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Genetic Variability, Character Association and Divergence Studies in Advance Generation Aromatic Rice

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ABSTRACT

Gangetic old alluvial zone in India has conserved many locally adapted aromatic rice landraces. In order to determine the extent of genetic divergence of twelve morphological characters, the study was conducted to examine thirty-five aromatic rice genotypes in *kharif* season of 2024-25 at the agriculture farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, Birbhum, West Bengal, India. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. A considerable degree of variation was noted for all the traits being investigated. Based on mean performance of 35 genotypes MED × Basmati and Baskota ×Gopalbhog crosses seem promising and its selection will be effective. Test weight and no. of spikelet/ panicle showed good GCV values in conjugation with heritability and genetic advance. From correlation coefficient analysis it was found that characters like plant height, flag leaf length, panicle length, no. of primary branches/ panicle, no. of secondary branches/ panicle, no. of spikelet/ panicle, spikelet fertility percentage and test weight showed positive and significant correlation with yield. Based on D^2 analysis values, all the genotypes were grouped into eight clusters in which cluster V had the largest intra cluster distance and cluster V & VIII had the largest inter cluster distance. Among the several genotypes of aromatic rice, the study assisted in identifying the superior germplasm that could be used as parents for subsequent breeding with desired traits.

Keywords Aromatic rice, Genetic divergence, Correlation coefficient analysis, Cluster analysis, Cluster distance.

INTRODUCTION

Oryza sativa, also known as Asian rice, or, less frequently, *Oryza glaberrima*, sometimes known as African rice, are grass species that produce rice. There are two species of rice that are grown. The primary species of rice grown worldwide is *Oryza sativa*, which is planted in Asia. West Africa is the

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primary location for the cultivation of African rice, *Oryza glaberrima.* Indica and Japonica are the two subspecies of rice that are grown in Asia. There are numerous varieties of rice, including brown rice, waxy rice, hybrid rice, wild rice and fragrant rice. A tiny but significant subgroup of the various types of rice, aromatic rice comes in two varieties: Long-grained (Basmati type) and short-grained (non-basmati type). Aromatic rice belongs to a limited yet unique category of rice that are regarded as having the highest quality. Most Indian-grown fragrant rice is tiny to medium-grained, despite the fact that long-grained aromatic rice is popular worldwide. India is the country that exports the majority of its basmati rice i.e. around two-thirds of its production. Actually, the Indian subcontinent received basmati rice as a gift from "Mother Nature" and it grows exclusively in the Indo-Gangetic plains. The Hindi word "Bas" means "aroma," while the Hindi word "Mati" means "full of." Thus, the phrase "basmati," which means "full of aroma. "The flavor and palatability of fragrant rice make it the preferred choice of consumers worldwide. The foundation of every breeding program is genetic variability, hence breeders have been very interested in determining the degree of genetic variation among the rice varieties or genotypes (Mondal *et al.* 2024). Breeding efforts may be improved by choosing parents with greater diversity for various yield and quality characteristics, which is influenced by genetic divergence across the genotypes. Because genetically varied parents are more likely to contribute desirable segregants and produce high heterotic crossings, the genetic divergence among the genotypes of aromatic rice is also a crucial tool for plant breeders looking to select parents for plant improvement (Bhogal *et al.* 2025). The genotypic and phenotypic coefficient of variation are much more useful in determining the variability in a trait (Mazal 2024). The main element of breeding programs for expanding the rice gene pool is genetic variability for agronomic parameters. In order to indirectly boost yield, plant breeders frequently choose for yield components. Predicting the gain under effective selection is made easier by heritability combined with genetic advance. Genetic advance and heritability are crucial selection criteria. When anticipating the gain under selection, heritability estimates in conjunction with genetic advancement are very much useful than heritability estimates alone. Two variables' mutual relationship is measured by correlation. It serves as a gauge for the degree of proximity and linearity between two variables. Correlation analysis can help plant breeders in understanding how enhancing one trait will concurrently enhance other traits. D^2 analysis is used to examine the genetic diversity of a population. This statistical technique determines the genetic variation present in a population. Assessing genetic diversity can reveal information on breeding program possibilities and the preservation of important genetic resources. D^2 analysis provides a more thorough picture of the genetic composition of a population and can pinpoint methods to increase its resilience and production.

MATERIALS AND METHODS

Experimental site

The Agriculture Farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, Birbhum, West Bengal, India, serves as the experimental location. The area, which is situated on the edge of the Chhotnagpur plateau, has a unique climate. The Summer temperatures range from 25.5°C to 41.5°C, and they are hot and dry. In the winter, temperatures can decrease by as much as 5°C. Rainfall during the monsoon season averages roughly 1400 mm. The area is located in the hot sub-humid to humid eco-region of West Bengal's laterite belt, according to the Indian Council of Agricultural Research's agroclimatic zonation. The plot's coordinates are 87°42'E longitude and 23°29'N latitude. The elevation is roughly 58.9 meters above mean sea level.

Experimental soil

The ferrous composition of the red soil causes the assigned experimental plot to be acidic. It is distinguished by lateritic formations and a sandy loam texture. The contents of phosphate and organic carbon are low to medium, whereas the potash amount is medium to high (Table 1). The fertilizer was applied sparingly and in accordance with the required dosages because the fertility is thought to be poor.

