Genetic variability, heritability and genetic advance for yield and yield related traits in rice (*Oryza Sativa* L.)

ABSTRACT

Aims:
To evaluate genetic variability, heritability, and genetic advance for key agronomic traits in rice to identify traits with high potential for selection and improvement in breeding programs.
Experimental Design:
The experiment was conducted in a randomized block design (RBD) with three replications.
Place and Duration of Study:
Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad, during the *kharif* 2022 season.
Methodology:
Eighteen Advanced Varietal Trial (AVT) entries were evaluated with a spacing of 20 cm × 15 cm. Data were recorded from five randomly selected plants per entry in each replication for agronomic and yield-related traits: days to 50% flowering (DFF), plant height (PH), panicle length, number of panicles per square meter, filled grains per panicle, 1000-grain weight, and grain yield per hectare (GY/ha). Analysis of variance (ANOVA) and genetic parameters, including environmental coefficient of variation (ECV), genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (h^2), and genetic advance as a percentage of the mean (GAM), were calculated using Windostat Version 9.1.
Results:
The ECV was low across all traits, indicating minimal environmental influence. GCV was low for DFF (4.957%) and PH (4.789%) but moderate for filled grains per panicle (15.874%) and 1000-grain weight (16.33%). PCV was slightly higher than GCV for most traits, confirming limited environmental effects. Heritability ranged from medium (37.4% for GY/ha) to very high (99.7% for 1000-grain weight). GAM was high for filled grains per panicle (31.96%) and 1000-grain weight (33.586%), indicating strong potential for genetic improvement.
Conclusion:
Traits with high heritability and genetic advance, such as filled grains per panicle and 1000-grain weight, are ideal for selection. These findings will aid in enhancing rice breeding programs through targeted genetic improvement.

Keywords: Rice breeding, Phenotypic variation, Genotypic variation, Yield improvement,

1. INTRODUCTION

Rice (*Oryza sativa* L.) is a fundamentally staple crop, sustaining more than half of the global population and serving as a cornerstone of global food security. India is the largest cultivator of rice, covering 46.5 million hectares, and ranks second in production, with an output of 137.8 million metric tons (MMT) in 2023–2024 (Statista and Directorate of Economics and Statistics, 2023). With the global population expected to reach 9.6 billion by 2050, a 70% increase in cereal food supply will be required to meet demand (Godfray et al., 2014). Despite the advancements of the Green Revolution, rice productivity has remained stagnated due to various biotic and abiotic stresses. Lack of adaptable varieties, stress, climate change, and poor agronomic practices are some of the major limiting factors affecting rice yield (Belayneh & Tekle, 2017). Hence, the developing rice varieties with high yield, high quality and high resistance to stress through conventional breeding system is economically affordable and possible way of crop improvement to increase rice productivity. Beside yield enhancement breeding is primarily done for improving grain quality traits.

Genetic variability is the foundation of plant breeding, enabling the selection of desirable traits and the development of superior cultivars (Allard, 1999). The success of any breeding program depends on the availability of a genetically diverse population that provides breeders with a broad spectrum of traits for selection (Frankham et al., 2002). The Variability in agronomic traits is crucial to improving crop yield, resistance to abiotic and biotic stresses, and adaptability to changing environmental conditions (Govindaraj et al., 2015). Understanding the extent and distribution of genetic variability in a population is, therefore, a prerequisite for effective breeding strategies (Falconer & Mackay, 1996). The Variability in a plant population arises due to differences in the genetic makeup of individuals or environmental fluctuations. A high degree of genetic variation among individuals in the breeding material enhances the efficiency of selection (Sumanth et al., 2017). The Heritability estimates the proportion of phenotypic variation that is genetically inherited, while genetic advance indicates the expected improvement in the mean genotypic value of the selected population compared to the original population. The combined use of heritability and genetic advance is more effective in predicting genetic gains under selection than heritability alone. Genetic variability and heritability studies revealed high phenotypic and genotypic coefficients of variation (PCV and GCV) for traits like grain yield per plant, underscoring significant genetic variability that can be leveraged in breeding programs (Bindu et al., 2024; Reddy et al., 2024). Traits such as plant height and grain yield per plant exhibited high heritability and genetic advance, indicating their potential for improvement through selection (Reddy et al., 2024). Furthermore, genetic diversity analyses among rice genotypes demonstrated substantial variability in traits like plant height, days to maturity and biological yield per plant (Singh et al., 2024).

