

Exploring Genetic Variability and Selection Parameters for Yield Improvement in Aromatic Rice

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ABSTRACT

Understanding genetic variability and the association among yield-related traits is essential for developing improved rice varieties. The present study evaluated 33 non-Basmati aromatic rice genotypes over two seasons to assess genetic variability, heritability, correlation, path coefficient and genetic divergence for ten quantitative traits. Analysis of variance revealed highly significant differences among genotypes for all traits, indicating substantial genetic variability. High genotypic and phenotypic coefficients of variation were observed for exsertion length, test weight, filled grains per panicle, grain yield per plant and total grains per panicle, suggesting considerable scope for effective selection. High heritability coupled with high genetic advance was recorded for plant

height, exsertion length, spikelet number per panicle, filled grains per panicle, fertility percentage and test weight, indicating the predominance of additive gene action. Grain yield per plant showed significant positive association with plant height, leaf area, fertility percentage and test weight at both genotypic and phenotypic levels. Path coefficient analysis identified fertility percentage, spikelet number per panicle, test weight and leaf area as major contributors to grain yield through strong positive direct effects. Mahalanobis' D^2 analysis grouped the genotypes into three clusters, demonstrating considerable genetic divergence. Test weight contributed most towards total divergence, followed by spikelet number per panicle. The findings highlight the potential of these traits for selection and hybridization in aromatic rice improvement programmes.

Keywords Aromatic rice, Genetic variability, Heritability, Path analysis, Correlation, Genetic divergence, D^2 statistics, Yield traits.

INTRODUCTION

Aromatic rice occupies a unique position in global agriculture because of its superior cooking quality, pleasant aroma and high market value. India possesses a rich repository of indigenous aromatic rice germplasm, particularly non-Basmati types adapted to diverse agro-ecological conditions (Touthang *et al.* 2025, Sunny *et al.* 2022). These traditional landraces are valued not only for their cultural importance but

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also for their potential use in crop improvement programmes. However, the replacement of traditional cultivars with modern high-yielding varieties during the Green Revolution led to a gradual erosion of valuable aromatic rice diversity (Acharjee *et al.* 2021). Yield improvement in rice depends largely on the availability and effective utilization of genetic variability present within breeding materials (Sen *et al.* 2026). The study of genetic variability, heritability and genetic advance provides valuable information regarding the nature and magnitude of gene action governing important agronomic traits. Likewise, correlation and path coefficient analyses help identify yield-contributing characters and determine their direct and indirect effects on grain yield. In addition, assessment of genetic divergence using multivariate techniques such as Mahalanobis' D² statistics facilitates the identification of genetically diverse parents for hybridization programmes (Nivedha *et al.* 2024).

The present investigation was therefore undertaken to evaluate the extent of variability, association among yield components and genetic divergence in 33 non-Basmati aromatic rice genotypes with the objective of identifying important selection criteria and promising parental combinations for rice improvement.

MATERIALS AND METHODS

Experimental Site

The field experiments were conducted during the two consecutive *kharif* seasons at the Agricultural Farm of the Institute of Agriculture, Visva-Bharati, Sriniketan, West Bengal, India. The experimental site is situated in the sub-humid lateritic agro-climatic zone at 23°19' N latitude and 87°42' E longitude, with an altitude of 58.9 m above mean sea level. The region experiences a subtropical humid climate with an average annual rainfall ranging from 1300 to 1600 mm. The experimental soil was sandy loam in texture, acidic in reaction and low to medium in fertility status, representing typical red and lateritic soil of the region. The physico-chemical properties of the soil were as follows: available nitrogen 227.5 kg ha⁻¹, available phosphorus 17.7 kg ha⁻¹, available potassium 168.2 kg ha⁻¹, organic carbon 0.56%, soil

pH 5.5, sand 58%, silt 11.7% and clay 31.3%.

Experimental materials and design

Thirty-three non-Basmati aromatic rice genotypes collected from different regions of West Bengal, North-East India and other rice-growing areas were used in the study. The experimental materials were obtained from the Department of Genetics and Plant Breeding, Visva-Bharati; Government Training Centre, Phulia, West Bengal; Rice Sub-Research Station, Chakdaha, Bidhan Chandra Krishi Viswavidyalaya (BCKV), Nadia; and other regional sources. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each experimental plot consisted of five rows of 3 m length with a spacing of 25 cm between rows and 15 cm between plants. Standard agronomic practices recommended for rice cultivation in the region were followed uniformly throughout the crop growth period.