Table 1. Physico-chemical properties of the soil in the experimental field.

Chemical composition					Physical composition		
Available N (kg/ha)	Available P (kg/ha)	Available K (kg/ha)	Organic carbon (%)	pH	Sand %	Silt %	Clay %
223.3	16.2	171.5	0.61	5.6	55	10.7	31.6

Table 2. List of genotypes from different cross combination used in the experiment.

Sl. No.	Cross combination	No. of genotype
1	MED × PST-5	9
2	MED ×Basmati	7
3	MED × Pakbas	4
4	MED × T-Basmati	1
5	Baskota × Gopalbhog	3
6	Baskota × Tulaipanji	2
7	Baskota × Dehradunpahari	2
8	Baskota × Gobindobhog	1
9	PB-1 × BM-24	3
10	MSD-1 × PST-5	3
Total		35

Experimental material

Table 2 shows the thirty-five families developed from 10 cross combinations with 13 different parents belonging Basmati type, Non-Basmati type and Mutant type were used in the experiment and its description given in Table 3. Families were grown separately during the *kharif* season of 2024-25 from the seeds of distinct plants from the F_5 families.

Experimental procedure

The experiment was undertaken during the *kharif*

Table 3. Description of parents.

Sl. No.	Parents	Description of parents
		Basmati type
1	Basmati	Broad erect leaf, lodging resistance, sturdy stem, medium height, dark green leaves
2	Pakistan basmati (Pakbas)	Medium awn, long and slender grain, medium broad and erect leaf, medium height, early duration
3	Pusa basmati-1 (PB-1)	Slender grain, awned, early
4	Taraori basmati (TB)	Well exerted panicle, stem height medium to tall, slender, long and bold grains, golden yellow hull, awn less, susceptible to stem borer, late maturity
5	BM-24	Medium tall, erect leaf, medium slender grain with short awn, light green leaf, lodging susceptible, medium broad flag leaf
6	Pusa sugandh type-5 (PST-5)	Bold grain, pointed tip of grain looks like awn, broad erect leaf
		Non-basmati type
7	Baskota	Medium slender grain, long awn, erect broad leaves, sturdy stem, medium height
8	Gopalbhog	Medium height, broad erect leaf, medium bold grain, no awn, brown husk, lodging susceptible
9	Gobindobhog	Short grain, medium broad leaf, medium tall, lodging susceptible, no awn, light green leaf, used for preparation of sweet dishes and ritual offerings
10	Dehradunpahari	Bold grain, brown husk, broad erect leaf, dark green
11	Tulaipanji	Narrow leaved, long awned, medium slender grain, medium tall, light green leaf
		Mutant type
12	Mutant early duration (MED)	Induced by 300Gy gamma rays on Badshahbhog. Height is 150 cm, well exerted panicle, 88% spikelet fertility, 10.5 g test weight, medium flag leaf
13	Mutant semi dwarf 1 (MSD 1)	Induced by 300Gy gamma rays on Badshahbhog. Medium height of 130 cm, 10 cm panicle exertion, 85% spikelet fertility, large flag leaf, slender grain, high yield

period of 2024–2025. On June 28th, 2024, 35 families' seeds were planted separately in a nursery bed. On July 28th, 2024, thirty-day-old seedlings were moved to the main field in RCBD with three replications, with a spacing of 20 cm between rows and 15 cm between plants. Four rows were maintained in each plot with 20 plants, and throughout the crop growth period, the suggested agronomic procedures & measures were observed to ensure a good harvest. Ten plants were randomly chosen from the middle rows of each plot to record the parameters.

Characters studied

For each of the three replications, the growth data of the 35 genotypes were obtained from all ten plants. The 12 traits that were examined included days to 50% flowering, plant height, flag leaf length, flag leaf breadth, no. of panicles/ plant, panicle length, no. of primary branches/ panicle, no. of secondary branches/ panicle, no. of spikelet/ panicle, spikelet fertility %, test weight and grain yield/ plant.

Statistical analysis

The best gain traits for selecting and breeding aromatic rice were evaluated according to correlation, heritability and genetic variability. Analysis of variance (ANOVA) was estimated by using the standard procedure of (Panse & Sukhatme 1954). (Burton and Devane's 1953) approach were used to estimate the genetic parameters, such as the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV). According to (Sivasubramanian and Madhavamenon 1973), the PCV and GCV values for each feature were separated into three groups: 20% (high), 10%–20% (moderate), and less than 10% (low). (Hanson 1956) formula was used to quantify heritability in the broadest sense, while Johnson *et al.* (1955) method was used to determine genetic advance. The basic categories of heritability were low (<30%), medium (30–60%), and high (60%). Additional classifications for the genetic advance were low (0–10%), moderate (10–20%), and high (>20%) (Robinson *et al.* 1949, Johnson *et al.* 1955). Following the procedure outlined by (Miller 1958), the data were examined in order to calculate the correlation coefficients. Divergence analysis (cluster analysis) was performed using the R studio. The cluster distance was measured by Euclidean clustering method. A hierarchical clustering dendrogram was constructed by using the WARD method in R studio.

RESULTS AND DISCUSSION

All of the traits showed a great deal of variability, and the genotypes under study showed a broad spectrum of ranges. These characters' mean, minimum, maximum, and coefficient of variation have all been tabulated appropriately. There was notable diversity among the 35 genotypes, according to the analysis of variance (ANOVA).

