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ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD, YIELD ATTRIBUTES AND QUALITY TRAITS IN ADVANCED RICE BREEDING LINES

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ABSTRACT

Genetic variability is the foundation of any successful crop improvement programme, as it facilitates the identification and selection of superior genotypes for yield and grain quality traits. The present investigation was conducted during *Rabi*, 2025-2026 at the Seed Research and Technology Centre (SRTC), Rajendranagar, Hyderabad, to assess genetic variability, heritability and genetic advance in 40 F† advanced breeding lines of rice (*Oryza sativa* L.). The experiment was laid out in a Randomized Block Design (RBD) with two replications. Fourteen traits, including yield components and grain quality parameters, were evaluated and genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability and genetic advance as per cent of mean (GAM) were estimated. Analysis of variance revealed significant differences among the breeding lines for all the characters studied, indicating the presence of substantial genetic variability. High PCV and GCV were recorded for number of filled grains per panicle while, 1000-grain weight, plant height, grain yield per plant, milling percentage and head rice recovery exhibited moderate variability. High heritability coupled with high genetic advance was observed for plant height number of filled grains per panicle, 1000-grain weight, grain yield per plant, milling percentage and head rice recovery, suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection. These traits may therefore serve as reliable selection criteria for developing high-yielding rice cultivars with improved grain quality.

Key words : Rice, Variability, Heritability, Genetic advance.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and serves as the principal food source for more than half of the global population. Besides meeting the dietary requirements of billions of people, rice cultivation provides employment and income to millions of farming families, particularly in developing countries. Asia dominates both rice production and consumption, contributing the largest share of the world's rice output and accounting for the majority of global rice consumption (FAO, 2020).

The demand for rice is expected to increase steadily over the coming decades due to continuous population growth and changing food requirements. According to Food and Agricultural Policy Research projections, global rice demand is anticipated to rise from 496 million tonnes in 2020 to approximately 555 million tonnes by 2035. (Jasmine *et al*., 2022). Likewise, with the world's population projected to approach 10 billion by 2050, ensuring an adequate supply of rice has become a major challenge for researchers, breeders and policymakers.

Rice is often described as "Rice is Life" because of

its indispensable role in ensuring food security and sustaining the livelihoods of nearly 120-150 million rural households. (Sandeep *et al.*, 2018). The crop contributes not only to nutritional security but also to the social and economic well-being of millions of people who depend on rice cultivation and its associated industries. Consequently, enhancing rice productivity has become an important priority to meet future food demands.

In India, the requirement for rice is also projected to increase substantially in the coming years. Estimates suggest that the national demand may reach 121.2 million metric tonnes by 2030, 129.6 million metric tonnes by 2040 and approximately 137.3 million metric tonnes by 2050. To satisfy this increasing demand without expanding the area under cultivation, productivity must be enhanced considerably. According to the (CRRI Vision 2050) report, average rice productivity needs to increase from the current level of about 2.4 t ha^{-1} to nearly 3.4 t ha^{-1}, while maintaining the existing cultivated area. Therefore, the development of high-yielding and superior rice varieties through efficient breeding approaches has become increasingly important.

Genetic improvement of rice largely depends on the availability of sufficient genetic variability within the breeding population. Variability provides the basic foundation for selection and enables plant breeders to identify desirable genotypes possessing superior agronomic and quality traits. However, selection based solely on observable plant performance may not always be reliable because environmental factors can significantly influence the expression of quantitative traits. As a result, superior phenotypes observed in one generation may not necessarily retain their performance in subsequent generations (Akshay *et al.*, 2022).

To improve the efficiency of selection, genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are widely employed. The genotypic coefficient of variation indicates the extent of heritable genetic variability present for a trait, whereas heritability estimates the proportion of observed variation that is genetically controlled. When considered together with genetic advance, these parameters provide valuable information regarding the expected response to selection and help identify traits predominantly governed by additive gene action, making them suitable targets for crop improvement (Burton, 1952).

Keeping these aspects in view, the present investigation was undertaken to assess the magnitude of genetic variability, estimate heritability and genetic advance and identify promising advanced breeding lines possessing desirable yield and quality attributes. The study was conducted using 40 advanced breeding lines to generate information that would facilitate effective selection and support the development of high-yielding rice cultivars with improved grain quality.

