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GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERGENCE STUDIES OF F_6 FAMILIES OF AROMATIC RICE

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ABSTRACT

The study evaluated 40 F_6 families from 13 diverse Basmati, non-Basmati, and mutant aromatic rice crosses to assess variability, trait associations, and genetic divergence. Genotypic and phenotypic coefficients of variation (GCV & PCV), heritability, and genetic advance as a percent of mean were calculated to identify traits under strong genetic control. A large PCV, GCV gap in traits like flag leaf length, panicles per plant, spikelet fertility, and grain yield indicated significant environmental influence. High heritability with high genetic advance in spikelets per panicle, test weight, and primary and secondary branches per panicle suggested additive gene action, making these traits suitable for selection. Genetic divergence analysis grouped genotypes into 11 clusters, revealing substantial variation. Superior lines with desirable traits such as high test weight, spikelet fertility, and grain yield were identified. These genotypes may serve as potential parents in breeding programs focused on improving yield and related traits.

***Keywords*:** Aromatic rice**,** Genetic variability, Correlation and Cluster analysis

Introduction

Aromatic rice which popular for its fragrance and other culinary attributes. The first reference to the existence of aromatic rice was discovered in the Susrutha text (c. 400 BC), the great Indian pioneer in medicine and surgery (Kizhakkeveettil *et al.,* 2024). The aromatic rice genotypes are categorised into three distinct categories based on their shape of grain and degree of aroma found in the grain. These groups are the basmati, jasmine and other aromatic rice group (Behera *et al.,*2024, Singh *et al.,*2000). Aerial plant components in aromatic rice create fragrant compounds, which are then stored in mature grain. Almost 100 volatile chemicals have been identified as the cause of aroma. (Hussain *et al.,* 1987; Zhao *et al.,* 2023). 2-Acetyl-1-pyrroline (2AP), a principal aroma compound has been detected in all aerial plant parts of aromatic rice (Yoshihashi *et al.,* 2002, Fayaz *et al.,* 2024).

Many other non-Basmati scented cultivars are grown in different part of India and they are superior than basmati rice in many aspects like high 2-AP concentration, grain/width ratio and taste. Non-Basmati scented rice are location specific and can perform better in particular environment. It has wider genetic base, more tolerance to biotic and abiotic stresses. Therefore, it becomes important to develop new variety by using non-basmati aromatic landraces as a parent in hybridisation programme. An effort was made to expand the genetic variety of aromatic rice by using traditional non-Basmati landrace and improved Basmati variety. Presently experimental work has advanced to the F_6 generation, focusing on blending favourable traits.

A crucial first step in successful selection is evaluating the genetic variability between the genotypes, particularly for variables relevant to yield. Estimates of genetic diversity and selection scope are aided by estimates of heritability, genetic advancement, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV). A good breeding programme requires great genetic variation, high heritability, and high genetic advancement.

The breeder can choose to wait rigorous selection until later generations, when progenies are almost homozygous, or close to choose favourable genotypes in early generations which accomplish this goal. It is quite challenging to make precise yield projections in the early phases of breeding operations. To determine the nature of the relationship between yield and variables that contribute to yield, as well as to evaluate the degree of genetic progress, heritability, and diversity.

Materials and Methods

Forty F_6 genotypes, which were developed from cross combinations involving three types of parents that are well-known non-Basmati aromatic genotypes, established Basmati types, and mutant derived from Badshabhog were employed in this investigation.

Experimental site

The Agricultural Farm, Institute of Agriculture, Visva-Bharati, Sriniketan, which is situated in a sub-humid lateritic environment, was the site of the field tests. The experimental site is 58.9 meters above sea level and is situated at 23°19' N latitude and 87°42' E longitude. The climate is subtropical and humid, with an average rainfall of 1300 to 1600 mm. The experimental plot's soil texture is sandy loam, and its fertility level ranges from medium to low. The acidity of the soil is indicative of lateritic and red soils. The following Table 1 showed the experimental field's physicochemical characteristics.

Table 1 : Experimental field's physicochemical characteristics.

