

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(5): 01-11
www.biochemjournal.com
Received: 15-01-2026
Accepted: 20-02-2026

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Genetic variability, heritability and genetic advance for yield and grain quality traits in advanced breeding lines of rice (*Oryza sativa* L.)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i5Sa.8296>

Abstract

The present investigation, entitled “Genetics and association studies for yield and its attributing characters in advanced breeding lines of rice (*Oryza sativa* L.)”, was conducted during *Kharif* 2024 at the Research cum Instructional Farm, IGKV, Raipur. The study evaluated 38 genotypes (35 advanced breeding lines and 3 checks) in a Randomized Block Design (RBD) with two replications to assess genetic variability, character association, and genetic divergence for 10 yield and 20 grain quality traits. Analysis of variance revealed highly significant differences among genotypes for all traits, indicating substantial genetic variability. High heritability (h^2) coupled with high genetic advance as percent of mean (GAM) was recorded for 1000-seed weight, gel consistency, alkali spreading value, amylose percentage, and head rice recovery, suggesting the predominance of additive gene action and the effectiveness of direct selection. Genotypic correlation analysis showed significant positive associations between grain yield per plant and biological yield, spikelet fertility, effective tillers, filled grains, harvest index, and 1000-seed weight. Path coefficient analysis identified biological yield per plant as the primary direct contributor to grain yield, followed by harvest index and 1000-seed weight. Genetic divergence analysis grouped the genotypes into four distinct clusters, with plant height contributing the maximum toward total divergence. The genotype R 2698-100-1 was identified as the most promising line for grain yield and biological yield. These findings suggest that biological yield, harvest index, and 1000-seed weight serve as reliable selection indices for developing high-yielding, quality rice varieties.

Keywords: Genetic variability, heritability and genetic advance, correlation and path analysis, genetic divergence, rice yield traits

Introduction

Rice (*Oryza sativa* L., $2n = 24$) is one of the most important staple food crops worldwide and serves as the primary source of nutrition for more than half of the global population, particularly in Asia. Globally, rice is cultivated on about 168-170 million hectares with an annual production exceeding 540 million metric tons (milled basis). India is the second largest producer and the largest exporter of rice, cultivating the crop on approximately 51.42 million hectares with a production of about 225 million metric tons (Anonymous, 2025). The increasing global population is expected to raise rice demand to nearly 584 million tons by 2050, necessitating sustained yield improvement along with quality enhancement (Samal *et al.*, 2022) [5, 35].

In addition to yield, grain quality traits such as milling percentage, hulling percentage, grain dimensions, gel consistency, alkali spreading value, and amylose content are of increasing importance due to changing consumer preferences and market demand (Babu *et al.*, 2011) [7]. Therefore, modern rice breeding programmes aim at simultaneous improvement of yield and grain quality traits without compromising productivity. The foundation of any crop improvement programme lies in the availability of adequate genetic variability. Genetic variability provides the raw material for selection and determines the scope of genetic gain (Shivani *et al.*, 2021) [38]. Quantitative traits such as yield and its components are governed by multiple genes and are influenced by environmental factors. Hence, evaluation of variability parameters is essential before initiating effective selection strategies. The magnitude of variability present in a population is commonly assessed through genotypic

coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). A small difference between PCV and GCV indicates minimal environmental influence on trait expression, whereas a wider gap suggests greater environmental effects (Dhanwani *et al.*, 2013; Verma *et al.*, 2023) [16, 48]. Several researchers have reported substantial variability for yield and quality traits in rice, indicating considerable scope for improvement (Bhargavi *et al.*, 2021; Yashwanth *et al.*, 2021; Heera *et al.*, 2023) [10, 21, 50]. However, variability alone is insufficient to predict response to selection. Heritability estimates the proportion of phenotypic variation that is genetically controlled and transmissible to subsequent generations. High heritability indicates that selection based on phenotype will be effective (Bhinda *et al.*, 2017; Sudeepthi *et al.*, 2020) [11, 42]. Nevertheless, heritability should be considered along with genetic advance, as high heritability coupled with high genetic advance suggests predominance of additive gene action and greater effectiveness of direct selection (Akshay *et al.*, 2022; Valla *et al.*, 2024) [3]. Numerous studies have demonstrated that traits such as effective tillers per plant, grain yield per plant, test weight, biological yield, gel consistency, alkali spreading value, and amylose percentage exhibit high heritability along with high genetic advance, indicating their suitability as reliable selection indices in rice improvement programmes (Rashmi Sai *et al.*, 2025; Charu *et al.*, 2025; Sharmila *et al.*, 2025). Advanced breeding lines represent stabilized and genetically refined material developed through successive cycles of selection. Evaluation of such material for genetic variability parameters enables identification of superior genotypes and efficient selection criteria. Therefore, a systematic assessment of genetic variability, heritability, and genetic advance for yield and grain quality traits is essential to enhance genetic gain and improve both productivity and quality in rice.

In view of the above considerations, the present investigation was undertaken to estimate the magnitude of genetic variability, heritability, and genetic advance for yield and grain quality traits in advanced breeding lines of rice (*Oryza sativa* L.) with the objective of identifying traits amenable to effective selection and genetic improvement.

Materials and method: The present investigation was conducted during Kharif 2024 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, India. The experimental site is situated in the dry tropical sub-humid agro-climatic zone with an average annual rainfall of approximately 1200-1400 mm. The experimental material comprised 38 rice genotypes, including 35 advanced breeding lines and three check varieties namely Narendra 359, Karma Mahsuri, and IGKV R 1244. These genotypes were selected to assess genetic variability for yield and grain quality traits. The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each genotype was grown in uniform plot size following recommended agronomic practices for rice cultivation. Standard cultural practices, including irrigation, fertilization, and plant protection measures, were followed to ensure a healthy crop stand.

Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) was carried out following the method described by Cochran and Cox (1950) [14] for Randomized Complete Block Design (RBD) to test the significance of differences among the genotypes.

The statistical model used was:

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

Where,

- Y_{ij} = phenotypic observation of the i th genotype in the j th replication
- μ = general mean
- g_i = effect of the i th genotype
- r_j = effect of the j th replication
- e_{ij} = random error associated with the i th genotype in the j th replication

The significance of mean squares was tested at 5% and 1% levels of probability against the error degrees of freedom using F-table values as given by Fisher and Yates (1963) [18].

