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## GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN RICE GENOTYPES

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### ABSTRACT

The presence and critical assessment of genetic variability are fundamental prerequisites for initiating an effective crop improvement programme and for identifying appropriate selection strategies. Accordingly, a study was conducted during *Rabi* 2018–19 to assess the extent of genetic variability among forty-eight rice genotypes. Analysis of variance revealed highly significant differences for all sixteen characters, confirming the existence of substantial genetic variability among the genotypes. For most traits, phenotypic coefficient of variation (PCV) values were marginally higher than the corresponding genotypic coefficient of variation (GCV), suggesting minimal environmental influence on trait expression and indicating good prospects for genetic improvement through direct selection. Moderate PCV and GCV estimates were observed for number of productive tillers per plant, test weight and kernel length-to-breadth ratio, implying a relatively greater environmental influence on these traits. High estimates of heritability coupled with high genetic advance were recorded for panicle weight, number of grains per panicle, pollen fertility, grain yield per plant and test weight, indicating the predominance of additive gene action and suggesting that selection for these traits would be effective for genetic improvement.

**Keywords** : Rice, genetic variability, heritability, genetic advance, PCV, GCV, additive gene action, quantitative traits, direct selection.

### Introduction

Rice (*Oryza sativa* L.) is the world's most important staple food crop, providing primary caloric intake to more than half of the global population and forming the cornerstone of food security in many developing countries (FAO, 2023). It is cultivated across diverse agro-ecological regions in more than 100 countries. Global rice production reached about 533.8 million tonnes (milled basis) during 2024–25, reflecting steady gains from genetic improvement, expansion of irrigated area and improved crop management practices (USDA, 2024).

India occupies a pivotal position in the global rice economy, contributing nearly 28-30% of total world production (FAO, 2023). During 2024-25, the country produced approximately 149 million tonnes of rice

from an area of 51.4 million hectares, with an average productivity of 2,899 kg ha<sup>-1</sup> (DES, 2024). Rice plays a vital role in India's agricultural economy by supporting rural livelihoods, ensuring food security through public distribution systems and contributing to export earnings.

In recent years, Telangana has emerged as India's leading rice-producing state, registering a remarkable increase in both area and productivity. The state recorded an estimated production of 170.94 lakh tonnes during 2024–25, accounting for nearly 12% of national rice output (Government of Telangana, 2025). Rice is cultivated over about 47 lakh hectares, with productivity levels ranging from 4.0 to 6.0 t ha<sup>-1</sup>, which is substantially higher than the national average and second only to Punjab. The impressive rise in

productivity can be attributed to the expansion of assured irrigation through major projects, rejuvenation of traditional tanks under Mission Kakatiya, adoption of high-yielding and short-duration varieties, increased mechanization, effective extension services and favourable procurement policies.

Despite these achievements, sustaining and further enhancing rice productivity under increasing climatic variability requires continuous genetic improvement. In this context, the study of genetic variability, heritability, and genetic advance is fundamental to crop improvement programs. Genetic variability provides the raw material for selection, heritability estimates indicate the proportion of phenotypic variation attributable to genetic causes and genetic advance predicts the expected response to selection (Falconer and Mackay, 1996). Together, these parameters help breeders identify traits governed predominantly by additive gene action and select superior genotypes effectively. Therefore, assessment of genetic variability, heritability and genetic advance for grain yield and its component traits is essential for identifying superior genotypes and facilitating the development of high-yielding, stable and climate-resilient rice varieties under intensive irrigated production systems.

### Materials and Methods

The material for this study comprised 32 hybrids, 12 parents (8 restorers and 4 CMS lines) and four checks, which were evaluated for yield and component traits during *Rabi* 2018-19 in Randomized Block Design (RBD) with three replications at Rice Research Institute, ARI, Rajendranagar, Hyderabad. Thirty days old seedlings were transplanted by adopting a spacing of 15 cm between plants and 20 cm between rows. Recommended agronomic and plant protection measures for raising a healthy nursery and main crop were taken up during the experiment.

