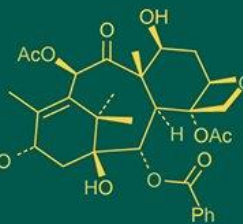
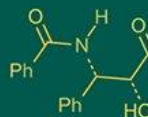


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 1544-1546
www.biochemjournal.com
Received: 15-05-2026
Accepted: 19-06-2026

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Evaluation of genetic variability for yield and yield contributing traits in advanced breeding lines of rice (*Oryza sativa* L.)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sq.9624>

Abstract

Thirty-four rice genotypes, including three check varieties, were evaluated and significant variation was observed for all yield and grain quality traits. The PCV values were higher than the corresponding GCV values for all traits, indicating environmental influence. High heritability was recorded for days to 50% flowering, panicle length, 1000 seed weight and several quality traits, indicating that these traits are predominantly governed by genetic factors. High heritability coupled with high genetic advance was recorded for panicle length, 1000-seed weight, paddy L/B ratio, kernel L/B ratio, gel consistency and alkali spreading value, suggesting the predominance of additive gene action.

Keywords: Rice, breeding lines, yield traits, quality traits, genetic parameters, variability

Introduction

Rice (*Oryza sativa* L.) is one of the world's most important staple food crops and serves as the primary food source for more than half of the global population (Roy *et al.*, 2013) [12]. Improving grain yield remains a major objective of rice breeding due to the increasing demand for food. Grain yield is a complex quantitative trait controlled by several component characters and influenced by both genetic and environmental factors. Therefore, the assessment of genetic variability is essential for the effective selection of superior genotypes. Johnson *et al.*, (1955) [7] reported that heritability coupled with genetic advance provides a reliable basis for selection.

Materials and Methods

Thirty-four rice genotypes, including three check varieties (Narendra 359, Karma Mahsuri and IGKV R 1244), were evaluated during *kharif* 2025 in a Randomized Block Design (RBD) with two replications at the Research-cum-Instructional Farm, Department of Genetics and Plant Breeding, IGKV, Raipur. Observations were recorded on twenty-one traits comprising eleven yield and yield-contributing traits and ten grain quality traits. Data for yield and yield-contributing traits were recorded from the mean of five randomly selected plants in each replication, except days to 50% flowering, which was recorded on a plot basis. Analysis of variance (ANOVA) was conducted separately for each character under a randomized block design (RBD) as suggested by Panse and Sukhatme (1978) [11]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to Burton and De Vane (1953) [6]. Broad-sense heritability were computed following the method of Allard (1960) [2] and genetic advance as percent of mean were computed using Johnson *et al.*, (1955) [7].

Results and Discussion

The results of the analysis of variance are presented in Table 1. All the traits included in the study were found to be highly significant at the 1% level of significance. Kondi *et al.*, (2022) investigated forty scented rice genotypes to assess genetic variability. The analysis of variance revealed highly significant differences for all the forty-one characters, indicating the existence of substantial genetic variability among the genotypes.

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The mean performance and range of the twenty-one studied traits are presented in Table 2. The PCV estimates were consistently higher than the corresponding GCV values for all the traits, indicating the influence of environmental factors on trait expression. Among the grain quality traits, the highest GCV and PCV were recorded for alkali spreading value, followed by gel consistency, which was in agreement with the findings of Barik *et al.*, (2026). Moderate GCV and PCV were observed for panicle length, 1000-seed weight, biological yield per plant, paddy L/B ratio, brown rice L/B ratio and kernel L/B ratio, corroborating the reports of Meher *et al.*, (2025) [9], Bhardwaj *et al.*, (2025) [5] and. The traits exhibiting high heritability included days to 50% flowering, panicle length, 1000 seed weight, paddy L/B ratio, brown rice L/B ratio, kernel L/B ratio, milling percentage, hulling percentage, head rice recovery, elongation ratio and alkali spreading

value. The predominance of genetic control over these traits suggests that selection based on phenotype would be effective for their improvement. Similar results have been documented by Sao *et al.*, (2024) [14] and Akhil *et al.*, (2025) [1]. High heritability coupled with high genetic advance as percent of mean was recorded for 1000-seed weight, panicle length, paddy L/B ratio, kernel L/B ratio, gel consistency and alkali spreading value, indicating the predominance of additive gene action and the effectiveness of direct selection. Similar findings were reported by Singh *et al.*, (2021) [15], Awad-Allah *et al.*, (2022) [3] and Naotia *et al.*, (2021). Head rice recovery, brown rice L/B ratio and elongation ratio exhibited high heritability with moderate genetic advance, suggesting the involvement of both additive and non-additive gene effects, which agreed with the findings of Sahu *et al.*, (2024) [15] and Singh *et al.*, (2021) [15].

