



Genetic Variability, Heritability, and Genetic Advance for Yield and Milling Quality Traits in Rice (*Oryza sativa* L.) Germplasm

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Genetic variability is the foundation of effective selection in crop improvement. Fifty rice germplasm lines were evaluated during the kharif season of 2025 at the Regional Agricultural Research Station, Polasa, Jagtial, Telangana, India, using a randomised block design with two replications. Ten yield and milling-quality traits were assessed: days to 50% flowering, plant height, panicle length, productive tillers per plant, grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percentage, and head rice recovery. Analysis of variance indicated highly significant differences among genotypes for all traits.

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Phenotypic coefficients of variation exceeded the corresponding genotypic coefficients for every trait, although the differences were generally small for days to 50% flowering, plant height, 1000-grain weight, head rice recovery, and grain yield per plant. High phenotypic and genotypic variability was observed for grains per panicle, head rice recovery, and grain yield per plant. Broad-sense heritability was high for nine traits and moderate for panicle length. High heritability accompanied by high genetic advance as a percentage of the mean was recorded for plant height, productive tillers per plant, grains per panicle, 1000-grain weight, head rice recovery, and grain yield per plant. These estimates identify traits with a favourable expected response to phenotypic selection within the evaluated material. Because the experiment was conducted in one season and one location, the stability of the estimates and the performance of individual germplasm lines should be confirmed through multi-environment evaluation before selections are advanced.

Keywords: *Broad-sense heritability; genetic advance; genotypic coefficient of variation; head rice recovery; phenotypic coefficient of variation; rice breeding.*

1. Introduction

Rice (*Oryza sativa* L.) is a principal staple crop and an important component of food and livelihood security across Asia and increasingly in other regions. Sustained genetic improvement of yield, adaptation, and grain quality therefore remains a central objective of rice breeding programmes (Muthayya et al., 2014). Germplasm collections provide the allelic and phenotypic diversity required to broaden the genetic base of breeding populations, but their value depends on reliable characterisation of variation for agronomically and commercially important traits. Studies of diverse rice materials have repeatedly demonstrated that grains per panicle, productive tiller number, 1000-grain weight, grain yield, and grain-quality traits can display substantial exploitable variation (Roy & Shil, 2020; Tuhina-Khatun et al., 2015).

Observed phenotypic variation reflects both genetic and environmental components. The phenotypic coefficient of variation (PCV) describes total observable variation relative to the trait mean, whereas the genotypic coefficient of variation (GCV) estimates the relative magnitude of genetic variation. Comparison of these coefficients helps indicate the extent to which environmental effects contribute to trait expression. Heritability further quantifies the proportion of phenotypic variance attributable to genetic differences within the evaluated population and environment. Genetic advance complements heritability by expressing the expected improvement under a specified selection intensity (Burton & DeVane, 1953; Johnson et al., 1955).

Heritability estimates must nevertheless be interpreted in relation to the population, experimental design, and target environment. Broad-sense heritability includes additive, dominance, and epistatic components and does not, by itself, separate the portion transmitted predictably through selection. Consequently, joint consideration of heritability and genetic advance is more informative than either statistic alone, and estimates from a single environment should not be assumed to remain unchanged across seasons or locations (Holland et al., 2003; Piepho & Möhring, 2007). Recent rice studies have used this combined approach to identify traits with favourable selection potential while recognising environmental and population-specific effects (Arpitha et al., 2025; Chaudhary et al., 2023; Soundharya et al., 2024).

However, the combined variability, heritability, and expected genetic advance of yield and milling-quality traits had not been characterised within this set of 50 rice germplasm lines under the stated experimental conditions.

The present investigation evaluated 50 rice germplasm lines for ten yield and milling-quality traits. The objectives were to quantify phenotypic and genotypic variability, estimate broad-sense heritability and expected genetic advance, and identify traits that may respond effectively to selection within the evaluated material.

2. Materials and Methods

2.1 Experimental Material and Field Design

The experimental material comprised 50 rice germplasm lines obtained from the Regional Agricultural Research Station, Polasa, Jagtial, Telangana, India. The field experiment was conducted during the kharif season of 2025 in a randomised block design with two replications, as indicated by the replication degrees of freedom in the

analysis of variance. Thirty-day-old seedlings of each germplasm line were transplanted manually in two rows, each 2 m in length. Row-to-row and plant-to-plant spacing were maintained at 20 cm and 15 cm, respectively.

