Plant Archives Vol. 26, Supplement 1, 2026 pp. 288-292 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.037

GENETIC VARIABILITY FOR IMPORTANT AGRONOMIC TRAITS AMONG ADVANCED BREEDING LINES OF RICE (*ORYZA SATIVA* L.)

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(Date of Receiving : 23-08-2025; Date of Acceptance : 28-10-2025)

ABSTRACT

Using twelve yield and related traits as a basis, the study sought to evaluate the genetic variability among sixteen rice advanced breeding lines. Two replications of the experiment were conducted using a Randomized Complete Block Design. The research was performed in the College of Agriculture, Navile, Shivamogga, which is part of the Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences (KSNUAHS), Shivamogga, during the Kharif season of 2024. The experimental material included four standard checks (Tunga, KHP-13, KPR-1, and Sahyadri Jalamukti) from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, as well as six lines from the cross Tunga × KHP-13 and ten lines from the cross KPR-1 × KHP-13. R software was utilized to statistically evaluate the recorded data for each attribute. Across all assessed attributes, the analysis of variance showed a substantial difference between the advanced breeding lines. In terms of traits such as the number of tillers, productive tillers per plant, grain count, filled grain count per panicle, and length-to-breadth ratio, moderate values were observed for both the genotypic and phenotypic coefficients of variation. High heritability and a significant genetic advance as a percentage of the mean were also recorded.The aforementioned results highlight how crucial it is to prioritize important attributes in breeding methods aimed at increasing yield. By highlighting these characteristics, rice yield potential might be greatly increased and increased food security could be supported.

***Keywords* :** GAM, heritability, rice.

Introduction

Rice (*Oryza sativa* L.) is a highly important cereal crop with 2n = 24 chromosomes and is widely cultivated worldwide. It is a member of the genus Oryza, within the tribe *Oryzeae* and the family Poaceae. The genus comprises 24 species, of which only two-*Oryza sativa* and *Oryza glaberrima* are cultivated, while the remaining 22 exist in the wildform. As a primary food source, rice sustains over half of the global population and represents a key economic resource in numerous Asian nations. Grown in more than 100 countries over approximately 154 million hectares of land, Asia alone accounts for 90 *per cent* of the total rice production worldwide (Bista, 2018).

Assessing genetic variability is a key component of any breeding programme. Variability among traits is crucial for identifying optimal genetic material needed to develop high-yielding varieties, which is a core objective in plant breeding (Tiwari *et al.*, 2019). A comprehensive understanding of genetic parameters, such as PCV, GCV, broad-sense heritability, and GAM is vital for effectively improving the genetic potential of a genotype (Kishore *et al.*, 2015). These parameters are fundamental for achieving successful genetic improvement. Heritability analyses combined with genetic advance typically perform better at predicting the outcome of selection than heritability estimates alone (Paul *et al.*, 2006).

Material and Methods

During the Kharif season of 2024, the study had been carried out at the Zonal Agricultural and Horticultural Research Station (ZAHRS), Navile, Shivamogga with geographical coordinates of 13.9722470, 75.5772481. A Randomized Complete Block Design with two replications was used to analyze six F6 lines from the cross Tunga × KHP-13, ten F_6 lines from KPR-1 × KHP-13, and four checks (Tunga, KHP-13, KPR-1, and Sahyadri Jalamukthi). Single seedlings per hill, spaced 20 × 15 cm apart, were manually transplanted from 21-day-old seedlings.

The data were subjected to analysis of variance (ANOVA) following RCBD to test the significance of differences among genotypes. The 'F' test was used to assess statistical significance at 5% and 1% probability levels. Further statistical analyses included the estimation of genetic variability parameters such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability (h^2), and genetic advance as per cent mean (GAM).

The genotypic and phenotypic coefficients of variation were estimated following the procedures outlined by Lush (1940) and Chaudhary and Prasad (1968).