Recording of observations and statistical analysis

Observations were recorded from five randomly selected plants from the middle rows of each replication to minimize border effects. Data were collected on the following quantitative traits: Plant height (cm), Main panicle length (cm), Exsertion length (cm), Flag leaf area (cm²), Total effective tillers plant⁻¹, Spikelet number panicle⁻¹, Filled grains panicle⁻¹, Spikelet fertility (%), Test weight (g), Grain yield plant⁻¹ (g),

The mean data obtained from replicated observations were subjected to statistical analysis using Windostat version 8.6 (Indostat Services, Hyderabad, India). Analysis of variance (ANOVA) was performed to assess the significance of differences among genotypes. Genotypic coefficient of variation (GCV) was calculated by the formula given by Burton and DeVane (1952).

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

phenotypic coefficient of variation (PCV) was calculated by the formula given by Burton and DeVane (1952)

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100 = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

Broad-sense heritability was estimated according to Lush (1940).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}}$$

and

Genetic advance was computed according to the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = k \times h^2 \times \sigma_p$$

Where,

k = A constant, the value equal to 2.06 at 5% selection intensity

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

Genetic Advance as Percentage of Mean (GA %):

$$\text{Genetic advance as percentage of mean} = \frac{GA}{\bar{X}} \times 100$$

Where, GA = Genetic advance were estimated following standard biometrical procedures.

Genotypic and phenotypic correlation coefficients were estimated following Al-Jibouri *et al.*

$$(1958) \text{ Correlation coefficients at genotypic } r_g = \frac{GCovxy}{(GV_x \times GV_y)^{1/2}}$$

$$\text{and phenotypic levels } r_p = \frac{PCovxy}{(PV_x \times PV_y)^{1/2}}$$

were calculated to determine the association among traits. Path coefficient analysis (Dewey and Lu 1959) was carried out to partition the correlation coefficients into direct and indirect effects on grain yield. Genetic divergence among genotypes was estimated using Mahalanobis' (1936) D^2 statistics, and clustering of genotypes was performed following Tocher's method.

RESULTS AND DISCUSSION

Pooled analysis of variance across two seasons revealed highly significant differences among the 33 aromatic rice genotypes for all ten quantitative characters, indicating the presence of substantial genetic variability (Table 1). Significant seasonal effects and genotype $\times$ season interactions further suggested differential performance of genotypes under varying environmental conditions. Similar observations of wide variability in rice were reported in earlier studies.

The existence of significant variation among genotypes provides opportunities for effective selection and genetic improvement of yield and associated traits. Wide range of variation in rice was reported by Faysal *et al.* (2022), Demeke *et al.* (2023), Sahoo *et al.* (2025), Kumar *et al.* (2025).

Table 1. ANOVA (Mean Square) for ten characters in thirty three rice genotypes.

Characters df	Mean Squares (MS)				Error 160
	Season (S) 1	Replication (R) 2	R X S 2	Genotype (G) 32	
Plant Height	9904.65 ***	24.76	101.82	2184.89 ***	51.13
Main Panicle Length	15.43 ***	0.435	0.18	25.78 ***	1.93
Exortion	32.07 ***	0.316	0.972	147.06 ***	2.51
Leaf Area	48.6	40.7	27.75	297.14 ***	22.39
Total Effective Tillers	9.96	33.14 **	9.75	20.8 ***	5.04
Spikelet number/Panicle	10626.6 ***	3099.66 ***	190.45	8190.24 ***	99.18
Filled Grain/Panicle	21054.88 ***	3934.91 ***	592.8 *	7522.42 ***	163.7
Fertility %	1189.77 ***	129.81 **	85.67 *	482.57 ***	20.01
Seed Yield/Plant	22.91	10.62	38.47	122.56 ***	18.12
Test weight	0.013 **	0.036	0.015	10.34 ***	0.006

*, **, ***: Significant at $p=0.05, 0.01$ and $.001$ respectively.