Assessment of Variability

Range

Range was calculated as the difference between the maximum and minimum values for each trait:

Range = Maximum value - Minimum value

Mean ($\bar{X}$)

The mean was calculated using the formula:

$$\bar{X} = \frac{\sum X}{N}$$

Where,

- $\bar{X}$ = Mean
- $\sum X$ = Sum of individual observations
- N = Total number of observations

Genotypic and Phenotypic Coefficient of Variation (GCV% and PCV%)

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated to quantify the magnitude of genetic and total variability present in the population, respectively. While PCV accounts for both genetic and environmental influences, GCV reflects only the genetic component of variability.

Genotypic and phenotypic coefficients of variation were computed as:

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100 \quad PCV = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

- σ_g = Genotypic standard deviation
- σ_p = Phenotypic standard deviation
- $\bar{X}$ = Grand mean of the trait

The magnitude of GCV and PCV was categorized following Sivasubramanian and Madhavamenon (1973) [40] as:

- Less than 10% - Low
- 10-20% - Moderate
- Greater than 20% - High
- Heritability in Broad Sense (h_{bs}^2)

Heritability in the broad sense estimates the proportion of total phenotypic variance that is attributable to genetic variance. It provides insight into the transmissibility of traits from one generation to the next.

Heritability in broad sense was estimated as:

$$h_{bs}^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h_{bs}^2 = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_e^2 = Environmental variance

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Heritability estimates were classified according to Johnson *et al.* (1955)^[22] as:

- Low: 0-30%
- Moderate: 30-60%
- High: Above 60%

Genetic Advance as Percent of Mean (GAM)

Genetic advance as percent of mean predicts the expected improvement in a trait under selection pressure and helps determine the effectiveness of selection. It complements heritability estimates by indicating the nature of gene action involved.

Genetic advance as percent of mean was calculated using the formula given by Robinson and Comstock (1949)^[32]:

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

- GAM = Genetic advance as percent of mean
- GA = Genetic advance under selection
- $\bar{X}$ = Grand mean of the trait

Genetic advance as percent of mean was categorized following Johnson *et al.* (1955)^[22] as:

- Low: 0-10%
- Moderate: 10-20%
- High: $\geq 20\%$

Genetic Diversity Analysis

Genetic diversity among genotypes was assessed through agglomerative hierarchical clustering to evaluate the degree of divergence based on multiple quantitative traits.

Euclidean distance was used as a measure of dissimilarity between genotypes.

The Euclidean distance between two genotypes was calculated as:

$$ED_{jk} = \sqrt{\sum_{i=1}^n (X_{ij} - X_{ik})^2}$$

Where,

- ED_{jk} = distance between genotypes j and k
- X_{ij} and X_{ik} = phenotypic value of the i th trait for genotypes j and k , respectively
- n = number of traits considered

The distance matrix was used to construct a dendrogram using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). Intra-cluster and inter-cluster distances were estimated based on average distances among genotypes within and between clusters.

Results and discussion

The present investigation was conducted on thirty-five advanced breeding lines of rice along with three check varieties under the title "Genetics and association studies for yield and its attributing characters in advanced breeding lines of rice (*Oryza sativa* L.)". The field experiment was carried out at the Research and Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.), using a Randomized Block Design (RBD) with two replications to evaluate yield and its component traits. Quality parameters were analyzed separately at the Quality Laboratory, Department of Genetics and Plant Breeding, RRL, IGKV, Raipur (C.G.). Observations were recorded for ten yield-related traits and twenty quality traits, based on the mean of five randomly selected plants per genotype in each replication, except for days to 50 per cent flowering which was recorded on a plot basis.

The recorded data were analyzed to estimate genetic parameters of variability in order to assess the extent of genotypic differences among the breeding lines. Correlation analysis was carried out to determine the association between grain yield and its component traits. Since correlation alone does not clearly explain the cause-and-effect relationships among characters, path coefficient analysis was employed to partition the correlation coefficients into direct and indirect effects of different traits on grain yield. In this analysis, grain yield per plant was considered as the dependent variable, while the remaining characters were treated as independent variables. In addition, genetic divergence among the breeding lines was assessed through cluster analysis, which helped to determine the extent of variability and the contribution of different traits to the overall genetic divergence. This analysis also facilitated the identification of genetically diverse parents that could be utilized in future breeding programmes.

ANOVA: The differences observed among the breeding lines for each trait were examined through analysis of variance (ANOVA), which was employed to assess the magnitude and significance of variation present in the experimental material. The ANOVA results pertaining to

yield and quality traits are presented in, respectively. For all the yield-related as well as quality traits taken under study, the analysis of variance revealed highly significant differences among the 33 advanced breeding lines evaluated. This clearly demonstrates that a considerable amount of genetic variation exists within the material, which can be effectively exploited in future selection and breeding programs. The F-test values obtained for all recorded traits further confirmed that the mean sum of squares was highly significant at the 1% level of significance. The presence of

such highly significant variability emphasizes that the breeding lines under investigation possess ample genetic diversity, making them a valuable resource for identifying superior genotypes with desirable combinations of yield and quality traits.

Significant genetic variability for various yield and quality related traits in rice was also documented by Kuna *et al.*, (2025), Sahithi *et al.*, (2023), and Singh *et al.*, (2021)^[26, 34, 39].

Table 1: Analysis of variance for yield attributing and grain quality traits in advanced breeding lines of rice

S. No	Sources of variance	Mean sum of squares		
		Replication (df=1)	Genotypes (df=32)	Error (df=32)
1	Days to 50% flowering	18.12	94.46**	9.84
2	Plant height (cm)	5.27	1023.18**	6.24
3	Panicle length (cm)	1.19	11.30**	0.34
4	Number of effective tillers per plant	3.04	1.19**	0.17
5	Filled grains per panicle	6.84	169.53**	15.68
6	Spikelet fertility percent	39.98	25.20**	9.95
7	1000 seed weight (g)	6.92	33.30**	1.80
8	Biological yield per plant (g)	14.59	49.57**	11.27
9	Harvest Index (%)	3.71	29.81**	9.24
10	Grain yield per plant (g)	0.35	9.84**	2.13
11	Hulling percentage	7.009	30.903**	5.352
12	Milling percentage	21.206	28.426**	4.995
13	Paddy length (mm)	0.152	0.989**	0.043
14	Paddy breadth (mm)	0.046	0.071**	0.019
15	Paddy L/B ratio	0.006	0.180**	0.051
16	Brown rice length (mm)	0.053	0.590**	0.037
17	Brown rice breadth (mm)	0.047	0.069**	0.030
18	Brown rice L/B ratio	0.039	0.287**	0.085
19	Kernel length (mm)	0.053	0.726**	0.028
20	Kernel breadth(mm)	0.645	0.066**	0.015
21	Kernel L/B ratio	0.076	0.190**	0.034
22	Kernel length after cooking (mm)	0.058	1.122**	0.107
23	Kernel breadth after cooking (mm)	0.103	0.150**	0.026
24	Cooked rice L/B ratio	0.208	0.206**	0.041
25	Elongation ratio	0.008	0.035**	0.002
26	Elongation index	0.058	1.122**	0.107
27	Gel consistency	43.230	486.341**	9.273
28	Alkali spreading value	0.118	3.037**	0.281
29	Amylose percentage	4.406	29.022**	2.041
30	Head rice recovery (%)	21.158	93.656**	5.329