- Genotypic co-efficient of variation (GCV): $\sigma_g / \bar{x} \times 100$
- Phenotypic co-efficient of variation (PCV): $\sigma_p / \bar{x} \times 100$

Where,

σ_p = phenotypic standard deviation

σ_g = genotypic standard deviation

$\bar{x}$ = mean

Three kinds of variability were identified using Shivasubramanian and Menon's (1973) classification: low (less than ten percent), moderate (10% to 20%), and high (>twenty percent).

Heritability in broad sense ($h^2_{(bs)}$) (Lush ,1945) was calculated by the formula:

$$h^2_{(bs)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$h^2_{(bs)}$ = heritability (Broad sense) expressed in *per cent*

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

while heritability can be classified as low (less than 30%), medium (30 to 60%), and high (greater than 60%), as proposed by Robinson *et al.* (1949).

Falconer and Mackay (1996), proposed the formula for estimating genetic advance as a percentage of the mean (GAM) as follows:

$$\text{GAM}(\%) = \frac{\text{Genetic advance}(\text{GA})}{\text{Grand mean}(\text{GM})} \times 100$$

According to the criteria proposed by Johnson *et al.* (1955) GAM values have been defined into three categories: low (less than 10 percent), medium (10 to 20%), and high (greater than 20 percent)

Statistical Analysis

The mean of observations recorded from five randomly selected plants was used for statistical analysis. Variability parameters were computed using R software.

Results and Discussion

ANOVA (Analysis of variance)

The analysis of variance revealed highly significant differences between the genotypes for the following traits: spikelet fertility (%), test weight (g), grain length breadth ratio, plant height (cm), number of tillers and number of productive tillers per plant, panicle length (cm), number of grains count per panicle, number of filled grains count per panicle, days to 50% flowering, and days to maturity. Such fluctuation indicates substantial genetic heterogeneity among the advanced breeding lines and confirms the genotype selection used in this study. Similar results have been noted by Singh *et al.* (2025) and Kumar *et al.* (2025). The analysis of variance for each of the twelve qualities is shown in Table 1.

Phenotypic coefficient of variance (PCV) and Genotypic coefficient of variance (GCV)

Table 2 displays the mean values and ranges for each assessed attribute. The GCV and PCV for all traits are shown in Table 2. Low levels of variability were observed in the following variables: plant height (5.29%;6.79%), days to 50% flowering (5.28%;5.36%), pikelet fertility (1.96%;2.95%), grain yield per plant (8.65%;11.15%), and panicle length (7.25%;8.94%). In a study at ICAR-IIRR, Hyderabad, Reddy *et al.* (2023) observed decreased GCV and PCV for parameters like plant height, panicle length, days to 50% flowering, and days to maturity. Furthermore, features including panicle length and days to 50% flowering were reported to have decreased GCV and PCV by Reddy *et al.* (2024).

Moderate levels of variability were reflected by the moderate GCV and PCV values observed for traits such as grain length-to-breadth ratio (11.96%; 12.72%), test weight (10.54%; 11.73%), number of tillers per plant (14.46%; 18.01%), number of productive tillers per plant (14.86%; 19.01%), number of grains per panicle (12.76%; 14.90%), and number of filled grains per panicle (13.78%; 16.14%). Comparable patterns for test weight, grain count per panicle, and filled grain count per panicle were also reported by Kerketta *et al.* (2024). In all traits, phenotypic variance exceeded genotypic variance, indicating the influence of environmental factors on trait expression.

Heritability and Genetic Advance as per cent of mean (GAM).

The percentage of genetic variation that is carried down from one generation to the next is known as heritability, according to Lush (1949). In order to find superior genotypes based on their phenotypic appearance, heritability estimation is essential. The efficiency of selection is increased when qualities primarily controlled by additive gene action are chosen using high GAM combined with high broad-sense heritability (Johnson *et al.*, 1955).

The possible improvement in a trait anticipated by selection is shown by GAM. GAM values have been defined into three categories: low (less than 10 percent), medium (10 to 20%), and high (greater than 20 percent), Table 2 displays the heritability and GAM estimates for every trait under study.

