phenotypic variance

As suggested by Johnson *et al.* (1955) [12] heritability values are categorized as

State Heritability
Low <30%
Moderate 30-60%
High >60%

2.2.6 Genetic advance as percent of mean (GAM)

Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.* (1955) [12].

$$\text{GAM} = \frac{GA}{\bar{X}}$$

Where,

GA = Genetic advance,

$\bar{X}$ = General mean

Genetic advance as percent of mean was categorized as per the formula suggested by Johnson *et al.* (1955) [12].

0-10 % = Low

10-20 % = Moderate

>20 % = High

2.2.7 Cluster analysis

The *D*² statistics was developed by Mahalanobis (1936) [18] and Rao (1952) [24] suggested the application of this technique for genetic diversity assessment between the populations. Between any two populations, the generalized distance is given by formula,

$$\Delta = \Sigma \lambda ij \sigma i \sigma j$$

Where,

D^2 = Generalized distance square,

λij= Reciprocal of the common dispersal matrix,

σi = (μi1-μi2),

σj = (μj1-μj2),

μ = General mean

The distance matrix from phenotype traits was used to construct Dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of Dendrogram.

3. Results and Discussion

3.1 Analysis of Variance

The results of the analysis of variance demonstrate in Table 2. All of the traits under consideration were determined to be highly significant (i.e., at 1 percent level of significance). Harshitha *et al.* (2023) [10] carried out investigations to know the extent of genetic variability present in thirty-four genotypes of rice. Analysis of variance revealed highly significant differences for all the 12 characters, indicating the presence of genetic variability among the genotypes.

Table 2: Analysis of variance (ANOVA) for different grain yield & attributing traits

S. No.	**Source of variation**	**Mean sum of square (MSS)**		
		Replication	**Treatment**	**Error**
		Degree of freedom		
		1	**60**	**60**
1.	Days of 50% flowering	5.12	77.57**	3.04
2.	Plant height (cm)	4.17	217.94**	12.12
3.	No. of total tillers per plant	2.45	2.43**	1.12
4.	No. of effective tillers per plant	0.07	2.51**	1.03
5.	Panicle length (cm)	7.53	5.28**	1.89
6.	No. of filled grains per panicle	17.49	740.12**	227.60
7.	No. of unfilled grains per panicle	40.39	132.71**	20.12
8.	Spikelet fertility (%)	27.38	109.30**	27.42
9.	Test weight (g)	1.91	22.93**	2.18
10.	Biological yield per plant (g)	42.61	147.90**	34.00
11.	Harvest index (%)	1.63	180.45**	30.46
12.	Grain yield per plant (g)	24.61	30.09**	4.76

**Significant at 1% probability level

3.2 Assessment of Genetic Variability

The range for number of days to 50 % flowering was 108 DAS with the varies from 92 DAS (R2845-KH-23-LST-C6-60-1) to 120 (DAS) (Pooja), the range for plant height varies from 93.6 cm (R2845-KH-23-LST-C6-60-1), to 136.57 cm (R2882-KH-23-LST-C53-83-1) with a mean of 114.33 cm, the varies for effective tillers per plant varies from 4.10 (R2865-KH-23-LST-C34-40-1) to 9.70 (R2853-KH-23-LST-17-37-1), with a mean of 6.73, the varies from panicle length varies from 21.89 cm (R2843-KH-23-LST-C4-29-1) to 29.23 cm NDR 8002 (29.23) with a mean of 25.98 cm, the varies from number of filled grains per panicle was with the varies from 63.3 (R2853-KH-23-LST-17-33-1) to 141.4 (R2856-KH-23-LST-C20-27-1) with a mean of 105.1, the range of spikelet fertility was with the varies from 50.85 % (R2843-KH-23-LST-C4-29-1) to 91.3 % (R2853-KH-23-LST-C17-54-1) with a mean of 78.62, the range for test weight varies from 16.15 g (R2851-KH-23-LST-C14-80-1) to 34.95 g (R2871-KH-23-LST-C41-63-1), with a mean of 22.69 g, the range of harvest index was with the varies from 14.7 % (R2893-KH-23-LST-C64-80-1) to 61.5 % (R2844-KH-23-LST-C5-57-1) with a mean of 39.64 % and the range grain yield per plant was with the range of 6.4 g (R2845-KH-23-LST-C6-60-1) to 26.5 g (R2869-KH-23-LST-C38-1-1) with a mean of 15.14 g.

