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GENETIC VARIABILITY STUDIES FOR YIELD AND YIELD ATTRIBUTING TRAITS IN RICE (*Oryza sativa* L.) GENOTYPES

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ABSTRACT

Genetic variability plays a pivotal role in crop improvement by providing the essential foundation for effective selection and the development of superior cultivars. The present study was undertaken during Summer 2025 at the Hill Millet Research Station, Navsari Agricultural University, Waghai, South Gujarat, to evaluate the extent of genetic variability among thirty rice (*Oryza sativa* L.) genotypes. The experiment was conducted in a Randomized Complete Block Design with three replications and twelve yield and grain quality traits were assessed. The analysis of variance revealed highly significant differences among the genotypes for all the characters, confirming the existence of considerable genetic variation in the experimental material. For all the traits, the phenotypic coefficient of variation was slightly higher than the corresponding genotypic coefficient of variation, indicating that environmental influence on trait expression was comparatively low. High variability was observed for grains per panicle, whereas productive tillers per plant, 100 grain weight, grain yield per plant, straw yield per plant, kernel breadth and kernel L/B ratio exhibited moderate levels of variation. High heritability coupled with high genetic advance as per cent of mean for these traits suggested the predominance of additive gene action and indicated that substantial genetic improvement could be achieved through direct phenotypic selection. The findings highlight the availability of adequate genetic variability among the evaluated rice genotypes and emphasize their potential for use in future breeding programmes aimed at developing high-yielding rice cultivars.

Key words : Rice, Genetic variability, GCV, PCV, Heritability and Genetic advance.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and serves as the staple food for more than half of the global population (Bellon *et al.*, 1998). It belongs to the family *Poaceae*, is predominantly a self-pollinated crop with a chromosome number of $2n = 24$ and is believed to have originated in Southeast Asia. More than 90 per cent of the world's rice is cultivated and consumed in Asia, where nearly 60 per cent of the global population depends on rice as a primary source of dietary energy.

India occupies a prominent position in global rice production and export. During 2025-26, the country

recorded an all-time high rice production of 154.024 million tonnes, surpassing China to become the world's leading rice-producing nation (Anonymous, 2026).

The success of any crop improvement programme largely depends on the availability and effective utilization of genetic diversity. Genetic diversity provides the basic raw material for selection and hybridization, enabling breeders to identify superior genotypes possessing desirable agronomic, physiological and quality traits. A broad genetic base enhances the probability of obtaining superior recombinants with improved yield potential, earliness, adaptability and resilience to biotic and abiotic stresses.

The magnitude of genetic variability present in breeding materials largely determines the efficiency of selection and the potential genetic gain achievable through breeding. Therefore, assessment of variability for grain yield and its component characters is an essential step in formulating an effective breeding strategy. Genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance provide valuable information regarding the nature and magnitude of variability present in a population (Singh *et al.*, 2011). Since the present investigation emphasizes the identification of early-maturing rice genotypes, particular attention is given to days to 50 per cent flowering and days to maturity, which determine crop duration and adaptation to hill ecosystems. Simultaneous consideration of heritability and genetic advance provides a more reliable estimate of the expected response to selection than heritability alone (Konate *et al.*, 2016). Furthermore, variability studies involving flowering and maturity traits facilitate the identification of promising early-maturing genotypes suitable for future breeding programmes (Maruti and Singh, 2025).

Materials and Methods

The present study was carried out during Summer 2025 at the Hill Millet Research Station, Navsari Agricultural University, Waghai, Gujarat, to evaluate the extent of genetic variability among rice (*Oryza sativa* L.) genotypes. A total of thirty genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was grown in plots measuring 3.30×2.80 m with a planting geometry of 20×15 cm. Observations were recorded from five randomly selected competitive plants in each replication for twelve quantitative and grain quality traits, namely days to 50 per cent flowering, days to maturity, plant height, panicle length, productive tillers per plant, grains per panicle, 100 grain weight, grain yield per plant, straw yield per plant, kernel length, kernel breadth and kernel L/B ratio. The average values of the selected plants across replications were subjected to statistical analysis.

The experimental data were analyzed using analysis of variance (ANOVA) following the procedure described by Panse and Sukhatme (1978) to determine the significance of differences among the genotypes. Estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed according to the method proposed by Burton (1952). The magnitude of variability was categorized as low, medium and high following the classification

suggested by Sivasubramanian and Menon (1973). Broad-sense heritability [h^2_{bs}] was estimated using the method described by Allard (1960) and the estimates were interpreted based on the classification of Johnson *et al.* (1955). Genetic advance (GA) was calculated as outlined by Allard (1960), while genetic advance as per cent of mean (GAM) was estimated according to Johnson *et al.* (1955) to assess the expected improvement through selection.

Results and Discussion

The analysis of variance revealed highly significant differences among the rice genotypes for all the characters studied, indicating the presence of considerable genetic variability (Table 1). Assessment of genetic variability through genotypic and phenotypic coefficients of variation (GCV and PCV) is essential to distinguish the relative contribution of genetic and environmental factors to trait expression, as reported by Akinwale *et al.* (2011). In the present study, the phenotypic coefficient of variation was only marginally higher than the corresponding genotypic coefficient of variation for all the traits, suggesting that environmental influence was comparatively low and that the observed variability was predominantly governed by genetic factors.