Observations were recorded on five randomly selected plants in each genotype in each replication for sixteen traits *viz.*, days to 50% percent flowering, plant height(cm), number of productive tillers per plant, panicle length(cm), panicle weight (g), number of grains per panicle, pollen fertility, spikelet fertility, Test weight (g), grain yield per plant yield (g), kernel length, kernel breadth, kernel L/B ratio, hulling percent, milling percent and head rice recovery percent. The mean of five plants for each metric trait was considered for statistical analysis using WINDOSTAT software version 9.2. The analysis of variance (ANOVA) was done on the basis of model described by Cochran and Cox (1950) for randomized

complete block design. The genotypic and phenotype variances were calculated as per the formulae proposed by Burton and Devane, 1953. Heritability in broad sense ( $h^2$ ) was calculated by the formula given by Lush, 1949 as suggested by Johnson *et al.* (1955). From the heritability estimates, the genetic advance (GA) was calculated by the formula given by Johnson *et al.* (1955).

### Results and Discussion

Analysis of variance revealed highly significant differences among the 48 genotypes for all the 16 characters (Table 1), indicating the presence of adequate amount of genetic variability among the genotypes assessed.

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for forty-eight genotypes and the details are furnished in table 2. The variability parameters are depicted graphically in Fig 1 and Fig 2.

The present investigation revealed that the estimates of PCV were slightly higher than GCV for all the characters studied indicating less influence of environmental factors on the expression of traits. As the characters were less influenced by the environment, the traits can be used for selection.

Moderate phenotypic and genotypic coefficients of variation were recorded for number of productive tillers per plant, test weight and kernel L/B ratio, indicating the presence of adequate genetic variability with moderate environmental influence. The close association between PCV and GCV suggests limited environmental effects and the involvement of both additive and non-additive gene action. These traits offer reasonable scope for improvement through selection in advanced generations, and the adoption of breeding approaches such as recurrent selection and multi-environment testing may enhance genetic gains. These findings are in agreement with Naga Durga Rao *et al.* (2020), Chacko *et al.* (2023), Dheeraj *et al.* (2023) and Vallala *et al.* (2024).

High estimates of GCV and PCV were observed for pollen fertility, number of grains per panicle and grain yield per plant. Similar findings were reported for pollen fertility by Sonu Kumar *et al.*, (2018), Aswin *et al.*, (2021) and Saha *et al.* (2024), Babu & Thouseem (2024), Margam Bharath Kumar *et al.* (2024), for number of grains per panicle, Sravani *et al.* (2022), Prasanna *et al.* (2022), Sheeba *et al.* (2023), Margam BharathKumar *et al.* (2024), Boda Srividhya *et al.* (2025) and Hyndhavi *et al.* (2025). For grain yield per plant, Khaire *et al.* (2022), Alahari *et al.* (2023), Singh *et al.* (2024) Maruti *et al.* (2025) and Hyndhavi *et al.*

(2025). In similar to our findings, the above reported observations for high GCV and PCV estimates in different set of genotypes including early segregating and advanced generation for important yield component traits, does indicate the possibility for genetic improvement through direct selection for these traits.

Low PCV and GCV were observed for days to 50% flowering, plant height, panicle length, spikelet fertility, kernel length, kernel breadth, hulling, milling and head rice recovery percentage, indicating limited genetic variability among the genotypes for these traits. The narrow difference between PCV and GCV suggests negligible environmental influence on trait expression and reflects a high level of genetic fixation due to prolonged selection in rice improvement programmes (Suresh *et al.*, 2019; Jitendra Kumar *et al.*, 2020; Rukmini Devi *et al.*, 2021). These traits generally exhibited low to moderate genetic advance despite moderate to high heritability, implying the predominance of non-additive gene action and reduced effectiveness of direct phenotypic selection (Sravani *et al.* (2022), Prathiksha *et al.* (2022), Vinay *et al.* (2023). The findings are in conformity with the reports of Patel *et al.* (2025) and Prateek Kerketta *et al.* (2024). Therefore, improvement of these traits may necessitate the creation of additional variability through hybridization, mutation breeding or the application of molecular and genomic breeding approaches to achieve meaningful genetic gains.

Heritability measures the contribution of genetic variability to the phenotypic variability and is a good index of the transmission of characters from parents to their offspring. The estimates of heritability can be utilized for prediction of genetic gain, which indicates the genetic improvement that would result from selection of best individuals. Genetic advance (GA) is the measure of genetic gain under selection. Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

High heritability coupled with high genetic advance was recorded for panicle weight, number of grains per panicle, pollen fertility, grain yield per plant

and test weight, demonstrating the predominance of additive gene action and indicating greater potential for improvement through simple phenotypic selection. These results are in agreement with the findings of Hyndhavi *et al.* (2025), Maruti *et al.* (2025), Shirisha *et al.* (2025), Soundharya *et al.* (2024) and Sravani *et al.* (2022). The high heritability along with substantial genetic advance suggests low environmental influence on the expression of these traits, thereby enabling effective selection. Grain yield, being a complex trait, is governed by the cumulative and interactive effects of various yield-contributing components.