The estimated genotypic and phenotypic efficient of variation for each attribute are shown in Table 3. On average, both genotypic and phenotypic coefficients of variation were higher for quantitative traits, such as number of unfilled grains per panicle (GCV 29.61%, PCV 34.50%), harvest index % (GCV 21.85%, PCV 25.91%) and grain yield per plant (g) (GCV 23.50%, PCV 27.57%). The high magnitude of genetic variability for number of unfilled grains per panicle and harvest index % was also noted by Singh *et al* (2021) [28]. Traits showing moderate GCV and PCV values were the number of total productive tillers per plant (GCV 15.23% and PCV 19.79%) and test weight (g) (GCV 14.20% and PCV 15.62%). These findings align with the previous reports by Sao *et al*. (2024) [26], Sharada *et al*. (2024) [27] and Vilas *et al*. (2024) [31].

High heritability values demonstrating that the observed variation was primarily under genetic control and was little impacted by the environment, signaling that phenotypic based selection will be beneficial for these traits. These findings are consistent with earlier estimates by Sao *et al*. (2024) [26] for days to 50% flowering and plant height, by Faysal *et al*. (2022) [9] for days to 50% flowering (92.46%), plant height (cm) (89.46%), test weight (g) (82.58%), number of unfilled grains per panicle (73.67%), grain yield per plant (g) (72.68%), harvest index (%) (71.11) and biological yield per plant (g) (62.61). Srujana *et al*. (2017) and Sao *et al*. (2024) [26] also noted high heritability estimates for biological yield per plant (g) and grain yield per plant (g).

High heritability, along with a higher genetic advance as a percentage of the mean, were recorded for quantitative characters was number of total grains per panicle, test weight, biological yield per plant, number of unfilled grains per panicle and harvest index. Similar result was found by Jadhav *et al*. (2020) [11], Noatia *et al*. (2021) [20], Demeke *et al*. (2023), Kumar *et al*. (2023) and Kerketta *et al*. (2024).

A greater [7] mean genetic advance percentage was observed for the number of unfilled grains per panicle (52.36%), grain yield per plant (g) (41.27%), harvest index (%) (37.95%), biological yield per plant (g) (31.06%), test weight (g) (26.57%), and number of filled grains per panicle (22.83%). Singh *et al*. (2021) [28] and Maruti *et al*. (2025) [19] also found comparable outcomes for biological yield per plant and grain yield per plant (g).

Plant height (17.29%), number of total productive tillers per plant (17.04%), spikelet fertility (%) (12.97%), number of total tillers per plant (12.36%) and days to 50% flowering (11.22%) were the attributes that showed the most modest genetic advancements as a percentage of mean. Comparable results were found for plant height (cm) by Barhate *et al*. (2021) [15] and Khatun *et al*. (2024) [14].