**Significance at 1% level of probability

Estimation of Genetic Parameters of Variability

The mean performance of 38 genotypes was estimated and genetic parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as percent of mean were computed for yield and grain quality traits. These parameters provide an understanding of the magnitude of variability present among the genotypes and help in determining the potential effectiveness of selection in breeding programs. The detailed estimates of these parameters are presented.

For yield and yield-related traits, days to 50% flowering ranged from 96.00 to 109.00 days with an overall mean of 101.47 days. Plant height showed variation from 96.42 to 134.79 cm with an average value of 116.22 cm. Panicle length ranged between 22.95 and 32.15 cm with a mean of 27.30 cm. The number of effective tillers per plant varied from 4.90 to 8.00 with a mean value of 6.88.

The number of filled grains per panicle ranged from 72.7 to 124.9 with a mean value of 111.25 grains. Spikelet fertility

varied from 87.56% to 94.73%. Test weight ranged from 18.77 to 33.67 g with a mean of 25.22 g. Biological yield per plant ranged from 30.40 to 62.19 g with a mean value of 40.56 g, while harvest index ranged from 35.56% to 49.14% with an average value of 43.70%. Grain yield per plant varied from 11.59 to 28.84 g with a mean value of 17.70 g. In general, PCV estimates were slightly higher than the corresponding GCV values for most of the studied traits, indicating that environmental factors had some influence on the expression of these characters. However, several traits exhibited moderate to high heritability along with appreciable genetic advance, suggesting the predominance of additive gene effects and the possibility of improving these traits through effective selection.

Considerable variation was also observed for grain quality parameters. Hulling percentage ranged from 70.00% to 85.40% with a mean value of 76.49%, while milling percentage varied from 61.45% to 74.39% with an average of 68.04%. Paddy length ranged from 7.30 to 10.10 mm

with a mean of 8.72 mm, whereas paddy breadth ranged from 2.00 to 2.85 mm with a mean value of 2.42 mm. Kernel length ranged from 5.30 to 7.60 mm, while kernel breadth ranged from 1.70 to 2.50 mm. Variation was also recorded for elongation ratio, alkali spreading value, amylose content and gel consistency, indicating considerable diversity among the genotypes with respect to cooking and eating quality characteristics.

Head rice recovery varied widely from 28.88% to 66.62% with an average value of 49.01%. Thirteen genotypes recorded head rice recovery above 50%, namely R2758-5-1, R2745-12-1, R2761-56-1, R2406-187-1-114-1, R2370-96-2-9-1, R2404-164-2-87-1, R2545-C4-6-468-1, R2699-25-1, R2771-14-1, R2734-14-1, R2037-22-1-19-1, Narendra 359 and Karma Mahsuri. All the genotypes recorded milling percentage above 65%. Higher elongation ratio was observed in genotype R2545-C4-6-468-1 followed by R2761-55- and R2544-C3-1-456-1.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated to measure the magnitude of variability among the studied characters. In general, PCV values were slightly higher than the corresponding GCV values for all traits, suggesting the presence of environmental influence on trait expression. Similar trends have also been reported earlier by Chacko *et al.* (2023) and Khatun *et al.* (2015)^[13, 25].

Moderate levels of variability were observed for traits such as 1000-seed weight (PCV: 16.61; GCV: 15.74), number of effective tillers per plant (PCV: 11.96; GCV: 10.37) and grain yield per plant (PCV: 9.01; GCV: 6.33). Days to 50% flowering (PCV: 11.25; GCV: 9.15), panicle length (PCV: 8.83; GCV: 8.57) and plant height (PCV: 15.01; GCV: 14.87) also showed moderate variation.

Among the grain quality traits, comparatively higher variability was observed for gel consistency (PCV: 48.36; GCV: 45.21), alkali spreading value (PCV: 25.55; GCV: 23.29) and amylose content (PCV: 16.43; GCV: 15.31). In contrast, relatively lower variability was recorded for hulling percentage (PCV: 5.56; GCV: 4.67), milling percentage (PCV: 6.00; GCV: 5.03) and kernel length after cooking (PCV: 9.53; GCV: 9.17).

Based on the magnitude of variability, the traits were categorized into low (0-10%), moderate (10-20%) and high (>20%) classes. High variability was observed for gel consistency and alkali spreading value, which corroborates the findings of Pushpa *et al.* (2018) and Pillai *et al.* (2020)^[30]. Moderate variability was recorded for days to 50% flowering, effective tillers per plant, plant height, 1000-seed weight, biological yield per plant, brown rice L/B ratio, head rice recovery and amylose content, which is in agreement with earlier reports of Behera *et al.* (2018), Rukmini *et al.* (2016), Gupta *et al.* (2022) and Yadav *et al.* (2020)^[9, 20, 33, 49].

Low variability was observed for several traits including panicle length, spikelet fertility, grain yield per plant, harvest index, hulling percentage, milling percentage, paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice breadth, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, elongation ratio and cooked rice L/B ratio. Similar observations were reported earlier by Singh *et al.* (2005), Singh *et al.* (2021) and Rukmini *et al.* (2016). The overall trends of GCV and PCV for yield and quality traits are illustrated in Figures^[33, 39].

Heritability is an important genetic parameter that measures the proportion of genetic variance present in the total phenotypic variance. Broad-sense heritability indicates the total heritable portion of variation and provides insight into the effectiveness of selection for improving specific traits.

