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Genetic variability and trait association studies for grain yield improvement in rice (*Oryza sativa* L.)

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Abstract

Rice (*Oryza sativa* L.) is one of the world's most important staple food crops and a major contributor to global food security, making the improvement of grain yield a key objective of rice breeding programmes. The present study was undertaken to assess genetic variability and to determine relationships among yield-associated traits in diverse rice breeding materials to identify effective selection criteria for grain yield improvement. Analysis of variance revealed significant differences among genotypes for all the traits studied, indicating substantial genetic variability. Relatively high coefficients of variation were observed for test weight (15.05%), productive tillers (13.96%) and grain yield per plant (8.74%). The highest PCV and GCV were recorded for test weight (25.61% and 20.72%, respectively), followed by productive tillers (23.71% and 19.17%) and grain yield per plant (20.86 and 18.94%). Broad-sense heritability was high for all traits and high heritability coupled with high genetic advance as per cent of mean was observed for most traits, indicating substantial genetic control and good potential for improvement through selection. Grain yield per plant exhibited the strongest positive correlation with panicle length ($r = 0.36$), followed by plant height ($r = 0.30$) and productive tillers ($r = 0.22$). Path analysis revealed positive direct effects of all eight component traits, with the highest direct effects for spikelet fertility (0.87), test weight (0.78) and grain length (0.73). The findings indicate that spikelet fertility, test weight, grain length, panicle length and productive tillers can be prioritized as selection criteria for improving grain yield, providing useful implications for selection and development of high-yielding rice varieties.

Keywords: Rice, *Oryza sativa* L., genetic variability, grain yield, heritability

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops and serves as a major source of food and energy for more than half of the world's population. With the continuous increase in population, changing climatic conditions and the growing demand for food, improving rice productivity remains a major objective of rice breeding programmes. Grain yield is a complex quantitative trait governed by several component traits and is considerably influenced by environmental conditions. Therefore, understanding the magnitude of genetic variability and the relationships among yield-associated traits is essential for developing effective selection strategies (Singh Yadav *et al.*, 2024; Jambhulkar *et al.*, 2014) ^[26, 11].

Diverse breeding materials, including germplasm accessions, maintainer lines, improved varieties and advanced breeding lines, represent valuable sources of genetic variation for rice improvement. Germplasm accessions can contribute novel genetic variation, whereas improved varieties and advanced breeding lines provide elite genetic backgrounds with desirable agronomic characteristics. Maintainer lines are also important components of rice breeding programmes, particularly in hybrid rice development, and may possess useful variation for yield and its component traits. Evaluation of such diverse genetic materials for agronomic, yield and grain characteristics is therefore essential for identifying superior genotypes and desirable trait combinations. Previous studies involving diverse rice genetic materials have reported significant variation for yield and its component traits, highlighting the potential of such materials for selection and crop improvement (Rekha *et al.*, 2026; Pathak *et al.*, 2024) ^[20, 18].

Assessment of genetic variability is an important initial step in any crop improvement programme because the effectiveness of selection depends on the magnitude of heritable variation present in the breeding material (Spoorthi *et al.*, 2026)^[27]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are useful parameters for quantifying the extent of phenotypic and genetic variability, respectively. The relative difference between PCV and GCV also provides an indication of the influence of environmental factors on trait expression (Burton and DeVane, 1953)^[3]. Greater GCV generally indicates greater scope for genetic improvement through selection, particularly when accompanied by high heritability and genetic advance.

Heritability is an important genetic parameter that indicates the proportion of phenotypic variation attributable to genetic differences among individuals. However, heritability alone is not sufficient to predict the response to selection because it does not indicate the nature of the genetic variance or the expected magnitude of improvement. Therefore, heritability should be considered together with genetic advance, particularly genetic advance as per cent of mean (GAM), to obtain a better indication of the potential effectiveness of selection (Johnson *et al.*, 1955)^[12]. High heritability coupled with high genetic advance is generally considered indicative of the predominance of additive gene action and suggests good prospects for improvement through selection (Panse, 1957; Johnson *et al.*, 1955)^[17, 12]. Several studies in rice have demonstrated the usefulness of these parameters in identifying traits with substantial genetic variability and selection potential (Bagudam *et al.*, 2018; Shivani *et al.*, 2021)^[2, 25].