Materials and Methods

The present study was conducted during *Rabi*, 2025-2026 at the Seed Research and Technology Centre (SRTC), Rajendranagar, Hyderabad, Telangana, India. The experimental material comprised 40 F_6 advanced breeding lines, which were evaluated to estimate the extent of genetic variability and genetic parameters for yield, yield attributing and grain quality traits. The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each breeding line was planted in three rows of 2 m length, maintaining a spacing of 15 cm × 15 cm between rows and plants. All the experimental plots were managed under uniform agronomic conditions by following the recommended package of practices to ensure normal crop growth and development.

Observations on days to 50% flowering were recorded on a plot basis for each breeding line. At physiological maturity, five healthy and representative plants were selected randomly from each genotype in every replication for recording observations on yield and its associated traits. The traits studied included plant height (cm), number of productive tillers per plant, panicle length (cm), panicle weight (g), number of filled grains per panicle, 1000-grain weight (g) and grain yield per plant (g). In addition, important grain quality parameters such as hulling percentage, milling percentage, head rice recovery percentage, kernel length (mm), kernel breadth (mm) and kernel length-to-breadth (L/B) ratio were also recorded.

The observations obtained from the five sampled plants were averaged to obtain a mean value for each genotype. These mean values were subsequently used for statistical analysis. Analysis of variance (ANOVA) for all the characters was performed separately following the procedure for a Randomized Block Design as described by Panse and Sukhatme (1978) to determine the significance of differences among the breeding lines.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated using the method proposed by Burton and Devane (1953). Based on the classification suggested by Sivasubramanian and Madhavamenon (1973), the magnitude of variability was categorized as low (0-10%), moderate (10-20%)

and high (>20%). Broad-sense heritability (H^2) was estimated according to the procedure outlined by Allard (1960). The heritability estimates were classified as low (0-30%), moderate (30-60%) and high (>60%), following the criteria proposed by Johnson *et al*. (1955). The expected genetic advance (GA) under selection was calculated using the method suggested by Burton (1952). Genetic advance was further expressed as genetic advance as per cent of mean (GAM) and the estimates were categorized as low (<10%), moderate (10-20%) and high (>20%) according to the classification given by Johnson *et al*. (1955).

Results and Discussion

The effectiveness of any plant breeding programme largely depends on the availability of adequate genetic variability for the traits of interest and the extent to which these traits are genetically inherited. A broad range of genetic variation provides greater opportunities for identifying superior genotypes through selection. Therefore, the assessment of variability, heritability, and expected genetic advance for yield, yield-attributing traits and grain quality parameters is an essential step in developing improved cultivars. As emphasized by Falconer (1981), the presence of sufficient genetic variability within a breeding population is a prerequisite for effective selection and sustained genetic improvement. Furthermore, evaluating variability in segregating breeding populations offers valuable information for identifying desirable lines and formulating efficient selection strategies.

The analysis of variance (ANOVA) performed on 40 advanced breeding lines of rice revealed significant differences among the genotypes for all the characters studied, namely days to 50% flowering, plant height, panicle length, panicle weight, number of productive tillers per plant, number of filled grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth and kernel length-to-breadth (L/B) ratio. The observed significance indicates the existence of substantial genetic variation among the breeding lines for these traits. Such variability provides ample scope for effective selection and further genetic improvement of desirable genotypes in the breeding programme.

The mean performance of the advanced breeding lines for all the traits evaluated is presented in Table 1. Estimates of genetic variability, including the genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance as per cent of mean, are summarized in Table 3. These parameters were used to assess the extent of genetic variation and to identify traits with greater potential for improvement through selection.

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for the studied traits are presented in Table 3. The PCV values varied from 2.70% for hulling percentage to 21.66% for number of filled grains per panicle, while the GCV values ranged from 2.14% for hulling percentage to 21.04% for number of filled grains per panicle, indicating differences in the extent of genetic variability among the characters evaluated.