Observations were recorded on five randomly selected plants from each genotype for ten quantitative traits: days to 50% flowering (DFF), plant height (PH; cm), panicle length (PL; cm), number of productive tillers per plant (PTP), number of grains per panicle (GPP), 1000-grain weight (TGW; g), hulling percentage (HULL), milling percentage (MILL), head rice recovery (HRR; %), and grain yield per plant (GYP; g).

2.2 Statistical analysis

Analysis of variance was performed for the randomised block design to test differences among germplasm lines. Genotypic variance (σ^2_g) was estimated as $(MS_g - MSe)/r$, where MS_g is the genotype mean square, MSe is the error mean square, and r is the number of replications. Phenotypic variance (σ^2_p) was estimated as $\sigma^2_g + \sigma^2_e$, where σ^2_e is the error variance. The genotypic and phenotypic coefficients of variation were calculated as $GCV (\%) = (\sqrt{\sigma^2_g}/\bar{x}) \times 100$ and $PCV (\%) = (\sqrt{\sigma^2_p}/\bar{x}) \times 100$, respectively, where $\bar{x}$ is the trait mean (Burton & DeVane, 1953).

Broad-sense heritability was calculated as $h^2_{bs} (\%) = (\sigma^2_g/\sigma^2_p) \times 100$. Expected genetic advance at a 5% selection intensity was estimated as $GA = k \times \sqrt{\sigma^2_p} \times h^2$, where $k = 2.06$ and h^2 is expressed as a proportion. Genetic advance as a percentage of the mean was calculated as $GAM = (GA/\bar{x}) \times 100$. PCV, GCV, and GAM values were interpreted as low (<10%), moderate (10-20%), or high (>20%), while heritability was considered low (<30%), moderate (30-60%), or high (>60%) following the conventional categories described by Johnson et al. (1955). Critical differences at the 5% probability level were calculated from the error variance of the randomised block design.

3. Results

3.1 Analysis of Variance

The analysis of variance revealed highly significant differences ($p < 0.01$) among the 50 germplasm lines for all ten traits (Table 1). The significant genotype mean squares confirmed the presence of measurable variability for flowering, plant architecture, yield components, milling quality, and grain yield. Error mean squares were comparatively small for most traits, supporting the estimation of genetic parameters from the experiment.

Table 1. Analysis of variance for ten yield and milling-quality traits in 50 rice germplasm lines

No.	Trait	Replication MS (df = 1)	Genotype MS (df = 49)	Error MS
1	Days to 50% flowering	0.640	149.571**	2.620
2	Plant height (cm)	58.676	444.378**	9.885
3	Panicle length (cm)	1.608	4.612**	1.318
4	Productive tillers per plant	3.675	4.497**	0.899
5	Grains per panicle	69.456	3710.250**	216.632
6	1000-grain weight (g)	0.077	32.971**	0.911
7	Hulling (%)	6.538	20.373**	2.507
8	Milling (%)	14.661	32.633**	2.256
9	Head rice recovery (%)	0.013	169.045**	3.466
10	Grain yield per plant (g)	11.445	44.348**	3.322

Note. MS = mean square; ** $p < 0.01$

3.2 Trait Ranges and Experimental Precision

The germplasm displayed broad ranges for several agronomic and quality traits (Table 2). Days to 50% flowering ranged from 85.50 to 121.00 days, plant height from 83.30 to 153.80 cm, grains per panicle from 113.70 to 287.00, 1000-grain weight from 11.35 to 28.25 g, and grain yield per plant from 14.70 to 35.25 g. Head rice recovery varied from 30.03% to 59.88%. Experimental coefficients of variation ranged from 1.60% for days to 50% flowering to 8.63% for productive tillers per plant, indicating acceptable precision for the measured traits.