The present investigation revealed that there is adequate genetic variability present in the material studied. Among all the characters, panicle weight, number of grains per panicle, pollen fertility, grain yield per plant and test weight recorded high heritability as well as high genetic advance, indicating the presence of considerable variation and additive gene effects. Hence, improvement of these characters could be effective through phenotypic selection.

### Conclusion

The study revealed substantial genetic variability among the rice genotypes, indicating wide scope for genetic improvement through selection. The narrow differences between phenotypic and genotypic coefficients of variation for several traits suggested minimal environmental influence and strong genetic control. High heritability estimates coupled with high genetic advance as a percentage of the mean for important yield related traits indicated the predominance of additive gene action, making these traits amenable to effective selection in early generations. Traits showing high heritability with low genetic advance suggested the involvement of non-additive gene effects, emphasizing the need for alternative breeding strategies. These findings provide valuable genetic insights for sustaining yield improvement under intensive irrigated ecosystems. Overall, the integration of variability, heritability and genetic advance analyses offers a reliable framework for identifying superior genotypes and refining breeding strategies aimed at developing high-yielding, stable and climate-resilient rice varieties.

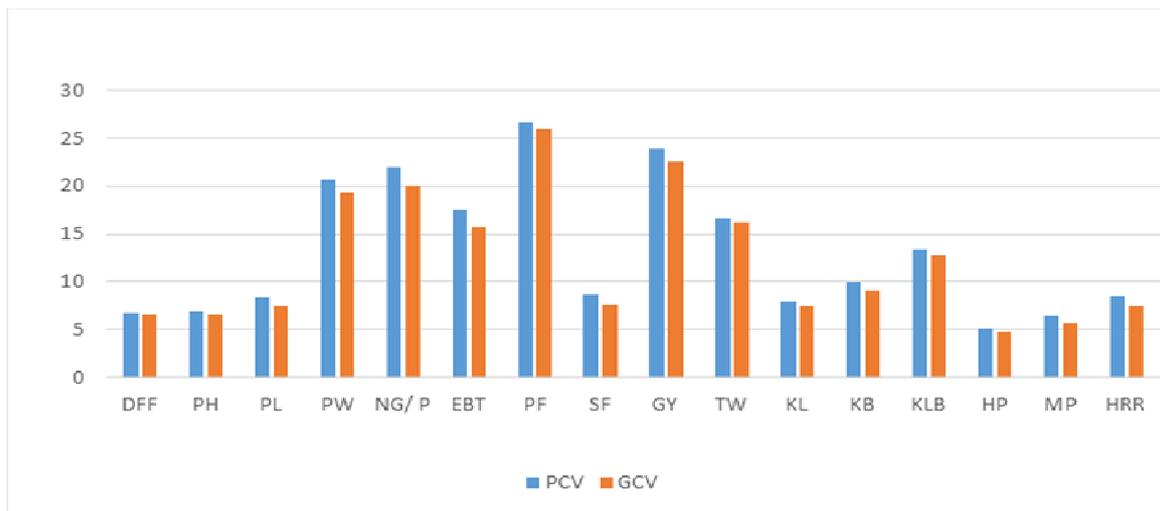
**Table 1:** Analysis of variance for yield and its component traits among rice genotypes

Characters	DF	DFF	PH	PL	PW	NG/P	EBT	PF	SF	GY	TW	KL	KB	KLB	HP	MP	HRR
Replications	1	0.51	8.64	0.02	0.06	176.04	2.87	2.04	24.83	23.44	0.42	0.04	0.01	0.02	1.23	5.42	18.2
Treatments	47	91.47**	95.13**	7.59**	1.77**	4047.67**	13.09**	805.44**	91.59**	169.73**	25.30**	0.50**	0.08**	0.31**	29.87**	34.96**	43.098**
Error	47	2.34	4.211	0.87	0.12	358.57	1.34	21.06	12.83	9.17	0.66	0.03	0.00	0.01	2.34	4.46	5.32