High estimates of both PCV and GCV were observed for number of filled grains per panicle (21.66% and 21.04%, respectively). The high magnitude of variation observed for the trait suggests the presence of substantial genetic variability with comparatively less environmental influence, indicating good scope for improvement through selection. Similar observations for number of filled grains

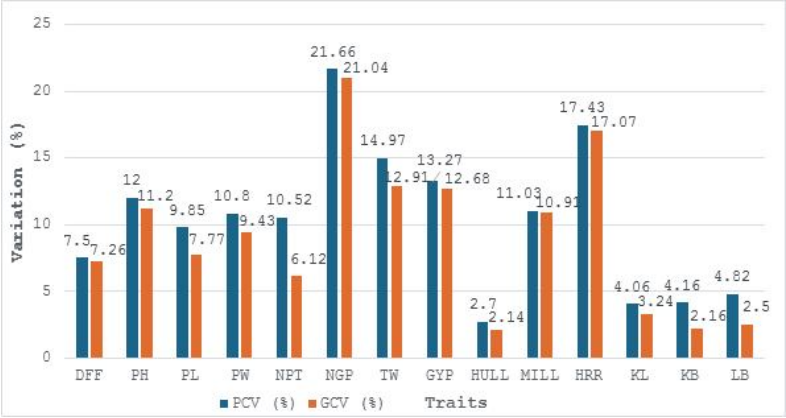


Fig. 1 : Graphical representation of PCV (%) and GCV (%) for yield, yield attributes and quality traits.

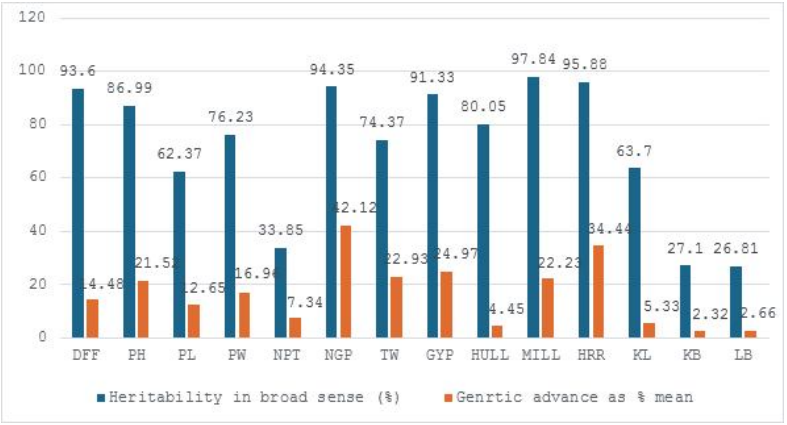


Fig. 2 : Graphical representation of heritability in broad sense and genetic advance as % of mean for yield, yield attributes and quality traits.

Table 1 : Mean performance of 40 advanced breeding lines for all the characters under study.

