



Assessment of Genetic Parameters and Correlation Analysis in Rice (*Oryza sativa* L.)

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ABSTRACT

The experiment was conducted during *kharif* season (July to November), 2022 at the Technology Park of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India to investigate genetic parameters and the correlation between grain yield and its contributing traits of 30 rice genotypes. The experiment was conducted with 30 genotypes in a Randomized Block Design (RBD). Observations were recorded for morphological traits, *viz.*, days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, grain per panicle, biological yield per plant, harvest index, test weight, and grain yield plant⁻¹. Analysis of variance found significant differences for all ten traits studied, indicating sufficient variability among the material used in the present study. High GCV and PCV were observed for the number of effective tillers plant⁻¹, biological yield plant⁻¹ and harvest index. High heritability, coupled with high genetic advance percent of the mean, was observed for grain panicle⁻¹, plant height, number of effective tillers plant⁻¹, biological yield plant⁻¹, panicle length, harvest index, and grain yield plant⁻¹. Grain yield exhibited significant and positive correlation with test weight, plant height, grain panicle⁻¹, biological yield plant⁻¹, panicle length, number of effective tillers plant⁻¹ and days to maturity at phenotypic as well as genotypic level. Vallabh Basmati-23, Sugandha-3, and Pusa Basmati-1509 recorded the highest values for effective tillers plant⁻¹, plant height with grains panicle⁻¹, and grain yield plant⁻¹, respectively, indicating their potential as promising parents for future breeding programmes.

KEYWORDS: Rice, variability, heritability, genetic advance, correlation

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1. INTRODUCTION

Rice is the most important food crop with regard to human nutrition and caloric intake, providing more than one-fifth of the calories consumed worldwide by humans (Smith, 1998) and is the primary source of food for 57% of the world population. India is the second-largest producer of rice after China. The world population is increasing and will reach the 10 billion mark by 2050, then the demand for rice will grow faster than for other crops. To feed the growing population, high-yielding varieties of crop plants will be required. Yield is an outcome of the multiplicative interaction of component characters. Breeders usually face the problem of selecting desirable parents. In general, parents are selected based on their performance, but many times a high-yielding genotype may/ may not transmit its superiority to progeny. Hence, critical choice of parents is most importance, particularly for the improvement of complex quantitative characters such as yield and its components. Breeders and growers of rice would profit from robust genotypes with improved morphological and yield-related characteristics (Al-Daej, 2022; Bagati et al., 2016). Grain quality traits are very crucial in rice breeding as it is predominantly consumed as a whole grain. Any successful hybridization programme for varietal development relies heavily on the selection of parents with high variability, allowing for the selection of desirable character combinations to increase grain quality and yield (Asante et al., 2019; Konate et al., 2016). The success of breeding programmes can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Ganesh et al., 2022). Heritability measures how much of a trait is passed down to subsequent generations, while genetic advance measures the difference between the mean genotypic values of the selected population and those of the original population (Tiwari et al., 2019; Saha et al., 2019). Heritability estimates combined with genetic advance are more accurate than heritability alone in predicting the genetic gain under selection (Benny et al., 2021; Birtucan et al., 2023). Genetic diversity analysis using multivariate approaches such as cluster analysis and D² statistics is essential to identify divergent genotypes for use as parents in hybridization programmes (Edukondalu et al., 2024; Katkani et al., 2023). Further, since grain yield depends on various component characters, the knowledge of correlation among yield, yield components, and quality traits, in addition to identification of direct and indirect effects of the yield and quality traits on grain yield, would help in effective yield improvement (Gupta et al., 2020; Zayed et al., 2023). Rice genotypes differ significantly in their response to abiotic stresses such as water stress, which influences morpho-physiological plasticity and root trait

dynamics, thereby affecting yield potential (Manikanta et al., 2020; Rejeth et al., 2020). Understanding such physio-morphological variability alongside agronomic performance is therefore critical in developing stress-resilient, high-yielding varieties (Gunasekaran et al., 2023; Kandibanda et al., 2023). Therefore, to keep the above facts in view, the present investigation was carried out to assess genetic parameters, i.e., genetic variability, heritability, genetic advance and correlation between grain yield and its contributing traits of 30 rice genotypes.