In addition to genetic parameters, understanding the association among grain yield and its component traits is essential for formulating an effective selection strategy. Grain yield is a complex quantitative trait influenced by several interrelated agronomic characteristics. Correlation analysis provides information on the direction and magnitude of associations among traits and helps identify characters that may be useful for indirect selection (Dewey and Lu, 1959)^[6]. Positive associations between yield and its component traits may facilitate simultaneous improvement of these characters; however, the observed correlation may result from both direct and indirect effects of other traits (Spoorthi and Immadi, 2026)^[28].

Path coefficient analysis provides a further understanding of trait relationships by partitioning correlation coefficients into direct and indirect effects. Originally developed by Wright (1921)^[30] and subsequently applied in plant breeding by Dewey and Lu (1959)^[6], path analysis enables the identification of traits that exert a strong direct influence on grain yield. Traits exhibiting high positive direct effects, particularly when supported by positive correlations with yield, can be considered important selection criteria for improving grain yield. Thus, the combined analysis of variability, heritability, genetic advance, correlation and path coefficients provides a comprehensive understanding of the genetic potential and interrelationships of yield-associated traits.

Considering the importance of diverse breeding materials and the complex genetic control of grain yield, the present study was undertaken to evaluate maintainer lines, germplasm accessions, improved varieties and advanced breeding lines for important agronomic, yield and grain traits; to assess the magnitude of phenotypic and genetic variability; to estimate heritability and genetic advance; and to determine the association and direct and indirect effects of component traits on grain yield per plant. The findings of the present study would aid in identifying key traits for effective selection and provide valuable information for

developing breeding strategies aimed at improving grain yield in rice.

2. Materials and Methods

The experimental material consisted of 30 rice genotypes, comprising ten maintainer lines, nine germplasm accessions, six improved varieties and five advanced breeding lines (Table 1). These genotypes were evaluated in a randomized block design (RBD) for grain yield and its associated traits during summer 2022 at the Zonal Agricultural Research Station (ZARS), V. C. Farm, Mandya. Each genotype was transplanted under puddled conditions in an area of one square metre, with a spacing of 20 cm between rows and 15 cm between plants, accommodating 42 plants per genotype. Observations were recorded on five randomly selected competitive plants for plant height (PH, cm), productive tillers (PT, cm), panicle length (PL, g), spikelet fertility (SF, %), test weight (TW, g), grain length (GL, cm), grain width (GW, cm), grain length-to-width ratio (L/B), and grain yield per plant (GD/P, g).

Analyses were performed using R version 4.5.1 (R Core Team, 2025) in RStudio (RStudio Team, 2025). Analysis of variance (ANOVA) was performed following the method of Cochran and Cox (1957)^[5] using the metan package (Olivoto and Lúcio, 2020)^[15]. Phenotypic and genotypic variances were calculated as suggested by Cochran and Cox (1957)^[5]. Variance components obtained from the ANOVA were used to estimate the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic advance as a percentage of the mean (GAM) to assess the extent of genetic variability. The genotypic and phenotypic coefficients of variation were calculated according to Burton and Devane (1953)^[3]. Pearson's correlation analysis was performed using the *corr.test* function of the *psych* package (Revelle, 2024)^[21]. Path coefficient analysis was performed using the *lavaan* (Rosseel, 2012)^[23] and *semPlot* (Epskamp, 2015)^[7] packages in R to know the direct and indirect effects of yield components on grain yield as suggested by Wright (1921)^[30] and illustrated by Dewey and Lu (1959)^[6].