Table 1: Analysis of Variance (ANOVA) for yield and its contributing traits in advanced breeding lines of rice

S. No.	Source of variation	Mean Sum of Square (MSS)		
		Replication	Treatment	Error
		Degree of Freedom		
		1	33	33
1.	Days of 50% flowering	0.235	51.774**	3.872
2.	Plant height (cm)	15.889	96.483**	95.601
3.	Panicle length (cm)	6.547	24.459**	2.132
4.	No. of effective tillers per plant	2.118	1.256**	0.535
5.	Number of filled grains per panicle	218.165	282.022**	143.513
6.	Number of total grains per panicle	208.250	206.309**	198.523
7.	Spikelet fertility (%)	4.488	32.360**	19.662
8.	1000 seed weight (g)	2.447	28.388**	0.634
9.	Biological yield per plant(g)	12.359	55.448**	18.565
10.	Grain yield per plant (g)	0.119	12.756**	3.502
11.	Harvest index (%)	7.840	27.488**	7.412
12.	Paddy L/B ratio	0.003	0.350**	0.020
13.	Hulling%	2.153	4.213**	1.015
14.	Milling%	5.011	7.177**	1.467
15.	Head rice recovery (%)	2.813	32.779**	2.691
16.	Brown rice L/B ratio	0.034	0.275**	0.038
17.	Kernel L/B ratio	0.274	0.283**	0.01
18.	Elongation ratio	0.052	0.016**	0.012
19.	Gel consistency	4.765	162.893**	0.643
20.	Alkali spreading value	0.235	3.371**	0.144
21.	Amylose percentage	7.399	7.417**	1.906

Table 2: Genetic variability parameters of yield and its contributing traits

S. No.	Traits	Mean	Range		GCV%	PCV%	h ² (bs)	GA as% Mean
			Min.	Max.				
1.	Days to 50% flowering	102.500	94.000	111.000	4.710	5.079	86.085	9.007
2.	Plant height (cm)	113.500	99.000	128.000	5.080	8.801	41.700	4.360
3.	Panicle length (cm)	24.500	18.000	31.000	13.948	15.222	83.966	26.329
4.	Number of effective tillers per plant	8.000	6.000	10.000	8.287	13.057	40.288	10.836
5.	Number of filled grains per panicle	106.000	86.000	126.000	8.954	14.304	38.300	7.850
6.	Number of total grains per panicle	123.500	104.000	143.000	15.630	21.270	54.360	17.400
7.	Spikelet fertility (%)	83.000	76.000	90.000	18.000	25.600	49.400	18.300
8.	1000 seed weight (g)	23.000	17.000	29.000	15.987	16.348	95.630	32.290
9.	Biological yield per plant (g)	35.305	24.830	45.780	12.325	17.459	49.840	17.930
10.	Grain yield per plant (g)	14.500	9.500	19.500	15.872	21.037	56.930	24.680
11.	Harvest index (%)	41.875	33.230	50.520	8.152	10.748	57.530	12.730
12.	Paddy L/B ratio	3.990	2.980	5.000	10.931	11.560	89.408	21.292
13.	Hulling%	77.320	73.790	80.850	1.607	2.054	61.184	2.589
14.	Milling%	66.850	62.780	70.920	2.486	3.059	66.055	4.163
15.	Head rice recovery (%)	51.640	42.410	60.870	7.389	8.023	84.824	14.020
16.	Brown rice L/B ratio	3.040	2.280	3.800	10.797	12.399	75.833	19.369
17.	Kernel L/B ratio	3.020	2.330	3.710	11.788	12.194	93.443	23.473
18.	Elongation ratio	1.440	1.240	1.630	5.968	6.145	94.321	11.941
19.	Gel consistency	44.750	25.000	64.500	25.799	25.901	99.213	52.937
20.	Alkali spreading value	4.750	2.500	7.000	26.657	27.824	91.785	52.609
21.	Amylose percentage	26.530	23.000	30.060	5.498	7.151	59.110	9.440

Note: Max = Maximum, Min = Minimum, GCV (%) = Genotypic Coefficient of Variation, PCV (%) = Phenotypic Coefficient of Variation, h² (bs) = Heritability in broad sense, GA as% of mean = Genetic advance as percentage of mean.

Conclusion

The study revealed substantial genetic variability among the rice genotypes. High heritability with high genetic advance for panicle length, 1000-seed weight, paddy L/B ratio, kernel L/B ratio, gel consistency and alkali spreading value indicated their suitability for selection. The genotypes R2875-KH-23-LST-C46-37-1, R2874-KH-23-LST-C44-50-1, R2879-KH-23-LST-C50-40-1, R2888-KH-23-LST-C59-63-1 and R2884-KH-23-LST-C55-22-1 were identified as promising high-yielding genotypes for further evaluation and use in rice breeding programmes.

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