2. MATERIALS AND METHODS

The experiment was conducted in July, 2022 at the Technology Park of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India. The experiment was conducted with 30 genotypes (Basmati and Non- Basmati) in a Randomized Block Design (RBD) with 3 replications. The soil type of the experimental site was sandy loam and fertile. The seeds were sown on 8th July 2022 in separate plots and 25 days (July, 2022) old seedlings were transplanted as single seedlings in a two-row plot of 3 m length, following 20 cm inter-row and 15 cm intra-row spacing. All the recommended cultural practices were followed to raise a good crop. The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorous and 60 kg potash per hectare through urea, DAP, and murate of potash, respectively. Half a dose of nitrogen and a full dose of phosphorus and potash were applied at the time of planting. The rest of the half dose of nitrogen was applied in two split doses as top dressing at the tillering stage and at the panicle initiation stage of crop growth. This study consisted of 30 genotypes of rice collected from different sources. These genotypes exhibited a wide spectrum of variability for various agronomic and morphological characters, as represented in Table 1. The genotypes included traditional Basmati varieties such as Punjab Basmati-2 (PAU), Type-3 (Uttarakhand), Pusa Basmati-1509, Pusa Basmati-1718, Vallabh Basmati-21, -22, -23, and -24 (SVPUAT); aromatic non-Basmati types viz. Sugandha-3, Sugandha-4, Sugandha-5, and Kasturi (IARI/BHU); high-yielding varieties viz. Jaya, Ratna, BPT-5204 (Andhra Pradesh), Govind (CVRC, Pantnagar), and Pusa-44 (IARI); salt-tolerant lines viz. CSR-10, CSR-23, and CSR-30 (ICAR-CSSRI); IRRI-developed lines viz. IR-29, IR-64, and IR-85893 (IRRI, Philippines); varieties from NDUAT viz. Narendra-2064, Narendra-359, and Sarjoo; and varieties from Pantnagar viz. Pant-100, Pant-60, and Pant Dhan-4. This diverse assemblage ensured a wide genetic base, representing material from premier national institutes including IARI, ICAR-CSSRI, NDUAT, SVPUAT, PAU, and CVRC, as well as the International Rice Research Institute (IRRI), Philippines, thus providing

Table 1: List of rice genotypes

Sl. No.	Variety	Origin
1.	Punjab Basmati-2	PAU
2.	Type-3	Uttarakhand
3.	IR-29	IRRI, Philippines
4.	IR-64	IRRI, Philippines
5.	IR-85893	IRRI, Philippines
6.	Sundari	Kerala
7.	Sarjoo	NDUAT
8.	CSR-10	ICAR-CSSRI
9.	CSR-23	ICAR-CSSRI
10.	CSR-30	ICAR-CSSRI
11.	Pant-100	Pantnagar
12.	Pant-60	Pantnagar
13.	Narendra-2064	NDUAT
14.	Sugandha -5	IARI
15.	Pusa Basmati-1509	IARI
16.	Pusa Basmati-1718	IARI
17.	Jaya	INDIA
18.	BPT-5204	Andhra Pradesh
19.	Ratna	INDIA
20.	Govind	CVRC, Pantnagar
21.	Kasturi	BHU
22.	Sugandha-4	IARI
23.	Sugandha-3	IARI
24.	Narendra-359	NDUAT
25.	Pusa-44	IARI
26.	Pant Dhan-4	Pantnagar
27.	Vallabh Basmati-21	SVPUAT
28.	Vallabh Basmati-22	SVPUAT
29.	Vallabh Basmati-23	SVPUAT
30.	Vallabh Basmati-24	SVPUAT

ample opportunity for identification of superior genotypes and trait associations.