In the present investigation, heritability estimates for yield and quality traits ranged from moderate to high. Among yield attributes, plant height recorded the highest heritability (94.56%), whereas spikelet fertility exhibited the lowest value (43.40%). Among grain quality parameters, kernel length recorded the highest heritability (92.57%), while the lowest heritability was observed for brown rice breadth (38.76%).

High heritability (>60%) was observed for several yield traits including days to 50% flowering, plant height, number of effective tillers per plant, panicle length and 1000-seed weight. Among quality traits, high heritability was recorded for hulling percentage, paddy length, brown rice length, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, elongation ratio, gel consistency, alkali spreading value, amylose content and head rice recovery. These findings indicate that these characters are predominantly governed by genetic factors and can therefore be improved effectively through selection.

Moderate heritability (30-60%) was observed for spikelet fertility, grain yield per plant and harvest index among yield parameters, and for paddy breadth, paddy L/B ratio, brown rice breadth and milling percentage among grain quality traits. Similar findings have been reported by Akhila *et al.* (2025), Dhanwani *et al.* (2013), Allam *et al.* (2019), Deep *et al.* (2017), Sharma *et al.* (2021) and Adjah *et al.* (2020)^[1, 2, 4, 16, 37].

Genetic advance as percentage of mean provides an estimate of the expected progress from selection by integrating the magnitude of variability and heritability of a trait. In the present study, genetic advance values ranged from low to high for both yield and grain quality characters.

Among the yield attributes, the highest genetic advance as percent of mean was recorded for 1000-seed weight (30.71%), whereas the lowest value was observed for spikelet fertility (5.08%). Among grain quality traits, gel consistency recorded the highest genetic advance (62.03%), while hulling percentage showed the lowest value (8.08%).

High genetic advance (>20%) was observed for 1000-seed weight among yield traits and for gel consistency, alkali spreading value, amylose percentage and head rice recovery among grain quality traits. Similar results were reported by Sao *et al.* (2019) for alkali spreading value, gel consistency and amylose content, Vange and Ojo (1997) for 1000-seed weight, and Reddy *et al.* (2025) for 1000-seed weight and head rice recovery^[31, 36, 47].

Moderate genetic advance (10-20%) was recorded for plant height, panicle length, number of effective tillers per plant, biological yield per plant and grain yield per plant. Among grain quality traits, moderate genetic advance was observed for paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice L/B ratio, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, cooked rice L/B ratio, elongation ratio and elongation index. Similar findings were reported by Tripathi *et al.* (2019), Sao *et al.* (2019) and Sharma *et al.* (2025)^[36, 37, 44].

Low genetic advance (<10%) was observed for days to 50% flowering and harvest index among yield traits, and for

hulling percentage, milling percentage and brown rice breadth among grain quality traits. Comparable observations were reported by Reddy *et al.* (2025) and Adjah *et al.* (2020) [1, 31].

The combined assessment of heritability and genetic advance provides a more reliable estimate of the nature of gene action governing a trait and the expected response to selection. Traits exhibiting high heritability along with high genetic advance are generally controlled by additive gene action and can therefore be improved effectively through direct selection, as suggested by Panse and Sukhatme (1967). Similar conclusions were also drawn by Kavadi *et al.* (2025) [23, 29], who emphasized that the combined evaluation of heritability and genetic advance is more reliable than heritability alone for predicting selection response.

In the present study, high heritability coupled with high genetic advance was observed for 1000-seed weight, gel consistency, alkali spreading value, amylose percentage and head rice recovery, indicating the predominance of additive gene action and a high scope for improvement through selection. Similar findings were reported by Bandi *et al.* (2018), Keerthiraj *et al.* (2020) and Tripathi *et al.* (2024) [8, 24, 43].

Several traits exhibited high heritability along with moderate genetic advance, including plant height, panicle length, spikelet fertility, number of effective tillers per plant,

biological yield per plant and grain yield per plant, along with many grain quality parameters such as paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice L/B ratio, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, cooked rice L/B ratio, elongation ratio and elongation index. This suggests the involvement of both additive and non-additive gene effects and indicates that selection may be moderately effective. Similar results were reported by Dhanwani *et al.* (2013), Manivelan *et al.* (2022) and Archana Patel *et al.* (2018) [6, 16, 28].

High heritability coupled with low genetic advance was observed for days to 50% flowering, hulling percentage and brown rice breadth, suggesting the predominance of non-additive gene action. Under such conditions, direct selection may be less effective and heterosis breeding could be a more suitable approach. Similar observations were reported by Edukondalu *et al.* (2017), Yadav *et al.* (2022) and Tuwar *et al.* (2013) [17, 45, 49].

Moderate heritability combined with low genetic advance was recorded for harvest index and milling percentage, indicating a stronger environmental influence on the expression of these characters and a relatively limited response to phenotypic selection. Similar findings were reported by Demeke *et al.* (2023) and Edukondalu *et al.* (2017) [15, 17].