Table 2. Mean, range, coefficient of variation for quantitative characters of thirty-three genotypes.

	Genotypes	Plant height (cm)	Main panicle length (cm)	Exortion (cm)	Leaf area (cm ²)	Total effective tillers	Spikelet number/ panicle	Filled grains per Panicle	Fertility %	Test weight (gram)	Seed yield per plant (gram)
1	Gopalbhog	155.63	26.92	3.2	43.18	9.6	211.66	168.99	79.8	4.88	21.56
2	BM-24	162.77	25.5	2.19	35.72	11.03	157.05	140.87	89.71	4.91	22.18
3	Govindobhog	160.23	26.84	14.92	24.51	9.43	226.53	196.28	86.53	2.39	14.63
4	Tulaipanji	151.02	29.01	12.63	28.95	18.03	110.44	100.73	91.32	3.47	13.44
5	Dehradun Pahari	124.30	25.63	3.49	36.70	11.4	146.24	135.08	92.47	5.38	25.44
6	Pusa Basmati-1	122.82	31.55	4.59	25.17	10.47	109.98	76.58	69.68	5.64	15.01
7	Baskota	118.63	30.97	6.69	21.19	11.60	142	101.29	71.22	5.54	21.05
8	Normal Joha	170.76	26.24	12.59	19.77	11.70	133.37	113.99	85.40	3.22	14.85
9	Kanda Band Sugandi	177.55	23.71	7.49	37.29	9.57	143.55	119.53	83.32	2.86	15.72
10	Dudheswar	186.35	23.73	4.27	31.39	8.87	145.20	132.58	91.31	4.4	19.54
11	Dehradun	178.04	25.62	4.34	39.39	11.83	147.64	131.49	88.98	4.75	30.46
12	Sugandha	169.05	25.33	14.50	26.58	9.03	177.58	159.59	89.75	2.67	15.43
13	Pusa Sugandhi Type-5	122.74	25.31	5.87	29.44	12.33	129.51	91.09	70.37	6.22	13.91
14	Black Joha	171.13	26.61	18.44	30.65	11.37	186.74	156.23	83.53	3.26	13.07
15	Tulsi Bhog	177.75	28.82	13.12	31.72	10.5	191.8	155.34	80.76	2.98	17.30
16	Gandeswari	156.48	29.11	9.16	31.08	9.87	229.73	190.17	82.23	3.19	19.19
17	Khas Dhan	175.55	23.39	9.58	35.25	11.83	218.48	180.18	82.20	2.78	21.71
18	Joha	178.46	28.65	12.54	29.04	9.33	127.09	114.83	89.97	4.32	15.96
19	Kalo Namak	182.89	29.21	11.71	25.27	9.87	160.65	104.72	64.65	3.28	17.58
20	China Kamini	169.34	25.09	14.01	24.45	10.1	195.52	163.7	83.34	2.73	19.83
21	Jamai Nadu	185.42	28.44	3.81	38.14	13.37	141.61	104.47	73.35	3.79	19.7
22	Manipuri Black Rice	171.20	23.97	2.45	41.29	8.53	111.18	89.22	80.29	5.82	15.14
23	Sona Mukhi	164.92	27.01	15.11	23.41	12.3	231.39	192.99	82.91	2.32	11.11
24	Katari Bhog	168.1	27.01	12.06	24.82	14.7	172.72	138.52	79.84	3.41	13.65
25	Shanti Bhog	185.38	26.95	6.65	50.06	9.6	156.91	123.98	78.61	7.64	27.34
26	Kalo Nunia	182.26	28.93	16.01	32.39	11.07	172.86	126.33	72.91	3.28	16.94
27	Radhatilok	154.14	28.98	8.92	25.59	11.93	205.74	175.8	85.41	2.78	19.49
28	Balam	185.27	26.65	2.99	32.32	11.47	164.64	131.77	79.87	4.11	21.22
29	Badsa Bhog	162.46	26.95	17.35	22.36	11.3	187.3	158.39	84.39	2.67	18.67
30	Bahadurbhog	169.01	27.07	16.89	27.3	12.37	191.7	155.19	80.59	2.55	21.22
31	88(8)	143.05	26.48	7.62	21.81	12.67	98.96	76.99	77.22	2.9	11.92
32	Danarguri	159.13	24.59	12.17	26.95	12.6	182.13	161.79	88.73	2.67	19.98
33	Pakbas	158.01	29.43	6.34	41.17	11.33	133.29	65.55	49.13	4.64	11.36
	Mean	163.63	26.96	9.51	30.98	11.24	164.88	134.37	80.9	3.86	18.05
	Range	118.63 to 186.35	23.39 to 31.55	2.19 to 18.44	19.77 to 50.06	8.53 to 18.03	98.96 to 231.39	65.55 to 196.28	49.13 to 92.47	2.32 to 7.64	11.11 to 30.46
	CV	4.37	5.15	16.68	15.27	19.97	6.04	9.52	5.53	2.04	23.59
	SE	2.92	0.567	0.647	1.93	0.917	4.07	5.22	1.83	0.032	1.74

