A-6402
[1-8]

RESEARCH ARTICLE Indian Journal of Agricultural Research

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

Suman Kumar[1], Jayasudha S.[1], Rajani[1], S.K. Singh[1]

10.18805/IJARe.A-6402

ABSTRACT

Background: Rice plays a vital role in ensuring global food security, being a staple crop that feeds more than half of the global population. With rising food demand, improving its yield and quality is a prior demand that tends to meet the current changing scenarios and market demands. Unlocking its hidden genetic variability offers immense potential to breed superior varieties. Exploring heritability and genetic advance can accelerate the development of high-performing quality-rich rice cultivars to fulfill the need of future food demands and consumer preferences.

Methods: A study aimed to evaluate twenty-eight rice genotypes during *Kharif* 2023 for genetic variability, heritability and genetic advance as per cent of mean for twenty-two yield and quality traits was conducted at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi.

Result: ANOVA showed highly significant differences in the twenty-eight genotypes suggesting that considerable variability exists at the genotype levels. Test weight displayed high genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) followed by effective number of tillers per plant. For quality traits, alkali digestion value displayed the highest GCV and PCV, followed by gel consistency, elongation index and length-breadth ratio before cooking. The existence of considerable genetic variability in the genotypes studied for twenty-two traits was evident. All twenty-two traits exhibited higher heritability levels with varying degree of genetic advance. The traits PH, PL, SFP, TW, KLBC, KBBC, LBBC, ER, HRR, ADV, AC, GC and ADV showed high heritability values along with high genetic advance as per cent of mean. These traits have evidence of additive gene action and can be improved using direct selection methods.

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

INTRODUCTION

Rice (*Oryza sativa* L.) a monocot plant of the genus *Oryza* under tribe Oryzeae in the grass family Gramineae or Poaceae is recognized as the staple for more than 100 countries across the world. Hence, it is quoted as “global cereal” (Muthayya *et al.,* 2014). It is the primary source of food and crucial dietary source of people of many Asian countries (Satya and Rao, 2022). Rice is a food that supplies 80% of the energy needs for nearly 2 billion people in Asia (Bhattacharjee *et al.,* 2020). It is composed of approximately 80% carbohydrates, 7-8% protein, 3% fat and 3% fiber (Burton and De Vane, 1953). In rice-dependent nations, per capita consumption ranges from 62 to 192 kg per year, contributing about 20% of daily energy and 13% of dietary protein (Bollinedi *et al.,* 2020). Although rice is cultivated worldwide, there is an urgent need to boost its production to meet the demands of a population that is projected to exceed nine billion (Paillard *et al.,* 2014).

At present, the cultivated land is decreasing day by day. In the other scenario the global population is increasing at an alarming rate. To feed such a vast population the ultimate goal is to increase yield on decreasing piece of land. So, the most economical measure is to enhance the productivity through genetic variability studies. Genetic variability is essential for breeding programs aimed at developing new rice varieties (Chandramohan *et al.,* 2021). Breeders can cross genetically diverse parents to create offspring with improved traits, such as higher yield, better quality, disease resistance, or tolerance to environmental stresses (Swarup *et al.,* 2021). Different genotypes exhibit variations in yield potential and quality traits such as grain size, cooking quality and taste. Genetic variability studies help identifies promising genotypes with desirable traits that can feed increasing population, meet consumer preferences and market demands. By preserving and studying genetic variability, researchers and breeders can ensure the long-term productivity and resilience of rice cultivation, thus contributing significantly to global food production and agricultural sustainability (Begna and Begna, 2021).

---

[1]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, Uttar Pradesh, India.

Corresponding Author: Suman Kumar, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, Uttar Pradesh, India.
Email: suman16096@gmail.com

How to cite this article: Kumar, S., Jayasudha, S., Rajani and Singh, S.K. (2025). Genetic Variability, Heritability and Genetic Advance for Yield and Quality Traits in Rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research*. 1-8. doi: 10.18805/IJARe.A-6402.

Submitted: 19-04-2025 **Accepted:** 14-10-2025 **Online:** 28-10-2025

A population characterized by high variability offers ample opportunities to select and develop varieties with a multitude of desirable traits (Glenn *et al.,* 2017). Understanding the extent and nature of this variability, as well as factors like heritability and genetic advance, is vital for designing effective breeding programs aimed at developing improved varieties (Choudhary *et al.,* 2018). The present research is expected to provide information that can improve breeding methods, speed up the development of better rice varieties and help improve food security in the face of climate change and changing market demands.