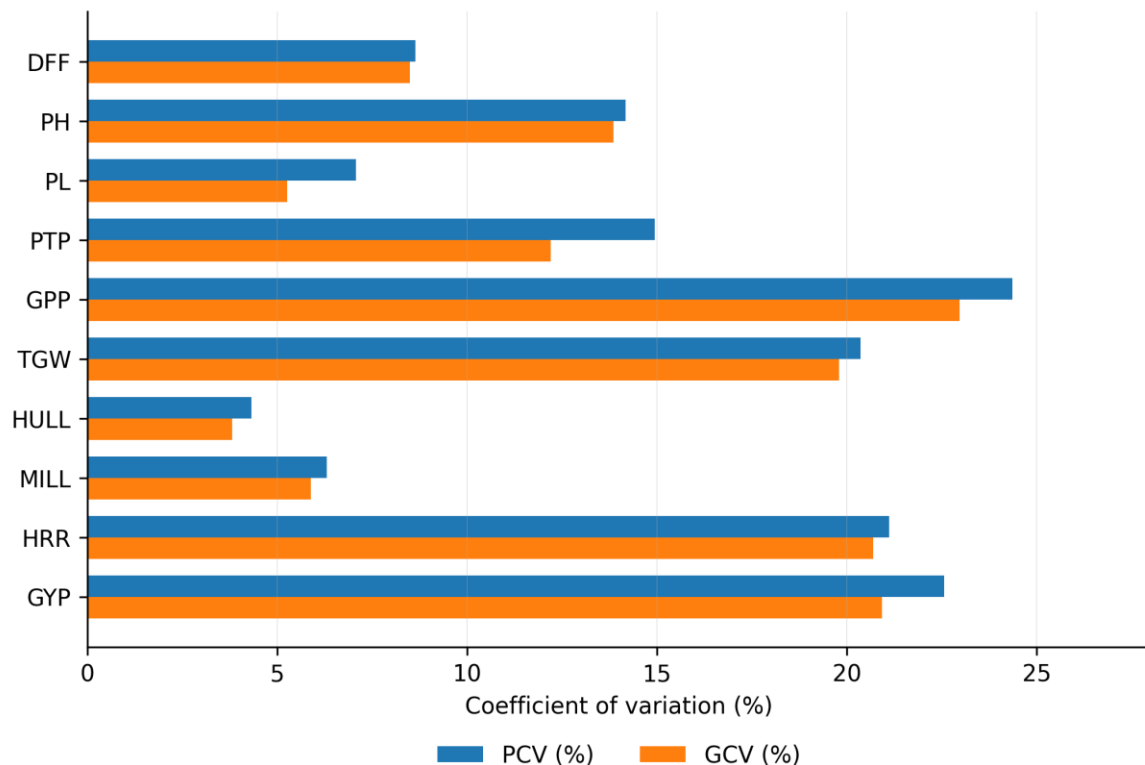
Table 2. Range, mean, coefficient of variation, and critical difference for ten traits in rice germplasm

No.	Trait	Minimum	Maximum	Mean	CV (%)	CD (5%)
1	Days to 50% flowering	85.50	121.00	100.98	1.60	3.25
2	Plant height (cm)	83.30	153.80	106.37	2.96	6.32
3	Panicle length (cm)	22.00	29.80	24.35	4.71	2.31
4	Productive tillers per plant	8.50	14.20	10.99	8.63	1.91
5	Grains per panicle	113.70	287.00	181.94	8.09	29.58
6	1000-grain weight (g)	11.35	28.25	20.22	4.72	1.92
7	Hulling (%)	69.16	89.17	78.31	2.02	3.18
8	Milling (%)	57.08	76.10	66.18	2.27	3.02
9	Head rice recovery (%)	30.03	59.88	43.98	4.23	3.74
10	Grain yield per plant (g)	14.70	35.25	21.64	8.42	3.66

Note. CV = experimental coefficient of variation; CD = critical difference

3.3 Variability, Heritability and Genetic Advance

PCV exceeded GCV for every trait (Table 3 and Fig. 1). The differences were narrow for days to 50% flowering, plant height, 1000-grain weight, head rice recovery, and grain yield per plant, indicating that environmental variance was relatively small in relation to genetic variance for these traits within the experiment. High PCV and GCV were observed for grains per panicle, head rice recovery, and grain yield per plant. The PCV for 1000-grain weight was high, while its GCV was moderate and close to the high threshold. Plant height and productive tillers per plant showed moderate PCV and GCV. Low coefficients were recorded for days to 50% flowering, panicle length, hulling percentage, and milling percentage.