2. MATERIALS AND METHODS

The experiment was conducted with 18 AVT entries at the Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad. The trial was laid out in a Randomized Block Design (RBD) with a spacing of 20 cm x 15 cm and three replications. Data were recorded from five randomly selected plants per entry across all three replications. Observations were made for key agronomic and yield-related traits, including days to 50% flowering (DFF), plant height (PH), panicle length, number of panicles per square meter, filled grains per panicle, 1000-grain weight (g), and grain yield (kg/ha). The collected data were statistically analyzed to determine the relative performance of the tested entries. Analysis of variance (ANOVA) and genetic parameter estimation were carried out using Windostat Version 9.1, developed by Indostat Services.

Genotypic and phenotypic coefficients of variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer, (1981).

Genotypic coefficient of variation= (Genotypic standard deviation/Mean) ×100

phenotypic coefficient of variation = (Phenotypic standard deviation/Mean) ×100 Categorization of the range of variation was affected as proposed by Sivasubramanian and Madhavamenon (1973).

<10%: low

10-20 %: moderate

>20%: high

Heritability and genetic advance

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

As suggested by Johnson et al. (1955) (h^2) estimates were categorized as:

Low: 0–30%

Medium: 30–60%

High: Above 60%

Genetic advance (Expected)

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$GA=K.h^2(b).\ \sigma p$

Where,

GA=Expected genetic advance

K=Selection differential, the value of which is 2.06 at 5% selection intensity

σp =Phenotypic standard deviation

h^2 (b)=Heritability in broad sense

Genetic advance as per cent of mean=(GA/Grand mean)×100 The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955).

Low: less than 10%

Moderate: 10–20%

High: more than 20%

3. RESULTS AND DISCUSSION

The analysis of variance for seven characters showed highly significant differences among the lines for days to 50% flowering, plant height, panicle length, panicle length, No. of Panicles/m2, filled grains/panicle, 1000 grain weight (gm) and Grain Yield (kg/ha) Table 1. The analysis of mean and range for seven traits presented in Table 2. Days to 50% flowering ranged from 86.67 to 108.00 days, with a mean of 94.48 days. Plant height varied between 103.33 cm and 126.33 cm, with an average of 115.50 cm, while panicle length ranged from 20.67 cm to 28.67 cm, averaging 23.72 cm. The number of panicles per square meter, ranging from 266.00 to 419.33, with a mean of 354.81. Filled grains per panicle ranged from 130.33 to 251.67, with an overall mean of 192.20. The 1000-grain weight varied widely from 11.40 g to 27.37 g, averaging 18.15 g. Grain yield demonstrated a range of 6970.44 to 8867.00 kg/ha, with an overall mean of 7772.23 kg/ha.

Table 1. Analysis of variance for yield and yield attributes in rice

S.NO	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=17)	Error (d.f.=34)
1	Days to 50% flowering	0.241	66.283***	0.476
2	Plant height (cm)	20.722	114.559***	22.781
3	Panicle length (cm)	1.556	11.422***	0.81
4	No. of Panicles/m2	140.796	5691.656***	164.483
5	Filled grains/panicle	168.574	2836.084***	43.594

6	1000 grain weight (gms)	0.15	26.391***	0.028
7	Grain Yield (kg/ha)	22845.69	975521.7**	349446.8

Significance Levels: ***: Highly significant ($p < 0.001$), **: Significant ($p < 0.01$)

The genetic variability estimates such as the phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV), broad sense heritability and genetic advance as percent of means 5% are presented in Table 2.

Days to 50% Flowering (DFF)

ECV (0.73%): The environmental coefficient of variation is very low, indicating that environmental factors have minimal influence on the variability of this trait. GCV (4.957%): The genotypic coefficient of variation is low, suggesting limited genetic diversity for DFF. However, there is potential for improvement through breeding. PCV (5.011%): The phenotypic coefficient of variation is slightly higher than the GCV, but the difference is minimal, implying that environmental factors have a negligible impact compared to genetic factors. h^2 (0.979): The broad-sense heritability is very high (97.9%), indicating that most of the variation in DFF is due to genetic factors, making it highly heritable. Gen. Adv as % of Mean (10.103%): The genetic advance as a percentage of the mean is moderate, indicating that selection for early flowering is moderately effective and can lead to genetic gains.