Observations on the 10 characters *viz*; days to 50% flowering, days to maturity, plant height, number of tillers plants⁻¹, panicle length, grain panicle⁻¹, biological yield plant⁻¹, grain yield plant⁻¹, test weight and harvest index were recorded based on five plants randomly selected and tagged from each row except for days to 50% flowering and days to maturity, which were recorded on the plot basis.

Analysis of variance was studied among 30 rice genotypes. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p),

genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broad sense (h^2_b), genetic advance (GA), and genetic advance as a percentage of means (GAM) were estimated. Phenotypic correlations, genotypic correlations, principal component analysis, path analysis, and cluster component analysis were done for all the rice genotypes using Windows Stat 9.2.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance (ANOVA)

The analysis of variance was highly significant for all the characters under study. It demonstrated that the mean sum of squares owing to the genotypes were highly significant for all the characters under study, namely, days to 50% flowering, days to maturity, plant height, number of effective tillers plants⁻¹, panicle length, grain panicle⁻¹, biological yield plant⁻¹, grain yield plant⁻¹, test weight and harvest index, indicating the existence of large genetic variation among the individuals. This indicates that genotypes are highly variable, especially for traits that showed significant differences. Thus, the possibility of genetic improvement through selection is highly promising. High variability of breeding materials will increase the probability of producing desirable recombinants in successive generations. This indicated that genotypes were highly variable, especially for traits that showed significant differences. Thus, the possibility of genetic improvement through selection was highly promising. High variability of breeding materials increased the probability of producing desirable recombinants in successive generations Adhikari et al. (2018), Maurya et al. (2022), Srinivas et al. (2023), and Gupta et al. (2020) also reported highly significant genotypic differences for grain yield and its component traits in rice, attributing this variability to the diverse genetic background of the genotypes evaluated in their respective studies (Table 2).

3.2. Mean performance of genotypes

The mean performance of 30 rice genotypes for ten morphological and yield-contributing traits was presented in Table 3. Days to 50% flowering ranged from 81.33 to 101.33 days (mean 89.40 days), with Sugandha-4 being the earliest and Vallabh Basmati-22 the latest to flower. Days to maturity varied from 109.33 to 133 days (mean 120.17 days), with IR-85893 maturing earliest and Vallabh Basmati-22 maturing latest. Plant height ranged from 63.98 cm to 112.76 cm (mean 85.01 cm), CSR-23 being the shortest and Sugandha-3 the tallest genotype. The number of effective tillers plant⁻¹ varied from 4.60 to 13.86 (mean 8.60), with the minimum in Sundari and the maximum in Vallabh Basmati-23. Panicle length ranged from 18.26 cm to 29.01 cm (mean 24.42 cm), being least in Sundari and highest in IR-64. Grains panicle⁻¹ ranged from 52.93 to 99.33 (mean 73.83), with the maximum in Sugandha-3

Table 2: Analysis of variance (ANOVA) for different characters in rice

Source of variation	DF	50% flowering	Maturity	Plant height (cm)	No. of eff. tillers plant ⁻¹	Panicle length (cm)	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%).	Test weight (g).	Grain yield plant ⁻¹ (g).
Replication	2	1.73	7.47	17.03*	0.98*	1.97	6.26	56.70	9.41	0.01	0.25
Treatments	29	90.12**	119.30	296.97**	16.07**	19.35**	445.51**	757.24**	109.33**	10.92**	41.88**
Error	58	8.00	8.55**	4.06	0.31	0.64	2.59	18.60	3.72	0.01	2.34