Fertility status				Mechanical composition			
Available N(Kg/ha)	Available P (Kg/ha)	Available K(Kg/ha)	Organic Carbon (%)	pH	Sand (%)	Silt (%)	Clay (%)
227.7	17.2	167	0.53	5.6	58	11.7	30.3

Experimental Procedure

In 2024, during the kharif season (June–December), the F_6 genotypes were raised alongside their parents in a duplicated study. The 40 unique F_6 genotypes were planted separately in the seed bed. In the main field, thirty-day-old seedlings were moved using a randomized complete block design (RCBD) with three replications, with a 20 cm space between rows and a 15 cm distance between plants. Each experimental plot comprises four rows, each containing 20 uniformly spaced plants. To ensure a satisfactory harvest, the suggested agronomic procedures and crop protection measures were adhered to during the period of crop growth. Five randomly chosen plants from each plot in each replication were subjected to biometric observations.

Characters under observation

11 quantitative characters were studied, including Days to 50% flowering, plant height(cm), flag leaf length (cm), panicle length (cm), number of panicles per plant, number of primary branches per panicle, number of secondary branches per panicile, number of spikelets per panicle, spikelet fertility percentage, test weight (g), and grain yield per plant (g).

Statistical analysis

The evaluation of yield enhancement through selection and breeding was conducted by examining genetic variability, heritability, and correlation. Analysis of variance, along with the assessment of phenotypic and genotypic variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic advance as a percentage of the mean were carried out using standard procedures (Singh and Chaudhary, 1979). The differences in mean, correlation coefficient were tested by R statistical software (Lüdecke *et al.,* 2021). According to Sivasubramanian and Madhavamenon's (1973) suggestion, the PCV and GCV are divided into three groups < 10% (low), 10-20% (moderate), and > 20% (high). In general, heritability was divided into three categories: low (<30%), medium (30–60%), and high (>60%). Also, the genetic advancement was categorized as high (>20), moderate (10–20%), and low (0–10%) (Robinson *et al.,* 1949; Johnson *et al.,* 1955). Tocher's approach was used to group the genotypes into various clusters.

Results and Discussion

Result of experiment 'Genetic diversity in F_6 generation of aromatic rice' conducted during Kharif season of 2024 is discussed below considering 11 quantitative characters. The information gathered was used to undertake statistical analyses for average performance, genetic variation, correlation, and divergence studies.

Analysis of variance (ANOVA)

For 11 quantitative characters, including days to 50% flowering, plant height (cm), flag leaf length (cm), panicle length (cm), number of panicle per plant, number of primary branches per panicle, number of secondary branches per panicle, number of spikelet per panicle, spikelet fertility percentage, test weight (g), and grain yield per plant (g), the analysis of variance of 40 F6 families derived from 13 crosses is shown in Table 2. Most of the characters are significant at 0.1% level except flag leaf length and number of panicles per plant, these are significant at 1% level.

Variability of mean performance in characters

The mean performance of 40 F_6 families resulting from 13 crosses for 11 quantitative characters is shown in Table 3.

The average days to 50% flowering was 98.65 days and it ranged from 92.33 to 104 days. The earliest flowering family was MED × T-Basmati-1, whereas MED × Basmati-7 was the last flowering genotype. The plant height varied from 82.40 cm to 139.40 cm. The shortest family was MED × Pakbas-1 and the tallest family was Baskota × Gobindobhogh-3. Average number of panicle per plant was 12.60 and it ranged from 5.60 to 16.33. MED × kalikasha exhibited lowest number of panicle/plant and MSD-1 × Baskota had highest panicle length ranged from 19.09 to 26.43 with a mean average of 21.76. Baskota × Gobindobhogh-3 has the highest panicle length and MED × Basmati-3 has the lowest. Average number of primary branches per panicle was 7.98 and it ranged from 5.36 in MED × Basmati-12 to 10.62 in Baskota × Gobindobhogh-3. Number of secondary branches per panicle range from 14.58 in MED × Basmati-2 to 31.51 in Baskota × Gobindobhogh-3 with an average of 20.19. Average spikelet per panicle is 226.54 with a range from 136.73 to 367.60. Baskota × Gobindobhogh-3 and PB-1 × BM-24-1 had highest and lowest number of spikelet per panicle respectively. Average spikelet fertility percentage was 88.09%. It ranged from 72.61% to 93.55% in MED × Basmati-1 and MED × Basmati-7 respectively. Test weight ranged from 10.79 g to 21.53 g with average of 17.52 g. MED × Basmati-9 and Baskota × gobindobhogh-1 had highest and lowest test weight respectively. Grain yield per plant ranged from 10.04 g to 22.06 g with an average of 14.76 g. MED × Basmati-1 and MED × Pakbas-2 had highest and lowest grain yield per plant respectively. From the CV value, high variability was observed in Grain yield per plant followed by number of spikelet per panicle, number of secondary branches per panicle, test weight, number of panicle per plant, flag leaf length, plant height, panicle length, spikelet fertility percentage, and days to 50% flowering.