MATERIALS AND METHODS

Experimental material and design

The study was carried out at the Agriculture Research Farm of Banaras Hindu University in Varanasi, Uttar Pradesh during the *kharif 2023*. The experiment involved twenty-eight rice genotypes, including both landraces and varieties (Table 1). A randomized complete block design was laid with two replications and a planting arrangement of 20 cm between rows and 15 cm between plants was followed. Recommended agronomic practices were followed to raise good crop.

Table 1: List of genotypes used in the study.

S. no.	Genotype
1.	HUR 3022
2.	HUR 1304
3.	Sarjoo 52
4.	Gautam
5.	HUR 4-3
6.	Malviya 36
7.	NDR-359
8.	Shiya
9.	Chintu
10.	Sampurna
11.	KRH-4
12.	MSN 99
13.	Higenic
14.	BB 11
15.	Moti
16.	Dhaniya
17.	BPT-5204
18.	MTU-7029
19.	Vijetha
20.	Yamuna
21.	Denim
22.	Syamjeera
23.	Damini
24.	Suvarna
25.	HUR 917
26.	Improved sambha mahsuri
27.	Swarna Sub-1
28.	HUR 105

The farm is located at an altitude of 123.23 meters above sea level, 25° 18′ north latitude and 83° 03′ east longitude. The soil in the area is Indo-Gangetic alluvial loam soil, known for its good fertility. The nursery was sown on a uniform raised bed. Twenty-five days old seedlings were transplanted to the main research field. The observations were recorded for twenty-two yield and quality traits as outlined in the following steps: The first border row is rejected; inner middle rows of each plot were used to randomly select five plants in both the replications. In each replication, the data was collected from five tagged plants from each accession. Tagging of plants was done before flowering.

Data collection

Data were recorded for 22 yield and quality traits: Days to 50% flowering (DFF), days to maturity (DTM), plant height (PH), effective number of tillers per plant (ET), panicle length (PL), spikelet fertility percentage (SFP), test weight (TW), grain yield per hectare (GY), amylose content (AC), gel consistency (GC), alkali digestion value (ADV), kernel length before cooking (KLBC), kernel breadth before cooking (KBBC), length-breadth ratio before cooking (LBBC), kernel length after cooking (KLAC), kernel breadth after cooking (KBAC), length-breadth ratio after cooking (LBBC), elongation ratio (ER), elongation index (EI), brown rice recovery (HUL), milled rice recovery (MIL) and head rice recovery (HRR). Observations for traits such as days to 50% flowering and days to maturity were recorded on a per-plot basis. Grain yield data were initially collected as per plot basis and subsequently converted to quintals per hectare (Q/ha) using an appropriate conversion factor. Test weight was determined by weighing 1000 kernels from each genotype in grams.

Statistical analysis

The data of mean value for all the characters were subjected to statistical analysis to assess variability. Analysis of Variance (ANOVA) was performed using R software (version 4.4.3) under a randomized complete block design (RCBD) to evaluate the significance of differences among genotypes. The procedure followed the methodology described by Panse and Sukhatme (1985) and the significance of F-values was determined using critical values from Yates' F-distribution table (Yates, 1967). Phenotypic and genotypic coefficient of variation were estimated following the method suggested by Burton and Devane (1953). Heritability in a broad sense (h^2b), genetic advance (GA) and genetic advance as per cent of means (GAM) were also estimated using the same analysis software.

RESULTS AND DISCUSSION

Mean performance and ANOVA

The mean performance of twenty-eight rice genotypes across twenty-two yield and quality traits is summarized in

Table 2a: ANOVA table for all the twenty-two traits.

Source of variation	d.f	Mean sum of square										
		DFF (days)	DTM (days)	PH (cm)	ET (No.)	PL (cm)	SFP (%)	TW (gm)	GY (Q/ha)	AC (%)	GC (mm)	ADV
Replication	1	0.643	0.643	1.059	3.500*	0.0001	1.995	0.228	3.250	5.792	5.786	0.003
Treatments	27	186.767**	203.963**	259.679**	4.534**	9.641**	128.866**	56.123**	231.408**	16.267**	612.275**	6.313**
Error	27	3.495	7.051	3.937	0.574	0.915	1.816	0.307	3.626	1.973	27.212	0.162

* Significance at 5% level of significance, **significance at 1% level of significance.