S. No	Traits	Mean	Range		Coefficient of Variation		h ²	GA as % of mean
			Max	Min	GCV	PCV		
1.	Days to 50% flowering	101.47	109.00	96.00	9.15	11.25	85.12	9.42
2.	Plant height (cm)	116.22	134.79	96.42	14.87	15.01	94.56	26.15
3.	Panicle length (cm)	27.30	32.15	22.95	8.57	8.83	94.12	17.13
4.	Number of effective tillers per plant	6.88	8.00	4.90	10.37	11.96	75.20	18.53
5.	Filled grains per panicle	111.25	124.90	72.70	7.88	8.65	83.07	14.80
6.	Spikelet fertility percent	83.26	87.56	70.98	3.32	5.04	43.40	4.50
7.	1000 seed weight (g)	25.22	33.67	18.77	15.74	16.61	89.72	30.71
8.	Biological yield per plant (g)	40.56	62.19	30.40	10.57	14.42	56.67	17.84
9.	Harvest Index (%)	43.70	49.14	35.55	5.43	9.54	49.38	8.48
10.	Grain yield per plant (g)	17.70	28.84	11.59	6.33	9.01	53.24	10.26
11.	Hulling percentage	76.49	85.40	70.00	4.67	5.57	70.48	8.08
12.	Milling percentage	68.04	74.40	61.46	5.03	6.01	70.11	8.68
13.	Paddy length (mm)	8.73	10.10	7.30	7.88	8.23	91.68	15.54
14.	Paddy breadth (mm)	2.43	2.85	2.00	6.64	8.72	58.07	10.43
15.	Paddy L/B ratio	3.62	4.31	2.90	7.01	9.40	55.64	10.77
16.	Brown rice length (mm)	6.81	7.85	5.75	7.73	8.23	88.13	14.94
17.	Brown rice breadth (mm)	2.20	2.50	1.75	6.31	10.13	38.76	8.09
18.	Brown rice L/B ratio	3.17	4.49	2.57	10.01	13.61	54.12	15.17
19.	Kernel length (mm)	6.44	7.60	5.30	9.18	9.54	92.57	18.19
20.	Kernel breadth(mm)	2.13	2.50	1.70	7.46	9.45	62.31	12.12
21.	Kernel L/B ratio	2.96	3.76	2.33	9.45	11.32	69.59	16.23
22.	Kernel length after cooking (mm)	9.29	10.95	7.90	7.67	8.44	82.52	14.35
23.	Kernel breadth after cooking (mm)	2.97	3.70	2.40	8.39	9.97	70.78	14.54
24.	Cooked rice L/B ratio	3.13	3.93	2.40	9.19	11.26	66.62	15.46
25.	Elongation ratio	1.45	1.76	1.13	8.81	9.45	86.86	16.91
26.	Elongation index	8.29	9.95	6.90	8.59	9.46	82.52	16.08
27.	Gel Consistency	39.25	61.50	27.00	45.22	48.36	89.81	62.03
28.	Alkali spreading value	5.04	7.00	1.00	23.30	25.56	83.09	43.75
29.	Amylose percentage	23.98	35.68	19.83	15.32	16.43	86.86	29.40
30.	Head rice recovery (%)	49.02	66.62	28.88	13.56	14.35	89.23	26.38

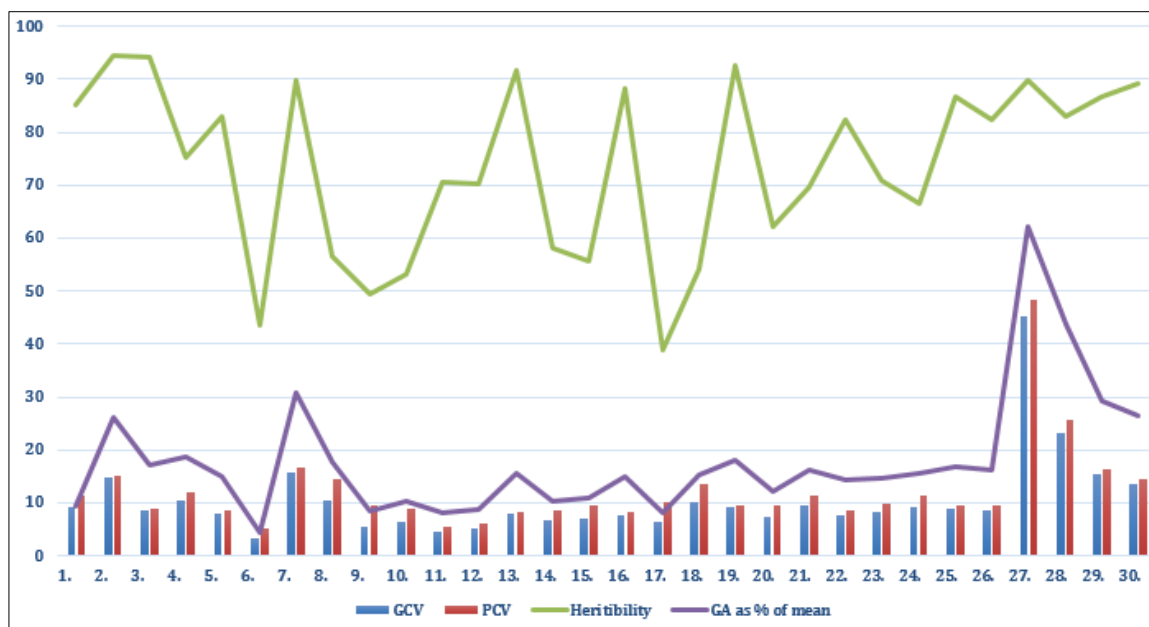


Fig 1: Diagrammatic representation of genetic parameters (GCV, PCV, heritability and genetic advance as% of mean)

1. Days to 50% flowering, 2. Plant height (cm), 3. Panicle length (cm), 4. Number of effective tillers per plant, 5. Filled grains per panicle, 6. Spikelet fertility percent, 7. 1000 seed weight (g), 8. Biological yield per plant (g), 9. Harvest Index (%), 10. Grain yield per plant (g), 11. Hulling percentage, 12. Milling percentage, 13. Paddy length (mm), 14. Paddy breadth (mm), 15. Paddy L/B ratio, 16. Brown rice length (mm), 17. Brown rice breadth (mm), 18. Brown rice L/B ratio, 19. Kernel length (mm), 20. Kernel breadth (mm), 21. Kernel L/B ratio, 22. Kernel length after cooking (mm), 23. Kernel breadth after cooking (mm), 24. Cooked rice L/B ratio, 25. Elongation ratio, 26. Elongation index, 27. Gel consistency, 28. Alkali spreading value, 29. Amylose percentage, 30. Head rice recovery (%).

Genetic Diversity

Classification of genotypes based on multiple traits is essential for identifying genetically similar and divergent lines for breeding programs. Analysis of variance revealed significant differences among the 38 genotypes for all the

traits studied, indicating the presence of considerable genetic variability. The existence of such variability provides opportunities for selecting genetically diverse parents for hybridization aimed at improving yield and grain quality.

Based on generalized Euclidean distances, the 38 genotypes were grouped into four clusters using Tocher's method. The clustering pattern reflected varying levels of genetic divergence among the genotypes, where those within the same cluster exhibited greater similarity while genotypes belonging to different clusters showed higher levels of divergence.

Cluster analysis grouped the 38 advanced breeding lines into four clusters. Cluster I was the largest, comprising 30 genotypes (78.94%), followed by Cluster II with 6 genotypes (15.70%). Clusters III and IV each contained a single genotype (2.63%). The occurrence of solitary clusters indicates the presence of highly divergent genotypes possessing unique genetic characteristics.

