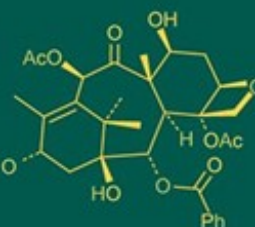
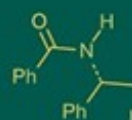


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Genetic variability, heritability and genetic advance for yield and yield-contributing traits in promising rice (*Oryza sativa* L.) hybrids

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ABSTRACT

Grain yield in rice (*Oryza sativa* L.) is a complex, polygenic quantitative trait governed by tight gene-environment interactions. Elucidating the magnitude of genetic variability, broad-sense heritability (h^2_{bs}) and genetic advance is crucial for establishing effective selection criteria. In this study, sixteen rice genotypes comprising twelve experimental F₁ hybrids and four standard checks (Sahyadri 3, Sahyadri 4, Karjat 7 and Konkan Sanjay) were evaluated in a Randomized Block Design (RBD) with three replications during the Kharif 2025 season on the research farm of Regional Agricultural Research Station, Karjat, Maharashtra. Quantitative profiling was conducted for fifteen yield and yield contributing traits. Analysis of variance (ANOVA) revealed highly significant differences ($p < 0.01$) among genotypes across all evaluated traits, establishing the presence of robust genetic diversity. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all characters, indicating minor environmental modulations on trait expression. Grain yield per plant exhibited moderate GCV (12.33%) and PCV (14.04%), coupled with high broad sense heritability (77.07%) and high genetic advance as a percentage of mean ($GAM = 22.30\%$). Notably, grain protein content manifested the highest heritability (97.13%) integrated with high genetic advance (23.29%). High heritability coupled with high genetic advance was also recorded for plant height and amylose content, indicating predominant regulation by additive gene action. Conversely, spikelet fertility, hulling percentage and milling percentage showed moderate heritability and low genetic gains, suggesting non-additive gene influence. These results provided useful information on the genetic contribution to phenotypic variation and the relative variability of these traits among the evaluated rice hybrids and checks.

Keywords: *Oryza sativa* L., Genetic Variability, Broad-Sense Heritability, Genetic Advance, Protein Content, Amylose Content

Introduction

Rice (*Oryza sativa* L., $2n = 24$) is the primary dietary staple for over half of the global population. Global rice production during the 2025/26 cycle was estimated at approximately 545.51 million metric tons of milled grain (USDA, 2025) [1]. Although India commands the largest acreage and contributes roughly 28% to global production, its average productivity ($\sim 4.39 \text{ t ha}^{-1}$) remains substantially lower than leading producers like China ($\sim 7.19 \text{ t ha}^{-1}$) (USDA, 2025) [1]. This yield gap highlights the critical need to design high-yielding varieties and experimental F₁ hybrids. In the high-rainfall Konkan ecosystem of Maharashtra, rice serves as a socio-economic anchor; however, production is constrained by fragmented landholdings, escalating labor scarcity, and minimal mechanization, necessitating the development of robust, high-yielding hybrids tailored to local agro-ecologies.

The phenotypic expression of complex quantitative traits is an interactive function of the genotype and prevailing environmental parameters. Effective selection requires partitioning total phenotypic variance into genotypic (GCV) and phenotypic (PCV) components to gauge the relative environmental influence. While broad-sense heritability (h^2_{bs}) quantifies the proportion of phenotypic variance attributable to genetic variations, it lacks predictive accuracy regarding absolute selection gain when confounded by non-additive gene action (epistasis and dominance). Consequently, the concurrent estimation of heritability and genetic advance as a percentage of mean (GAM) serves as a superior index to predict the response to directional selection, confirming whether a trait is governed by additive or non-additive genetic components. This investigation evaluates the genetic architecture, heritability parameters, and expected genetic gain for fifteen morphophysiological and biochemical parameters in twelve promising experimental rice hybrids under the agro-climatic conditions of Karjat, Maharashtra.