Variability in mean performance of 12 quantitative characters

The mean performance of 35 families derived from 10 crosses for 12 Quantitative characters is given in the following (Table 4).

Taking into account the values of CV grain yield/ plant showed maximum CV values followed by flag leaf length, no. of panicles/ plant, panicle length and test weight. Based on the mean performance table of 35 rice genotypes (Table 4) we can say that the cross-MED × Basmati-5 showed good test weight and MED × Basmati-7 exhibited good response for grain yield/ plant. The cross Baskota ×Gopalbhog showed a combination of good characters like plant height, flag leaf length, panicle length and no. of spikelet/ panicle, but in this case certain measures can be taken or we can go for appropriate breeding methods for reducing the height of the plant as it gives a very high yield. Based on mean performance of 35 genotypes and heat map MED × Basmati and Baskota ×Gopalbhog crosses seem promising and its selection will be effective.

Genetic parameters of variation

Table 5 shows the estimated genotypic variance, phenotypic variance, broad sense heritability, genotypic (GCV) and phenotypic (PCV) coefficient of variation, and genetic advance as a percentage of mean (GAM) for 35 aromatic rice genotypes.

Table 4. Mean performance for 12 quantitative characters of 35 genotypes of F_6 families of rice.

No. of geno-types	Family	Genotypes within families	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	No. of panicles/ plant	Panicle length (cm)
1	MED × PST-5	1	101.67	89.40	25.43	0.54	15.53	16.71
2		2	106.67	108.60	25.00	0.68	15.40	18.18
3		3	98.00	108.80	25.40	0.49	14.07	16.93
4		4	100.00	107.64	25.73	0.53	13.06	29.79
5		5	101.00	124.00	25.73	0.91	10.80	20.96
6		6	95.00	136.87	34.80	1.08	15.13	19.91
7		7	97.00	115.73	33.18	0.69	16.07	18.93
8		8	101.67	102.26	30.73	1.85	12.53	20.53
9		9	94.33	108.86	35.93	1.09	13.26	21.73
10	MED× Basmati	1	94.00	94.03	31.18	0.76	17.80	17.49
11		2	95.33	104.53	39.47	0.52	14.73	15.51
12		3	97.67	94.24	21.87	0.89	16.62	19.82
13		4	99.33	109.67	35.60	0.79	14.47	18.62
14		5	98.67	100.30	28.33	0.68	14.13	19.67
15		6	96.67	97.20	21.60	0.58	17.27	18.11
16		7	98.00	106.20	32.33	0.79	15.93	21.53
17	MED×Pakbas	1	95.33	96.27	30.80	0.95	17.33	17.66
18		2	91.33	102.80	29.33	0.63	15.73	18.04
19		3	95.33	121.00	38.40	0.71	19.27	20.62
20		4	98.33	104.80	14.33	1.07	14.59	17.71
21	MED×T-Basmati		91.33	106.20	31.00	0.73	14.27	17.71
22	Baskota×Gopalbhog	1	98.00	173.13	48.13	0.95	15.13	30.67
23		2	96.00	90.60	18.07	0.57	15.60	22.89
24		3	94.00	117.33	20.27	0.57	13.00	19.96
25	Baskota ×Tulaipanji	1	99.67	104.60	22.53	0.80	12.67	26.61
26		2	106.00	114.27	23.20	0.48	12.80	20.33
27	Baskota×Dehradun-pahari	1	103.33	106.20	29.53	0.79	14.53	18.49
28		2	104.67	104.40	26.94	0.51	10.07	17.18
29	Baskota ×Gobindo-bhog		99.67	153.40	41.00	0.99	13.07	20.84
30	PB-1× BM-24	1	95.00	114.73	24.20	0.53	15.87	15.33
31		2	92.33	119.00	25.67	0.51	15.93	16.51
32		3	91.67	121.07	35.13	0.99	16.53	17.38
33	MSD-1 × PST-5	1	96.00	103.60	33.67	1.12	12.67	21.49
34		2	105.00	105.47	26.76	1.13	11.27	22.22
35		3	100.00	109.40	23.60	0.69	13.80	19.62
	Range (max)		106.67	173.13	48.13	1.85	19.27	30.67
	Range (min)		91.33	89.40	14.33	0.48	10.07	15.33
	Grand mean		97.94	110.76	29.00	0.79	14.60	19.88
	Coefficient of variance		4.12	14.73	19.78	15.53	13.58	17.09
	Standard error of mean		0.89	3.46	3.25	0.14	1.22	0.94
	Critical difference at 5%		2.50	9.77	9.16	0.38	3.45	2.65
	Critical difference at 1%		3.32	12.98	12.17	0.51	4.58	3.52

Table 4. Continued.

No. of geno-types	Family	Genotypes within families	No. of primary branches /panicle	No of secon-dary branches/ panicle	No. of spike-let/panicle	Spikelet fertility %	Test weight (g)	Grain yield/ plant (g)
1	MED × PST-5	1	9.33	26.93	209.67	86.71	14.99	14.49
2		2	9.71	28.31	217.67	87.06	12.79	13.36
3		3	7.91	25.69	201.73	84.72	16.43	12.91

Table 4. Continued.