Table 2: Clustering pattern among 38 advance breeding lines of rice for both yield and quality traits

Cluster Number	No. of genotypes	Percent of genotypes	Advanced breeding lines
I	30	78.94%	R2758-5-1, R2761-55-, R2701-8-1, R2699-25-1, R2733-27-1, R2734-14-1, R2735-10-1, R2735-24-1, R2735-25-1, R2738-97-1, R2748-14-1, R2751-32-1, R2751-50-1, R2751-61-1, R2752-34-1, R2760-61-1, R2764-55-1, R2765-31-1, R2741-101-1, R2698-100-1, R2370-96-2-9-1, R2037-22-1-19-1, Narendra 359 (C), R2404-164-2-87-1, R2544-C3-1-456-1, R2545-C4-6-468-1, R2550-C9-3-500-1, Karma Mahsuri (C), R2406-187-1-114-1, R2506-485-1-584-1]
II	6	15.70%	R2737-26-1, R2745-12-1, R2745-74-1, R2771-14-1, IGKV R 1244 (C), R2406-182-2-107-1
III	1	2.63%	R2754-60-1
IV	1	2.63%	R2761-56-1

The concentration of a large number of genotypes in Cluster I suggests a high degree of genetic similarity among these lines, possibly due to common ancestry or similar selection history. Comparable clustering patterns in rice germplasm were also reported by Bose and Pradhan (2010) and

Senapati and Kumar (2019)^[12], where most genotypes were grouped into one major cluster while a few genotypes formed distinct solitary clusters representing genetically divergent resources.

Table 3: Average intra-cluster (diagonal) and inter-cluster distance values

Cluster Number	I	II	III	IV
I	118.31	424.65	345.04	208.42
II		111.49	365.61	293.57
III			0.00	427.80
IV				0.00

The intra- and inter-cluster distances among clusters are presented in Table 3. The highest inter-cluster distance was observed between Cluster III and Cluster IV (427.80), followed by Cluster I and Cluster II (424.65), indicating maximum genetic divergence among these clusters. Such widely separated clusters are desirable for hybridization as they are expected to produce greater heterosis and wider variability in segregating generations.

The lowest inter-cluster distance was observed between Cluster I and Cluster IV (208.42), suggesting relatively closer genetic relationships among the genotypes belonging to these clusters. Similar findings were reported by Garg *et al.* (2011) ^[19], who observed that smaller inter-cluster distances indicate closer genetic similarity and may result in limited heterotic response.

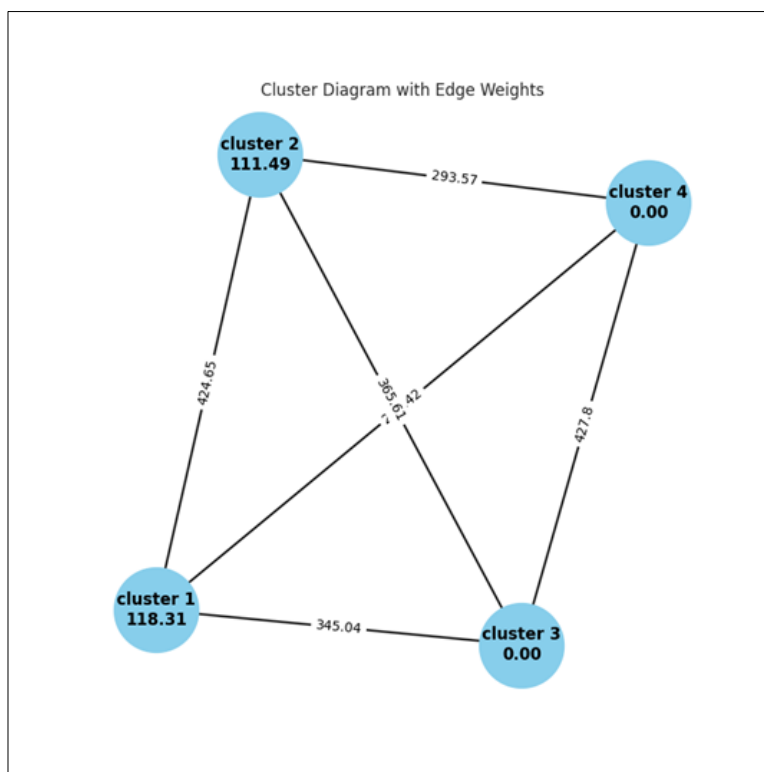


Fig 2: A set of 38 advanced breeding lines underwent cluster analysis using the Tocher method to group genetically similar lines based on the measured parameters

In general, intra-cluster distances were lower than inter-cluster distances, indicating that genotypes within the same cluster were more similar to each other than those belonging to different clusters. The intra-cluster distance ranged from 111.49 in Cluster II to 118.31 in Cluster I. Therefore, hybridization between genotypes belonging to clusters separated by larger inter-cluster distances may generate greater genetic variability and useful recombinants. Cluster mean analysis revealed considerable variation among clusters for different traits. Cluster I recorded higher

mean values for panicle length (27.75 cm), number of effective tillers per plant (9.44), and biological yield (47.97 g).

Cluster IV exhibited the highest mean values for several yield attributes including days to 50% flowering (116.00), plant height (164.90 cm), filled grains per panicle, spikelet fertility (90.10%), 1000-seed weight (38.00 g), harvest index (31.40%) and grain yield per plant. The superior performance of Cluster IV indicates its potential as a valuable source of desirable traits for yield improvement.

Table 4: Average performance of advanced breeding lines for each cluster for different characters along with percent contribution of traits towards genetic divergence

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Percentage contribution
1.	112.82	108.25	96.00	116.00	0.98%
2.	161.01	111.12	148.20	164.90	39.44%
3.	9.44	9.23	9.10	7.40	2.77%
4.	27.75	25.16	26.90	25.05	10.17%
5.	112.54	112.53	72.70	123.70	8.07%

6.	86.88	88.80	86.25	90.10	11.27%
7.	31.65	26.58	33.50	38.00	9.46%
8.	47.97	34.93	47.50	35.00	5.98%
9.	24.36	26.09	22.85	31.40	0.60%
10.	12.92	11.45	11.90	13.10	3.86%

Note: Bold digits represent highest mean values for that particular traits and mean values which are not favorable are not bold.

1. Days to 50% flowering, 2. Plant height (cm), 3. Number of effective tillers per plant, 4. Panicle length (cm), 5. filled grains per panicle, 6. Spikelet fertility percent, 7. 1000 seed weight (g), 8. Biological yield per plant (g), 9. Harvest Index (%), 10. Grain yield per plant (g).