Plant Height (PH)

ECV (4.132%): The environmental coefficient of variation is low, indicating that environmental factors have a small impact on the variability of this trait. GCV (4.789%): The genotypic coefficient of variation is low, suggesting limited genetic variability for plant height. PCV (6.325%): The phenotypic coefficient of variation is higher than the GCV, indicating some influence of environmental factors. h^2 (0.573): The broad-sense heritability is medium (57.3%), showing that both genetic and environmental factors contribute to the observed variation. Gen. Adv as % of Mean (7.469%): The genetic advance as a percentage of the mean is low, suggesting that selection for plant height may result in slow genetic improvement.

Panicle Length

ECV (3.795%): The environmental coefficient of variation is low, indicating minimal environmental influence on this trait. GCV (7.928%): The genotypic coefficient of variation is low, but higher than DFF and PH, suggesting some genetic variability for panicle length. PCV (8.789%): The phenotypic coefficient of variation is slightly higher than the GCV, suggesting a minor environmental impact. h^2 (0.814): The broad-sense heritability is high (81.4%), showing that most of the variation is genetically determined. Gen. Adv as % of Mean (14.731%): The genetic advance as a percentage of the mean is moderate, indicating that selection for panicle length is likely to result in moderate genetic gains.

Number of Panicles per m^2

ECV (3.615%): The environmental coefficient of variation is low, indicating minimal environmental influence on this trait. GCV (12.097%): The genotypic coefficient of variation is moderate, suggesting considerable genetic variability. PCV (12.626%): The phenotypic coefficient of variation is slightly higher than the GCV, suggesting a small environmental influence. h^2 (0.918): The broad-sense heritability is high (91.8%), indicating that most of the variation is due to genetic factors. Gen. Adv as % of Mean (23.877%): The genetic advance as a percentage of the mean is high, indicating that selection for this trait is likely to result in significant genetic improvement.

Filled Grains per Plant

ECV (3.435%): The environmental coefficient of variation is low, indicating minimal environmental influence. GCV (15.874%): The genotypic coefficient of variation is moderate, indicating substantial genetic variability. PCV (16.241%): The phenotypic coefficient of variation is slightly higher than the GCV, indicating a small environmental influence. h² (0.955): The broad-sense heritability is high (95.5%), suggesting that most of the variation is genetic. Gen. Adv as % of Mean (31.96%): The genetic advance as a percentage of the mean is high, indicating that selection for this trait is likely to be very effective, resulting in substantial genetic gains.

1000-Grain Weight (1000GW)

ECV (0.916%): The environmental coefficient of variation is very low, indicating negligible environmental influence. GCV (16.33%): The genotypic coefficient of variation is moderate, suggesting good genetic variability. PCV (16.355%): The phenotypic coefficient of variation is almost equal to the GCV, indicating minimal environmental effects. h² (0.997): The broad-sense heritability is very high (99.7%), indicating that almost all observed variation is genetic. Gen. Adv as % of Mean (33.586%): The genetic advance as a percentage of the mean is high, suggesting that selection for this trait will result in substantial genetic improvement.

Grain Yield per kg (GY/kg)

ECV (7.606%): The environmental coefficient of variation is low, indicating a moderate environmental influence. GCV (5.878%): The genotypic coefficient of variation is low, indicating limited genetic variability. PCV (9.612%): The phenotypic coefficient of variation is higher than the GCV, suggesting some environmental effects. h² (0.374): The broad-sense heritability is medium (37.4%), indicating that both genetic and environmental factors contribute to the observed variation. Gen. Adv as % of Mean (7.404%): The genetic advance as a percentage of the mean is low, suggesting that genetic improvement for this trait through selection may be slow.

Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all studied traits indicates the environmental influence on the expression of these traits. Similar results were presented by (Malimar et al., 2015; Rashid et al., 2017; Gyawali et al., 2018). The difference between the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) shows how much the environment affects the traits. In this study, the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all traits, implying that environmental factors have a considerable impact on the expression of these traits.