*, ** significant at ($p=0.05$) and ($p=0.01$) level, respectively

Table 3: Mean performance of genotypes for ten characters in rice

Sl. No.	Varieties	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers plant ⁻¹	Panicle length (cm)	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%)	Test weight (g)	Grain yield plant ⁻¹ (g).
1.	Punjab Basmati-2	96.66	128.33	72.43	5.40	25.83	58.10	45.56	43.95	18.73	20.03
2.	Type-3	93.33	122.33	79.39	10.26	21.61	69.40	64.56	36.76	20.83	23.77
3.	IR-29	87	121.33	87.38	8.53	24.60	79.36	88.73	27.9	20.76	24.80
4.	IR-64	99.33	132.33	90.96	7.13	29.01	84.06	89.43	23.56	19.63	21.13
5.	IR-85893	83	109.33	84.90	9.86	25.73	80.36	70.86	32.65	19.96	23.16
6.	Sundari	84	113.66	70.13	4.60	18.26	56.40	45.36	44.10	18.23	20.03
7.	Sarjoo	90.33	119.33	80.38	8	24.11	67.40	65.83	36.36	22.76	23.96
8.	CSR-10	87.33	115.33	82.42	8.66	23.93	72.83	60.56	32.68	18.03	19.80
9.	CSR-23	91.66	122	63.98	13.40	19.18	52.93	43.16	44.73	18	19.33
10.	CSR-30	85.66	113	77.74	8.06	22.58	62.70	72.43	34.13	20.80	24.76
11.	Pant-100	84.66	113.33	75.36	6.93	21.26	56.53	53.4	42.3	19.76	22.56
12.	Pant-60	85.66	119.33	82.10	10.46	24.24	69	70.56	30.13	19.13	21.23
13.	Narendra-2064	90.33	123.33	76.50	7.63	24.33	60.26	62.5	37.56	19.96	19.33
14.	Sugandha -5	100	131	91.26	6.40	28.43	80.33	89.9	22.96	18.36	20.70
15.	Pusa Basmati-1509	88	122.33	101.10	11.60	25.26	97.80	85.76	38.10	24.06	32.73
16.	Pusa Basmati-1718	90.33	120.33	82.93	8.56	27.60	72.66	61.23	37.16	19.56	22.80
17.	Jaya	87.33	122	86.56	8.33	25.96	74.13	52.66	41.99	20.63	22.46
18.	BPT-5204	85	116.66	84.28	5.66	24.81	74.83	67.60	36.33	22.23	24.60
19.	Ratna	93	124.66	95.53	7.06	25.03	82.83	97.73	25.53	21.66	25
20.	Govind	90	123	94.00	8	22.46	83.73	94.33	25.10	21.53	23.70
21.	Kasturi	87.66	120.66	96.73	11.93	24.23	85.83	83.56	31.30	21.80	26.23
22.	Sugandha-4	81.33	110.33	81.36	9.40	21.38	71	55.50	37.50	18.43	20.83
23.	Sugandha-3	90.33	115.66	112.76	11.26	28.03	99.33	75.10	41.76	24.23	31.43
24.	Narendra-359	86.33	117	78.63	5.33	23.06	58.66	63.46	38.50	19.96	24.46

Table 3: Continue...

Sl. No.	Varieties	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers plant ⁻¹	Panicle length (cm)	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%)	Test weight (g)	Grain yield plant ⁻¹ (g).
25.	Pusa-44	85.33	112.33	80.33	10.53	24.26	67.43	66.93	31.40	18.03	21.03
26.	Pant Dhan – 4	84	116.33	77.23	6.93	23.46	61.80	55.53	37.26	18.83	20.73
27.	Vallabh Basmati-21	86.66	120.66	94.70	8.13	27.16	86.66	92.50	33.93	24.26	31.46
28.	Vallabh Basmati-22	101.33	133	88.76	7.06	24.59	80.63	81.93	32.26	21.10	25.43
29.	Vallabh Basmati-23	100.66	129.66	87.13	13.86	24.76	81.13	67.60	38.73	21.96	26.23
30.	Vallabh Basmati-24	85.66	116.66	93.28	8.93	27.43	86.76	91.83	33.63	23.06	30.93
Mean		89.40	120.17	85.01	8.60	24.42	73.83	70.54	35.01	20.54	23.82
CV		3.16	2.43	2.37	6.50	3.29	2.18	6.11	5.51	0.55	6.42
F ratio		11.25	13.94	73.07	51.41	29.81	171.88	40.70	29.33	855.36	17.88
SEm±		1.63	1.68	1.16	0.32	0.46	0.92	2.49	1.11	0.06	0.88
CD ($p=0.05$)		4.62	4.78	3.29	0.91	1.31	2.63	7.04	3.15	0.18	2.50
Range lowest		81.33	109.33	63.98	4.60	18.26	52.93	43.16	22.96	18	19.33
Range highest		101.33	133	112.76	13.86	29.01	99.33	97.73	44.73	24.26	32.73