Table 2b: ANOVA table for all the twenty-two traits.

Source of variation	d.f	Mean sum of squares										
		KLBC (mm)	KBBC (mm)	LBBC	KLAC (mm)	KBAC (mm)	LBAC	ER	EI	Hulling (%)	Milling (%)	HRR (%)
Replication	1	0.001	0.011	0.049	0.0001	0.0001	0.0002	0.001	0.006	1.215	7.029	0.564
Treatments	27	1.593**	0.188**	0.762**	0.970**	0.240**	0.408**	0.119**	0.080**	26.902**	51.330**	87.191**
Error	27	0.021	0.016	0.066	0.059	0.028	0.033	0.004	0.011	6.05	1.818	2.847

* Significance at 5% level of significance, **significance at 1% level of significance.

Table 3, while the extent of variability among genotypes is visually depicted through box plots (Fig 1). Notably, the variation in alkali digestion value-a key indicator of cooking quality is illustrated separately in Fig 2. The ANOVA results based on a randomized block design for all 22 traits are detailed in Tables 2a and 2b. From these results, a highly significant sum of squares due to genotypes for all traits shows a highly significant range of genetic variability indicating the potential of effective selection and genetic improvement from this diverse rice set. Similar results were also observed by Priyanka *et al.,* (2017) and Hasan *et al.,* (2022) in rice for different yield and yield-related traits.

The classification of genotypic and phenotypic coefficients of variation (GCV and PCV) was based on the scale proposed by Robinson *et al.,* (1949), wherein values exceeding 20% are considered high, those between 10% and 20% moderate and below 10% low. By using this criterion, the present study detected considerable genetic variability based on GCV and PCV values (Table 4) ranging from low to high across the traits evaluated. For all the traits that were evaluated, GCV values differed only slightly from their corresponding PCV values, suggesting that the environmental factors have a minimal (non-significant) influence and a predominance of genetic control. Among yield traits, test weight exhibited the highest GCV and PCV values, followed by ET. For quality traits, ADV showed the highest GCV and PCV values, followed by GC, EI and LBBC. High genetic variability for these traits indicates they will respond favorably to direct selection. Overall, considerable variability between genotypes indicates the potential for genetic improvement by trait-specific selection in the future. These findings imply that genotypes in the study possess a wide genetic variability, presenting opportunities for genetic enhancement through targeted selection of these traits. Similar results were obtained in rice by Kushwah *et al.,* (2021), Akshay *et al.,* (2022), Mahesh *et al.,* (2022) and Paramanik *et al.,* (2023).

Heritability

Heritability is crucial in plant breeding as it indicates the extent to which genetic factors contribute to trait variation. High heritability allows breeders to efficiently select and predict trait expression, guiding better breeding strategies to achieve genetic gain. Ultimately, heritability enhances breeding success by focusing efforts where genetic potential for improvement is greatest, ensuring more productive and adaptable crop varieties. Among yield and associated traits, plant height (97.01%), days to 50% flowering (96.33%), days to maturity (93.32%), spikelet fertility percentage (97.20%) and grain yield per hectare (96.90%) had a very high heritability, indicating they have more strong genetic control and low environmental influence. Notably, test weight (98.91%) exhibited the highest heritability along with exceptionally high genetic advance as a percent of mean (63.09%), making it a key selection trait for grain yield improvement. Effective tillers per plant (77.52%) showed moderately high heritability, indicating that while genetic control is substantial, environmental effects may still play a role.

For grain quality traits, alkali digestion value recorded 95.00% heritability suggesting that selection for this trait would be highly efficient. Other traits such as gel consistency (91.50%), kernel length before cooking (97.40%) and head rice recovery (93.68%) also exhibited high heritability making them suitable for direct selection in breeding programs targeting cooking and processing quality. Traits such as length breadth ratio after cooking (84.10%), kernel breadth before cooking (84.30%) and elongation index (75.10%) had moderate to high heritability, suggesting that it is possible to achieve improvements, but a certain level of environmental influences should also be expected. These results are consistent with those reported by Satya *et al.,* (2022), Dinesh *et al.,* (2023) and Paramanik *et al.,* (2023). High heritability of these traits helps breeders to allocate resources effectively and prioritize traits for improvement.

