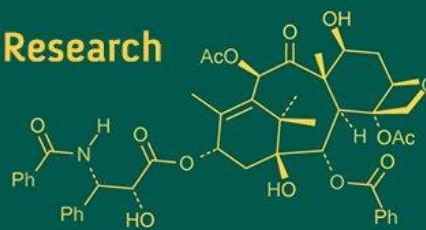


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Study on variability and genetic advance for yield and its attributing traits in rice genotypes (*Oryza sativa* L.) over the five environments of Chhattisgarh

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Abstract

The present work was carried out in two consecutive years of *Kharif* (wet season) season during 2022 and 2023 at five different locations of Chhattisgarh State. The variability parameters were estimated for 12 agro-morphological and 15 grain quality traits. The mean sum of square in analysis of variance for environment revealed that all the morphological and quality traits showed highly significant variation and also for the grain quality except for alkali spreading value, gel consistency and amylose content. In the combined analysis over five environments and over two seasons, the top values of genotypic and phenotypic coefficients of variation were found moderate for morphological traits viz., total number of tillers per plant (15.63 and 17.32) and quality trait head rice recovery (11.96 and 13.65). The high heritability coupled with high genetic advance was found highest for the morphological trait total number of tillers per plant ($h^2(b) = 81.41\%$, $GA = 29.05\%$) and for quality trait head rice recovery ($h^2(b) = 76.85\%$, $GA = 21.61\%$). The high heritability coupled with high genetic advance is desirable as the traits get transfer from generation after generation in high frequency with high rate of genetic improvement as they are governed with additive gene action.

Keywords: Rice, genetic variability, heritability and genetic advance

Introduction

The global population and two-thirds of the population in India rice serves as a primary food source (Rout *et al.*, 2020) ^[10]. India is one of the world's leading producers and exporters of rice and therefore, plays a vital role in ensuring global food security. During 2025-26, the India rice production was estimated at a record 154.02 million tonnes, and was reported to have surpassed China as the world's largest rice-producing nation (Press Information Bureau, 2026) ^[13]. Chhattisgarh is popularly known as Rice Bowl of India. Rice is grown on 68.8 percent (32.85 lakh hectares in *Kharif* and in addition to this, approx. 5 lakh hectares is sown during summer paddy during December to May) to the total of 47.75 lakh hectares agricultural land of the state. The agricultural land is 34 percent of the state's total geographical area (Panda, 2025) ^[12].

The world population is projected to reach a peak of 10.4 billion by the 2080s, with approximately 9.7 billion people anticipated by 2050 (Norman *et al.*, 2022) ^[9]. This possesses a significant challenge in feeding the world's population within the planet's ecological boundaries (Rockström *et al.*, 2020) ^[15]. The national average yield of India is anticipated approximately to 2.7-3.0 t ha⁻¹, which remains substantially lower due to the continued cultivation of older inbred varieties, fragmented landholdings, limited quantity of quality seed access, and suboptimal agronomic practices (FAO, 2022). These problems can be managed to a great extent by screening and developing rice varieties having traits such as higher yields, shorter maturity period, better input efficiency, efficient land use and climate resilience varieties.

In the state, Indira Gandhi Krishi Vishwavidyalaya, Raipur maintains the 23,250 rice germplasm which were collected and conserved from various locations of Chhattisgarh, Madhya Pradesh and adjoining state of Odisha. The existence of sufficient genetic variability is considered to be essential for any effective crop improvement initiative. In rice cultivation, relying solely on phenotypic selection based on performance can

sometimes be misleading, as environmental factors may obscure the true genotypic potential, resulting in subpar performance in later generations. Thus, to attain consistent genetic enhancement, it is vital to select genotypes using genetic metrics such as heritability and genetic advance. The genotypic coefficient of variation (GCV) is a dependable measure for assessing the level of genetic variability and indicates the percentage of variation due to genetic factors (Maruti *et al.*, 2025) [7]. Analysing genetic variability measures alongside heritability and genetic advance aids in forecasting the expected genetic gain from selection (Burton, 1952) [1]. In this contest, the present study was carried out using nine rice genotypes including two checks, subjected to multilocation trail in five environments for two consecutive seasons.