Table 3: Estimation of variability parameters for quantitative traits

S. No.	Characters	Mean	Min.	Max.	GCV%	PCV%	$h^2(b_s)$	GA as % mean
			Range					
1.	Days to 50% flowering	107.76	92.5	120.5	5.67	5.89	92.46	11.22
2.	Plant height (cm)	114.33	93.6	136.57	8.87	9.38	89.46	17.29
3.	No. of total tillers/plant	8.16	6.5	10.9	9.91	16.35	36.70	12.36
4.	No. of total productive tillers/plant	6.73	4.1	9.7	12.79	19.79	41.81	17.04
5.	Panicle length (cm)	25.98	21.89	29.23	5.01	7.29	47.30	7.10
6.	No. of filled grains/panicle	105.10	63.3	141.4	15.23	20.93	52.96	22.83
7.	No. of unfilled grains/panicle	25.34	9.7	42.4	29.61	34.50	73.67	52.36
8.	Spikelet fertility (%)	78.62	50.85	91.3	8.14	10.52	59.88	12.97
9.	Test weight (g)	22.69	16.15	34.95	14.20	15.62	82.58	26.57
10.	Biological yield/plant (g)	39.60	20	63.9	19.06	24.08	62.61	31.06
11.	Harvest index (%)	39.64	14.7	61.5	21.85	25.91	71.11	37.95
12.	Grain yield/plant (g)	15.14	6.4	26.5	23.50	27.57	72.68	41.27

Note- GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, $h^2(b_s)$ = Heritability in broad sense, GA as % of mean = Genetic advance as % of mean.

3.3 Genetic Divergence Analysis

Sixty-one entries were grouped into 5 clusters. Parents from various clusters are used in the hybridization procedure. 61 genotypes genetic divergence is displayed in Tables 4.

Table 4: Clustering of 61 rice genotypes into five clusters

Cluster number	Number of genotypes	Genotypes names
I	**19**	R2848-KH-23-LST-C9-70-1, R2885-KH-23-LST-C56-92-1, R2893-KH-23-LST-C64-40-1, R2893-KH-23-LST-C64-80-1, R2840-KH23-LST-C1-4-1, R2841-KH23-LST-C3-21-1, R2856-KH-23-LST-C20-31-1, R2869-KH-23-LST-C38-31-1, R2856-KH-23-LST-C20-20-1, R2865-KH-23-LST-C34-50-1, R2876-KH-23-LST-C47-80-1, R2882-KH-23-LST-C53-55-1, R2865-KH-23-LST-C34-40-1, R2854-KH-23-LST-C18-6-1, R2856-KH-23-LST-C20-35-1, R2880-KH-23-LST-C51-4-1, R2846-KH-23-LST-C7-1-1, R2848-KH-23-LST-C9-86-1, R2845-KH-23-LST-C6-20-1
II	**6**	R2851-KH-23-LST-C14-80-1, R2848-KH-23-LST-C9-45-1, R2844-KH-23-LST-C5-57-1, R2843-KH-23-LST-C4-22-1, Swarna, Chhattisgarh Dhan 1919
III	**9**	R2869-KH-23-LST-C38-48-1, R2853-KH-23-LST-17-39-1, R2853-KH-23-LST-17-20-1, R2843-KH-23-LST-C4-29-1, R2856-KH-23-LST-C20-14-1, R2845-KH-23-LST-C6-60-1, R2844-KH-23-LST-C5-4-1, R2853-KH-23-LST-C17-54-1, NDR 8002
IV	**15**	R2871-KH-23-LST-C41-60-1, R2856-KH-23-LST-C20-82-1, R2853-KH-23-LST-17-37-1, R2856-KH-23-LST-C20-27-1, R2871-KH-23-LST-C41-63-1, R2882-KH-23-LST-C53-78-1, R2852-KH-23-LST-C16-80-1, R2864-KH-23-LST-C33-25-1, R2851-KH-23-LST-C14-95-1, R2892-KH-23-LST-C63-50-1, R2853-KH-23-LST-C17-70-1, R2869-KH-23-LST-C38-79-1, R2869-KH-23-LST-C38-1-1, R2856-KH-23-LST-C20-32-1, R2864-KH-23-LST-C33-45-1
V	**12**	R2882-KH-23-LST-C53-83-1, R2846-KH-23-LST-C7-80-1, R2853-KH-23-LST-17-26-1, R2849-KH23-LST-C1-52-1, R2853-KH-23-LST-17-33-1, R2851-KH-23-LST-C14-96-1, R2893-KH-23-LST-C64-79-1, R2840-KH23-LST-C1-11-1, R2872-KH-23-LST-C42-8-1, R2853-KH-23-LST-17-31-1, R2864-KH-23-LST-C33-10-1, Pooja