No. of geno-types	Family	Genotypes within families	No. of primary branches/ panicle	No. of secon-dary branches/ panicle	No. of spike-let /panicle	Spikelet fertility %	Test weight (g)	Grain yield/ plant (g)
4		4	11.45	34.39	102.60	87.84	10.01	13.51
5		5	9.96	29.02	288.73	87.62	21.95	19.75
6		6	10.18	28.00	272.80	90.59	18.48	22.82
7		7	8.78	25.98	235.21	88.53	16.62	17.76
8		8	9.02	25.71	280.67	89.96	16.77	18.63
9		9	7.91	23.09	339.07	86.73	10.41	13.98
10	MED× Basmati	1	9.35	28.78	204.33	87.66	18.77	20.13
11		2	8.42	27.56	205.20	90.18	19.85	19.24
12		3	8.54	26.15	235.20	86.31	13.76	15.79
13		4	9.53	28.67	234.60	86.01	21.22	21.07
14		5	9.82	28.67	207.67	87.11	22.12	16.84
15		6	9.60	28.42	269.04	83.68	16.17	19.03
16		7	9.38	25.47	292.80	92.67	17.17	24.39
17	MED×Pakbas	1	9.18	26.80	95.98	93.47	14.96	14.41
18		2	8.24	22.82	178.20	62.94	10.44	10.03
19		3	10.24	26.89	289.33	90.79	18.85	31.27
20		4	9.18	22.13	293.40	91.25	15.70	20.18
21	MED×T-Basmati		7.31	17.31	212.17	57.53	9.72	10.54
22		1	9.89	28.13	370.80	92.81	18.45	29.65
23	Baskota×Gopalbhog	2	9.04	22.31	197.27	77.39	15.46	12.64
24		3	10.24	29.27	220.73	83.09	20.85	16.58
25	Baskota ×Tulaipanji	1	9.52	26.33	84.38	85.13	14.56	15.08
26		2	9.14	26.44	271.65	89.48	16.40	17.59
27	Baskota×Dehradun-pahari	1	9.01	24.93	297.48	90.15	10.78	13.63
28		2	8.00	23.53	246.13	90.80	13.29	10.31
29	Baskota ×Gobindobhog		11.18	29.84	288.87	89.67	18.84	22.02
30		1	8.60	20.47	87.64	87.19	10.22	12.38
31	PB-1× BM-24	2	7.80	26.22	172.93	78.87	12.10	11.98
32		3	9.33	24.62	195.40	80.73	9.94	10.15
33		1	10.29	30.55	280.60	92.53	19.73	21.12
34	MSD-1 × PST-5	2	9.62	24.60	308.10	89.78	17.77	20.56
35		3	9.27	28.40	288.13	88.83	17.86	21.77
	Range (max)		11.45	34.39	370.80	93.47	22.12	31.27
	Range (min)		7.31	17.31	84.38	57.53	9.44	10.03
	Grand mean		9.26	26.36	233.61	86.17	15.81	17.30
	Coefficient of variance		9.73	11.80	18.09	8.58	16.61	20.37
	Standard error of mean		0.48	1.10	15.64	3.02	0.92	2.46
	Critical difference at 5%		1.36	3.10	44.15	8.52	2.59	6.93
	Critical difference at 1%		1.81	4.12	58.63	11.31	3.43	9.21

GCV and PCV

The characteristics such as plant height and days to 50% flowering showed a negligible difference between GCV and PCV, indicating that they will be effective for selection as the environment will have less of an impact Bhogal *et al.* (2025). Three groups are used to classify GCV and PCV values: Low (<10%), moderate (10–20%), and high (>20%). Flag leaf length, flag leaf breadth & no. of spikelet/ panicle (Salunkhe *et al.* 2024), test weight Tiwari *et al.* (2025), grain yield/plant Balakrishnan *et al.* (2025) has high GCV and PCV (Fig. 1). Characters like plant height (Sadhu *et al.* 2025 & Tiwari *et al.* 2025), no. of panicles/ plant (Acharjee *et al.* 2021), panicle length & no. of secondary branches/ panicle Tiwari

Table 5. Genotypic and phenotypic coefficient of variation, heritability and genetic advance for 12 quantitative characters of F_6 families of Rice.

Characters	Grand mean	Range		Coefficient of variation (%)		Heritability (%)	Genetic advance	Genetic advance as a percent of mean
		Min	Max	GCV	PCV			
Days to 50% flowering	97.94	91.33	106.67	4.08	4.37	87.12	7.68	7.84
Plant height (cm)	110.76	89.40	173.13	14.61	15.58	87.93	31.26	28.23
Flag leaf length (cm)	29.00	14.33	48.13	21.38	28.86	54.84	9.46	32.61
Flag leaf breadth (cm)	0.79	0.48	1.85	30.50	42.66	51.11	0.35	44.90
No. of panicles/plant	14.60	10.07	19.27	10.95	18.16	36.37	1.99	16.60
Panicle length (cm)	19.88	15.33	30.67	16.68	18.58	80.62	6.13	30.86
No. of primary branches/ panicle	9.26	7.31	11.45	8.39	12.32	46.35	1.09	11.76
No. of secondary branches/panicle	26.36	17.31	34.39	11.22	13.35	70.70	5.12	19.44
No. of spikelet/panicle	233.61	84.38	370.80	28.75	31.00	86.00	128.29	54.92
Spikelet fertility %	86.17	57.53	93.47	7.97	10.02	63.31	11.25	13.06
Test weight (g)	15.78	9.44	22.12	23.24	25.32	84.23	6.93	43.93
Grain yield/plant (g)	17.04	4.96	31.27	29.51	38.65	58.28	7.91	46.40

et al. (2025), Balakrishnan *et al.*(2025), Biswas *et al.* (2024) has moderate GCV and PCV (Fig. 1), no. of spikelet/panicle (Balakrishnan *et al.* 2025) and no. of primary branches/panicle (Biswas *et al.* 2024) has Low GCV and Moderate PCV (Fig. 1). Days to 50% flowering (Sadhu *et al.* 2025) has Low GCV and PCV (Fig. 1).