Materials and Methods

The field experiment was conducted in two consecutive *Kharif* (wet season) seasons during 2022 and 2023 at five different locations. The five different locations were College of Agriculture, IGKV, Raipur, KVK Dhamtari, KVK Bhatapara, KVK Balod and KVK Kanker. The experimental material comprises of nine genotypes of rice laid out in Randomized Complete Block Design (RCBD) with four replications. The plot size was 2 m x 5 m. A spacing of 20 cm between rows and 15 cm between plants was maintained throughout the experiment. The recommended agronomic and plant-protection practices were applied uniformly to all experimental plots during the crop-growth period to minimize non-experimental variation and ensure the establishment of a healthy and uniform crop stand.

Observations were recorded on five randomly selected plants per replications for twelve morphological traits, namely days to 50 per cent flowering, plant height (cm), total number of tillers per plant, number of effective tillers per plant, number of panicles per plant, panicle length (cm), total number of spikelets per panicle, number of fertile spikelets per panicle, spikelet fertility percent, grain yield per plant (g), grain yield per ha on plot basis (q) and harvest index and fifteen quality traits *i.e.* test weight, hulling percent, milling percent, head rice recovery, paddy length, paddy breadth, paddy length to breadth ratio, length of milled rice, breadth of milled rice, length to breadth ratio of milled rice, length of cooked kernel, kernel elongation ratio, Alkali spreading value, Gel consistency and Amylose content. The data were pooled over five locations in each *Kharif* season *i.e.* *Kharif* 2022 and *Kharif* 2023. The pooled data of individual season was then again pooled over the two seasons for the analysis of variation including genetic parameters like phenotypic coefficient of variation, genotypic coefficient of variance, heritability in broad sense and genetic advance as percent of mean. The genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated using the formula given by (Burton, 1952) [1]. The PCV and GCV values were categorized as low (0-10%), moderate (10-20%), and high (>20%) following (Sivasubramanian and Madhavamenon, 1973) [16]. Heritability in a broad sense (h^2b) was estimated following the method of (Khush, 2013) [5] and (Hanson *et al.*, 1956) [4]. The genetic advance as a percentage of the mean was calculated as per (Burton & De Vane, 1953) [1]. These genetic parameters provided insight into the variability present in the genotypes screened and provide the scope for improvement through selection (Murti *et al.*, 2025).

Estimation of Variability Parameters

- a) **Genotypic variance:** It is the variance contributed by genetic causes or the occurrence of differences among the individuals due to their genetic makeup.

$$V_g = \frac{MSg - MSe}{r}$$

Where,

V_g = Genotypic variance, MSg = Treatment mean square, MSe = Error mean square, and r = Number of replications

- b) **Phenotypic variance:** It is the sum of variances contributed by genetic causes and environmental factors and was computed as;

$$VP = V_g + MSe$$

Where,

V_p = Phenotypic variance, V_g = Genotypic variance and MSe = Error mean square

- c) **Genotypic coefficient of variation (GCV):** The magnitude of genetic variation existing in the trait was estimated by the formula;

Where,

$$GCV = \frac{\sqrt{V_g}}{\bar{x}} \times 100$$

V_g = Genotypic variance, $\bar{x}$ = Population mean of the character

- d) **Phenotypic coefficient of variation (PCV):** The magnitude of phenotypic variation existing in a trait was estimated by using the following formula;

$$PCV = \frac{\sqrt{V_p}}{\bar{x}} \times 100$$

Where,

V_p = Phenotypic variance, $\bar{x}$ = Population mean of the character

- e) **Heritability (broad sense):** The proportion of total phenotypic variance that is attributed to genetic variance in a population.

$$h^2(bs) = (\sigma_g^2 / \sigma_p^2) \times 100$$

Where,

$h^2(bs)$ = Broad sense heritability, σ_g^2 = genotypic variance and σ_p^2 = phenotypic variance

- f) **Genetic Advance (GA):** The expected improvement in a trait from one generation of selection based on phenotypic performance.

$$GA = k \times \sigma_p \times h^2(bs)$$

Where, k = selection differential (standard value for 5% selection intensity is 2.06),