and the minimum in CSR-23. Test weight varied from 18.00 g to 24.26 g (mean 20.54 g), with the highest value in Vallabh Basmati-21 and the lowest in CSR-23. Biological yield plant⁻¹ ranged from 43.16 g to 97.73 g (mean 70.54 g), being highest in Ratna and lowest in CSR-23. Harvest index ranged from 22.96% to 44.73% (mean 35.01%), with Sugandha-5 recording the lowest and CSR-23 the highest value. Grain yield plant⁻¹ varied from 19.33 g to 32.73 g (mean 23.82 g), with the maximum yield recorded in Pusa Basmati-1509 and the minimum in both CSR-23 and Narendra-2064. This range of variation for the traits studied was in close agreement with the findings of Patel et al. (2022), Lakshmi et al. (2022), and Yadav et al. (2024), who also reported wide variation for yield and yield-contributing traits among diverse rice genotypes.

3.3. Estimate of genetic parameters

The phenotypic variance was found to be higher than the genotypic variance for all ten characters that were studied (Table 4). Genotypic and phenotypic variances were observed in the range of 3.63 to 246.2 and 3.65 to 264.8, respectively. The highest estimates of GCV and PCV were recorded in the number of effective tillers per plant (26.65 and 27.43), followed by biological yield per plant (22.24 and 23.07), indicating that a large amount of variation was present among the genotypes. This showed that these characters were major contributors to the total variability.

The results revealed that the characters harvest index (16.94 and 17.8), grain panicle⁻¹ (16.45 and 16.6), grain yield plant⁻¹ (15.23 and 16.53), plant height (11.62 and 11.86), and panicle length (10.22 and 10.74) had moderate PCV and GCV values, indicating selective breeding could be done for these characters. Low (<10%) GCV and PCV were recorded for the traits *viz.*, test weight, days to 50% flowering, and days to maturity (5.05 and 5.61), respectively. Small differences between PCV and GCV values were recorded for all the traits studied in the present investigation, indicating a little influence of environment and additive gene effects, indicating genotypes can be improved and selected for these characters. Similar results were also obtained by Bharti et al. (2021), Beena et al. (2021), Jasmine et al. (2022), and Caleb et al. (2023), who similarly recorded moderate genotypic and phenotypic coefficients of variation for grain yield and yield-contributing traits in rice. High GCV and PCV for effective tillers and biological yield were also reported by Bhargavi et al. (2021), Benny et al. (2021), Patel et al. (2022), and Lakshmi et al. (2022), attributing the high variability observed for these traits to the substantial genetic diversity present among the genotypes evaluated in their respective studies. Similarly, Debsharma et al. (2022), Faysal et al. (2022), and Burman et al. (2023) noted comparable magnitudes of genotypic and phenotypic variation for yield-associated traits across multiple environments.