Mean performance of genotypes

Considerable variation was observed among the genotypes for all studied traits. Plant height ranged from 118.63 cm to 186.35 cm with an overall mean of 163.63 cm (Table 2). Dudheswar recorded the maximum plant height, whereas Baskota was the shortest genotype. Semi-dwarf genotypes such as Pusa Sugandhi Type-5 and Pusa Basmati-1 may serve as useful donors in breeding programmes aimed at

developing lodging-resistant high-yielding cultivars.

Main panicle length varied from 23.39 cm to 31.55 cm, with Pusa Basmati-1 possessing the longest panicle. Exsertion length exhibited wide variation ranging from 2.19 cm to 18.44 cm, indicating substantial diversity among genotypes (Table 2).

Leaf area ranged from 19.77 cm² to 50.06 cm². Shantibhog exhibited the highest leaf area, while

Normal Joha recorded the lowest value. Total effective tillers per plant ranged from 8.53 to 18.03, with Tulaippanji producing the highest number of tillers.

Substantial variability was also observed for spikelet number per panicle and filled grains per panicle. Sonamukhi produced the highest number of spikelets per panicle, whereas Govindobhog recorded the maximum number of filled grains. Fertility percentage ranged from 49.13% to 92.47%, with Dehradun Pahari showing the highest spikelet fertility.

Test weight varied considerably among genotypes, ranging from 2.32 g to 7.64 g. Shantibhog recorded the highest test weight. Grain yield per plant ranged from 11.11 g to 30.46 g, with Dehradun exhibiting superior yield performance followed by Shantibhog and BM-24 (Table 2).

The wide range of variation observed for yield and associated traits indicate the potential for effective selection and crop improvement. Considerable amount of genotypic variability in rice was reported by Debsharma *et al.* (2022), Gebrie *et al.* (2022) and Lakshmi *et al.* (2022) for days to flowering; Umadevi *et al.* (2023), Kulsum *et al.* (2022) and Paramanik *et al.* (2023) for culm length; Sahoo *et al.* (2025), Kumar *et al.* (2025), for panicle number plant⁻¹; Debsharma *et al.* (2022), Paramanik *et al.* (2023) for panicle length; Lakshmi *et al.* (2022) for spikelet number panicle⁻¹, Sahoo *et al.* (2025) for grain number panicle⁻¹, Kumar *et al.* (2025) for spikelet fertility; Sahoo *et al.* (2025), Kumar *et al.* (2025), for test weight; and Umadevi *et al.* (2023), Kulsum *et al.* (2022) and Paramanik *et al.* (2023) for seed yield plant⁻¹.

Genotypic and phenotypic coefficients of variation

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits, indicating the influence of environment on trait expression. High GCV and PCV values were observed for exsertion length, test weight, filled grains per panicle, grain yield per plant and spikelet number per panicle, suggesting the presence of substantial genetic variability for these traits (Table 3). These findings are in agreement with Madhuri *et al.* (2024), Sahoo *et al.* (2025).

Moderate variability was observed for plant height and fertility percentage, whereas panicle length exhibited relatively low GCV and PCV values, indicating greater environmental stability and lower genetic variability.