σ_p = phenotypic standard deviation, $h^2(bs)$ = heritability in broad sense

- g) **Genetic Advance as Percentage of Mean (GAM):** Genetic advance expressed as a percentage of the

population mean, indicating the potential for genetic improvement.

$$GAM = (GA / GrandMean) \times 100$$

Results and discussion

In the present investigation, analysis of variance pooled over five locations for two seasons were worked out which revealed significant mean squares for all the morphological characters and quality traits except for alkali spreading value, gel consistency and amylose content for genotypes. The highly significant mean square for environment was observed in all traits under study as revealed in Table 3 & Table 4. The mean sum of square for genotypes were also found highly significant for traits days to 50% flowering, plant height, total number of tillers per plant, number of effective tillers per plant, number of panicle per plant, panicle length, total number of spikelets per panicle, number of filled spikelets per panicle, spikelets fertility percent, grain yield per plant, grain yield per ha on plot basis, harvest index, test weight, hulling percent, milling percent, head rice recovery, paddy length, paddy breadth, paddy length to breadth ratio, breadth of milled rice, length of cooked rice, kernel elongation ratio (Table 3 & Table 4). The significant mean sum of square for genotypes was obtained in length of milled rice and length to breadth ratio of milled rice. Beside this the non-significant mean sum of square was obtained for the trait's alkali spreading value, gel consistency and amylose content. Further, for replication and replication with environment interaction analysis of variance revealed no significant mean sum of squares for all the morphological and quality traits in rice genotypes (Table 3 & Table 4).

Analysis of variance in case of genotype with environment interaction reveals that mean sum of square was highly significant for the traits like total number of tillers per plant, number of effective tillers per plant, number of panicle per plant, panicle length, total number of spikelets per panicle, number of filled spikelets per panicle, spikelets fertility percent, grain yield per plant, grain yield per ha on plot basis, harvest index, test weight, hulling percent, milling percent, head rice recovery, paddy length, paddy breadth, paddy length to breadth ratio, breadth of milled rice, length of cooked rice (Table 3 & Table 4). The mean sum of square was significant for the quality traits like alkali spreading value and gel consistency, while for the traits like days to 50% flowering, plant height, length of milled rice, length to breadth ratio of milled rice, kernel elongation ratio and amylose content were found non-significant for genotype with environment interaction.

The above results clearly indicate that there was sufficient variability for almost all the characters among the nine genotypes. The traits like days to 50% flowering, plant height, length of milled rice, length to breadth ratio of milled rice, kernel elongation ratio and amylose content were found non-significant for genotype with environment interaction. It revealed that environment is not creating significant variation in the such traits. The genotypes for such traits superseded the effects of environments for such traits.

In the combined analysis of variance over five environments and over two seasons, the values of genotypic and phenotypic coefficients of variation were moderate for morphological traits viz., total number of tillers per plant

(15.63 and 17.32) followed by number of panicles per plant (11.96 and 13.06), total number of spikelets per panicle (11.55 and 13.47) and number of filled spikelets per panicle (11.38 and 14.10); quality traits viz., head rice recovery (11.96 and 13.65) (Table 5). Similar finding was reported for moderate GCV and PCV for characters by total number of tillers per plant and number of filled spikelets per panicle were reported by Gupta *et al.*, 2021^[3].

Further, study revealed that the low genotypic and moderate phenotypic coefficient of variation was observed by number of effective tillers per plant (9.51 and 12.10), harvest Index (9.01 and 10.49) and spikelet fertility per cent (8.23 and 10.91) (Table 5). Similar observations of low GCV for low GCV for spikelet fertility was noted by Mohanty *et al.*, 2020^[8] and Sreewongchai *et al.*, 2010^[17] and Murti *et al.*, 2025; for panicle length by Gupta *et al.*, 2021^[3]. The fact that PCV values were greater than GCV values across all traits suggests that, there is significant genetic variability, the influence of environmental factors should be over looked in the expression of these traits.