The genotype R2761-56-1, belonging to Cluster IV, possessed several favourable trait means and may therefore be considered a promising parent for hybridization as well as for direct selection. Similar utilization of cluster mean analysis for identifying superior genotypes has been reported by Sree *et al.* (2023), Bose and Pradhan (2010) and Mahesh *et al.* (2022) [12, 27, 41].

The contribution of different traits towards total genetic divergence revealed that plant height contributed the highest proportion (39.44%), followed by spikelet fertility (11.27%), panicle length (10.17%), 1000-seed weight (9.46%) and number of filled grains per panicle (8.07%). These traits played a major role in differentiating the genotypes into distinct clusters.

Moderate contributions were recorded for biological yield per plant (5.98%) and grain yield per plant (3.86%), indicating that yield variation was largely influenced by its component traits. In contrast, effective tillers per plant (2.77%), days to 50% flowering (0.98%) and harvest index (0.60%) contributed relatively less to genetic divergence.

Overall, traits with higher percentage contributions played a dominant role in genetic differentiation and should therefore be prioritized during parent selection and hybridization programs aimed at improving rice yield and grain quality.

Conclusion

The present study revealed the existence of substantial genetic variability among the advanced breeding lines of rice for both yield and grain quality traits, indicating ample scope for effective selection and crop improvement. Analysis of variance confirmed highly significant differences among genotypes for all the characters studied. The estimates of genetic parameters indicated that several traits exhibited moderate to high variability with relatively higher PCV than GCV, suggesting the influence of environmental factors on trait expression.

High heritability coupled with high genetic advance as percent of mean was observed for traits such as 1000-seed weight, gel consistency, alkali spreading value, amylose percentage, and head rice recovery, indicating the predominance of additive gene action and the effectiveness of direct selection for these characters. Correlation analysis revealed significant positive associations of grain yield per plant with biological yield, spikelet fertility, number of effective tillers, filled grains per panicle, harvest index, and 1000-seed weight, suggesting that improvement in these component traits would lead to enhanced grain yield. Path coefficient analysis further indicated that biological yield per plant had the highest direct effect on grain yield, followed by harvest index and 1000-seed weight,

highlighting their importance as reliable selection criteria in rice breeding programs.

Genetic divergence analysis grouped the 38 genotypes into four distinct clusters, indicating the presence of considerable genetic diversity among the evaluated lines. The maximum inter-cluster distance observed between certain clusters suggested that hybridization between genotypes from these clusters may produce superior recombinants with greater variability. Among the studied genotypes, R 2698-100-1 emerged as the most promising line for grain yield and biological yield, while R2761-56-1 also showed superior cluster mean performance for several yield-related traits.

Overall, the findings of this study indicate that biological yield, harvest index, and 1000-seed weight can be effectively utilized as reliable selection indices for improving grain yield, while traits such as gel consistency, alkali spreading value, amylose content, and head rice recovery can be targeted for improving grain quality. The identified genetically diverse and superior genotypes may serve as valuable parental lines in future rice breeding programs aimed at developing high-yielding varieties with desirable grain quality traits.

Disclaimer (artificial intelligence)

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

Competing interests

Authors have declared that no competing interests exist.

References

1. Adjah KL, Abe A, Adetimirin VO, Kizito EB. Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (*Oryza sativa* L.). *Physiol Mol Biol Plants*. 2020;26:1309-1317.
2. Akhila A, Krishna L, Sameer Kumar CV, Kiranbabu T. Genetic variability and correlation analysis for yield attributing traits in rice (*Oryza sativa* L.). *J Exp Agric Int*. 2025;47(7):667-674.
3. Akshay M, Rukmini K, Yadla H, Chandra B, Devi K. Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). *Pharma Innov J*. 2022;11:167-172.
4. Allam TE, Nagaraja, Shivakumar N. Studies on variability, heritability and genetic advance in parental lines of hybrid rice (*Oryza sativa* L.). *Int J Curr Microbiol Appl Sci*. 2019;8(9):879-888.
5. Anonymous. FAOSTAT database. Food and Agriculture Organization of the United Nations; 2025.
6. Archana RS, Rani MS, Vardhan KMV, Fareeda G. Estimation of genetic variability for grain yield, yield components and nutritional traits in rice (*Oryza sativa* L.). *Green Farming*. 2018;9(4):596-599.
7. Babu VR, Shreya K, Dangi KS, Usharani G, Shankar AS. Correlation and path analysis studies in popular