Heritability and genetic advance

Heritability values are categorized into low (0-30%), moderate (30-60%), and high (>60%). Estimates of heritability in broad sense were very high for traits like days to 50% flowering (Sao *et al.* 2024), plant height (Bhogal *et al.* 2025), panicle length, no. of secondary branches/panicle, no. of spikelet/ panicle & no. of spikelet/ panicle (Kole & Deo 2024) and test weight (Tiwari *et al.* 2025). Traits having high heritability are less influenced by environment and exhibit greater correspondence between phenotypic and breeding values. Moderate heritability (Fig. 1) was found in grain yield/ plant, flag leaf length & flag leaf breadth (Tiwari *et al.* 2025), no. of panicles/ plant & no. of primary branches/ panicle (Adhikari *et al.* 2018). Genetic advanced over mean is generally grouped into three categories: Low (0–10%), moderate (10–20%), and high (above 20%). In this study,

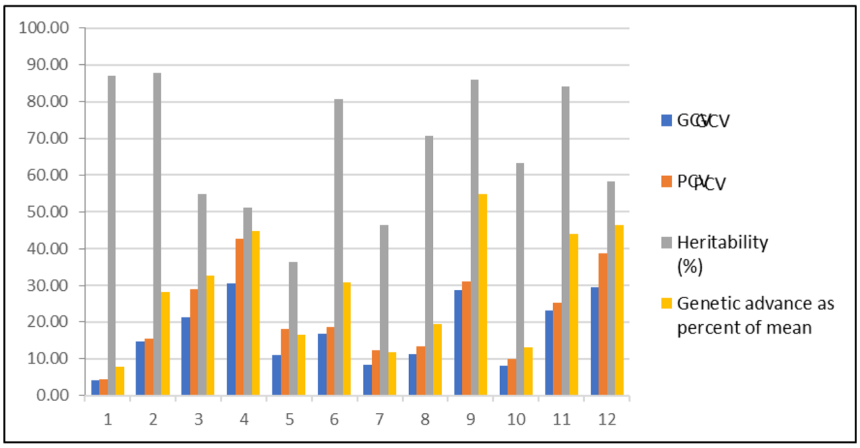


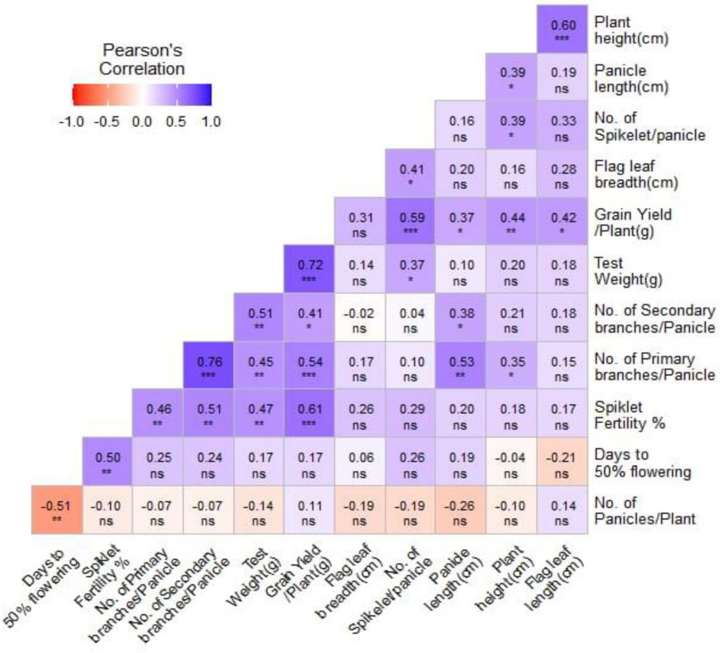
Fig. 1. Graph showing GCV, PCV, heritability and genetic advance as a percent of mean.

Table 6. Genotypic (G) and phenotypic (P) correlation for twelve quantitative characters in F_6 families of rice.