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Materials and methods

Experimental plant material

The experimental germplasm consisted of sixteen genotypes: twelve experimental F₁ hybrids developed *via* a three-line breeding system utilizing the cytoplasmic male-sterile (CMS) line IR-58025A crossed with distinct restorer lines, to get the respective hybrids. The checks included two hybrid checks (Sahyadri 3 and Sahyadri 4) and two varietal checks (Karjat 7 and Konkani Sanjay), procured from the Regional Agricultural Research Station, Karjat. The experimental lines evaluated were designated as KJTRH-2101, KJTRH-2205, KJTRH-2232, KJTRH-2243, KJTRH-2314, KJTRH-2334, KJTRH-2347, KJTRH-2353, KJTRH-2411, KJTRH-2414, KJTRH-2422 and KJTRH-2446.

Field layout and crop management

The field trial was conducted in a Randomized Block Design (RBD) with three replications during the *Kharif* 2025 season at RARS, Karjat, Raigad, Maharashtra. Seedlings were transplanted at a standard spacing of 15 cm × 15 cm. Agronomic interventions, crop protection protocols and fertilizer applications were executed uniformly across all plots as per standard package of practices.

Phenotypic and biochemical phenotyping

Quantitative and qualitative measurements were recorded from five randomly selected competitive plants per genotype per replication. Observations were recorded for fifteen distinct traits *viz* days to 50% flowering (DFF), plant height (PH, cm), panicle length (PL, cm), number of tillers per plant (NTP), number of productive tillers per plant (NPP), spikelet fertility (SF, %), test weight (TW, g), grain yield

per plant (GYP, g), straw yield per plant (SYP, g), harvest index (HI, %), hulling percentage (HLP, %), milling percentage (MLP, %), protein content (PC, %), amylose content (AC, %), and length-to-breadth ratio (LBR). Biochemical analyses for grain protein content (via total nitrogen determination) and amylose concentration were executed using standard colorimetric and analytical biochemistry methodologies.

Statistical and biometrical computations

Raw field data were subjected to Analysis of Variance (ANOVA) using standard linear models for RBD. Genotypic and phenotypic variances were estimated utilizing the mean expectation values according to [Weber et al. \(1952\)](#) [2]. The genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated following [Burton et al. \(1953\)](#) [3] and classified as low (< 10%), moderate (10–20%), and high (> 20%) based on [Sivasubramanian and Madhava Menon \(1973\)](#) [4]. Broad-sense heritability (h^2_{bs}) was derived using the genetic-to-phenotypic variance ratio. Genetic advance (GA) and genetic advance as a percentage of mean (*GAM*) were computed according to [Johnson et al. \(1955\)](#) [5]. All biometrical analyses were processed *via* R software platforms.

Results and discussion

Analysis of variance (ANOVA)

The structured analysis of variance ([Table 1](#)) demonstrated highly significant differences ($p < 0.01$) among the sixteen evaluated genotypes across all fifteen traits. This confirms the presence of extensive genetic variability within the breeding material, establishing the empirical validity for further partitioning into genotypic and phenotypic components.

Table 1. Analysis of Variance (ANOVA) for Yield, Yield-Contributing, and Biochemical Traits

Source	d.f.	DFF	PH (cm)	PL (cm)	NTP	NPP	SF (%)	TW (g)	GYP (g)	SYP (g)
Replication	2	0.44	36.53	5.06	2.97	6.42	17.56	1.94	6.71	2.58
Treatments	15	101.82**	415.30**	18.07**	10.37**	6.29**	41.25**	16.38**	50.23**	60.00**
Error	30	1.59	27.44	2.47	3.07	2.10	13.51	2.36	4.53	9.72

** Significant at the 1% probability level ($p < 0.01$). DFF: Days to 50% flowering; PH: Plant height; PL: Panicle length; NTP: Number of tillers/plant; NPP: Number of productive tillers/plant; SF: Spikelet fertility; TW: Test weight; GYP: Grain yield/plant; SYP: Straw yield/plant.

Table 1. Continued...