Genetic advance

The estimates of genetic advance (GA) and genetic advance as percent of mean (GAM) presented in this study highlight the selection and expected genetic gain potential. The trait with highest GAM was alkali digestion value (110.89%), followed by test weight (63.09%) and gel consistency (59.17%) indicating that additive gene action is the main contributor in these traits and there will be significant effect of selection on these traits. Other traits such as length breadth ratio before cooking (36.36%), kernel length before cooking (35.63%), elongation index (34.69%), kernel breadth before cooking (32.86%) and length breadth ratio after cooking (28.99%) also exhibited a high GAM value, which suggests a good opportunity for breeding improvements. Moderate genetic advance was observed in traits like head rice recovery (25.89%), plant height (24.69%) and kernel breadth after cooking (21.76%), while days to 50% flowering (17.11%), days to maturity (13.90%) and panicle length (16.72%) showed relatively lower GAM,

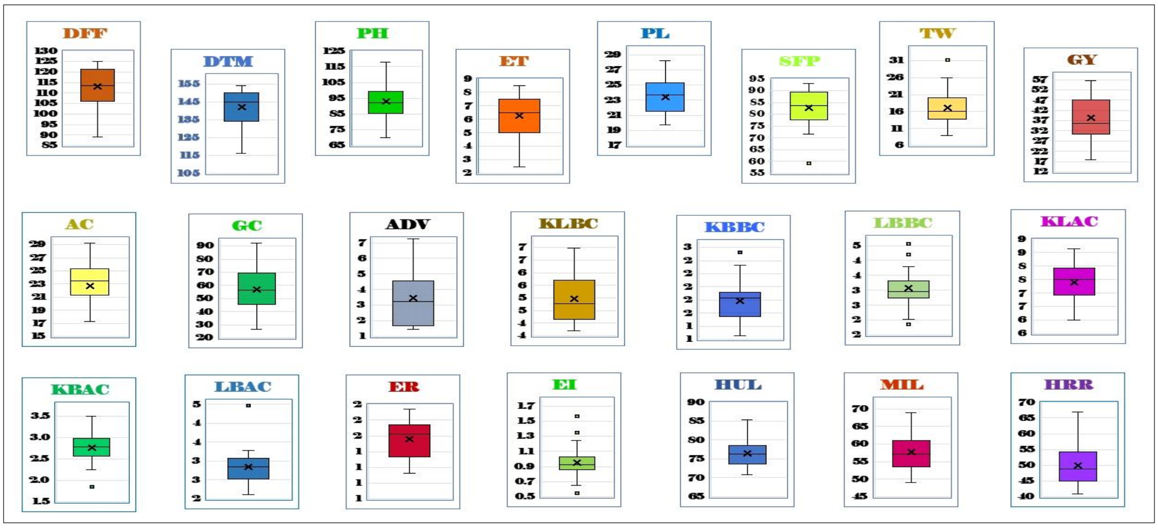

Fig 1: Boxplot showing the variation of traits among the 28 genotypes.

Fig 2: Variation in alkali digestion value among the genotypes.

Table 3: Mean performance of the 28 genotypes for yield and quality traits.