The low genotypic and phenotypic coefficient of variation was obtained in the morphological traits viz., panicle length (8.24 and 8.63), grain yield per plant (7.32 and 8.06), plant height (3.83 and 4.01) and days to 50% Flowering (0.80 and 0.95); the quality traits viz., gel consistency (7.35 and 8.66), followed by length of cooked kernel (5.21 and 6.16), test weight (3.53 and 3.84), Paddy length to breadth ratio (3.34 and 3.57), hulling percent (3.22 and 3.80), paddy length (2.99 and 3.75), breadth of milled rice (2.82 and 3.45), milling percent (2.49 and 2.67), kernel elongation ratio (2.04 and 2.35), alkali spreading value (1.73 and 2.20), paddy breadth (1.64 and 1.89), amylose content (1.17 and 1.48), length of milled rice (0.94 and 1.13) and length to breadth ratio of milled rice (0.90 and 1.03) (Table 3). Similar observations of low GCV for days to 50% flowering were reported by Saha *et al.*, 2019^[11] and Sivasubramanian & Madhavamenon, 1973 and Murti *et al.*, 2025^[16].

Considerable variability was observed in the estimates of broad-sense heritability and genetic advance as a percent of mean (GAM) among morphological yield traits and grain quality traits. Very high (>90%) heritability was observed for days to 50% flowering days {h²(b)=91.46%}, Plant height (cm) {h²(b)=91.46%}, suggesting strong genetic control and a high probability of success through direct selection. High heritability (60%-90%) was observed for the morphological traits like grain yield per ha on plot basis {h²(b)=84.45%}, number of panicles per plant {h²(b)=83.87%}, grain yield per plant {h²(b)=82.45%}, total number of tillers per plant {h²(b)=81.41%}, harvest index {h²(b)=73.73%}, total number of spikelet per panicle {h²(b)=73.58%}, number of effective tillers per plant {h²(b)=61.83%} and while, the quality traits paddy length to breadth ratio {h²(b)=87.31%}, milling percent {h²(b)=86.70%}, test weight {h²(b)=84.26%}, length to breadth ratio of milled rice {h²(b)=77.13%}, head rice recovery {h²(b)=76.85%}, kernel elongation ratio {h²(b)=75.80%}, paddy breadth {h²(b)=75.74%}, gel consistency {h²(b)=72.16%}, hulling percentage {h²(b)=71.87%}, length of cooked kernel {h²(b)=71.72%}, length of milled rice {h²(b)=69.25%}, breadth of milled rice {h²(b)=66.66%}, paddy length {h²(b)=63.85%}, amylose content percent {h²(b)=62.24%} and alkali spreading value {h²(b)=62.03%}. High heritability (>60%) was recorded for most traits, indicating the predominance of genetic factors

over environmental influences. Moderate heritability (30-60%) was noted for spikelet fertility percent $\{h^2(b) = 56.92\}$ indicating a higher influence of environmental factors. High GAM (>20%) was observed for total number of tillers per plant $\{GAM = 29.05\}$ %, number of panicles per plant $\{GAM = 22.56\}$ %, grain yield per ha on plot basis $\{GAM = 21.06\}$ % and total number of spikelets per panicle $\{GAM = 20.41\}$ % while, the quality traits head rice recovery $\{GAM = 21.61\}$ %. High magnitude of heritability was observed for plant height, grain yield per plant, harvest index and 1000 seed weight. It is in accordance with Gupta *et al.* 2021 [3] and Kujur *et al.*, 2023 [6]. High heritability was observed for effective tillers per plant, days to 50 percent flowering and number of filled grains per panicle in accordance with Rashmi *et al.*, 2017 and Gupta *et al.* 2021 [2, 14]. The high

heritability coupled with high genetic advance is the desirable as the traits features gets transfer to generation after generation in high frequency with high rate of genetic improvement as they are tightly linked with additive gene of action. In comparison, the noted moderate heritability and moderate genetic gain per generation for morphological traits such as spikelet fertility percent $\{h^2(b) = 56.92\}$, $GA = 12.79\}$ % indicate that simple selection processes are unlikely to yield significant genetic improvements. This challenge arises from the intricate genetic makeup of these traits, which are controlled by multiple minor genes and are unresponsive to environmental variations. While yield-related traits can be effectively enhanced through straightforward phenotypic selection.