**Fig. 1. Phenotypic and genotypic coefficients of variation for ten rice traits**

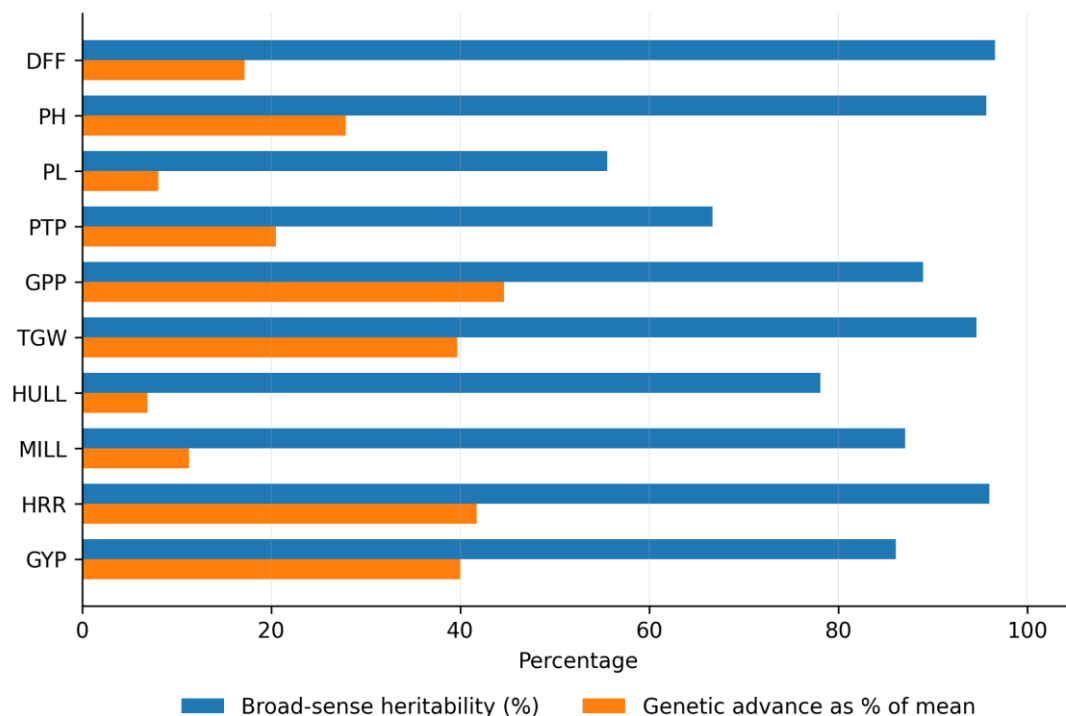
DFF = days to 50% flowering; PH = plant height; PL = panicle length; PTP = productive tillers per plant; GPP = grains per panicle; TGW = 1000-grain weight; HULL = hulling percentage; MILL = milling percentage; HRR = head rice recovery; GYP = grain yield per plant

Table 3. Phenotypic and genotypic coefficients of variation, broad-sense heritability, and genetic advance for ten traits

No.	Trait	PCV (%)	GCV (%)	h^2_{bs} (%)	GAM (%)
1	Days to 50% flowering	8.64	8.49	96.56	17.18
2	Plant height	14.17	13.86	95.65	27.92
3	Panicle length	7.07	5.27	55.56	8.09
4	Productive tillers per plant	14.94	12.20	66.67	20.52
5	Grains per panicle	24.36	22.97	88.97	44.64
6	1000-grain weight	20.36	19.80	94.62	39.68
7	Hulling percentage	4.32	3.82	78.09	6.95
8	Milling percentage	6.31	5.89	87.07	11.32
9	Head rice recovery	21.12	20.69	95.98	41.75
10	Grain yield per plant	22.56	20.93	86.06	40.00

Note. PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; h^2_{bs} = broad-sense heritability; GAM = genetic advance as a percentage of the mean

Broad-sense heritability was high for all traits except panicle length, which displayed moderate heritability of 55.56% (Table 3 and Fig. 2). The highest estimates were recorded for days to 50% flowering (96.56%), head rice recovery (95.98%), plant height (95.65%), and 1000-grain weight (94.62%). High GAM was observed for grains per panicle (44.64%), head rice recovery (41.75%), grain yield per plant (40.00%), 1000-grain weight (39.68%), plant height (27.92%), and productive tillers per plant (20.52%). Days to 50% flowering and milling percentage showed moderate GAM, whereas panicle length and hulling percentage showed low GAM.

**Fig. 2. Broad-sense heritability and genetic advance as a percentage of the mean for ten rice traits. Trait abbreviations are defined in Fig. 1**

4. Discussion

The significant genotype effects for all traits demonstrated that the germplasm set contained measurable phenotypic diversity. The generally small differences between PCV and GCV indicated that environmental effects did not obscure genetic differences for several traits under the conditions of this experiment. Similar

patterns, in which PCV modestly exceeds GCV, have been reported across rice germplasm and breeding populations (Anuhya & Lavanya, 2022; Islam et al., 2015; Soundharya et al., 2024). The magnitude of the coefficients nevertheless varied among traits, showing that selection opportunities were not uniform across traits.