Characters		Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	No. of panicles/plant	Panicle length (cm)	No. of primary branches/panicle
Days to 50% flowering	G	-0.0342	-0.2566	0.0586	-0.6094**	0.2034	0.3082
	P	-0.0509	-0.1470	0.0627	-0.4325**	0.1656	0.1837
Plant height (cm)	G		0.6704**	0.1660	-0.1730	0.4007*	0.3758*
	P		0.5047**	0.1441	-0.0135	0.3705**	0.3161**
Flag leaf length (cm)	G			0.3166	0.1921	0.2353	0.2139
	P			0.2336*	0.0957	0.1361	0.0769
Flag leaf breadth (cm)	G				-0.3038	0.2535	0.2625
	P				-0.0955	0.1433	0.0806
No. of panicles/plant	G					-0.3837*	-0.1693
	P					-0.1431	0.0154
Panicle length (cm)	G						0.6134**
	P						0.4395**
No. of primary branches/panicle	G						
	P						
No. of secondary branches/panicle	G						
	P						
No. of spikelet/panicle	G						
	P						
Spikelet fertility %	G						
	P						
Test weight (g)	G						
	P						

Table 6. Continued.

Characters		No. of secondary branches/panicle	No. of spikelet/panicle	Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)
Days to 50% flowering	G	0.2676	0.2717	0.554 **	0.1749	0.2138
	P	0.2035*	0.2356*	0.4183**	0.1534	0.1023
Plant height (cm)	G	0.2204	0.4063*	0.2263	0.2032	0.4871**
	P	0.1833	0.3558**	0.1222	0.194*	0.3764**
Flag leaf length (cm)	G	0.2616	0.4012*	0.2202	0.2186	0.5579**
	P	0.0785	0.2438*	0.1076	0.1400	0.2682**
Flag leaf breadth (cm)	G	-0.0236	0.4514**	0.2725	0.1484	0.3526*
	P	-0.0057	0.3585**	0.2379*	0.1403	0.2548**
No. of panicles/plant	G	-0.1640	-0.2837	-0.2014	-0.1841	-0.0911
	P	0.0147	-0.1022	-0.0123	-0.0961	0.2893**
Panicle length (cm)	G	0.4073*	0.1642	0.2174	0.1030	0.3945*
	P	0.3501**	0.1544	0.1654	0.0830	0.3339**
No. of primary branches/panicle	G	0.8554**	0.1138	0.6039**	0.5768**	0.6926**
	P	0.6606**	0.0919	0.3148**	0.3137**	0.3826**
No. of secondary branches/panicle	G		0.0290	0.5979**	0.5582**	0.4449**
	P		0.0452	0.3899**	0.449**	0.3638**
No. of spikelet/panicle	G			0.3060	0.3945*	0.605**
	P			0.2742**	0.3244**	0.571**
Spikelet fertility %	G				0.5079**	0.6729**
	P				0.4106**	0.5234**
Test weight (g)	G					0.7051**
	P					0.6109**



ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Fig. 2. Pearson correlation matrix.

traits such as plant height & flag leaf length (Sao *et al*. 2024), flag leaf breadth & no. of spikelet/ panicle (Biswas *et al.* 2024), panicle length (Chowdhury *et al.* 2023), test weight & grain yield/ plant (Bhogal *et al.* 2025) showed high genetic advance (Fig. 1). Moderate values were observed for no. of panicles/ plant & no. of secondary branches/ panicle (Adhikari *et al*. 2018), no. of primary branches/ panicle (Biswas *et al.* 2024), no. of spikelet/ panicle (Bhogal *et al.* 2025). To summarize the overall results of examining GCV and PCV values in conjunction with heritability and genetic advancement, we can state that the following qualities demonstrated high genetic advance, high heritability and strong GCV,- test weight and no. of spikelet/ panicle. According to this, these characteristics are mostly governed by additive genetic factors and are amenable to selection, which makes them desirable targets for breeding program enhancement.

Genotypic and phenotypic correlation coefficient genotypic correlation coefficient analysis

In genotypic correlation coefficient analysis (Table 6) maximum number of characters showed +ve and significant correlation with grain yield/plant except days to 50% flowering (Satturu *et al.* 2023) and no. of panicles/plant (Mondal *et al.* 2024). Number of panicles/plant exhibited negative correlation with grain yield/plant.

Phenotypic correlation coefficient analysis

In phenotypic correlation coefficient analysis, all the characters are positively and significantly correlated with grain yield/plant except days to 50% flowering (Table 6). Days to 50% flowering is positively correlated with grain yield/plant but not significant (Chowdhury *et al.* 2023), Mondal *et al*. (2024).

From the correlation studies and Pearson correlation matrix (Fig. 2) we got to know that the characters like plant height, flag leaf length, panicle length, No. of primary branches/panicle, No. of secondary branches/panicle, No. of spikelet/panicle, spikelet fertility percentage and test weight showed positive and significant correlation with yield.

Multivariate analysis of genetic divergence

The choice of genetically distinct parents in a hybridization program is done using D^2 statistics analysis. It was in 1928 that P.C. Mahalanobis first invented the idea of D^2 statistics. Rao employed this method to evaluate genetic diversity in plant breeding. All 35 test genotypes were classified into eight groups using Tocher's approach based on the relative magnitude of D^2 values, the various genotypes included in each cluster are discussed below (Table 7). Within the experimental population, eight unique clusters were found using cluster analysis. Our present grouping pattern is supported by Satturu *et al.* (2023) who got eight clusters in his prior investigations. The biggest cluster was Cluster I supporting twenty-two genotypes then four in Cluster II, two in each in Cluster III, IV & V, and one in each of Cluster VI, VII and VIII. In our current experiment three solitary clusters have been formed. In those three clusters (VI, VII & VIII) Pusa Sugandha type-5 (PST-5) is a common parent and in clusters VI and VII Mutant early duration (MED) is a common parent.