3. Results and Discussion

The analysis of variance revealed significant differences ($p < 0.01$) among the genotypes for all the traits studied, indicating the presence of substantial variability within the experimental material for both yield and grain related traits (Table 2). The significant genotypic variation observed for agronomic, yield and grain traits in the present study agrees with recent reports in rice, confirming the presence of exploitable variability for selection and breeding. Pathak *et al.*, (2024)^[18] reported substantial variability for plant height, productive tillers, grain yield and 100-grain weight among 60 rice germplasm accessions. Similar significant differences for growth, yield and grain traits were reported by Rezk *et al.* (2024)^[22] and Awad-Allah *et al.* (2022)^[1]. Thus, the observed variability provides a basis for estimating genetic parameters, assessing trait associations and identifying superior genotypes for grain yield improvement.

The mean values varied considerably among the traits, indicating variation in the phenotypic expression of the genotypes (Table 3). PH recorded a mean value of 108.16 cm, while PT and PL exhibited mean values of 13.14 and 24.77 cm, respectively. SF recorded a mean value of 88.44%. The mean TW was 17.66 g, whereas GL and GW recorded mean values of 7.89 mm and 2.33 mm, respectively. The mean L/B was 3.43, while GD/P recorded a mean value of 31.84 g. The observed variation in mean performance among the traits reflects the diverse phenotypic

characteristics of the genotypes and provides a basis for identifying promising genotypes for further selection and breeding.

Among the traits, a comparatively high coefficient of variation was observed for TW (15.05), followed by PT (13.96) and GD/P (8.74), indicating relatively greater variability among genotypes for these traits. The higher CV for TW suggests greater phenotypic dispersion for grain weight and may provide useful scope for selection of genotypes with desirable grain weight. Similarly, the relatively higher variability for PT and GD/P indicates the presence of appreciable variation for these traits. In contrast, traits with lower CV values like GL (1.67) exhibited comparatively less phenotypic variation among the genotypes, suggesting greater uniformity for these characters.

The observed variability in mean performance and CV across traits is important for crop improvement, as traits exhibiting greater variation provide a wider range of phenotypes for selection. In particular, the substantial variation observed for TW, PT and GD/P could be exploited to identify superior genotypes and improve yield-related attributes through selection. However, CV represents the relative magnitude of variation and should be interpreted together with estimates of genotypic and environmental variance, heritability and genetic advance to assess the actual potential for effective selection.

The PCV estimates were consistently higher than the corresponding GCV estimates for all the traits, indicating that environmental effects contributed to the observed phenotypic variation, although the relatively narrow differences between PCV and GCV for several traits suggested a substantial genetic contribution to their expression (Table 4). Similar trends, with PCV slightly exceeding GCV, have been reported in rice germplasm, indicating relatively limited environmental influence on several quantitative traits (Bagudam *et al.*, 2018)^[2].

The highest PCV and GCV were recorded for TW (25.61 and 20.72%, respectively), followed by PT (23.71% and 19.17%) and GD/P (20.86% and 18.94%), indicating comparatively greater variability for these traits. In contrast, PL exhibited the lowest PCV and GCV (6.65% and 5.39%), suggesting relatively lower variability. The relatively high GCV observed for TW, PT and GD/P indicates considerable genetic variation for these characters, which could be exploited in selection programmes. Similar observations of comparatively high variability for test weight and other yield-related traits have been reported in rice (Padmaja *et al.*, 2008)^[16].

Broad-sense heritability estimates were high for all the traits, ranging from 65.36% for PT to 97.84% for GL. The highest heritability was observed for GL (97.84%), followed by SF (97.31%), PH (96.73%) and L/B (94.80%), whereas the lowest was recorded for PT (65.36%). High heritability indicates that a large proportion of the observed phenotypic variation was attributable to genetic variance, suggesting that phenotypic selection may be effective for these traits. However, heritability alone does not provide sufficient information about the expected response to selection because it does not distinguish between additive and non-additive genetic effects. Therefore, heritability should be considered together with genetic advance for predicting selection response. This interpretation is consistent with earlier rice studies emphasizing the combined use of heritability and genetic advance in breeding decisions (Shivani *et al.*, 2021)^[25].