Genetic Parameters of Variation

GCV and PCV

GCV and PCV were estimated for 11 characters in the experimental population. GCV and PCV ranged from 2.39, 3.95 in days to 50% flowering to 19.46, 35.08 in grain yield per plant. (Table 4). Characters like grain yield per plant, number of secondary branches per panicle, flag leaf length, number of panicles per plant, and number of spikelet per panicle showed high PCV. Grain yield per plant, number of secondary branches per panicle, flag leaf length, number of panicles per plant, number of spikelet per panicle, test weight, number of primary branches per panicle, and plant height show moderate GCV. Spikelet fertility percentage, days to 50% flowering, and panicle length had low GCV and PCV. Test weight, plant height, and number of primary branches per panicle showed moderate PCV values. The estimates of GCV and PCV for flag leaf length, number of panicles per plant, Spikelet fertility percentage, and grain yield per plant showed higher differences, which indicated the greater role of environment. Low differences were observed for days to 50% flowering, number of primary branches per panicle, panicle length, plant height, and test weight, which indicates less sensitivity of these characters in the fluctuating environment. These characters are influenced by genetics and useful for selection.

Similar result of GCV and PCV for days to 50% flowering Mazal *et al.,* (2024); Das *et al.,*(2024); Bastola *et al.,* (2025); Dabhi *et al.,* (2025); Devi *et al.,* (2025), for plant height Demeke *et al.* (2023) Renuprasath *et al.,* (2023); Verma *et al.,* (2023); Pardhi *et al.,* (2025); Bastola *et al.,* (2025), for flag leaf length Thuy *et al.,* (2023), for number of panicles per plant Kole *et al.* (2008); Chacko *et al.,* (2023); Prakash *et al.,*(2024), for panicle length Thuy *et al.,* (2023) Verma *et al.,* (2023) Gupta *et al.,* (2023); Kole *et al.,* (2008); Das *et al.,* (2024), for primary branches per panicle Kole and Deo (2024); Singh *et al.,* (2022); Nath *et al.,* (2021), for secondary branches per panicle Hastini *et al.,* (2021); Chacko *et al.,* (2023); Singh *et al.,*(2022);

Nath *et al.,*(2021), for number of spikelet per panicle Naik *et al.,* (2022), for spikelet fertility percentage Renuprasath *et al.,*(2023)*;* Thuy *et al.,* (2023)*;* Quadri *et al.,* (2023)*;* Chouhan *et al.,* (2024), for test weight Faysal *et al.,* (2022) Ramachary *et al.,* (2022) Thuy *et al.,* (2023) Mazal *et al.,* (2024); Harshraj *et al.,* (2024); Salunkhe *et al.,* (2024); Saravanan *et al.,* (2024), for grain yield per plant Adhikari *et al.,* (2018); Cheabu *et al.,* (2024)

Heritability and genetic advance

Heritability values are categorized into low (0-30%), moderate (30-60%) and high (.60%). Estimates of heritability in a broad sense were very high for traits like panicle length (77.89%), number of primary branches per panicle (71.94%), number of secondary branches per panicle (66.40), test weight (63.80%), and spikelet per panicle (61.15%). Trait with high heritability is less influenced by environment and exhibit greater correspondence between phenotypic and breeding values. Moderate heritability was found for plant height (52.78%), days to 50% flowering (36.67%), spikelet fertility percentage (31.74%) and grain yield per plant (35.08%).

Genetic Advance as percent of Mean was high for number of spikelet per panicle (29.79%), number of secondary branches per panicle (29.47%), test weight (25.08%), number of primary branches per panicle (24.65%) and grain yield per plant (22.24%). Moderate values were observed for plant height (17.46%), panicle length (15.65%), number of panicle per plant (12.62%) and flag leaf length (11.03%). It was low for spikelet fertility percentage (4.39%) and days to 50% flowering (2.98%).