The highest number of genotypes appeared in cluster I, which contain 19 genotypes followed by cluster IV, which contain 15 genotypes followed by cluster V, which contain 12 genotypes followed by cluster III, which contain 9 genotypes followed by cluster II, which contain 6 genotypes. The pattern of group constellation proved the existence of significant amount of variability.

The mean cluster values showed a wide range of variations for all the 12 quantitative characters undertaken in the investigation and is summarized in Table 4.

Cluster I exhibited the highest mean values for plant height (120.47) and biological yield per plant (43.71), along with the lowest mean value for harvest index (36.38) and test weight (23.05). This combination suggests that genotypes within this cluster possess a desirable trait profile characterized by early flowering and high productivity.

The greatest mean values for spikelet fertility (85.82), harvest index (54.03), days to 50% flowering (112), and grain production per plant (17.88) were found in Cluster II. In contrast, it had the lowest mean values for test weight (18.8), panicle length (24.63), number of unfilled grain per panicle (15.56), total number of tillers per plant (7.43), number of productive tillers per plant (6.45) and biological yield per plant (33.76).

The mean numbers for the total number of tillers per plant (8.74) and the number of productive tillers per plant (6.89) were highest in Cluster III. The mean values for spikelet fertility (75.79), plant height (102.24) and days to 50% flowering (104.27) were the lowest, never the less.

Cluster IV exhibited highest mean values for panicle length (26.80), number of filled grain per panicle (126.26), number of unfilled grain per panicle (32.90) and test weight (23.54).

Cluster V recorded the lowest mean values for number of filled grain per panicle (78.95) and grain yield per plant (13.57).

Table 5: Cluster mean values of five clusters for various characters in distinct rice genotypes

		Clusters				
S. No.	**Characters**	**I**	**II**	**III**	**IV**	**V**
1.	Days to 50% flowering	106.00	**112.91**	104.27	109.53	108.37
2.	Plant Height	**120.47**	103.78	102.24	118.17	114.11
3.	Panicle length	25.83	24.63	25.06	**26.80**	26.55
4.	Total number of tillers per plant	8.14	7.43	**8.74**	8.07	8.22
5.	No. of productive tillers per plant	6.70	6.45	**6.89**	6.70	6.78
6.	No. of filled grain per panicle	108.27	115.53	91.02	**126.26**	78.95
7.	No. of unfilled grain per panicle	25.47	15.56	24.65	**32.90**	21.05
8.	Spikelet fertility	80.19	**85.82**	75.79	76.34	77.51
9.	Test weight (g)	23.05	18.84	23.46	**23.54**	22.40
10.	Biological yield per plant (g)	**43.71**	33.76	35.37	43.25	34.60
11.	Harvest Index (%)	36.38	**54.03**	39.92	37.18	40.43
12.	Grain yield per plant (g)	15.15	**17.88**	14.27	15.81	13.57

Note: Bold digits represent highest mean values for the particular traits.

The composition of the average intra and inter-cluster D^2 values among the five clusters is displayed in Table 6. Genetic diversity between the genotypes under study was of varying magnitude, while genotypes within a cluster showed little genetic divergence from one another with regard to the aggregate effect of 12 yield and yield attributing characters under study, according to average intra and inter-cluster distance assessments for five clusters.

An intra-cluster was found, ranging from 17.95 (cluster II) to 25.73 (cluster III). Highest inter-cluster distance was exhibited between cluster V and IV. The higher the distance between two clusters, the higher will be the genetic diversity within those clusters genotypes and such highly divergent high-performing genotypes would be quite useful in a recombination breeding programme to produce high yielding varieties.