Genotypes	DFF (days)	DTM (days)	PH (cm)	ET (No.)	PL (cm)	SFP (%)	TW (g)	GY (q/ha)	AC (%)	GC (mm)	ADV	KLBC (mm)	KBBC (mm)	LBBC	KLAC (mm)	KBAC (mm)	LBAC	ER	EI	HUL (%)	MIL (%)	HRR (%)
HUR 3022	111	144	80.80	8.5	25.50	72.61	22.96	45.63	25.85	43.50	4.07	6.30	1.80	3.50	8.05	2.50	3.23	1.28	0.92	71.96	57.85	42.25
HUR 1304	121	148	78.05	6.5	20.55	84.20	21.32	44.12	22.50	54.50	6.43	4.90	1.75	2.81	7.50	3.05	2.46	1.54	0.88	74.87	55.95	42.78
Sarjoo 52	106	132	91.75	5.0	24.25	83.01	25.92	33.41	25.47	50.50	5.16	6.26	2.23	2.82	8.65	2.96	2.93	1.39	1.04	71.85	57.77	48.60
Gautam	113	141	110.15	5.0	24.30	74.25	20.05	26.17	28.42	62.00	1.22	4.90	1.80	2.73	8.55	2.95	2.90	1.75	1.07	80.63	64.06	53.24
HUR 4-3	104	134	93.20	7.5	25.45	79.81	20.18	55.30	22.52	60.50	6.50	5.70	1.50	3.80	8.00	2.45	3.27	1.41	0.86	72.06	55.61	45.86
Malviya 36	113	142	105.80	6.0	21.55	88.79	16.30	47.11	21.28	65.00	1.43	4.80	1.45	3.32	8.25	1.85	4.47	1.72	1.35	76.09	59.98	46.25
NDR 359	105	134	94.78	5.0	25.50	90.73	31.30	53.92	25.68	45.25	4.07	7.08	2.43	2.93	8.95	2.85	3.14	1.27	1.08	76.83	58.07	48.92
Moti	92	119	92.10	5.5	24.10	80.09	14.69	30.30	23.87	70.50	2.85	3.95	1.35	2.93	6.35	2.35	2.71	1.61	0.93	78.75	56.74	48.52
Dhaniya	89	116	118.15	5.5	25.80	90.58	18.22	29.67	27.29	90.00	4.31	4.11	2.20	1.87	7.85	2.70	2.91	1.91	1.56	71.72	51.97	47.59
BPT 5204	123	151	77.40	5.0	21.10	91.00	14.01	51.55	24.00	26.75	4.07	5.87	1.83	3.22	7.40	2.25	3.29	1.26	1.03	77.67	56.15	54.46
MTU 7029	121.5	150	89.30	8.5	24.75	92.93	19.25	51.70	23.29	45.50	2.88	5.60	2.05	2.74	6.65	3.15	2.11	1.19	0.78	76.49	55.01	61.46
Vijetha	111	140	85.10	7.5	25.95	80.80	9.03	27.47	20.84	72.50	3.01	5.91	1.40	4.22	8.25	2.90	2.85	1.40	0.68	75.94	60.69	51.75
Yamuna	106	135	95.35	7.5	22.60	87.34	10.98	31.79	23.28	57.00	1.50	4.30	1.45	2.97	7.30	2.65	2.76	1.70	0.93	77.30	48.97	44.75
Denim	106	140	99.35	4.5	20.35	88.92	14.99	26.93	2.31	59.50	2.07	4.30	1.25	3.45	8.17	2.80	2.92	1.90	0.85	77.02	52.85	44.23
Shiya	123	152	70.15	8.0	19.75	59.08	9.37	18.02	19.12	78.00	1.22	4.15	1.50	2.78	7.40	2.60	2.85	1.79	1.03	72.18	49.22	40.84
Chintu	125	154	87.30	8.5	21.60	71.50	10.03	31.30	28.17	44.50	1.15	4.15	1.30	3.19	7.15	2.25	3.19	1.72	1.00	80.00	59.22	51.52
Sampurna	122	151	87.25	4.5	23.15	82.57	13.77	24.85	29.25	32.00	1.14	5.22	1.15	4.55	6.30	2.55	2.49	1.21	0.55	78.37	52.90	43.02
KRH 4	103	131	101.30	7.0	28.25	80.16	16.96	32.84	19.39	67.25	2.64	5.05	1.75	2.89	8.45	2.95	2.87	1.68	1.00	74.71	53.07	42.66
MSN 99	119	148	99.05	6.5	23.25	85.57	13.82	43.06	21.27	54.50	1.48	4.25	1.35	3.26	8.25	2.65	3.12	1.94	1.00	79.00	64.41	46.45
Higenic	120	150	85.50	5.5	24.05	78.28	11.78	30.53	20.16	83.00	1.36	3.80	1.90	2.03	7.20	2.90	2.48	1.89	1.24	83.82	61.10	54.85
BB 11	123	152	84.50	6.0	21.85	90.51	18.81	34.65	17.24	92.50	1.36	4.05	1.95	2.08	6.65	3.15	2.12	1.65	1.02	75.92	51.78	48.91
Syamjeera	105	129	82.30	4.5	21.05	77.41	15.06	54.45	22.30	70.00	1.40	4.75	1.75	2.74	7.75	3.15	2.47	1.64	0.91	75.74	56.41	48.92
Damini	112	146	85.90	2.5	20.30	93.09	15.37	32.30	23.10	51.75	3.97	4.55	1.70	2.69	8.15	3.10	2.63	1.79	0.98	73.42	54.70	46.86
Suvarna	122	150	106.90	6.5	26.80	89.73	19.77	39.72	23.96	47.00	6.93	4.85	1.65	2.97	6.95	2.60	2.68	1.44	0.91	82.08	60.85	56.61
HUR 917	120	148	99.50	8.0	24.15	87.06	13.26	40.67	25.05	26.50	4.17	5.85	1.78	3.29	7.74	2.67	2.91	1.32	0.89	85.30	66.66	66.91
Improved Sambha Mahsuri	121	150	97.00	6.5	23.20	87.22	15.88	46.66	23.77	30.00	3.42	4.78	1.75	2.73	7.95	3.50	2.29	1.66	0.84	70.82	64.06	57.60
Swarna Sub-1	121	150	89.85	6.5	24.65	73.91	24.07	36.65	23.97	59.00	4.50	5.50	1.70	3.25	8.15	3.00	2.75	1.49	0.86	76.97	68.95	62.95
HUR 105	114	143	113.60	8.0	21.85	74.48	23.20	56.42	24.02	56.00	4.67	6.71	1.60	4.20	7.55	2.75	2.76	1.13	0.66	75.20	63.88	52.21
C.D. at 5%	3.84	5.45	4.07	1.55	1.96	2.77	1.14	3.91	2.88	10.70	0.83	0.30	0.26	0.53	0.50	0.34	0.37	0.14	0.21	5.04	2.77	3.46
SE(m)	1.32	1.88	1.40	0.54	0.68	0.95	0.39	1.35	0.99	3.69	0.28	0.10	0.09	0.18	0.17	0.12	0.13	0.05	0.07	1.74	0.95	1.19
C.V.	1.65	1.87	2.14	12.05	4.09	1.63	3.23	4.95	5.98	9.16	12.68	2.85	7.55	8.35	3.15	5.96	6.37	4.23	10.95	3.21	2.35	3.37