The presence of high variability for several important yield components suggests good scope for improvement through selection

Heritability and genetic advance

Heritability estimates ranged from low to very high among the studied characters. Test weight exhibited the highest heritability, whereas total effective tillers showed comparatively lower heritability (Table 3).

High heritability coupled with high genetic advance as percentage of mean was observed for plant height, exsertion length, spikelet number per panicle, filled grains per panicle, fertility percentage and test weight. This combination indicates the predominance

Table 3. Phenotypic and genotypic coefficient of variability, heritability and genetic advance for different quantitative characters.

Characters	Grand mean	Range	GCV	PCV	Heritability (bs) %	GA (5%)	GA as % of mean (5%)
Plant Height	163.63	118.63 to 186.35	11.53	12.33	87.4	36.32	22.2
Main Panicle Length	26.96	23.39 to 31.55	7.4	9.01	67.3	3.37	12.5
Exsertion	9.51	2.19 to 18.44	51.63	54.26	90.6	9.62	101.21
Leaf Area	30.98	19.77 to 50.06	21.84	26.65	67.2	11.42	36.88
Total Effective Tillers	11.24	8.53 to 18.03	14.42	24.63	34.3	1.95	17.38
Spikelet number/Panicle	164.88	98.96 to 231.39	22.27	23.08	93.1	73.01	44.28
Filled Grain/Panicle	134.37	65.55 to 196.28	26.03	27.75	88.2	67.76	50.43
Fertility %	80.9	49.13 to 92.47	10.85	12.18	79.4	16.12	19.92
Seed Yield/Plant	18.05	11.11 to 30.46	23.12	33.03	49.0	6.02	33.33
Test weight	3.86	2.32 to 7.64	33.97	34.04	99.6	2.7	69.86

Table 4. Phenotypic and genotypic correlation coefficients among nine quantitative characters.

Character	Plant Height	Main Panicle Length	Exortion	Leaf Area	Total Effective Tillers	Spikelet number/ Panicle	Fertility %	Test Weight	Seed Yield/ Plant
Plant Height		-0.312 ***	0.203 **	0.226 **	-0.254 ***	0.228 **	0.161 *	-0.288 ***	0.168 *
Main Panicle Length	-0.226**		0.111	-0.2 **	0.225 **	-0.092	-0.518 ***	0.091	-0.212 **
Exortion	0.206**	0.098		-0.618 ***	0.166 *	0.448 ***	0.147 *	-0.693 ***	-0.417 ***
Leaf Area	0.212**	-0.04	-0.468***		-0.302 ***	-0.127	-0.147 *	0.653 ***	0.537 ***
Total Effective Tillers	-0.182*	0.134	0.092	-0.099		-0.193 **	0.019	-0.213 **	-0.376 ***
Spikelet number/ Panicle	0.2**	-0.058	0.421***	-0.096	-0.122		0.205 **	-0.517 ***	0.152 *
Fertility %	0.105	-0.375***	0.142*	-0.163*	0.025	0.199**		-0.246 ***	0.324 ***
Test Weight	-0.269***	0.075	-0.658***	0.542***	-0.120	-0.498***	-0.2159**		0.379 ***
Seed Yield/Plant	0.074	-0.082	-0.278 ***	0.371 ***	0.269 ***	0.127	0.206 **	0.276 ***	

*, **, ***: Significant at p= 0.05, 0.01 and .001 respectively.

Above diagonal values (**bold face**) are **genotypic correlation coefficients**

Below diagonals (normal face) are phenotypic correlation coefficients

Table 5. Genotypic path coefficients among nine quantitative characters.

	Plant Height	Main Panicle Length	Exortion	Leaf Area	Total Effective Tillers	Spikelet number/ Panicle	Fertility %	Test Weight	Seed Yield/ Plant
Plant Height	0.133	-0.065	-0.065	0.053	0.038	0.075	0.08	-0.081	0.168 *
Main Panicle Length	-0.042	0.208 **	-0.036	-0.047	-0.034	-0.030	-0.257 ***	0.026	-0.212 **
Exortion	0.027	0.023	-0.322 ***	-0.145 *	-0.025	0.148 *	0.073	-0.196 **	-0.417 ***
Leaf Area	0.03	-0.041	0.199 **	0.234 ***	0.046	-0.042	-0.073	0.184 **	0.537 ***
Total Effective Tillers	-0.034	0.047	-0.053	-0.071	-0.151 *	-0.064	0.009	-0.06	-0.376 ***
Spikelet number/ Panicle	0.03	-0.019	-0.144 *	-0.03	0.029	0.33 ***	0.102	-0.146 *	0.152 *
Fertility %	0.022	-0.108	-0.047	-0.034	-0.003	0.068	0.496 ***	-0.069	0.324 ***
Test Weight	-0.038	0.019	0.223 **	0.153 *	0.032	-0.171 *	-0.122	0.282 ***	0.379 ***