Table 7. Composition of cluster.

Clusters	Frequency	Name of the families
I	22	MED × PST-5 (1,4,5,7,8 & 9) MED × Basmati (4,5,6 & 7) MED × Pakbas (1,2 & 4) MED × T-Basmati Baskota × Gopalbhog (1 & 3) Baskota × Dehradunpahari (2) PB-1 × BM-24 (1,2 & 3) MSD-1 × PST-5 (2 & 3)
II	4	MED × Basmati (2 & 3) Baskota × Tulaipanji (1) Baskota × Dehradunpahari (1)
III	2	MED × PST-5 (6) MED ×Pakbas (3)
IV	2	MED × Basmati (1) Baskota × Gobindobhog
V	2	Baskota ×Gopalbhog (2) Baskota ×Tulaipanji (2)
VI	1	MED × PST-5 (2)
VII	1	MED × PST-5 (3)
VIII	1	MSD-1 × PST-5 (1)

Average inter and intra cluster values

Table 8 and Fig. 3 indicates maximum Inter Cluster Distance between Cluster V and Cluster VIII

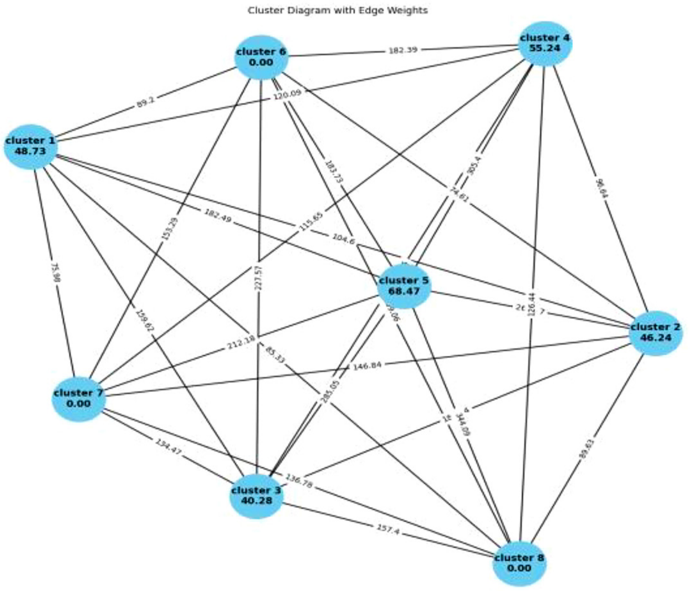


Fig. 3. Average inter and intra-cluster distances (D^2) among 35 rice genotypes in 8 clusters based on Euclidean values.

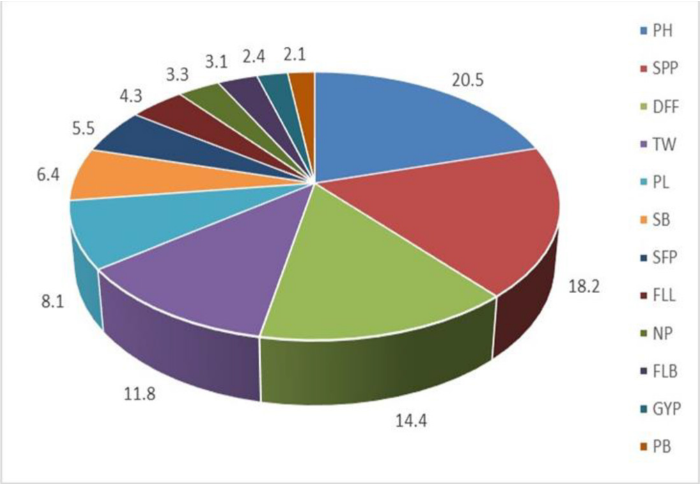


Fig. 4. Contribution of traits towards divergence shown using Pie chart.

Table 8. Average inter and Intra cluster values.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	48.73	104.60	159.62	120.09	182.49	89.20	75.98	85.33
II		46.24	185.14	96.64	266.57	74.61	146.84	89.63
III			40.28	102.50	285.05	227.57	134.47	157.40
IV				55.24	305.40	182.39	115.65	126.44
V					**68.47**	183.73	212.18	**344.09**
VI						**0.00**	153.29	109.06
VII							**0.00**	136.78
VIII								**0.00**

(344.09). The average inter-cluster distances were turned out to be > the average intra-cluster distances, proving that the 35 rice genotypes possess a greater degree of genetic diversity (Debata *et al.* 2020). A cross between genotypes with the greatest genetic distance from Clusters V and VIII would produce

Table 9. Cluster means and percentage contribution towards divergence of 12 quantitative characters in F$_6$ families of rice.