(DFF- days to 50% flowering; DTM- days to maturity; PH- plant height; ET- effective number of tillers per plant; PL- panicle length; SFP- Spikelet fertility percentage; TW- test weight; GY- grain yield; AC- amylose content; GC- gel consistency; ADV- alkali digestion value; KLBC- kernel length before cooking; KLBC- kernel breadth before cooking; LBBC- length breadth ratio before cooking; KLAC- kernel length after cooking; KBAC- kernel breadth after cooking; LBAC- length-breadth ratio after cooking; ER- elongation ratio; EI- elongation index; HUL-Hulling %; MIL- Milling%; HRR- head rice recovery%).

Table 4: Estimates of parameters of genetic variability.

Trait	Mean	Maximum	Minimum	CV	Genotypic variance	Phenotypic variance	Environmental variance	GCV	PCV	ECV	Heritability	Genetic advance	GA as % of mean
DFF (days)	113	127	87	1.65	91.64	95.13	3.49	8.47	8.63	1.65	96.33	19.35	17.11
DTM (days)	142	159	113	1.87	98.46	105.51	7.05	6.99	7.23	1.87	93.32	19.74	13.9
PH (cm)	92.91	119.5	68.2	2.14	127.87	131.81	3.94	12.17	12.36	2.14	97.01	22.94	24.69
ET (No).	6.29	9	2	12.05	1.98	2.55	0.57	22.39	25.42	12.05	77.52	2.55	40.58
PL (cm)	23.42	30	19.3	4.09	4.36	30	5.28	8.92	9.81	4.09	82.66	3.91	16.72
SFP (%)	82.69	93.18	58.36	1.63	63.525	65.34	1.82	9.64	9.77	0.97	97.20	16.19	19.57
TW (g)	17.15	31.69	8.95	3.23	27.91	28.22	0.31	30.8	30.97	3.23	98.91	10.82	63.09
GY(Q/ha)	38.47	58.3	17.90	4.95	113.89	117.52	3.63	27.74	28.18	3.63	96.9	21.64	56.25
AC (%)	23.48	30.20	16.45	5.98	7.15	9.12	1.97	11.39	12.86	5.98	78.40	4.88	20.77
GC (mm)	56.96	96	23	9.16	292.53	319.74	27.21	30.03	31.39	9.16	91.50	33.71	59.17
ADV	3.18	7	1	12.68	3.08	3.24	0.16	55.22	56.66	12.68	95.00	3.52	110.89
KLBC (mm)	5.06	7.12	3.8	2.85	17.53	17.76	0.02	17.53	17.76	2.85	97.40	1.80	35.63
KBBC (mm)	1.69	2.55	1.1	7.55	0.09	0.10	0.02	17.36	18.91	7.56	84.3	0.56	32.86
LBBC	3.07	4.82	1.81	8.35	0.35	0.41	0.07	19.23	20.98	8.35	84.10	1.12	36.36
KLAC (mm)	7.7	9	6.2	3.15	0.46	0.51	0.06	8.76	9.31	3.15	88.60	1.31	17.00
KBAC (mm)	2.75	3.7	1.8	5.96	0.11	0.13	0.02	11.84	13.22	5.96	78.81	0.60	21.76
LBAC	2.85	4.56	2	6.36	0.19	0.22	0.03	15.23	16.52	6.37	85.20	0.82	28.99
ER	1.56	1.96	1.08	4.23	0.05	0.06	0.01	15.32	15.98	4.21	92.30	0.47	30.36
EI	0.96	1.56	0.54	10.95	0.04	0.05	0.01	19.54	22.41	10.96	75.10	0.33	34.69
HUL (%)	76.52	86.22	68.73	3.21	10.43	16.48	6.05	4.22	5.3	3.21	63.28	5.29	6.92
MIL (%)	57.46	69.2	48.58	2.35	24.76	26.57	1.82	8.66	8.97	2.35	93.16	9.9	17.23
HRR (%)	50.03	68.51	40.45	3.37	42.17	45.02	2.85	12.98	13.41	3.37	93.68	12.95	25.89