Phenotypic and Genotypic Coefficients of Variation

Low PCV values were observed for traits such as Days to 50% Flowering (5.01%) and Plant Height (6.33%), indicating limited phenotypic variation. Results are similar with Prasanna et al. (2022), In contrast, moderate PCV values were noted for Number of Panicles per square meter (12.63%), Filled Grains per Plant (16.24%), and 1000 Grain Weight (16.36%). These results suggest moderate environmental influence on these traits, supported by closely aligned GCV values. Sheeba et al. (2023) also reported filled grains per panicle and hundred seed weight with high and moderate extent of PCV and GCV. Moderate genetic variation was observed for Number of Panicles per square meter (12.10%), Filled Grains per Plant (15.87%), 1000 Grain Weight (16.33%) and remaining traits showed low genotypic coefficient of variation Gyawali et al. (2018), Devkota et al., 2023. The Number of Panicles per square meter (GCV: 12.10%), Filled Grains per Plant (15.87%) and 1000 Grain Weight (16.33%) demonstrated minimal differences between PCV and GCV, indicating that genetic factors predominantly control their expression. Patel et al. (2019) also observed close alignment between PCV and GCV values for traits like Number of Panicles and 1000 Grain Weight, indicating that these traits are less influenced by environmental variation. Traits such as Plant Height and Grain Yield exhibited larger differences between PCV and GCV, suggesting higher environmental influence. These observations underscore the need to consider environmental factors in breeding programs for traits with low genetic variability.

Heritability and Genetic Advance

High broad-sense heritability values were observed for Days to 50% Flowering, Panicle Length, Number of Panicles per square meter, Filled Grains per Plant and 1000 Grain Weight, with values exceeding 60%. These traits are largely governed by genetic factors and are reliable for selection in breeding programs. The1000 Grain Weight, which exhibited high heritability (84.7%) and genetic advance as a percentage of mean (33.59%), indicates strong potential for improvement through selection. Similar findings were reported by Gyawali et al. (2018), Bandi et al. (2018), and Aditya and Bhartiya (2013) for traits such as days to flowering, maturity, and thousand-grain weight. Plant Height with moderate heritability (57.3%) and low genetic advance (7.47%), suggests that selection progress for this trait may be slower due to environmental influence. Similarly, Grain Yield, showing low heritability (37.4%) and genetic advance (7.40%), highlights significant environmental impact, complicating its improvement through direct selection. However, traits with lower heritability and genetic advance, such as Grain Yield, were similarly described as being challenging for selection due to substantial environmental effects. High to medium heritability for grain yield, as reported by Gyawali et al. (2018), Bandi et al. (2018), and Abebe et al. (2017), could be attributed to environmental influences, given that yield is a polygenic trait. The high heritability and genetic advance observed for traits like Panicle Length, Number of Panicles per square meter, and 1000 Grain Weight suggest that these traits are promising targets for genetic improvement. Conversely, traits such as Plant Height and Grain Yield may require advanced breeding strategies. Similar findings supported by Edukondalu et al., 2023, Adhikari et al., 2018

Table 2: Average, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability and genetic advance as a percentage of the mean (GAM) for seven traits.

	Range					Coefficient of variation				
Characters	**Lowest**	**Highest**	**Mean**	**C.V.**	**C.D. 5%**	**GCV**	**PCV**	**ECV**	**h2**	**GA: 5% of mean**
Days to 50% flowering	86.67	108.00	94.48	0.73	1.14	4.957	5.011	0.73	0.979	10.103
Plant height (cm)	103.33	126.33	115.50	4.13	7.92	4.789	6.325	4.132	0.573	7.469
Panicle length (cm)	20.67	28.67	23.72	3.80	1.49	7.928	8.789	3.795	0.814	14.731
No of panicles/m2	266.00	419.33	354.81	3.61	21.28	12.097	12.626	3.615	0.918	23.877
Filled grains/panicle	130.33	251.67	192.20	3.44	10.96	15.874	16.241	3.435	0.955	31.96
1000 GW (g)	11.40	27.37	18.15	0.92	0.28	16.33	16.355	0.916	0.997	33.586
Grain yield (kg/ha)	6970.44	8867.00	7772.23	7.61	980.89	5.878	9.612	7.606	0.374	7.404

4. CONCLUSION

The study provides valuable insights into the genetic variability, heritability, and genetic advance of key agronomic traits in rice, essential for enhancing breeding strategies. Traits like days to 50% flowering, 1000-grain weight and filled grains per plant exhibited high heritability and genetic advance, indicating their strong genetic control and potential for effective selection. Conversely, traits such as grain yield kg/ha with lower heritability and genetic advance, may require alternative breeding strategies, such as hybridization to achieve significant improvements.

Disclaimer (Artificial intelligence)

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

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

authors' contributions

Author BS contributed to the conceptualization, study design, data analysis, and interpretation. **Author BS & BE** was responsible for writing the original draft, reviewing and editing, as well as data analysis and interpretation, and also managed the analyses of the study. **Author BS, AD & GN** carried out the investigation and supervision, managed the analyses of the study and conducted the literature searches. All authors read and approved the final manuscript.

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