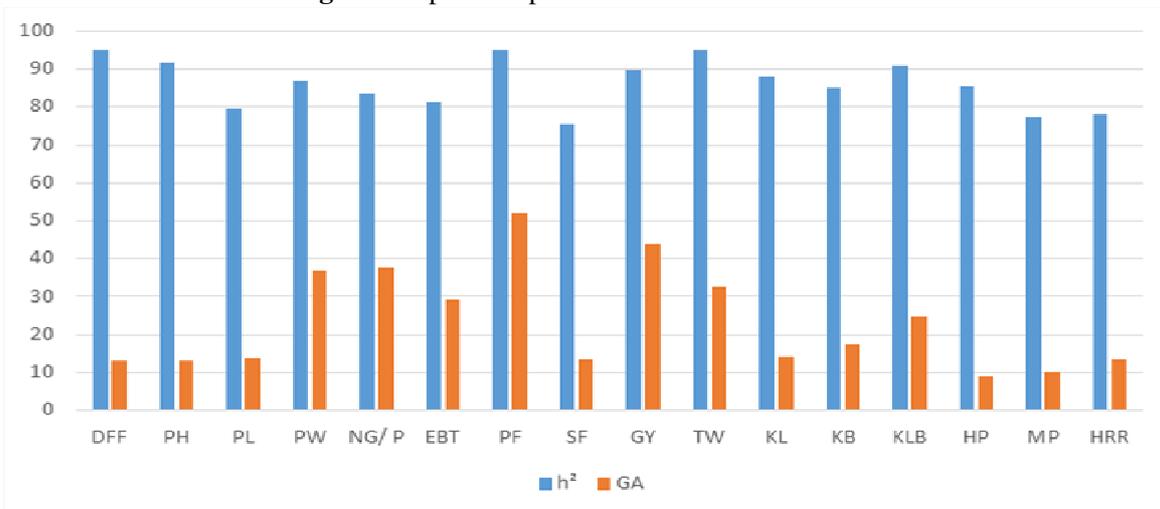
DF= Degrees of freedom, DFF=Days to 50% flowering, PH=Plant height, PL=Panicle length, PW=Panicle weight NG/P= No. of grains per panicle, EBT= No. of effective bearing tillers per plant, PF=Pollen fertility, SF= Spikelet fertility, GYP=Grain yield/ plant, TW= Test weight  
KL= Kernel length, KB= Kernel breadth, KLB= Kernel length breadth ratio, HP= Hulling %, MP= Milling %, HRR=Head rice recovery%

**Table 2:** Estimation of genetic parameters for yield and quality traits in rice genotypes

Characters	General Mean	Range	PCV	GCV	h <sup>2</sup> (Broad Sense)	Genetic advance as percent of mean (at 5%)
Days to 50% flowering	101	87-113	6.75	6.57	95.00	13.21
Plant height (cm)	101.98	84.9-118.7	6.91	6.61	91.50	13.02
Panicle length (cm)	24.57	20.80-28.40	8.37	7.46	79.40	13.69
Panicle weight (g)	4.72	3.39-6.95	20.60	19.22	87.00	36.94
No. of grains per panicle	213.70	99-334	21.96	20.09	83.70	37.88
No. of productive tillers per plant	15.35	8-23	17.50	15.79	81.30	29.33
Pollen fertility	76.35	30-99.50	26.62	25.93	94.90	52.05
Spikelet fertility	83.00	61.95-93.90	8.70	7.56	75.40	13.52
Grain yield/ plant(g)	39.67	23.75-62.89	23.83	22.58	89.70	44.07
Test weight (g)	21.60	12.66-28.82	16.68	16.24	94.90	32.60
Kernel length (mm)	6.55	5.54-7.93	7.90	7.41	88.00	14.32
Kernel breadth (mm)	2.17	1.76-2.67	9.92	9.15	85.20	17.40
Kernel length breadth ratio (mm)	3.04	2.35-4.49	13.36	12.74	90.80	25.01
Hulling %	77.43	68.15-84.90	5.18	4.79	85.50	9.12
Milling %	68.68	54.60-79.20	6.46	5.68	77.40	10.30
Head rice recovery%	58.19	44.05-66.10	8.45	7.46	78.00	13.58



**Fig. 1 :** Graphical representation of PCV and GCV



**Fig. 2 :** Graphical representation of heritability (broad sense) and genetic advance as per cent of mean (5%)

### 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.

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### Competing Interest:

The authors have declared that no competing interest exists.

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