Table 1: Classification of genetic parameters

Parameter	Classification	Range	Reference
GCV & PCV	Low	< 10%	(Sivasubramanian and Madhavamenon, 1973) [16]
	Moderate	10 - 20%	
	High	> 20%	
Heritability (h^2)	Low	0 - 30%	(Burton, G.W. and De Vane, 1953) [11]
	Moderate	30.1 - 60%	
	High	> 60%	
Genetic Advance (GAM)	Low	0 - 10%	(Khush, 2013) [5]
	Moderate	10.1 - 20%	
	High	> 20%	

Table 2: List of Genotypes used in the present study

S. No.	Genotype Designation	Genotype name
1.	G1	R 2054-685-1-205-1
2.	G2	R 2223-979-1-394-1
3.	G3	NPT-HR-505-1-1
4.	G4	CG Dhan 1919
5.	G5	MTU 1318
6.	G6	Vikram TCR
7.	G7	Swarna super
8.	G8	MTU 1010
9.	G9	Swarna

Table 3. ANOVA based on RCBD for morphological traits pooled over locations (five environments) and over two seasons viz. Kharif 2022 & Kharif 2023 in nine rice genotypes

Source of variation	df	Days to fifty percent Flowering	Plant height (cm)	Total number of tillers per plant	Number of effective tillers per plant	Number of Panicles per plant	Panicle length (cm)	Total number of spikelets per panicle	Number of filled spikelets per panicle	Spikelets fertility %	Grain Yield per plant (g)	Grain Yield per ha on plot basis (q)	Harvest Index (%)
Replication	3	13.97	49.261	2.272	0.709	1.349	5.025	278.449	170.972	54.568	34.351	8.075	24.394
Environment	4	37.999**	256.223*	44.117**	6.390**	19.180*	22.026**	3957.152**	3716.765**	223.476**	564.133*	419.472**	73.473**
Genotype	8	36.128**	803.257*	195.186*	73.283*	70.720*	165.288*	17822.767*	12304.253*	2992.018*	232.391*	1423.663*	638.578*
Replication x Environment	12	7.879	51.490	1.572	1.370	1.063	1.780	279.374	210.086	39.340	9.571	33.851	11.373
Genotype x Environment	32	10.341	68.586	36.288**	27.972*	11.408*	14.426**	4709.520**	4296.721**	1289.000*	40.795**	221.354**	167.782*
Error	120	11.144	63.870	2.082	1.735	1.401	2.652	337.415	233.860	53.421	14.103	38.590	15.849
CD at 5%		1.47	3.52	0.64	0.58	0.52	0.72	8.09	6.74	3.22	1.65	2.74	1.75
CV %		3.32	7.15	11.31	11.77	11.62	6.91	11.72	12.30	9.22	12.56	12.60	10.46
S.Em		0.53	1.26	0.23	0.21	0.19	0.26	2.90	2.42	1.16	0.59	0.98	0.63

**Significant at 0.1% level, *Significant at 5% level

Table 4. ANOVA based on RCBD for quality traits pooled over locations (five environments) and over two seasons viz. *Kharif 2022 & Kharif 2023* in nine rice genotypes

Source of variation	df	Test weight (g)	Hulling %	Milling %	Head Rice Recovery %	Paddy length (cm)	Paddy Breadth (cm)	Paddy length breadth ratio	Length of milled rice (cm)	Breadth of milled rice (cm)	Length to breadth ratio of milled rice	Length of Cooked rice (mm)	Kernel elongation ratio	ASV	GC	Amylose (%)
Replication	3	1.627	5.092	2.113	56.103	0.029	0.003	0.004	0.043	0.005	0.001	0.347	0.013	0.053	55.838	1.704
Environment	4	14.641*	57.044*	134.834**	170.233*	0.417*	0.030*	0.073*	0.292*	0.037*	0.046*	1.235**	0.060**	0.936*	107.392**	127.135**
Genotype	8	27.297*	342.508**	140.196**	2753.869**	3.725*	0.083*	0.575*	0.174*	0.174*	0.040*	13.133*	0.057**	0.647*	799.395**	3.340
Replication x Environment	12	1.039	3.778	7.766	20.872	0.045	0.004	0.014	0.033	0.002	0.009	0.228	0.009	0.149	18.835	1.312
Genotype x Environment	32	4.295**	96.348*	18.643*	637.387*	1.347*	0.020*	0.073*	0.053	0.058*	0.009	3.715**	0.014	0.246*	222.557**	0.540
Error	120	1.245	5.449	8.967	30.382	0.055	0.005	0.016	0.041	0.003	0.009	0.290	0.012	0.170	27.731	1.699
CD at 5%		0.49	1.03	1.32	2.43	0.10	0.03	0.06	0.09	0.02	0.04	0.24	0.05	0.18	2.32	0.57
CV %		5.19	3.03	4.27	9.07	2.88	2.95	3.73	3.49	2.82	3.11	5.78	6.78	7.14	10.20	5.74
S.Em		0.18	0.37	0.47	0.87	0.04	0.01	0.02	0.03	0.01	0.02	0.09	0.02	0.07	0.83	0.21