Days to 50% flowering exhibited low PCV and GCV but very high heritability and moderate GAM. This combination indicates limited relative variability within the evaluated material, yet a high proportion of the observed variation was genetic in the tested environment. Flowering time may therefore respond predictably to selection, although the expected proportional gain is smaller than for highly variable traits. Plant height showed moderate variability, very high heritability, and high GAM, suggesting a favourable response to selection. Comparable estimates for flowering time and plant height have been reported in rice populations evaluated across single and multiple environments (Arpitha et al., 2025; Chaudhary et al., 2023).

Panicle length had low coefficients of variation, moderate heritability, and low GAM. The relatively larger difference between PCV and GCV for this trait indicates a stronger environmental contribution than for most other characters. Direct phenotypic selection for panicle length would consequently be less efficient in this population unless supported by replicated evaluations across environments. Productive tillers per plant displayed moderate PCV and GCV, high heritability, and marginally high GAM. This pattern indicates useful variability, but its expression may be more environmentally responsive than that of plant height or grain weight. Recent rice studies have likewise reported variable heritability for panicle length and comparatively greater selection potential for productive tiller number (Hyndhavi et al., 2025; Kumar et al., 2026).

Grains per panicle, 1000-grain weight, and grain yield per plant were among the most promising yield-related traits. Grains per panicle and grain yield per plant had high PCV, high GCV, high heritability, and high GAM. The narrow PCV-GCV difference for grain yield per plant also suggests that genotype differences were expressed clearly under the test conditions. For 1000-grain weight, PCV was high and GCV was moderate but close to the high threshold; very high heritability and high GAM indicate substantial expected improvement under selection. Similar combinations of high heritability and high GAM for grain number, 1000-grain weight, and grain yield have been documented in diverse rice materials (Bakode et al., 2025; Maruti et al., 2025; Roy & Shil, 2020; Sudeepthi et al., 2020; Tuhina-Khatun et al., 2015).

The milling-quality traits differed markedly in their selection potential. Hulling and milling percentages showed low variability. Despite high broad-sense heritability, hulling percentage had low GAM and milling percentage had only moderate GAM, indicating limited proportional gain from direct selection in this germplasm set. In contrast, head rice recovery displayed high PCV and GCV, very high heritability, and high GAM. This combination supports head rice recovery as a useful quality-selection criterion. Studies incorporating rice milling and quality traits have similarly reported stronger variability and expected response for head rice recovery than for hulling percentage in some populations (Devi et al., 2022; Sadhana et al., 2022).

The joint occurrence of high broad-sense heritability and high GAM is compatible with a substantial transmissible component and favourable expected selection response, but it should not be interpreted as direct proof that additive gene action predominates. Broad-sense heritability combines additive and non-additive genetic variance, and the present design does not partition these components (Holland et al., 2003). Moreover, heritability is specific to the population and environmental conditions in which it is estimated. The two-replication, single-season, single-location design provides a useful initial assessment but does not quantify genotype $\times$ environment interaction. Multi-environment testing is therefore required to determine the stability of trait expression and to confirm the performance of individual germplasm lines before breeding selections are advanced (Piepho & Möhring, 2007).

5. Conclusion

The 50 rice germplasm lines exhibited significant variability for all ten yield and milling-quality traits. PCV was consistently higher than GCV, but the differences were small for several traits, indicating that useful genetic variation was expressed under the experimental conditions. Grains per panicle, head rice recovery, and grain yield per plant combined high PCV, high GCV, high broad-sense heritability, and high GAM. Plant height, productive tillers per plant, and 1000-grain weight also showed high heritability with high GAM and therefore represent additional selection targets. Panicle length and hulling percentage showed a comparatively limited

expected response to direct phenotypic selection. These results provide a quantitative basis for prioritising traits within the evaluated germplasm; however, selections should be validated across seasons and locations to assess stability and genotype $\times$ environment interaction.

6. Limitations

The study was conducted during a single season at one location with two replications. Consequently, genotype $\times$ environment interaction and the stability of the estimated genetic parameters across environments could not be assessed. Broad-sense heritability also combines additive and non-additive genetic variance and does not identify the proportion transmitted predictably through selection. Multi-season and multi-location evaluations are therefore necessary before individual germplasm lines are advanced in a breeding programme.

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Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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