Table 6: Estimates of intra (diagonal and bold) and their inter cluster distances among 5 clusters

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	22.11	30.78	29.19	36.99	47.05
Cluster II		17.95	34.51	46.41	53.75
Cluster III			25.73	58.31	29.67
Cluster IV				22.27	82.12
Cluster V					22.50

According to the data, inter crossing genotypes from several clusters that have shown superior mean performance would help produce a higher output. Similarly, results were found by Devi *et al*. (2019) [8], Sao *et al*. (2020) [25] and Arun Kumar *et al*. (2022) [4] for grain yield per plant; Koli *et al*. (2022) [15], Rahman *et al*. (2023) [23], Khatun *et al*. (2024) [14] and Lakshmeesha *et al*. (2024) [17] and for test weight and filled grain per panicle.

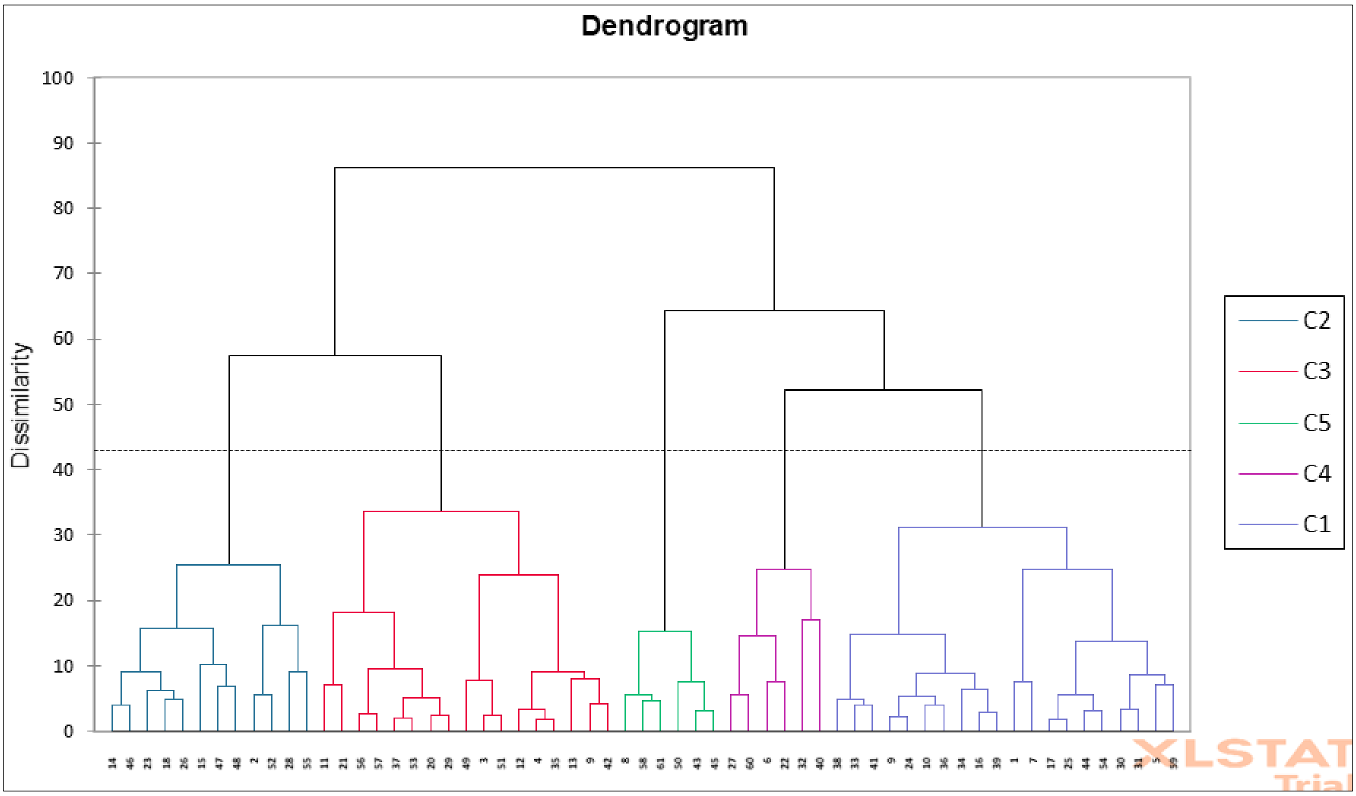

Fig 1: Dendrogram showing distance and relationship between rice genotypes

Conclusion

According to the analysis of variance, there was a high degree of meaningful variability in the quantitative attributes. Therefore, crop development initiatives have a sufficient opportunity to utilize and include a variety of traits. The genotypes viz., R2869-KH-23-LST-C38-1-1, R2848-KH-23-LST-C9-86-1, R2882-KH-23-LST-C53-78-1, R2848-KH-23-LST-C9-45-1 and R2865-KH-23-LST-C34-50-1, have been selected as the best genotype for higher yield. Highest inter-cluster distance was exhibited between cluster V and IV (82.12). The higher the distance between two clusters, the higher will be the genetic diversity within those clusters genotypes and such highly divergent high-performing genotypes would be quite useful in a recombination breeding programme to produce high genetic diversity.

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References

1. Adhikari BN, Joshi BP, Shrestha J, Bhatta NR. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). Journal of Agriculture and Natural Resources. 2018;1(1):149-160.
2. Akshay M, Chandra BS, Devi KR, Hari Y, Vamshi P. DUS characterization of traditional varieties and advanced cultivars of rice using 29 essential characters. Association of Rice Research Workers. 2022;:157-161.
3. Anonymous. Rice - statistics & facts, worldwide. [Internet]. 2025. Available from: www.fao.com
4. Arun Kumar M, Geetha S, Amudha K, Suresh R, Ravichandran V, Geetha K. Genetic diversity and QTL-marker association analysis of rice germplasm for grain number per panicle and its contributing traits. Electronic Journal of Plant Breeding. 2022;13(2):558-566.