Table 4: Genetic variability, heritability and genetic advance for yield and related traits

	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers plant ⁻¹	Panicle length (cm).	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%)	Test weight (g)	Grain yield plant ⁻¹ (g).
Var environmental	8.00	8.55	4.06	0.31	0.64	2.59	18.61	3.72	0.01	2.34
ECV	3.16	2.43	2.37	6.50	3.29	2.18	6.11	5.51	0.55	6.42
Var genotypical	27.37	36.91	97.63	5.25	6.23	147.60	246.20	35.20	3.63	13.18
GCV	5.85	5.05	11.62	26.65	10.23	16.46	22.24	16.95	9.28	15.24
Var phenotypical	35.38	45.47	101.70	5.56	6.88	150.20	264.80	38.93	3.65	15.52
PCV	6.65	5.61	11.86	27.43	10.74	16.6	23.07	17.82	9.29	16.54
h ² (Broad Sense)	0.77	0.81	0.96	0.94	0.90	0.98	0.93	0.90	0.99	0.84
Genetic advance 5%	9.47	11.27	19.94	4.58	4.89	24.81	31.17	11.62	3.92	6.89
Gen. Adv as % of Mean 5%	10.60	9.38	23.46	53.33	20.05	33.61	44.18	33.20	19.09	28.93

Highest heritability was recorded for test weight (0.99) followed by grain panicle⁻¹ (0.98), plant height (0.96), number of effective tillers plant⁻¹ (0.94), biological yield plant⁻¹ (0.93), panicle length (0.906), harvest index (0.904), grain yield plant⁻¹ (0.84), days to maturity (0.81) and days to 50% flowering (0.77). The highest value of genetic advance as percent mean was recorded for number of effective tillers plant⁻¹ (53.33) followed by biological yield plant⁻¹ (44.18), grain panicle⁻¹ (33.61), harvest index (33.2), grain yield plant⁻¹ (28.93), plant height (23.46), panicle length (20.05), test weight (19.09), days to 50% flowering (10.60) and days to maturity (9.38). High heritability coupled

with high genetic advance percent of mean was observed by grain panicle⁻¹, plant height, number of effective tillers plant⁻¹, biological yield plant⁻¹, panicle length, harvest index, and grain yield plant⁻¹, indicating that these traits were less influenced by the environment, additive gene activity influenced the inheritance of these features. It can easily be selected through phenotypic selection. Following a simple selection method, these traits can be improved. High heritability with moderate genetic advance was reported for test weight, indicating the importance of dominance and epistatic effects in its inheritance, and selection for it would be moderately effective. Similar findings were also

Table 5: Genotypic correlations among yield and yield components of thirty rice genotypes

Traits	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of effective tillers plant ⁻¹	Panicle length (cm)	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%)	Test weight (g)	Grain yield plant ⁻¹ (g)
Days to 50% flowering	1.000	0.915**	0.171	0.052	0.381**	0.214**	0.256*	-0.254*	0.048	-0.035
Days to maturity		1.000	0.200	-0.029	0.400**	0.248*	0.353**	-0.323**	0.109	0.004
Plant height (cm)			1.000	0.240*	0.654**	0.964**	0.776**	-0.435**	0.721**	0.765**
No. of effective tillers plant ⁻¹				1.000	-0.013	0.332**	0.056	0.087	0.217*	0.295**
Panicle length (cm)					1.000	0.661**	0.547**	-0.428**	0.384**	0.388**
Grain panicle ⁻¹						1.000	0.792**	-0.465**	0.699**	0.764**
Biological yield plant ⁻¹							1.000	-0.807**	0.574**	0.593**
Harvest index (%)								1.000	-0.033	-0.022
Test weight (g)									1.000	0.941**

Table 6: Phenotypic correlations among yield and yield components of thirty rice genotypes