indicating slower progress under selection. Traits like hulling percentage (6.92%) had the lowest genetic advance, suggesting limited scope for genetic improvement through direct selection. Overall, traits with relatively high heritability as well as high genetic advance *viz*., ADV, TW, GC and GY are ideal targets for effective genetic gains in rice breeding. These findings are in accordance with recent studies by Demeke *et al.,* (2023) which focuses on plant height and grain yield. Dinesh *et al.,* (2023) also reported high heritability along with high genetic advance for GC and other traits.

CONCLUSION

The evaluation of twenty-eight rice genotypes for twenty-two yield and quality traits revealed a high degree of genetic variability, providing a strong foundation for selection and crop improvement. Analysis of variance (ANOVA) showed highly significant differences among genotypes for all traits, emphasizing abundance of genetic variation within the material. Estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) further supported this variability, with traits like test weight, effective tillers per plant, alkali digestion value and gel consistency displaying notably high values. The differences between GCV and PCV for the traits observed were relatively small, suggesting that environmental effects are relatively low, indicating a strong genetic basis and making these traits highly suitable to direct selection. High heritability values recorded for key agronomic traits such as plant height, days to 50% flowering and days to maturity, spikelet fertility and grain yield confirm this genetic control and good prospects to achieve stable genetic gain.

Similarly, quality traits like alkali digestion value, gel consistency, kernel length before cooking and head rice recovery also demonstrated high heritability, reinforcing their significance in quality improvement programs. Traits like test weight and ADV, which exhibited both high heritability and high genetic advance as per cent of mean (GAM), emerged as ideal candidates for effective selection due to their additive gene action and PL and HUL may represent traits that will be difficult to enhance without multi-location evaluation, or more precise breeding objectives to capture the improvement potential. Overall, this study highlights the significant genetic potential of the evaluated genotypes and provides critical insights for targeted breeding strategies. These findings not only aid in the identification of superior genotypes for yield and quality traits but also support the development high performing and market preferred rice cultivars.

ACKNOWLEDGEMENT

The authors are sincerely thankful to the Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University for providing the necessary facilities, academic environment and support that enabled me to carry out this study effectively.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish or preparation of the manuscript.

REFERENCES

Akshay, M., Chandra, B.S., Devi, K.R. and Hari, Y. (2022). Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*. **11(5):** 167-172.

Begna, T. and Begna, T. (2021). Role and economic importance of crop genetic diversity in food security. *International Journal of Agricultural Science and Food Technology.* **7(1):** 164-169.

Bhattacharjee, M., Majumder, K., Kundagrami, S. and Dasgupta, T. (2020). Evaluation of recombinant inbred lines for higher iron and zinc content along with yield and quality parameters in rice (Oryza sativa L.). *Indian Journal of Agricultural Research*. **54(6):** 724-730. doi: 10.18805/IJARe.A-5454.

Bollinedi, H., Vinod, K.K., Bisht, K., Chauhan, A., Krishnan, S.G., Bhowmick, P.K. and Singh, A.K. (2020). Characterising the variability of grain nutritional and physico-chemical quality in Indian rice landraces by multivariate genetic analyses. *Indian Journal of Genetics and Plant Breeding*. **80(01):** 26-38.