- rice hybrids of India. *Int J Sci Res Publ.* 2011;2(3):158-165.
8. Bandi HRK, Satyanarayana PV, Babu DR, Chamundeswari N, Rao VS. Genetic variability estimates for yield and yield component traits and quality traits in rice (*Oryza sativa* L.). *Int J Curr Microbiol Appl Sci.* 2018;7(3):13-31.
 9. Behera B. Studies on genetic variability for some metric traits in slender grain rice genotypes. *J Appl Nat Sci.* 2018;10(1):375-378.
 10. Bhargavi M, Shanthi P, Reddy VLN, Reddy DM, Reddy BR. Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *Pharma Innov J.* 2021;10(5):507-511.
 11. Bhinda M. Estimates of genetic variability, heritability and genetic advance for yield contributing and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). *J Plant Dev Sci.* 2017;7:229-233.
 12. Bose LK, Pradhan SK. Genetic divergence in land races of rice (*Oryza sativa* L.). *Electron J Plant Breed.* 2010;1(2):199-204.
 13. Chacko A, Jayalekshmy VG, Shahiba AM. Studies on PCV, GCV, heritability and genetic advance in rice genotypes for yield and yield components. *Int J Plant Soil Sci.* 2023;35(16):324-330.
 14. Cochran WG, Cox GM. *Experimental designs.* New York: John Wiley and Sons; 1950.
 15. Demeke B, Tadesse Z, Bekele A. Genetic variability, heritability and genetic advance for yield and yield related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes. *J Agric Sci.* 2023;15(2):52-64.
 16. Dhanwani RK, *et al.* Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). *Bioscan.* 2013;8(4):1403-1407.
 17. Edukondalu B, *et al.* Studies on variability, heritability, correlation and path analysis for yield, yield attributes and quality traits in rice (*Oryza sativa* L.). *Int J Curr Microbiol Appl Sci.* 2017;6(10):2369-2376.
 18. Fisher RA, Yates F. *Statistical tables for biological, agricultural and medical research.* Edinburgh: Oliver and Boyd; 1963.
 19. Garg R, Singh R, Singh A, Gautam R. Genetic divergence in aromatic rice (*Oryza sativa* L.). *J Plant Breed Crop Sci.* 2011;3(4):58-62.
 20. Gupta P. A study of trends in rice production in India: Post millennium. *Int J Sci Res.* 2024;13(7):349-353.
 21. Heera P, Ram M, Kumar R, Murali S, Kumar A. Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in rice (*Oryza sativa* L.). *Ecol Environ Conserv.* 2023;29:160-163.
 22. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J.* 1955;47:314-318.
 23. Kavadi V, Umate SM, Kalpande HV. Genetic variability, heritability and genetic advance among elite wheat (*Triticum aestivum*) genotypes. *Int J Adv Biochem Res.* 2025;9(7):140-143.
 24. Keerthiraj B, Biju S. Assessment of genetic variability, heritability and genetic advance in F2 generation of rice (*Oryza sativa* L.). *Pharma Innov J.* 2021;10(10):138-142.
 25. Khatun M, Hanafi MM, Rafii MY, Wong MY, Salleh FM, Ferdous J. Genetic variation, heritability and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *Biomed Res Int.* 2015;2015:290861.
 26. Kuna S, Gauraha D, Sao A, Indumathi S, Nagaraju D. Exploring genetic variability and diversity in advanced breeding lines of rice for yield-attributing and grain quality traits. *J Adv Biol Biotechnol.* 2025;28(4):42-56.
 27. Mahesh D, Hari Y, Sudarshan M, Badri J, Srikanth R. Genetic variability, heritability and genetic advance for yield and grain quality traits in rice (*Oryza sativa* L.). *J Exp Agric Int.* 2022;44(9):1-8.
 28. Manivelan K, Manonmani S, Suresh R, Jeyaprakash P. Genetic variability and character association studies for yield and yield contributing traits in rice (*Oryza sativa* L.). *Pharma Innov J.* 2022;11(11):324-329.
 29. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers.* New Delhi: ICAR; 1985.
 30. Pushpa R, Suresh R, Iyyanar K, Mannimaran R, Sassikumar D. Study on gelatinization properties and amylose content in rice germplasm. *J Pharmacogn Phytochem.* 2018;7(15):2934-2942.
 31. Reddy MVS, Hari Prasanna K, Dinesh D. Genetic variability, heritability and genetic advance for yield and yield related traits in rice (*Oryza sativa* L.) genotypes. *Indian J Agric Res.* 2025.
 32. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. *Agron J.* 1949;41:353-359.
 33. Rukmini KD, Parimala K, Venkanna V, Lingaiah N, Hari Y, Chandra BS. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *Int J Pure Appl Biosci.* 2016;4(2):250-255.
 34. Sahithi M, Fiyaz RA, Kumar CVS, Laha GS. Genetic variability and character association studies for yield and yield related traits in rice (*Oryza sativa* L.). *Pharma Innov J.* 2023;12(9):598-602.
 35. Samal P, Babu S, Mondal B, Mishra S. The global rice agriculture towards 2050: An inter-continental perspective. *Outlook Agric.* 2022;51:164-172.
 36. Sao R, Sao R, Saxena RR, Singh N, Sahu PK. Genetic variation for morphological, grain yield and grain quality traits in rice landraces of Chhattisgarh. *Adv Biores.* 2019;10(1):128-132.
 37. Sharma S. Assessment of genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) genotypes. *J Plant Dev Sci.* 2021;13(4):201-206.
 38. Shivani D, Jabeen F, Supriya K, Sundaram RM, Kumar JA, Fiyaz RA. Genetic variability, heritability and genetic advance for yield and its component traits in germplasm lines of rice (*Oryza sativa* L.). *J Res PJTSAU.* 2021;49:25-29.
 39. Singh M, Shweta, Yadav VK, Yadav RK, Singh P, Singh AK. Genetic variability studies for yield and related attributes in rice genotypes (*Oryza sativa* L.). *Int J Curr Microbiol Appl Sci.* 2021;10(12):133-138.
 40. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. *Madras Agric J.* 1973;60:1093-1096.
 41. Sree KS, Sarma VVSS, Kumar RM. Genetic divergence studies in rice (*Oryza sativa* L.) genotypes for yield and quality traits using D² analysis. *Pharma Innov J.* 2023;12(4):1636-1640.

42. Sudeepthi K, Jyothula DPB, Umar SK, Kumar B, Thati S. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electron J Plant Breed. 2020;144-148.
43. Tripathi N, Kumar A, Tripathi MK. Studies on genetic variability, heritability and genetic advance for grain yield and its attributing traits in rice (*Oryza sativa* L.). Bioscan. 2024;19(1):101-105.
44. Tripathi N, Verma OP, Singh PK, Rajpoot P. Studies on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for yield and its components under salt affected soil. Int J Curr Microbiol Appl Sci. 2019;8(7):5316-5324.
45. Tuwar JC, Jaiswal JP, Vishwakarma SR. Appraisal of genetic variability for yield and its component traits in rice (*Oryza sativa* L.). Curr Int J Med Appl Sci. 2013;1(3):19-25.
46. Vallala G, Kumar JA, Mohan YC, Rathod S. Genetic variability and character association studies on yield attributing and grain quality traits in rice (*Oryza sativa* L.). J Sci Res Rep. 2024;30(8):562-572.
47. Vange T, Ojo AA. Variability and heritability estimates of yield and yield components in some Nigerian lowland rice genotypes. Int Rice Res Notes. 1997;22(3):6.
48. Verma Y, Tomar N, Saran D. Assessment of genetic variability for yield and its contributing traits in rice (*Oryza sativa* L.). Int J Environ Clim Change. 2023;13:36-39.
49. Yadav SK, Yuvraj R. Estimates of genetic variability and heritability in some promising rice genotypes. Pharma Innov J. 2022;11(7):2683.
50. Yashwanth JV, Shanthi P, Shekar MR, Reddy VLN, Kumari PL. Estimates of genetic variability, heritability and genetic advance for yield and its component traits in advanced breeding lines of rice (*Oryza sativa* L.). Pharma Innov J. 2021;10(8):1422-1425.