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers plant ⁻¹	Panicle length (cm)	Grain panicle ⁻¹	Biological yield plant ⁻¹	Harvest index (%)	Test weight (g)	Grain yield plant ⁻¹ (g)
Days to 50% flowering	1.000	0.919**	0.157	0.037	0.331**	0.191	0.223*	-0.215*	0.046	-0.018
Days to maturity		1.000	0.190	-0.029	0.356**	0.227*	0.310**	-0.276**	0.102	0.015
Plant height (cm)			1.000	0.235*	0.644**	0.946**	0.752**	-0.405**	0.712**	0.722**
No. of effective tillers plant ⁻¹				1.000	-0.022	0.335**	0.051	0.082	0.211*	0.273**
Panicle length (cm)					1.000	0.624**	0.545**	-0.396**	0.374**	0.386**
Grain panicle ⁻¹						1.000	0.749**	-0.425**	0.694**	0.705**
Biological yield plant ⁻¹							1.000	-0.791**	0.559**	0.573**
Harvest index (%)								1.000	-0.033	-0.023
Test weight (g)									1.000	0.875**

reported by Jasmine et al. (2022) and Caleb et al. (2023) in rice, who also recorded high heritability coupled with high genetic advance for grain yield and its component traits, attributing this to the predominance of additive gene action. Kumari et al. (2023), Bhargavi et al. (2021), Tiwari et al. (2019), Satturu et al. (2023) and Yadav et al. (2024) further confirmed that traits with narrow GCV-PCV differences were strongly governed by genetic rather than environmental factors, making them reliable targets for direct selection.

3.4. Genotypic and phenotypic correlation

The genotypic correlation coefficient revealed that grain yield plant⁻¹ was highly significant, positively correlated with test weight (0.941) followed by plant height (0.765), grain panicle⁻¹ (0.764), biological yield plant⁻¹ (0.593), panicle length (0.388), and number of effective tillers plant⁻¹ (0.295). The positive but non-significant correlation was observed for days to maturity (0.004), while a negative correlation with days to 50% flowering (-0.035) and harvest index (-0.022) was observed (Table 5). The phenotypic correlation coefficient revealed that grain yield plant⁻¹ was highly significant, positively correlated with test weight (0.875), followed by plant height (0.722), grain panicle⁻¹ (0.705), biological yield plant⁻¹ (0.573), panicle length (0.386), and number of effective tillers plant⁻¹ (0.273). A positive but non-significant correlation was observed for days to maturity (0.015), while negative correlations were observed with days to 50% flowering (-0.018) and harvest index

(-0.023) as shown in Table 6. The results of the correlation analysis revealed that grain yield exhibited significant positive correlations with test weight, plant height, grain panicle⁻¹, biological yield plant⁻¹, panicle length, number of effective tillers plant⁻¹, and days to maturity at both phenotypic and genotypic levels. Hence, these traits could be utilized as selection criteria for the yield improvement in rice. Improvement in 1000-grain weight character will lead to a reduction of grain yield or alteration in days to flowering or maturity duration as well as a change in plant height. Similar results were also derived earlier by Singh et al. (2018), Sreedhar et al. (2019), Saha et al. (2019), Sharma et al. (2020), and Jasmine et al. (2022) in rice, who similarly reported strong positive associations of grain yield with plant height, panicle length, and test weight, supporting the use of these traits as indirect selection criteria. Significant positive genotypic and phenotypic correlations of grain yield with plant height, grains per panicle, effective tillers, biological yield, panicle length, and test weight were also reported by Vennela et al. (2021) and Gupta et al. (2020). The preponderance of genotypic over phenotypic correlations for most trait pairs, as observed in the present study, was consistent with findings of Faysal et al. (2022), Salunkhe et al. (2024), and Kandibanda et al. (2023), indicating minimal environmental distortion and the reliability of these associations for breeding purposes.

4. CONCLUSION

Analysis of variance revealed significant variability among thirty rice genotypes for all ten traits. High GCV and PCV were observed for effective tillers, biological yield, and harvest index. High heritability with high genetic advance indicated additive gene effects for grain per panicle, plant height, effective tillers, biological yield, panicle length, harvest index, and grain yield, suggesting direct selection would be effective. Grain yield showed significant positive correlations with test weight, plant height, grains per panicle, biological yield, panicle length, effective tillers, and days to maturity, indicating that these characters would be helpful in the genetic improvement.

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