Residual = 0.6227; *, **, ***: Significant at p= 0.05, 0.01 and .001 respectively.

of additive gene action and suggests that direct phenotypic selection would be effective for improvement of these traits.

Moderate heritability along with moderate genetic advance was recorded for grain yield per plant,

panicle length and leaf area, indicating the involvement of both additive and non-additive gene effects. These findings are in agreement with Madhuri *et al.* (2024) for filled grains per panicle, Akhil *et al.* (2025) for Spikelet fertility, Kumar *et al.* (2026) and Soundharya *et al.* (2024) for Hundred grain weight, Sahoo

Table 6. Phenotypic path coefficients among nine quantitative characters.

	Plant Height	Main Panicle Length	Exortion	Leaf Area	Total Effective Tillers	Spikelet number/Panicle	Fertility %	Test Weight	Seed Yield/Plant
Plant Height	0.18 *	-0.003	-0.489 ***	0.026	-0.078	0.082	0.025	-0.110	0.074
Main Panicle Length	-0.041	0.013	-0.023	-0.005	0.057	-0.024	-0.090	0.031	-0.082
Exortion	0.037	0.001	-0.235 ***	-0.057	0.039	0.173 *	0.034	-0.269 ***	-0.278 ***
Leaf Area	0.038	-0.001	0.110	0.122	-0.042	-0.039	-0.039	0.222 **	0.371 ***
Total Effective Tillers	-0.033	0.002	-0.022	0.012	0.427 ***	-0.05	0.006	-0.049	0.269 ***
Spikelet number/Panicle	0.036	-0.001	-0.099	-0.012	-0.052	0.411 ***	0.048	-0.204 **	0.127
Fertility %	0.189 **	-0.005	-0.033	-0.02	0.011	0.082	0.241 ***	-0.088	0.206 **
Test Weight	-0.048	0.001	0.155 *	0.066	-0.051	-0.205 **	-0.052	0.41 ***	0.276 ***

Residual = 0.7403 *, **, ***: Significant at p= 0.05, 0.01 and .001 respectively.

et al (2025) for Single plant yield.

Correlation analysis

Genotypic correlation coefficients were generally higher than phenotypic correlations, indicating strong inherent associations among traits (Table 4).

Grain yield per plant showed significant positive association with plant height, leaf area, fertility percentage and test weight at both genotypic and phenotypic levels. These findings suggest that improvement in these traits would likely enhance grain yield. These

results are in agreement with the findings of Akhil *et al.* (2025) and Tripathy (2024) and Dinesh (2023) for culm length; Kumar *et al.* (2025) for spikelet number panicle⁻¹, Sahoo *et al.* (2025) for grain number panicle⁻¹, Tripathy (2024), Sahoo *et al.* (2025) for spikelet fertility and Kumar *et al.* (2025) for test weight.

Conversely, panicle length and exertion length exhibited significant negative association with grain yield, indicating that excessive increase in these traits may adversely affect productivity.

Positive interrelationships among important yield components such as spikelet number per panicle, fertility percentage and test weight further emphasize their importance in breeding programmes aimed at yield enhancement. The results are in agreement with the reports of Chang *et al.* (2024) for culm length with spikelet number panicle⁻¹, grain number panicle⁻¹, spikelet fertility; Kole *et al.* (2008) for spikelet number panicle with grain number panicle⁻¹ and spikelet fertility; Sahoo *et al.* (2025) for grain

Table 7. Cluster of thirty-three Genotypes of Rice.