Source	d.f.	HI (%)	HLP (%)	MLP (%)	PC (%)	AC (%)	LBR
Replication	2	0.89	10.40	2.43	0.02	0.73	0.01
Treatments	15	31.83**	8.26**	18.15**	1.68**	17.83**	0.25**
Error	30	2.15	2.94	4.93	0.02	1.47	0.01

** Significant at the 1% probability level ($p < 0.01$). HI: Harvest index; HLP: Hulling percentage; MLP: Milling percentage; PC: Protein content; AC: Amylose content; LBR: Length-to-breadth ratio.

Genetic variability parameters

Phenotypic coefficients of variation were uniformly higher than their corresponding genotypic counterparts across all parameters, signaling environmental interactions, though the margins remained minimal for most characters. Low-to-moderate variability coupled with narrow GCV-PCV margins were observed for days to 50% flowering (GCV = 6.22%, PCV = 6.36%), plant height (GCV = 9.13%, PCV = 10.05%), panicle length (GCV = 8.85%, PCV = 10.75%), harvest index (GCV = 7.19%, PCV = 7.93%), and L/B ratio (GCV = 9.22%, PCV = 9.65%). These findings align with [Nithya et al. \(2020\)](#) [6] and [Sala et al. \(2016\)](#) [7], confirming rigorous genetic control over these expressions. In contrast, the number of tillers per plant (GCV = 10.26%, PCV = 15.42%) and number of productive tillers per plant (GCV = 10.69%, PCV = 16.90%) exhibited wider GCV-PCV disparities, echoing the findings of [Ullah et al. \(2023\)](#) [8] and [Savitha et al. \(2015\)](#) [9], which point to environmental vulnerability regarding tillering processes. Economically vital parameters such as grain yield per plant

manifested moderate coefficients of variation (GCV = 12.33%, PCV = 14.04%), matching the conclusions of [Babu et al. \(2024\)](#) [10]. Grain milling properties, specifically hulling percentage (1.79%, 2.91%) and milling percentage (3.44%, 5.01%), presented the narrowest variation parameters, consistent with [Binodh et al. \(2006\)](#) [11].

Heritability and genetic advance as a percent of mean

Broad-sense heritability values exhibited wide variations, extending from 37.65% (hulling percentage) to a peak of 97.13% (grain protein content). In structural alignment with [Ojha et al. \(2018\)](#) [12], biochemical profiling demonstrated that protein content combined high heritability (97.13%) with high genetic advance (*GAM* = 23.29%). This highly favorable genetic framework was similarly recorded for grain yield per plant (h^2_{bs} = 77.07%, *GAM* = 22.30%), plant height (h^2_{bs} = 82.49%, *GAM* = 17.08%), and amylose content (h^2_{bs} = 78.81%, *GAM* = 18.98%). These traits are governed by additive gene action, as documented by [Akter et al. \(2019\)](#) [13] and [Akshay et al.](#)

(2022) [14], indicating that direct phenotypic selection will be highly effective.

Conversely, traits like days to 50% flowering (95.45%), L/B ratio (91.26%), and harvest index (82.12%) yielded high broad sense heritability but only low-to-moderate genetic advance values (12.51%, 18.14%, and 13.42%, respectively). This dynamic reflects the influence of non-additive gene actions (dominance/epistasis) and environmental interactions, corroborating Meena *et al.* (2020) [15] and Gour

et al. (2017) [16]. Furthermore, tillering parameters (NTP, NPP), spikelet fertility, and grain-recovery values (HLP, MLP) displayed low-to-moderate heritability integrated with limited genetic gains, matching the trends discovered by Divya *et al.* (2018) [17] and Kurmanchali *et al.* (2019) [18]. Heterosis breeding or multi-locational progeny tests across temporal scales remain necessary to bypass these genotype $\times$ environment blocks, as advanced by Fentie *et al.* (2021) [19] and Shrivastava *et al.* (2015) [20].