**Significant at 0.1% level, *Significant at 5% level

Table 5: General means, phenotypic range, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense and genetic advance as % mean pooled over locations (five environments) and two seasons i.e. *Kharif 2022* and *Kharif 2023*

Character parameter	General mean	Minimum	Maximum	GCV %	PCV %	h ² (b)	GA as % of mean
Days to 50% flowering	100.65	99.35	101.80	0.80	0.95	69.82	1.37
Plant Height (cm)	111.76	105.92	119.06	3.83	4.01	91.46	7.55
Total number of tillers per plant	12.75	10.30	16.69	15.63	17.32	81.41	29.05
Number of effective tillers per plant	11.19	9.78	13.69	9.51	12.1	61.83	15.41
Number of panicles per plant	10.18	8.82	12.35	11.96	13.06	83.87	22.56
Panicle Length (cm)	23.56	20.09	26.37	8.24	8.63	91.27	16.22
Total number of spikelets per panicle	156.72	127.72	190.25	11.55	13.47	73.58	20.41
Number of filled spikelets per panicle	124.35	101.47	153.83	11.38	14.1	65.08	18.91
Spikelet fertility %	79.30	69.48	93.61	8.23	10.91	56.92	12.79
Grain yield per plant (g)	29.89	27.50	33.86	7.32	8.06	82.45	13.7
Grain yield per ha (q)	49.28	41.11	58.26	11.12	12.1	84.45	21.06
Harvest Index (%)	38.08	29.81	44.05	9.01	10.49	73.73	15.94
Test weight (g)	21.50	20.36	22.77	3.53	3.84	84.26	6.67
Hulling Percent	77.07	69.98	79.70	3.22	3.8	71.87	5.62
Milling Percent	70.08	66.03	71.77	2.49	2.67	86.70	4.77
Head rice recovery	60.80	47.39	75.81	11.96	13.65	76.85	21.61
Paddy Length	8.15	7.89	8.62	2.99	3.75	63.85	4.93
Paddy breadth	2.42	2.32	2.47	1.64	1.89	75.74	2.94
Paddy length to breadth ratio	3.36	3.22	3.56	3.34	3.57	87.31	6.42
Length of milled rice	5.81	5.76	5.93	0.94	1.13	69.25	1.62
Breadth of milled rice	1.91	1.84	2.05	2.82	3.45	66.66	4.74
Length to Breadth ratio of milled rice	3.07	3.02	3.12	0.90	1.03	77.13	1.64
Length of cooked kernel	9.31	8.32	10.33	5.21	6.16	71.72	9.09
Kernel elongation ratio	1.61	1.55	1.65	2.04	2.35	75.8	3.66
Alkali spreading value	5.78	5.55	5.95	1.73	2.2	62.03	2.81
Gel consistency	51.64	43.56	56.76	7.35	8.66	72.16	12.87
Amylose content %	22.70	22.45	23.33	1.17	1.48	62.24	1.89

Table 6: Genetic variability, heritability and Genetic advance as percent of mean summary as per the present study