Burton, G.W. and De Vane, D.E. (1953). Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. *Agronomy Journal*. **45:** 478- 481.

Burton, G.W. and De Vane, D.E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal.* **45:** 478-481.

Chandramohan, Y., Srinivas, B., Thippeswamy, S. and Padmaja, D. (2016). Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian Journal of Agricultural Research*. **50(6):** 609-613. doi: 10.18805/ijare.v0iOF.10777.

Choudhary, M., Singh, R.P., Singh, P.K., Verma, R.L. and Jayasudha, S. (2025). Genetic variability and association studies for morpho-floral traits in backcross introgression lines of rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research*. **59(7):** 1031-1038. doi: 10.18805/IJARe.A-6272.

Demeke, B., Dejene, T. and Abebe, D. (2023). Genetic variability, heritability and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food and Agriculture*. **9(1):** 2157099.

Dinesh, K., Devi, M.S., Sreelakshmi, C. and Paramasiva, I. (2023). Exploring the genetic variability for yield and quality traits in indigenous landraces of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. **14(2):** 502-510.

Glenn, K.C., Alsop, B., Bell, E., Goley, M., Jenkinson, J., Liu, B. and Vicini, J.L. (2017). Bringing new plant varieties to market: Plant breeding and selection practices advance beneficial characteristics while minimizing unintended changes. *Crop Science*. **57(6):** 2906-2921.

Hasan, M.J., Kulsum, M.U., Paul, A.K., Biswas, P.L., Rahman, M.H., Ansari, A., Akter, A., Lipi, L.F., Mohiuddin, S.J. and Rafiq, M.Z.A. (2018). Assessment of variability for floral characteristics and out-crossing rate in CMS lines of hybrid rice. *Bangladesh Rice Journal.* **22(2):** 31-39.

Kushwah, A., Bhatia, D., Singh, G., Singh, I., Bindra, S., Vij, S. and Singh, S. (2021). Phenotypic evaluation of genetic variability and selection of yield contributing traits in chickpea recombinant inbred line population under high temperature stress. *Physiology and Molecular Biology of Plants*. **27(4):** 747-767.

Mahesh, G., Ramesh, T., Narendar Reddy, S., Meena, A., Rathod, S., Fiyaz, R.A. and Jukanti, A.K. (2022). Genetic variability, heritability, genetic advance and path coefficients for grain protein content, quality traits and grain yield in rice (*Oryza sativa* L.) germplasm lines. *The Pharma Innovation Journal*. **11(3):** 1836-1839.

Muthayya, S., Sugimoto, J.D., Montgomery, S. and Maberly, G.F. (2014). An overview of global rice production, supply, trade and consumption. *Annals of the new york Academy of Sciences.* **1324(1):** 7-14.

Paillard, S., Treyer, S. and Dorin, B. (Eds.). (2014). Agrimonde-scenarios and challenges for feeding the world in 2050. Springer Science and Business Media.

Panse, V.G. and Sukhatme, P.V. (1985). Statistical Methods for Agricultural Workers, ICAR, New Delhi.

Paramanik, S., Rao, M.S., Rashmi, K., Panda, K.K. and Chakraborty, A. (2023). Studies on genetic variability, heritability and genetic advance for quantitative traits and nutritional traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. **14(4):** 1527-1537.

Priyanka, R.M., Thiyagarajan, K., Bharathi, S.P. and Rajendran, R. (2017). Studies on genetic variability for floral and grain quality traits in rice (*Oryza sativa* L). *Electronic Journal of Plant Breeding.* **8(2):** 609-614.

Robinson, H.F.; Comstock, R.E. and Harvey, P.H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*. **41:** 353-359.

Satya, P. and Rao, L.V.S. (2022). Phenotypic assessment of rice landraces for genetic variability and studies under heat stress. *Oryza*. **59(1):** 31-38.

Satya, P. and Rao, L.V.S. (2022). Phenotypic assessment of rice landraces for genetic variability and studies under heat stress. *Oryza*. **59(1):** 31-38.

Swarup, S., Cargill, E.J., Crosby, K., Flagel, L., Kniskern, J. and Glenn, K.C. (2021). Genetic diversity is indispensable for plant breeding to improve crops. *Crop Science*. **61(2):** 839-852.

Yates, R.A. (1967). Studies on the irrigation of sugar-cane. *Australian Journal of Agricultural Research*. **18(6):** 903-920.