Genotypes	DFF	PH	PL	PW	NPT	NGP	TW	GYP	HULL	MILL	HRR	KL	KB	LB
RNR 57867	91	90	24.78	4.08	14.00	209	20.90	31.00	84.47	57.56	42.38	4.46	1.54	2.90
RNR 57868	89	88	25.53	4.03	13.00	162	18.00	25.28	83.00	59.45	44.47	4.68	1.60	2.92
RNR 57869	92	97	23.05	3.33	14.00	270	15.98	31.67	80.99	54.05	50.12	4.77	1.44	3.31
RNR 57870	105	75	21.33	2.98	12.00	175	13.27	22.43	80.14	68.04	43.95	4.81	1.49	3.23
RNR 57871	106	71	16.95	2.99	14.00	129	16.99	22.05	80.89	59.60	48.06	5.12	1.58	3.24
RNR 57872	105	71	19.30	2.98	12.00	141	16.47	22.37	80.91	57.64	38.72	4.81	1.53	3.14
RNR 57873	107	69	21.63	3.06	12.00	192	16.25	22.46	80.53	68.80	47.25	4.90	1.54	3.17
RNR 57874	104	67	22.42	3.11	13.00	153	15.94	23.11	80.69	67.83	45.60	5.15	1.60	3.21
RNR 57875	93	94	25.17	3.32	13.00	181	14.74	20.66	80.73	67.45	56.45	4.95	1.57	3.15
RNR 57876	92	98	25.27	3.60	12.00	237	14.01	21.19	80.81	77.16	65.64	4.87	1.59	3.06
RNR 57877	102	108	25.05	3.47	14.00	201	15.40	22.81	81.64	71.31	44.30	4.76	1.52	3.14
RNR 57878	93	95	23.43	3.24	13.00	268	13.60	21.43	82.42	64.85	54.42	4.90	1.60	3.06
RNR 57879	95	93	21.20	3.17	14.00	207	15.87	22.56	78.88	57.61	52.98	4.86	1.58	3.07
RNR 57880	101	96	24.17	4.14	14.00	221	16.42	27.46	80.46	64.31	44.65	4.63	1.55	2.98
RNR 57881	92	99	24.12	3.10	12.00	187	15.81	24.14	82.90	55.85	37.35	4.65	1.46	3.17
RNR 57882	93	86	25.18	3.14	12.00	283	16.67	31.93	79.34	57.51	54.61	4.78	1.50	3.19
RNR 57883	92	105	24.97	3.63	11.00	257	13.24	21.75	82.95	69.54	61.12	4.86	1.50	3.24
RNR 57884	102	103	24.53	3.76	11.00	218	13.63	21.84	83.97	68.59	61.52	4.87	1.45	3.36
RNR 57885	91	103	24.22	3.95	11.00	296	13.21	22.14	83.35	74.30	53.78	4.68	1.54	3.04
RNR 57886	92	98	23.28	3.82	12.00	203	16.74	23.09	80.25	70.39	42.00	4.75	1.62	2.92
RNR 57887	94	102	24.78	4.04	12.00	168	13.78	23.93	78.98	66.05	41.58	4.76	1.52	3.17
RNR 57888	95	98	23.37	4.01	12.00	271	15.57	27.13	84.34	65.57	40.65	4.81	1.59	3.01
RNR 57889	93	95	23.72	3.16	11.00	290	12.60	21.96	83.97	76.64	47.89	4.97	1.57	3.17
RNR 57890	92	94	20.95	3.81	12.00	183	13.02	20.95	82.59	76.87	48.39	4.91	1.55	3.18
RNR 57891	98	107	25.55	3.50	13.00	205	15.01	21.09	82.34	71.15	55.17	4.88	1.51	3.23
RNR 57892	98	97	23.80	3.85	14.00	230	14.16	22.12	81.98	71.68	44.57	4.86	1.56	3.11
RNR 57893	94	98	22.13	3.38	13.00	251	17.05	28.72	82.76	74.43	45.41	4.75	1.59	2.99
RNR 57894	102	99	25.33	3.26	12.00	209	14.94	21.07	82.24	72.59	63.32	5.07	1.53	3.30
RNR 57895	104	96	23.60	3.21	14.00	189	15.49	23.18	91.73	77.58	55.30	4.94	1.55	3.17
RNR 57896	110	96	18.88	3.22	17.00	220	13.84	25.47	85.38	76.98	56.95	5.05	1.53	3.28
RNR 57897	112	93	21.45	3.77	14.00	152	17.15	24.28	83.65	72.59	41.93	5.00	1.50	3.33
RNR 57898	110	101	22.37	3.37	13.00	163	15.31	23.74	83.87	67.09	34.25	4.79	1.53	3.13
RNR 57899	111	95	20.15	3.23	13.00	208	15.50	22.11	82.66	78.26	65.13	4.70	1.56	3.01
RNR 57900	108	102	22.80	3.24	14.00	213	13.93	22.11	80.40	72.81	38.23	4.65	1.45	3.20
RNR 57901	110	101	23.68	3.32	13.00	268	17.01	28.97	82.81	75.33	66.23	5.13	1.65	3.10
RNR 57902	107	101	25.42	3.30	13.00	225	16.63	24.25	83.34	60.64	46.49	5.00	1.56	3.21
RNR 57903	109	104	26.50	3.34	12.00	313	17.52	30.78	81.85	56.52	50.50	4.51	1.49	3.01
RNR 57904	110	120	21.70	3.15	13.00	183	16.53	20.46	81.14	74.82	48.11	5.20	1.56	3.31
RNR 57905	108	89	24.37	3.15	12.00	204	15.90	23.99	81.49	61.51	40.86	5.15	1.59	3.23
RNR 57906	110	101	25.15	3.39	14.00	174	15.80	23.22	82.12	67.70	41.25	4.82	1.49	3.23
RNR 15048	99	101	23.08	3.63	14.00	252	11.57	23.26	82.42	70.68	61.25	4.57	1.50	3.04
Mean	100	95	23.27	3.44	13.00	214	15.39	23.90	82.17	67.99	49.33	4.85	1.54	3.15
CD (%)	3.83	8.30	2.84	0.36	2.21	22.2	2.35	1.88	2.02	2.22	3.52	0.23	0.11	0.26
SE(m)	1.34	2.90	0.99	0.12	0.77	7.77	0.82	0.66	0.70	0.77	1.23	0.08	0.03	0.09
CV (%)	1.89	4.33	6.00	5.26	8.56	5.14	7.57	3.90	1.20	1.62	3.53	2.44	1.54	3.15