Cluster	No. of genotypes	Name of genotypes
I	22	Govindobhog, Tulaipangi, Radhatilok, China Kamini, Bahadurbhog, 88(8), Tulsi Bhog, Black Joha, Joha, Kalo Namak, Kalo Nunia, Jami Nadu, Sugandha, Normal Joha, Sonamukhi, Danarguri, Badsabhog, Kataribhog, Gandeswari, Khasdhan, Balam, Kanta Bandh Sugandhi.
II	10	Pusa basmati-1, Baskota, Pusa Sugandhi Type-5, Manipuri Black Rice, Dehradun Pahari, BM-24, Gopalbhog, Pakbas, Dehradun, Dudheswar.
III	1	Shantibhog.

Table 8. Average intra-and inter-cluster $\sqrt{D^2}$ values.

Cluster	I	II	III
I	28.27	183.23	652.29
II		44.60	199.79
III			0.00

Table 9. Cluster means of ten quantitative characters in aromatic rice.

	Plant height	Main Panicle Length	Exortion	Leaf Area	Total Effective Tillers	Spikelet number/ Panicle	Filled Grains Per Panicle	Fertility %	Seed Yield Per Plant	Test Weight
Cluster 1	168.82	27.01	11.98	28.16	11.56	175.02	144.43	82.19	16.94	3.07
Cluster 2	150.05	26.86	4.34	35.26	10.70	143.38	113.27	78.29	19.56	5.22
Cluster 3	185.38	26.95	6.65	50.06	9.60	156.91	123.98	78.61	27.34	7.64
Relative Contribution (%)	0.76	0.76	4.73	0	0.19	10.8	0.95	1.14	1.14	79.55

number panicle⁻¹ with panicle weight; Kumar *et al.* (2025) for test weight with panicle weight.

Path coefficient analysis

Path coefficient analysis partitioned the correlation coefficients into direct and indirect effects, providing clearer insight into the contribution of individual traits toward grain yield.

At the genotypic level, fertility percentage exerted the highest positive direct effect on grain yield, followed by spikelet number per panicle, test weight and leaf area (Table 5). These traits also exhibited positive correlations with yield, indicating their importance as reliable selection criteria. The results are in conformity with Sahoo *et al.* (2025) for panicle number plant⁻¹, Kumar *et al.* (2025) for test weight.

Exsertion length and total effective tillers showed negative direct effects on grain yield, suggesting that indiscriminate selection for these traits may not be beneficial.

Phenotypic path analysis also identified spikelet number per panicle, test weight and fertility percentage as major contributors to grain yield (Table 6). The consistency of results across genotypic and phenotypic analyses confirmed the importance of these characters in determining yield performance.

Genetic divergence analysis

Mahalanobis' D² analysis grouped the 33 genotypes

into three distinct clusters, reflecting substantial genetic diversity among the genotypes. Cluster I contained the maximum number of genotypes, while Cluster III consisted of a single highly divergent genotype, Shantibhog (Table 7).

The highest inter-cluster distance was observed between Clusters I and III, indicating the possibility of obtaining maximum heterosis and wider recombination by crossing genotypes belonging to these clusters (Table 8). The results are agreement with Tiwari *et al.* (2022), Bhoite (2023), Jangala *et al.* (2022).

Among all characters, test weight contributed the highest proportion towards total genetic divergence, followed by spikelet number per panicle. These traits therefore played a major role in differentiating the genotypes (Table 9).

Based on divergence pattern, cluster means and per se performance, crosses involving Baskota, Pusa Basmati-1, BM-24, Gobindobhog and Tulaipanji were identified as promising combinations for future breeding programmes.

CONCLUSION

The present investigation revealed substantial genetic variability among the evaluated non-Basmati aromatic rice genotypes. High heritability coupled with high genetic advance for several yield-related traits indicated the predominance of additive gene action and the effectiveness of direct selection. Correlation

and path coefficient analyses identified fertility percentage, spikelet number per panicle, test weight and leaf area as major determinants of grain yield. These traits should therefore receive greater emphasis in breeding programmes aimed at improving productivity in aromatic rice. Genetic divergence analysis demonstrated the existence of considerable diversity among genotypes and identified promising parental combinations for hybridization. The findings of the study provide valuable information for the development of high-yielding aromatic rice varieties with desirable agronomic traits.

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