Trait	GCV	Heritability (bs)	Genetic advance as % of mean (GAM)	Selection potential	Breeding Implications
Days to 50% flowering	Low	High(69.82%)	Low (~1.37)	Low	Despite high heritability slow progress expected due to low variability
Plant Height (cm)	Low	Very high (91.46%)	Low (~ 7.55)	Low	Despite high heritability slow progress expected due to low variability
Total number of tillers per plant	Moderate	High (81.41%)	High (~29.05)	High	Feasible improvement via selection, suitable for breeding
Number of effective tillers per plant	Low	High (61.83%)	Moderate (~15.41)	Moderate	Additive and non-additive effects; Low progress through selection
Number of panicles per plant	Moderate	High (83.87%)	High (~25.56)	High	Feasible improvement via selection, suitable for breeding
Panicle Length (cm)	Low	Very High (91.27%)	Moderate (~16.22)	Moderate	Selection response possible; additive effects moderately expressed
Total number of spikelets per panicle	Moderate	High (73.58%)	High (~20.41)	Moderate	Selection response possible; additive effects moderately expressed
Number of filled spikelets per panicle	Moderate	High (65.08%)	Moderate (~18.91)	Moderate	Selection response possible; additive effects moderately expressed
Spikelet fertility %	Low	Moderate(56.92%)	Moderate (~12.79)	Low	Environmental influence significant; indirect selection advisable
Grain yield per plant (g)	Low-Moderate	High (82.45%)	Moderate (~13.70)	Low-Moderate	Improvement via direct selection
Grain yield per ha (q)	Moderate	High (84.45%)	High (~21.06)	Moderate	Selection response possible; additive effects moderately expressed
Harvest Index (%)	Low	High (73.73%)	Moderate (~15.94)	Moderate	Selection response possible; additive effects moderately expressed
Test weight (g)	Low	High (84.26%)	Low (~6.67)	Low	Selection less effective; Environment influence manageable
Hulling Percent	Low	High (71.87%)	Low (~5.62)	Low	Selection less effective; Environment influence manageable
Milling Percent	Low	High (86.70%)	Low (~4.77)	Low	Selection less effective; Environment influence manageable
Head rice recovery	Moderate	High (76.85%)	High (~21.61)	Moderate	Selection possible; Environment influence manageable

Table 7: Genetic variability, heritability and Genetic advance as percent of mean summary as per the present study

Trait	GCV	Heritability (bs)	Genetic advance as % of mean (GAM)	Selection potential	Breeding Implications
Paddy Length	Low	High (63.85%)	Low (~4.93)	Low	Selection less effective
Paddy breadth	Low	High (75.74%)	Low (~2.94)	Low	Selection less effective
Paddy length to breadth ratio	Low	High (87.31%)	Low (~6.42)	Low	Selection less effective
Length of milled rice	Low	High (69.25%)	Low (~1.62)	Low	Selection less effective
Breadth of milled rice	Low	High (66.66%)	Low (~4.74)	Low	Selection less effective
Length to Breadth ratio of milled rice	Low	High (77.13%)	Low (~1.64)	Low	Selection less effective
Length of cooked kernel	Low	High (71.72%)	Low (~9.09)	Low	Selection less effective
Kernal elongation ratio	Low	High (75.80%)	Low (~3.66)	Low	Selection less effective
Alkali spreading value	Low	High (62.03%)	Low (~2.81)	Low	Selection less effective
Gel consistency	Low	High (72.16%)	Moderate (~12.87)	Low	Selection less effective
Amylose content %	Low	High (62.24%)	Low (~1.89)	Low	Selection less effective

4. Conclusion

The current investigation on nine rice genotypes revealed significant genetic variability for yield-attributing traits and grain quality traits based on mean performance and genetic variability parameters including GCV, heritability, and genetic advance. The moderate estimates of genotypic coefficient of variation (GCV), high broad-sense heritability and high genetic advance as percent of mean (GAM) for yield attributing traits like total number of tillers per plant, number of panicles per plant, total number of spikelets per panicle, grain yield per ha on plot basis and head rice recovery indicate the dominance of additive gene action, suggesting that genetic improvement can be effectively achieved through direct phenotypic selection. In contrast, high heritability coupled with moderate genetic advance for

traits, number of effective tillers per plant, panicle length, number of filled spikelets per panicle, grain yield per plant, harvest index and alkali spreading value points out that selection will be effective as additive genes are moderately expressed, forced to manage or control the environmental factors like management. While, only trait spikelet fertility percent showing moderate heritability with moderate genetic advance, points to complex genetic control and greater environmental influence, necessitating marker-assisted selection strategies.

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