Table 2. Genetic Parameters for Agro-Morphological and Biochemical Traits in Rice Genotypes

Sr.	Trait	Mean	Min	Max	GCV(%)	PCV(%)	$h^2_{bs}(\%)$	GA	GAM(%)
1	Days to 50% Flowering	93.00	81.00	101.00	6.22	6.36	95.45	11.63	12.51
2	Plant Height (cm)	124.52	91.36	147.24	9.13	10.05	82.49	21.27	17.08
3	Panicle Length (cm)	25.77	20.12	30.88	8.85	10.75	67.81	3.87	15.01
4	No. of Tillers/Plant	15.21	8.40	19.20	10.26	15.42	44.25	2.14	14.06
5	No. of Prod. Tillers	11.06	6.80	15.40	10.69	16.90	39.96	1.54	13.91
6	Spikelet Fertility (%)	84.12	72.96	91.41	3.61	5.67	40.64	3.99	4.75
7	Test Weight (g)	21.92	16.08	26.35	9.86	12.10	66.41	3.63	16.56
8	Grain Yield/Plant (g)	31.66	21.90	38.23	12.33	14.04	77.07	7.06	22.30
9	Straw Yield/Plant (g)	41.10	29.26	51.28	9.96	12.52	63.31	6.71	16.33
10	Harvest Index (%)	43.77	36.12	50.02	7.19	7.93	82.12	5.87	13.42
11	Hulling Percentage (%)	74.50	68.11	78.69	1.79	2.91	37.65	1.68	2.26
12	Milling Percentage (%)	61.04	50.60	67.33	3.44	5.01	47.21	2.97	4.87
13	Protein Content (%)	6.49	5.04	8.13	11.47	11.64	97.13	1.51	23.29
14	Amylose Content (%)	22.50	17.12	26.97	10.38	11.69	78.81	4.27	18.98
15	L/B Ratio	3.02	2.31	3.65	9.22	9.65	91.26	0.55	18.14

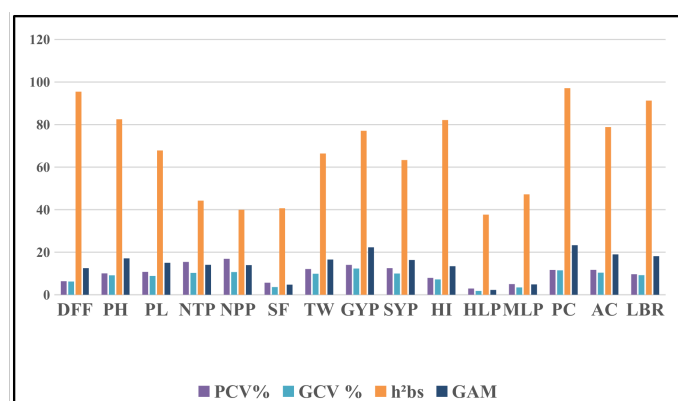


Figure 1. Pattern of PCV, GCV, heritability (broad sense) and genetic advance as percent of mean for various traits in 16 rice genotypes.

CHARACTERS: DFF-Days to fifty percent flowering, PH-Plant height (cm), PL-Panicle length (cm) NTP-No. of tillers per plant, NPP-No. of productive tillers per plant, SF-Spikelet fertility (%) TW-Test weight (g), GYP-Grain yield per plant (g) SYP- Straw yield per plant (g), HI-Harvest index (%), HLP-Hulling percentage (%), MLP-Milling percentage (%), PC-Protein content (%), AC-Amylose content (%), LBR-L/B ratio.

Conclusion

Extensive genetic variability was successfully characterized across the sixteen evaluated rice genotypes for all fifteen parameters. Traits such as grain yield per plant, protein content, plant height and amylose content exhibited high broad-sense heritability coupled with high expected genetic advance, indicating substantial genetic variability and good scope for effective selection among the evaluated hybrids. Conversely, tillering and milling parameters showed greater environmental influence and complex genetic control, emphasizing the need for multi-environment evaluation to assess hybrid stability and consistency. Overall, grain yield per plant, harvest index and protein content emerged as important traits for identifying superior hybrids and advancing promising rice hybrids under the agro-ecological conditions of Karjat, Maharashtra.

References

1. United States Department of Agriculture. World agricultural production. Foreign Agricultural Service, USDA, Washington, DC; 2025.
2. Weber CR, Moorthy BR. Heritable and nonheritable relationships and variability of oil content and agronomic characters in the F2 generation of soybean crosses 1. *Agron. J.* 1952;44(4):202-209.