According to Lush (1949), broad-sense heritability was computed. Every trait evaluated in the study had substantial heritability, with the exception of spikelet fertility. The factors that were most heritable were the following: days to maturity (98.10%), days to 50% flowering (96.86%), test weight (80.84%), grain length breadth ratio (88.52%), number of grains per panicle (73.37%), number of filled grains per panicle (73.37%), panicle length (65.72%), number of tillers per plant (64.41%), number of productive tillers per plant (61.11%), plant height (60.76%) and grain yield per plant (60.21%). Spikelet fertility has a rather low heritability (44.28%). These findings are in line with those of Kerketta *et al.* (2024), Chattar *et al.* (2024), and Maruti *et al.* (2025) for the following parameters: test weight, days to 50% flowering, days to maturity, plant height, panicle length, number of tillers per plant, number of productive tillers, number of grains count per panicle, number of filler grains count per panicle and grain yield per plant.

Table 1: Analysis of variance for yield and yield contributing traits in advanced breeding lines of rice

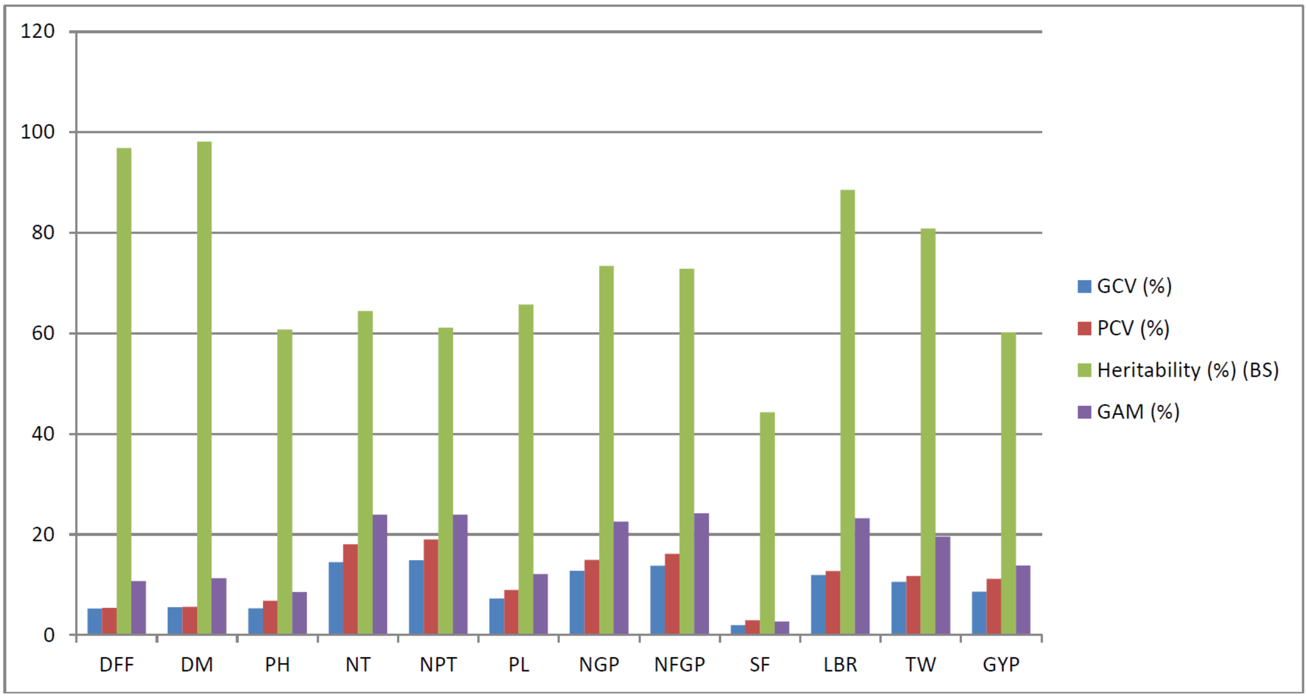
Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)
Mean sum of squares							
Replication	1	3.03	0.22	30.80	0.62	0.32	0.55
Genotype	19	80.87**	133.50**	166.85**	14.52**	14.39**	10.45**
Error	19	1.29	1.28	40.72	3.14	3.47	2.16
CV (%)		0.95	0.77	4.25	10.75	11.86	5.24