The GAM ranged from 9.00% for PL to 35.43% for GD/P. High GAM was recorded for GD/P (35.43%) followed by TW (34.53%) and PT (31.93%). PL showed comparatively low GAM (9.00%). The combination of high heritability and high GAM observed for PH, PT, SF, TW, GL, GW, L/B and GD/P suggests that these traits are likely to have a substantial additive genetic component and that selection based on phenotypic performance

could be effective for their improvement. Similar interpretations have been reported in rice, where high heritability coupled with high genetic advance was associated with the predominance of additive gene effects and greater effectiveness of selection (Kumar *et al.*, 2020)^[13].

Overall, the high heritability coupled with substantial genetic advance observed for most of the traits indicates the presence of exploitable genetic variability in the evaluated rice germplasm. Particularly, TW and PT appear to be important selection targets because of their relatively high genetic variability and expected response to selection. These findings demonstrate the usefulness of the evaluated germplasm as a source of variability for improving yield-associated and grain-related traits in rice breeding programmes.

Correlation analysis revealed that grain yield per plant (GD/P) exhibited predominantly positive associations with the agronomic and grain-related traits evaluated in the present study (Figure 1). The strongest positive correlation was observed between GD/P and PL ($r = 0.36$), followed by PH ($r = 0.30$). Weak positive correlations were observed with PT ($r = 0.22$), SF ($r = 0.15$), GL ($r = 0.15$), TW ($r = 0.14$), GW ($r = 0.11$) and L/B ratio ($r = 0.05$). Similar positive associations among yield and its component traits have been reported in rice, demonstrating the importance of evaluating inter-trait relationships for effective selection (Bagudam *et al.*, 2018; Shivani *et al.*, 2021)^[2, 25].

Grain yield per plant also showed a positive correlation with plant height ($r = 0.30$), indicates that genotypes with longer panicles tended to produce higher grain yield per plant. Panicle length is an important component of panicle architecture and may contribute to yield by providing greater space for spikelet development. Positive associations between panicle traits and grain yield have also been reported in rice, suggesting the potential usefulness of panicle characteristics as selection criteria for yield improvement (Bagudam *et al.*, 2018; Meena *et al.*, 2020)^[2, 14].

These findings indicate that panicle architecture and productive tillering may have greater relevance for improving grain yield in the studied genotypes. Nevertheless, correlation coefficients represent both direct and indirect relationships among traits and therefore cannot alone establish the relative importance of individual traits for selection. Path coefficient analysis is consequently useful for partitioning the observed correlations into direct and indirect effects and identifying traits that have the greatest direct contribution to grain yield (Dewey and Lu, 1959; Meena *et al.*, 2020)^[6, 14].

Path coefficient analysis partitioned the phenotypic association of the component traits with grain yield into direct and indirect effects (Figure 2), allowing the relative importance of individual traits to be assessed. The analysis revealed that all eight traits showed positive direct effects on grain yield, although their magnitudes varied considerably. The SF exhibited the highest direct effect (0.87), followed by TW (0.78) and GL (0.73), indicating that these traits were the major direct contributors to grain yield. The predominance of positive direct effects suggests that improvement of these traits could contribute positively to grain yield. The strong direct effects of TW and SF are consistent with recent rice studies, which have identified these traits as important selection criteria for yield improvement (Chattar *et al.*, 2024)^[4]. Similarly, recent path analysis in advanced rice breeding lines demonstrated that yield-associated traits with strong positive direct effects can serve as effective selection criteria for improving grain yield (Shende *et al.*, 2025)^[24]. Thus, the present findings suggest that SF, TW and GL should receive greater emphasis in selection for enhancing grain yield, while the contribution of the remaining traits may be exploited through their direct and indirect associations.