5. Barhate KK, Jadhav MS, Bhavsar VV. Genetic variability, heritability and genetic advance in aromatic lines of rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2021;10(3):360-362.
6. Chaudhary BK, Verma OP, Singh PK, Patel A. Assessment of genetic variability, heritability and genetic advance of rice genotypes (*Oryza sativa* L.). International Journal of Plant and Soil Science. 2023;35(19):1372-1378.
7. Demeke B, Dejene T, Abebe D. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotypes at Pawe, northwestern Ethiopia. Cogent Food & Agriculture. 2023;9(1):2157099.
8. Devi PS, Veni BK, Raja DS. Genetic diversity for yield components, physical and biochemical quality parameters in colored rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences. 2019;8(11):18-26.
9. Faysal ASM, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA. Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. Plants. 2022;11(21):2952.
10. Harshitha P, Jeyaprakash P, Geetha K, Selvam S, Vanniarajan C. Genetic analysis of quality traits in non-aromatic rice varieties for export potential. Electronic Journal of Plant Breeding. 2023;14(3):1174-1184.
11. Jadhav SP, Kunkerkar RL, Thorat BS, Gawai MP, Keluskar MH. Variability and genetic parameters studies in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2020;9(1):1375-1377.
12. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-318.
13. Kerketta P, Sao A, Ekka A, Sai R, Singh R. Application of genetic parameters for betterment of yield and yield contributing traits in rice (*Oryza sativa* L.). International Journal of Advanced Biochemistry Research. 2024;8(4):346-351.
14. Khatun SM, Naim J, Das B, Mim MH, Akter S, Yasmin S, *et al*. Genetic analyses of advanced breeding lines of rice for yield-attributing traits and salinity stress tolerance. Journal of Phytology. 2024;16:183-199.
15. Koli GK, Upadhyay S, Rathi SR, Gupta S, Kumawat G, Singh PK, *et al*. Study of genetic divergence for yield and yield attributing traits of wild germplasm in rice. Pharma Innovation Journal. 2022;11(2):472-474.
16. Kumar PAS, Delvadiya IR, Murali S, Ginoya AV. Unraveling the genetic architecture of rice (*Oryza sativa* L.) using variability, correlation, path analysis and diversity analysis: insights for crop improvement strategies. International Journal of Plant and Soil Science. 2023;35(15):32-39.
17. Lakshmeesha R, Mahesh HB, Basavaraj M, Pattanashetti KM, Harinikumar, Veena SA. Principal component analysis of yield and its attributing traits in recombinant inbred lines of rice under submerged condition (*Oryza sativa* L.). Archives of Current Research International. 2024;24(4):39-44.
18. Mahalanobis PC. On the generalized distance in statistics. Proceedings of the National Institute of Science of India. 1936;2:49-55.
19. Maruti KR, Prashanth K, Sruthi K, Chanuradha C. Assessment of genetic variability, heritability and genetic advance for yield and nutritional traits in rice (*Oryza sativa* L.) genotypes. Journal of Experimental Agriculture International. 2025;47(7):982-993.
20. Noatia P, Sao A, Tiwari A, Nair SK, Gauraha D. Genetic dissection of yield determinants in advance breeding lines (ABLs) of rice (*Oryza sativa* L.) under irrigated condition of Chhattisgarh, India. International Journal of Plant and Soil Science. 2021;33(20):119-131.
21. Pachauri AK, Gauraha D, Sahu SR, Pujari P, Saran D. Molecular diversity and population structure analysis in rice genotype using SSR marker. Environment and Ecology. 2023;41(3C):1883-1890.
22. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of Agricultural Research; 1978. p. 369.
23. Rahman MA, Islam MR, Islam AKMS, Munna NA, Razu MAU, Rana MM. Genetic analyses of advanced breeding lines of rice (*Oryza sativa* L.) based on morphological traits. Journal of Bioscience and Agriculture Research. 2023;30(2):2559-2569.
24. Rao CR. Advanced statistical methods in biometric research. New York: John Wiley & Sons; 1952. 390 p.
25. Sao A, Panigrahi P, Kumar P, Sahu H. Molecular distinguishness among rice (*Oryza sativa* L.) landraces of central India using microsatellite markers. International Journal of Chemical Studies. 2020;8(4):1046-1050.
26. Sao A, Singh G, Nair SK, Harish D, G. Estimation of genetic variability parameters for various yield attributing traits in germplasm collection of rice (*Oryza sativa* L.). International Journal of Plant and Soil Science. 2024;36(3):158-165.
27. Sharada HB, Kumar D, Krishnamurthy SL, Lakshmana D, Dhananjaya BC, Satish KM. Trait association and genetic variability study in rice MAGIC lines for yield related traits. Journal of Advances in Biology & Biotechnology. 2024;27(12):673-680.
28. Singh B, Gauraha D, Sao A, Nair SK. Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). Pharma Innovation Journal. 2021;10(8):1627-1630.

29. Sivasubramanian S, Madhavanmenon. Heterosis and inbreeding depression in rice. Madras Agricultural Journal. 1973;60:1139-1144.
30. Srujana G, Suresh BG, Lavanya GR, Ram BJ, Sumanth V. Studies on genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). Karnataka Journal of Agricultural Sciences. 2020;6(4):564-566.
31. Vilas GM, Shashidhara N, Uday G, Nethra P, Sainath K. Genetic evaluation of advanced breeding lines of rice (*Oryza sativa* L.) for grain yield and nutrient characters in upland condition. International Journal of Plant and Soil Science. 2024;36(7):997-1006.