3. Burton GW, De Vane EM. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal- material. *Agron. J.* 1953;45:478-481.
4. Sivasubramaniam S, Madhava Menon P. Heterosis and inbreeding depression in rice. *Madras Agric. J.* 1973;60(2):1134-1144.
5. Johnson HW, Robinson HF, Comstock R. Estimates of genetic and environmental variability in soybean. *Agron. J.* 1955;7(7):314-318.
6. Nithya N, Beena R, Stephen R, Abida PS, Jayalekshmi VG, Viji MM, Manju RV. Genetic variability, heritability, correlation coefficient and path analysis of morphophysiological and yield related traits of rice under drought stress. *Chem. Sci. Rev. Lett.* 2020;9(33):48-54.
7. Sala M, Shanthi P. Variability, heritability and genetic advance studies in F2 population of rice (*Oryza sativa* L.). *Agric. Res. J.* 2016;53(1):13-18.
8. Ullah MZ, Biswas P, Islam MS. Genetic Analysis of Agronomic Traits and Grain Anthocyanin and Micronutrient (Zinc and Iron) Content in Rice (*Oryza sativa* L.). *Trends Agric. Sci.* 2023;2:288-297.
9. Savitha P, Usha KR. Assessment of genetic variability and correlation studies among traditional land races and improved cultivars for segregating generations of rice (*Oryza sativa* L.). *Int. J. Sci. Nat.* 2015;6(2):135-140.
10. Babu H, Thouseem N. Genetic variability, correlation and path analysis of yield and its attributing traits in rice (*Oryza sativa* L.). *Int. J. Plant Soil Sci.* 2024;36(8):1029-1043.
11. Binodh AK, Kalaiyarasi R, Thiyagarajan K, Manonmani S. Physio-chemical and cooking quality characteristics of promising varieties and hybrids in rice (*Oryza sativa* L.). *Indian J. Genet. Plant Breed.* 2006;66(02):107-112.
12. Ojha GC, Sarawgi AK, Ojha N. Physico-chemical characterization of indigenous and exotic rice germplasm accessions for quality traits *Int. J. Chem. Sci.* 2018;6(2):3231-3236.
13. Akter A, Hasan MJ, Latif MA, Kulsum MU, Biswas PL, Rahman MH, Ara A. Genetic variability, heritability, correlation and path coefficient studies for yield and yield components of some promising rice hybrids. *Bangladesh Rice J.* 2019;23(2):27-34.
14. Akshay M, Chandra BS, Devi KR, Hari Y. Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). *Pharma Innov. J.* 2022;11(5):167-172.
15. Meena D, Kumar M, Sandhya KN, Yamini T, Meena AK. Assessment of correlation and path coefficient analysis for yield and its attributing traits in rice (*Oryza sativa* L.) genotypes. *Int. J. Curr. Microbiol. Appl. Sci.* 2020;9(7):3845-3851.
16. Gour L, Koutu GK, Singh SK, Patel DD, Shrivastava A, Singh Y. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *Pharma Innov. J.* 2017;6(11):693-696.
17. Divya J, Raju CD, Rao LS, Aparna K. Genetic Variability Studies in genetically diverse rice genotypes. *Int. J. Curr. Microbiol. Appl. Sci.* 2018;7(4):1169-1172.
18. Kurmanchali M, Kurmanchali N, Kukreti A, Sihag N, Chaudhary H, Karnwal MK. Study of genetic variability, heritability and genetic advance for various yield attributing and quality traits in basmati rice (*Oryza sativa* L.). *Int. J. Chem. Sci.* 2019;7(1):2486-2489.
19. Fentie BD, Bayuh Belay Abera BB, Ali HM. Association of Agronomic Traits with Grain Yield of Lowland Rice (*Oryza sativa* L.) Genotypes. *Int. J. Res. Agric. Sci.* 2021;8(3):2348-3997.
20. Shrivastava A, Mishra DK, Koutu GK. Estimation of genetic parameters of variability for yield and its attributing traits in parental lines of hybrid rice. *Plant Arch.* 2015;15(1):571-574.

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