Table 1: List of 30 rice genotypes evaluated for grain yield and associated traits

Sl. No	Maintainer line		
1	KCMS 62 B	16	EC 813187
2	APMS 6 B	17	EC 813136
3	1R68897 B	18	CR 2711-76
4	KCMS 61 B	19	CB 06-022
5	MSN-101 B	20	Improved varieties
6	KCMS 57 B	21	SIDDARANNA
7	KCMS 53 B	22	RAKSHA
8	KCMS 60 B	23	THANU
9	KCMS 55 B	24	JYOTHI
10	KCMS 63 B	25	JAYA
			BPT 5204
Sl. No	Germplasms	Sl. No	Advanced Breeding Lines
11	MSN 97	26	MSN 85 × PH 585 (7-1-1-1-1-1-1)
12	MSN 106	27	MSN 85 × PH 585 (46-2-2-2-1-1)
13	MSN 64	28	MSN 85 × PH 585 (39-1-1-1)
14	MSN 20-1	29	MSN 85 × PH 585 (44-2-1-1-1-1-1 B)
15	MSN 102	30	MSN 85 × PH 585 (39-1-1-2-1-1-1 B)

Table 2: Analysis of variance for grain yield and its associated traits among a set of rice genotypes

Source of Variation	df	Mean sum of squares								
		PH	PT	PL	SF	TW	GL	GW	L/B	GD/P
Genotypes	31	379.87**	16.05**	4.50**	290.61**	33.85**	1.58**	0.14**	0.54**	80.46**
Replication	1	77.29	1.23	3.91	3.90	4.90	0.07	0.001	0.02	1.22
Error	31	6.31	3.36	0.93	3.96	7.07	0.02	0.01	0.01	7.74

Whereas, ** - $p < 0.01$, * - $p < 0.05$

PH: Plant height (cm), PT: Productive tillers, PL: Panicle length, SF: Spikelet fertility percentage (%), TW: Test weight (g), GL: Grain length (cm), GW: Grain width (cm), L/B: Length to breadth ratio, GD/P: Grain yield per plant (g/plant)

Table 3: Perse performance of genotypes for grain yield and its associated traits among a set of rice genotypes

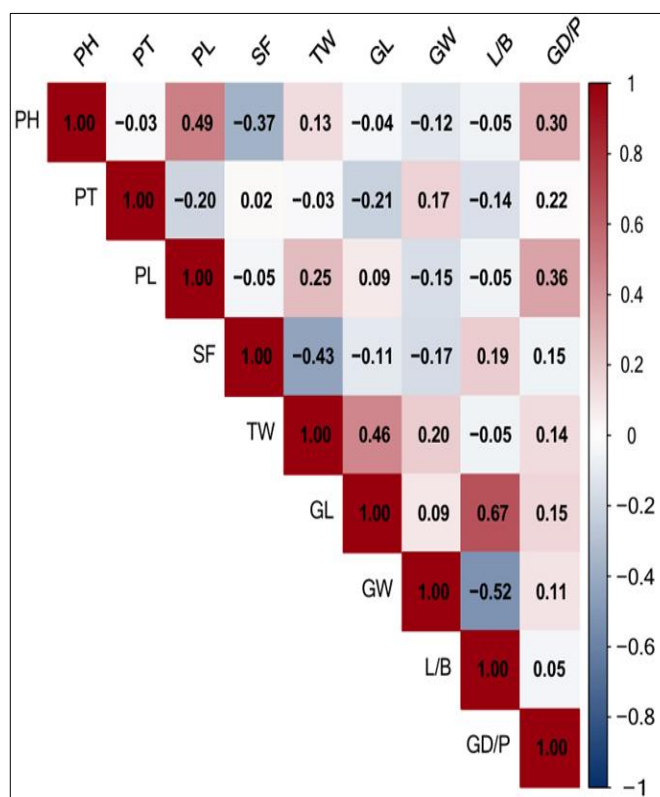
Trait	Mean	Range		CV
		Minimum	Maximum	
PH	108.16	91.33	141.83	2.32
PT	13.14	9.50	20.33	13.96
PL	24.77	20.50	27.33	3.90
SF	88.44	60.74	98.90	2.25
TW	17.66	12.07	26.14	15.05
GL	7.89	5.65	10.02	1.67
GW	2.33	1.83	2.86	4.72
L/B	3.43	2.20	4.49	3.49
GD/P	31.84	21.18	47.80	8.74

PH: Plant height (cm), PT: Productive tillers, PL: Panicle length, SF: Spikelet fertility percentage (%), TW: Test weight (g), GL: Grain length (cm), GW: Grain width (cm), L/B: Length to breadth ratio, GD/P: Grain yield per plant (g/plant).