DFF: Day to 50% flowering, **PH:** Plant height (cm), **PL:** Panicle length (cm), **PW:** Panicle weight (g), **NPT:** Number of productive tillers per plant, **NGP:** Number of filled grains per panicle, **TW:** 1000-grain weight (g), **GYP:** Grain yield per plant (g), **HULL:** Hulling (%), **MILL:** Milling (%), **HRR:** Head rice recovery (%), **KL:** Kernel length (mm), **KB:** Kernel breadth (mm), **L/B:** Kernel length /kernel breadth ratio.

Table 2 : Analysis of variance for yield, its components and quality traits.

S. no.	Characters	Mean sum of squares		
		Replications (d.f=1)	Treatments (d.f=41)	Error (d.f=41)
1.	Days to 50% flowering	3.95	107.34**	3.62
2.	Plant height (cm)	27.70	236.84**	16.88
3.	Panicle length (cm)	1.10	8.43**	1.97
4.	Panicle weight (g)	0.0022	0.252**	0.03
5.	No. of productive tillers per plant	0.0013	2.366*	1.19
6.	No. of filled grains per panicle	5.38	4368.46**	120.87
7.	1000- grain weight (g)	0.74	32.64**	1.36
8.	Grain yield per plant (g)	0.483	21.16**	0.87
9.	Hulling (%)	1.11	8.67**	0.98
10.	Milling (%)	1.84	114.02**	1.21
11.	Head rice recovery (%)	1.86	137.63**	3.04
12.	Kernel length (mm)	0.00	0.06**	0.014
13.	Kernel breadth (mm)	0.008	0.005*	0.003
14.	Kernel length/breadth ratio	0.03	0.02*	0.017

Table 3 : Mean, coefficient of variation, heritability (broad sense), genetic advance as per cent of mean for different characters.

Characters	Mean	Range		PCV (%)	GCV (%)	Heritability	Genetic advance as per cent mean
		Min	Max				
DFF	100.00	89.00	112.00	7.50	7.26	93.60	14.48
PH	95.00	67.00	120.00	12.00	11.20	86.99	21.52
PL	23.27	16.95	26.50	9.85	7.77	62.37	12.65
PW	3.44	2.98	4.14	10.80	9.43	76.23	16.96
NPT	13.00	11.00	17.00	10.52	6.12	33.85	7.34
FGP	214.00	129.00	313.00	21.66	21.04	94.35	42.12
TW	15.39	12.60	18.90	14.97	12.91	74.37	22.93
GYP	23.90	20.66	31.93	13.27	12.68	91.33	24.97
HULL	82.17	78.98	91.73	2.70	2.14	80.05	4.45
MILL	67.99	54.05	78.26	11.03	10.91	97.84	22.23
HRR	49.33	34.25	66.23	17.43	17.07	95.88	33.44
KL	4.85	4.46	5.20	4.06	3.24	63.70	5.33
KB	1.54	1.44	1.65	4.16	2.16	27.10	2.32
LB	3.15	2.90	3.36	4.82	2.50	26.81	2.66

per panicle were reported by Sudeepthi *et al*. (2020), Paramanik *et al*. (2023), Sahithi *et al*. (2023) and Maruti *et al*. (2025).