Source of variation	Degrees of freedom	Number of grains count per panicle	Number of filled grains count per panicle	Spikelet fertility (%)	Grain Length breadth ratio	Test weight (g)	Grain yield per plant (g)
Mean sum of squares							
Replication	1	101.12	80.09	0.63	0.09	2.74	6.56
Genotype	19	1273.01**	1295.01**	10.85*	0.37**	14.67**	52.10**
Error	19	195.50	203.56	4.19	0.02	1.55	12.94
CV (%)		7.69	8.41	2.20	4.31	5.13	7.03

** - Significant at 1% level *- Significant at 5% level

Table 2: Genetic variability for yield and yield contributing traits in advanced breeding lines of rice

SL NO	**Characters**	**Mean**	**Range**		**GCV (%)**	**PCV (%)**	**Heritability (%) (bs)**	**GAM (%)**
			Min	**Max**				
1	Days to 50 *per cent* flowering	119.53	102.00	132.00	5.28	5.36	96.86	10.70
2	Days to maturity	146.98	132.00	161.50	5.53	5.59	98.10	11.29
3	Plant height (cm)	150.12	128.15	163.90	5.29	6.79	60.76	8.49
4	Number of tillers per plant	16.50	11.70	20.10	14.46	18.01	64.41	23.90
5	Number of productive tillers per plant	15.72	11.30	19.50	14.86	19.01	61.11	23.93
6	Panicle length	28.07	23.35	32.45	7.25	8.94	65.72	12.11
7	Number of grains count per panicle	181.87	151.20	230.40	12.76	14.90	73.37	22.52
8	Number of filled grains count per panicle	169.57	138.60	219.90	13.78	16.14	72.83	24.22
9	Spikelet fertility	93.12	86.78	95.48	1.96	2.95	44.28	2.69
10	Grain Length breadth ratio	3.48	2.96	4.27	11.96	12.72	88.52	23.19
11	Test weight	24.28	19.82	29.43	10.54	11.73	80.84	19.53
12	Grain yield per plant	51.14	40.50	60.50	8.65	11.15	60.21	13.83



Where, DFF- Days to 50 *per cent* flowering, DM- Days to maturity, PH- Plant height (cm), NT- Number of tillers per plant, NPT- Number of productive tillers per plant, PL- Panicle length, NGP- Number of grains per panicle, NFGP- Number of filled grains per panicle, SF- Spikelet fertility (%), LBR- Length to breadth ratio, TW- Test weight (g), GYP - Grain yield per plant (g)

Fig. 1: Genetic variability for yield and yield contributing traits in advanced breeding lines of rice

The approach developed by Johnson *et al.* (1955) was used to calculate genetic advance. The number of productive tillers per plant, the number of tillers per plant, the number of filled grains per panicle, the grain length-to-breadth ratio, and the number of grains count per panicle all displayed high values. While days to 50% blooming, days to maturity, panicle length, test weight, grain yield per plant, and grain yield per hectare displayed moderate gam, plant height and spikelet fertility displayed low gam values. These findings are in line with those of Chattar *et al.* (2024) and Maruti *et al.* (2025) about the number of days till 50% flowering. The results were in line with those of Chattar *et al.* (2024) for the characteristics of spikelet fertility, number of grains counted per panicle and number of filled grains counted per panicle.

Conclusion

The study, which aimed to ascertain the level of genetic diversity, discovered significant variance among the advanced breeding lines for all yield and yield-related parameters examined. The genetic variability analysis showed low to moderate phenotypic and genotypic coefficients of variation, high heritability, and significant genetic advancement as a percentage of the mean for most traits, including the number of tillers per plant, the number of productive tillers per plant, the number of grains count per panicle, the number of filled grains count per panicle, and the grain length breadth ratio. Combining high heritability and genetic progress suggests that additive gene action plays a major role in the expression of these traits, indicating that selection based on these characteristics.

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