Cluster	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	No. of panicles/ plant	Panicle length (cm)	No. of primary branches/ panicle	No. of secondary branches/ panicle	No. of spikelet/ panicle	Spikelet fertility %	Test weight (g)	Grain yield/ plant (g)
I	98.94	107.71	28.29	0.80	14.41	19.20	9.31	26.90	256.06	88.57	17.53	18.90
II	94.33	108.86	35.93	1.09	13.26	21.73	7.91	23.09	339.07	86.73	10.41	13.98
III	106.67	108.60	25.00	0.68	15.40	18.18	9.71	28.31	217.67	87.06	12.79	13.36
IV	95.17	105.50	27.50	0.74	16.60	16.49	8.89	23.64	91.81	90.33	12.59	13.40
V	99.83	106.12	24.13	0.66	12.86	28.20	10.49	30.36	93.49	86.48	12.27	14.30
VI	91.67	112.27	30.28	0.72	15.62	17.41	8.17	22.74	189.68	70.02	10.30	8.41
VII	96.00	90.60	18.07	0.57	15.60	22.89	9.04	22.31	197.27	77.39	15.46	12.64
VIII	98.83	163.27	44.57	0.97	14.10	25.76	10.54	28.99	329.83	91.24	18.65	25.83
Percentage contribution	14.4	20.5	4.3	3.1	3.3	8.1	2.1	6.4	18.2	5.5	11.8	2.4

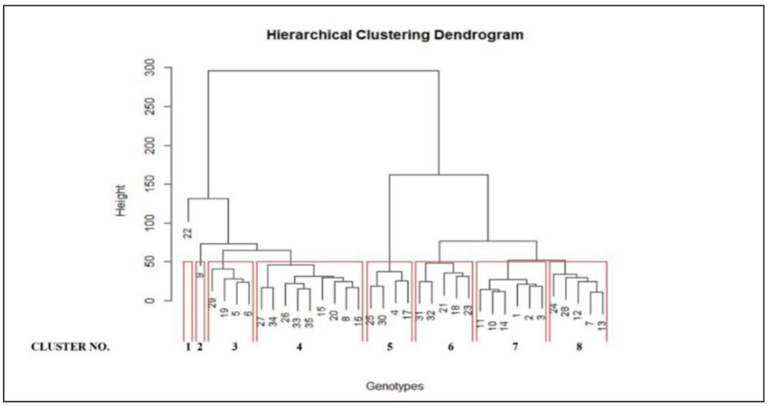


Fig. 5. Hierarchical wards method dendrogram of 35 rice genotypes (Serial no. 1-35 represents the 35 aromatic rice genotypes used and the corresponding crosses for 35 genotypes is same as represented in Table 4).

maximum heterosis (Nanda *et al.* 2025, Singh *et al.* 2016). Thus, it may be extremely beneficial to hybridize genotypes resulting from crosses Baskota ×Gopalbhog, Baskota ×Tulaipanji (Cluster V), and cross MSD-1 × PST-5 (Cluster VIII); but, crossing genotypes within a cluster would not lead to production of superior hybrids (Sharma *et al.* 2017). Maximum Intra Cluster distance was observed for Cluster V (68.47). Hence crosses can be performed between certain genotypes of this cluster. On basis of these Baskota ×Gopalbhog, Baskota ×Tulaipanji and MSD × PST-5 seems useful and can be used in the advanced generations.

Characteristic features of the clusters

Table 9 displays the cluster mean values derived from all twelve characters combined.

Cluster II exhibited good flag leaf breadth and no. of spikelet/panicle. Cluster IV has good no. of panicles/plant. Cluster V exhibited a good panicle length and no. of secondary branches/panicle. Cluster VI consisted of early flowering genotypes. Cluster VIII has many desirable characters like plant height, flag leaf length, panicle length, no. of primary branches/ panicle, spikelet fertility test weight and grain yield/ plant. We can sum up by saying that cluster VIII offered most of the highest values for the aforementioned characters, whereas cluster VI and VII displayed the majority of less significant values in which Cluster VI displayed less values for important characters like spikelet fertility %, test weight and grain yield/ plant.

Contribution of traits towards divergence

A pie chart (Fig. 4) is used to graphically depict each trait's percentage contribution. Plant height (20.5%) was found to contribute the most to diversity (Perween *et al.* 2022), followed by of spikelet/ panicle, days to 50% flowering, test weight, panicle length, no. of secondary branches/ panicle, spikelet fertility %, flag leaf length, no. of panicles/ plant, flag leaf breadth, grain yield/ plant & no. of primary branches/ panicle.

Hierarchical clustering using dendrogram

The Euclidean distance provides the basis for the intra and inter-cluster distance values in divergence analysis, while the Ward method was used to construct the hierarchical dendrogram (Fig. 5). Thus, the number of clusters created using both approaches is the same, i.e., 8. However, the cluster composition varies slightly between the two since they employ different methods to determine the distance values between and within clusters. Thirty-five rice genotypes have been divided into 8 clusters (Fig. 5) using the Ward method in R studio to create a dendrogram in which Cluster I & II consist of 1 genotype followed by Cluster III (4 genotypes), Cluster IV (9 genotypes), Cluster V (4 genotypes), Cluster VI (5 genotypes), Cluster VII (6 genotypes) and Cluster VIII (5 genotypes).

CONCLUSION

High degrees of variation were found in the study for characteristics such as grain yield/plant followed by flag leaf length, no. of spikelet/ panicle, panicle length and test weight. The best grain features that would aid in the transfer of traits like no. of spikelet/panicle & test weight through hybridization were identified as having a considerable impact on yield coupled with high variability, heritability, genetic advance, and minimal environmental influence. In the population of several aromatic rice genotypes, the study also assisted in identifying the potential germplasm that could be used as parents with advantageous traits for subsequent breeding. Furthermore, in order to provide high-quality planting material, only the elite germplasm should be multiplied.

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