Table 4: Genetic variability parameters for grain yield and its associated traits among a set of rice genotypes

Traits	PCV	GCV	h^2	GAM
PH	12.85	12.64	96.73	25.60
PT	23.71	19.17	65.36	31.93
PL	6.65	5.39	65.63	9.00
SF	13.72	13.54	97.31	27.51
TW	25.61	20.72	65.46	34.53
GL	11.32	11.20	97.84	22.82
GW	11.71	10.72	83.76	20.21
L/B	15.32	14.91	94.80	29.91
GD/P	20.86	18.94	82.45	35.43

PH: Plant height (cm), PT: Productive tillers, PL: Panicle length, SF: Spikelet fertility percentage (%), TW: Test weight (g), GL: Grain length (cm), GW: Grain width (cm), L/B: Length to breadth ratio, GD/P: Grain yield per plant (g/plant), PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h^2 : Broad sense heritability, GAM: Genetic advance as percent of mean.

**Fig 1:** Phenotypic correlation coefficients among grain yield and its associated traits among a set of rice genotypes. PH: Plant height (cm), PT: Productive tillers, PL: Panicle length, SF: Spikelet fertility percentage (%), TW: Test weight (g), GL: Grain length (cm), GW: Grain width (cm), L/B: Length to breadth ratio, GD/P: Grain yield per plant (g/plant)

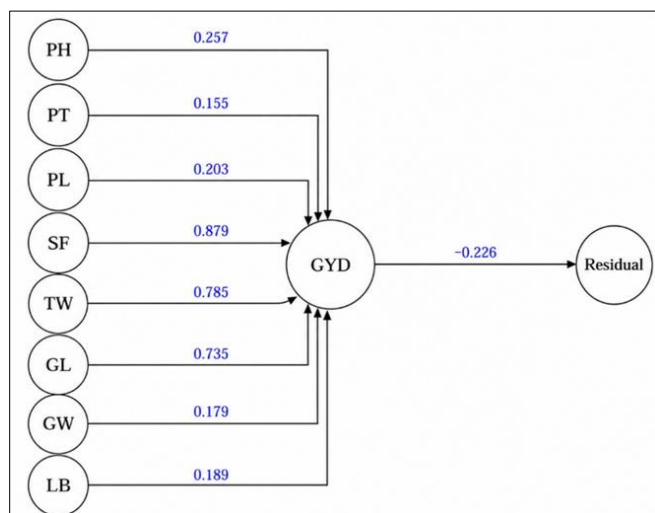


Fig 2: Path analysis depicting direct effects of yield component traits on grain yield among a set of rice genotypes. PH: Plant height (cm), PT: Productive tillers, PL: Panicle length, SF: Spikelet fertility percentage (%), TW: Test weight (g), GL: Grain length (cm), GW: Grain width (cm), L/B: Length to breadth ratio, GD/P: Grain yield per plant (g/plant).

4. Conclusion

The present study revealed substantial phenotypic and genetic variability among the evaluated rice genotypes, with significant genotypic differences for all traits. High heritability coupled with considerable genetic advance for most traits indicated good potential for improvement through selection. Test weight, productive tillers and grain yield per plant exhibited relatively high genetic variability and genetic gain. Grain yield per plant showed positive associations with all the evaluated traits, with the strongest correlations observed with panicle length, plant height and productive tillers. Path analysis identified spikelet fertility, test weight and grain length as the major traits with positive direct effects on grain yield. Therefore, spikelet fertility, test weight, grain length, panicle length and productive tillers can be prioritized as selection criteria for improving grain yield. The findings provide useful information for the identification and development of high-yielding rice varieties.

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