Moderate values of PCV and GCV were recorded for plant height (12.00% and 11.20%), test weight (14.97%, 12.91%), grain yield per plant (13.27% and 12.68%), milling percentage (11.03% and 10.91%), and head rice recovery (17.43% and 17.07%). These results indicate the existence of moderate genetic variability for these characters, suggesting that improvement through selection is feasible. Comparable findings for plant height were reported by Devi *et al*. (2022) and Anusha *et al*. (2024); for test weight by Anusha *et al*. (2024) and Modarresi *et al*. (2026); for grain yield per plant by Sudeepthi *et al*. (2020), Awad-allah *et al*. (2022) and Maruti *et al*. (2025); for milling percentage by Akshay *et al*. (2022) and Sadhana *et al*. (2022); and for head rice recovery by Sadhana *et al*. (2022) and Anusha *et al*. (2024).

Low PCV and GCV estimates were observed for days to 50% flowering (7.50% and 7.26%), panicle length (9.85% and 7.77%), hulling percentage (2.70% and 2.14%), kernel length (4.06% and 3.24%), kernel breadth (4.16% and 2.16%) and kernel length-to-breadth (L/B) ratio (4.82% and 2.50%). The relatively low estimates for these traits indicate limited genetic variability and a comparatively greater influence of environmental factors on their expression. Similar results for days to 50% flowering were reported by Sudeepthi *et al*. (2020), Anusha *et al*. (2024) and Nanda *et al*. (2026); for panicle length by Sadhana *et al*. (2022) and Shahin *et al*. (2023); for hulling percentage by Akshay *et al*. (2022) and Anusha *et al*. (2024). and for kernel length, kernel breadth by Nikki and Parmer (2020) and Nanda *et al*. (2026) and L/B ratio by Kumar *et al*. (2018) and Nikki and Parmer (2020).

Heritability values ranged from 26.81% for kernel length-to-breadth (L/B) ratio to 97.90% for milling

percentage, whereas the genetic advance as per cent of mean varied from 2.32% for kernel breadth to 47.16% for 1000-grain weight (test weight). Heritability and genetic advance are important genetic parameters that provide valuable information regarding the effectiveness of selection.

High heritability coupled with high genetic advance as per cent of mean was recorded for number of filled grains per panicle, plant height, grain yield per plant, 1000-grain weight (test weight), milling percentage and head rice recovery. This combination suggests that these traits are predominantly governed by additive gene action, making them highly amenable to improvement through direct phenotypic selection. Similar findings were reported by Nanda *et al*. (2026) and Maruti *et al*. (2025) for number of filled grains per panicle; Anusha *et al*. (2024) and Maruti *et al*. (2025) for plant height; Maruti *et al*. (2025) and Nanda *et al*. (2026) for grain yield per plant; Maruti *et al*. (2025) and Modarresi *et al*. (2026) for 1000-grain weight and Panika *et al*. (2022) and Anusha *et al*. (2024) for head rice recovery.

High heritability associated with moderate genetic advance as per cent of mean was observed for days to 50% flowering, panicle length and panicle weight. This pattern indicates that both additive and non-additive gene effects may be involved in the inheritance of these traits. It also suggests that, although these characters are highly heritable, the expected improvement through selection may be moderate because environmental factors and gene interactions also contribute to their expression. Similar observations were reported by Anusha *et al*. (2024) and Nanda *et al*. (2026) for days to 50% flowering; Pallavi *et al*. (2022), Shruti *et al*. (2023) and Anusha *et al*. (2024) for panicle length and Sadhana *et al*. (2022) and Edukondalu *et al*. (2017) for panicle weight.

High heritability coupled with low genetic advance as per cent of mean was observed for hulling percentage and kernel length. Such a combination indicates limited scope for improvement through simple phenotypic selection, as these traits are likely influenced by non-additive gene action and environmental factors despite their high heritability. Similar findings for hulling percentage were reported by Akshay *et al*. (2022) and Edukondalu *et al*. (2017).

Conclusion

The findings of the present investigation revealed the existence of considerable genetic variability among the advanced breeding lines for several yield and grain quality traits. Characters such as plant height, number of filled grains per panicle, 1000-grain weight, grain yield per plant milling percentage and head rice recovery percentage exhibited moderate to high levels of variability, along with high heritability and high genetic advance as per cent of mean. This combination indicates that these traits are predominantly controlled by additive gene action and can be effectively improved through direct phenotypic selection. Therefore, these characters may be considered reliable selection criteria in rice breeding programmes aimed at developing high-yielding genotypes with improved grain quality.

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