Moderate to high estimates of genotypic and phenotypic coefficients of variation were recorded for productive tillers per plant, grains per panicle, 100 grain weight, grain yield per plant, straw yield per plant, kernel breadth and kernel L/B ratio. The present findings are in agreement with those reported by Patel *et al.* (2025) and Tiwari *et al.* (2026) for productive tillers per plant and straw yield per plant, Akshay *et al.* (2022) and Periyasamy *et al.* (2026) for grains per panicle, 100 grain weight and grain yield per plant, Patel *et al.* (2025) and Periyasamy *et al.* (2026) for kernel breadth and kernel L/B ratio. The low value of GCV and PCV was found for days to 50 per cent flowering, days to maturity, plant height, panicle length and kernel length. These traits exhibited less variability, suggesting that selection based on them may not be fruitful. Allam *et al.* (2015) found similar results for days to 50 per cent flowering and days to maturity, Meena *et al.* (2015) and Tiwari *et al.* (2026) for plant height and panicle length, Akshay *et al.* (2022) for kernel length.

Fig. 1 depicts the magnitudes of broad sense heritability (h^2_{bs}) and genetic advance as per cent of mean for different traits. High heritability coupled with high genetic advance as per cent of mean was observed for grains per panicle, 100-grain weight, productive tillers per plant, grain yield per plant, straw yield per plant, kernel

Table 1 : Analysis of variance (mean sum of squares) for various characters in rice.

Source	df	DF	DM	PH	PL	PT	GPP
Replications	2	4.74	18.34	8.81	7.70	1.25	3.68
Genotypes	29	171.14**	163.80**	239.51**	8.68**	5.94**	2695.72**
Error	58	5.97	6.40	25.52	2.62	0.43	12.49
Source	df	HGW	GY	SY	KL	KB	LBR
Replications	2	0.011	7.91	16.55	0.06	0.009	0.02
Genotypes	29	0.50**	33.77**	76.32**	0.99**	0.17**	0.46**
Error	58	0.0036	3.45	9.98	0.02	0.0034	0.01

*Significant at 5% level, ** Significant at 1% level

DF = Days to 50 per cent flowering

DM = Days to maturity

PH = Plant height (cm)

PL = Panicle length (cm)

PT = Productive tillers per plant

GPP = Grains per panicle

HGW = 100 grain weight (g)

GY = Grain yield per plant (g)

SY = Straw yield per plant (g)

KL = Kernel length (mm)

KB = Kernel breadth (mm)

LBR = L/B ratio

Table 2 : Descriptive statistics and variability parameters for various characters in rice.

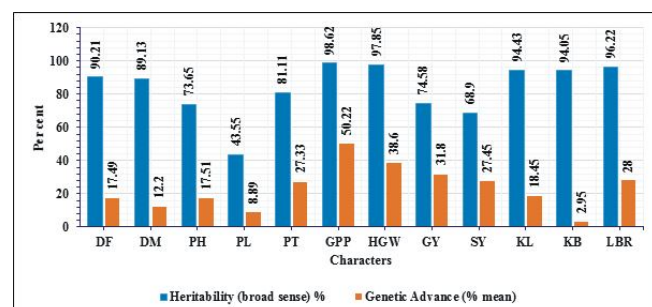
Traits	Mean	Range		GCV%	PCV%	h^2_{bs} (%)	GA as % of mean
		MIN.	MAX.				
DF	82.99	68.33	93.67	8.94	9.41	90.21	17.49
DM	115.46	103.67	129.67	6.27	6.54	89.13	12.20
PH	85.26	70.00	105.80	9.11	11.54	73.65	17.51
PL	21.73	18.40	24.80	6.54	9.91	43.55	8.89
PT	9.20	6.60	12.00	14.73	16.36	81.11	27.33
GPP	121.82	87.60	224.40	24.55	24.72	98.62	50.22
HGW	2.15	1.46	3.13	18.94	19.15	97.85	38.60
GY	17.79	13.06	26.66	17.87	20.70	74.58	31.80
SY	29.30	21.58	38.27	16.05	19.34	68.90	27.45
KL	6.18	5.01	6.87	9.22	9.48	94.43	18.45
KB	2.22	1.63	2.66	10.49	10.81	94.05	20.95
LBR	2.81	2.05	3.57	13.86	14.13	96.22	28.00

Where, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation

*Classes of Heritability (%): High >60%, Moderate 30-60%, Low <30%

*Classes of GA as % of mean at 5%: high >20%, Moderate 10-20%, Low <10%

*Classes of PCV (%), and GCV (%): high >20, Moderate 10-20, Low

**Fig. 1 :** Magnitudes of broad sense heritability [h^2_{bs}] and genetic advance as per cent of mean for different traits.

breadth and kernel L/B ratio, suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection. Similar findings were reported by Tiwari *et al.* (2026), Katkani

et al. (2023) and Pavani *et al.* (2024). High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50 per cent flowering, days to maturity, plant height and kernel length, indicating the involvement of both additive and non-additive gene effects, as also reported by Maurya *et al.* (2022), Mishu *et al.* (2016) and Kumar *et al.* (2024). In contrast, panicle length exhibited moderate heritability coupled with low genetic advance as per cent of mean, indicating the predominance of non-additive gene action and comparatively greater environmental influence, making direct selection less effective.

Conclusion

The evaluation of thirty rice genotypes revealed significant differences for all twelve traits, demonstrating

the existence of substantial genetic variability within the experimental material. Moderate to high estimates of genotypic and phenotypic coefficients of variation for plant height, productive tillers per plant, grains per panicle, 100 grain weight, grain yield per plant, straw yield per plant, kernel breadth and kernel L/B ratio indicated considerable scope for genetic improvement of these characters. In addition, the combination of high heritability and high genetic advance as per cent of mean for grains per panicle, 100 grain weight, productive tillers per plant, grain yield per plant, straw yield per plant, kernel breadth and kernel L/B ratio suggested that additive gene action predominantly governs these traits, making them suitable targets for improvement through direct phenotypic selection.

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