When combined with genetic advance estimates, heritability offers more information for choosing the finest individuals than when utilized alone, according to Jhonson *et al.,* (1955). High heritability with high genetic advance as percent of mean was observed for number of spikelet per panicle, test weight, number of primary branches per panicle, and number of secondary branches per panicle, indicating the predominance of additive gene action in the expression of these characters. Therefore selection of all these characters would be productive.

Similar finding of heritability for days to 50% flowering by Bhattachraya and Chakraborty (2019); Renuprasath *et al.,* (2023), for plant height Renuprasath *et al.,* (2023); Soundharya, B., *et al.,* (2024), for flag leaf length Abebe *et al.,* (2017), for number of panicle per plant Krishna *et al.,* (2014); Imsong *et al.,* (2015); Jia *et al.,*(2019), for panicle length Kole and Deo (2024); Prasanth *et al.,* (2024), for primary branches per panicle Faysal *et al.,* (2022); Kole and Deo (2024), for secondary branches per panicle Faysal *et al.,* (2022); Kole and Deo (2024); Guttikonda et al (2024), for number of spikelet per panicle Kole and Deo (2024), for spikelet fertility% Nath & Kole (2021), for test weight Renuprasath *et al.,* (2023), Sao *et al.,* (2024); Pavani *et al.,* (2025); Sharada *et al.,* (2025), for grain yield per plant Adhikari *et al.,* (2018).

Genotypic and Phenotypic correlation coefficient

To determine the association between each character, genotypic and phenotypic correlation coefficients were calculated for every character combination in the current study. Table 5 displayed the estimated genotypic and phenotypic correlation coefficients.

Grain yield/plant was found to be positively and significantly correlated with panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of spikelet per panicle, spikelet fertility percentage, and test weight. This suggested that using these traits for direct selection could increase grain yield. When choosing traits that are directly related to grain yield, it's also important to take into account how those traits relate to other traits. Panicle length, significantly and positively correlated with number of primary branches per panicle, number of secondary branches per panicle, and number of spikelet per panicle. Number of primary branches per panicle significantly and positively correlated with number of secondary branches per panicle, number of spikelet per panicle, and spikelet fertility percentage. Number of secondary branches per panicle significantly and positively correlated with number of spikelet per panicle. Number of spikelet per panicle and spikelet fertility percentage significantly and positively correlated with spikelet fertility percentage and test weight respectively. Days to 50% flowering, plant height, flag leaf length, number of panicle per plant are positively but non-significantly related with grain yield per plant. Significant negatively correlation was observed between days to 50% flowering and test weight; plant height and spikelet fertility percentage; number of panicle per plant and number of secondary branches per panicle.

Number of panicle per plant, panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of spikelet per panicle, spikelet fertility percentage, and test weight emerged as the most important character for selection in improving rice yield in the population under investigation.

Genetic divergence analysis

In the present study, 40 F_6 families were evaluated for genetic divergence based on 11 quantitative characters. Significant differences between the families for every character under examination were found by the analysis of variance.

Distribution of 40 families into various cluster

Cluster I contain maximum number of 22 families representing MED × Basmati (1,3,5,8,11 & 12), MED × Paklbas (1 & 2), MED × PST (2 & 3), Baskota × Dehradunpahari (1,2,3,4 & 5), Baskota × Gobindbhogh (3), Baskota × BM (2), MSD-1 × PST (1,2 & 3), PB-1 × BM (2 & 3).

Cluster II contain the next highest number of families (5) comprising of PB-1 × BM (1), PB-1 × Gopalbhogh (1 & 2), MED × Basmati (2), MED × Kailkasha.Cluster III had 3 families included Baskota × Gobindbhogh (1), Baskota × Gopalbhogh Baskota × BM (1).Cluster IV and cluster V both had only 2 families. In cluster IV included MED × PST (1) and MED × Basmati (10). In cluster V included Baskota × Gobindbhogh (2) and MED × Basmati (9). Cluster VI, VII, VIII, IX, X and XI were solitary cluster containing MSD-1 × Baskota, MED × T-Basmati (1), MED × Basmati (4), MED × Basmati (6), MED × Basmati (7), and MED × T-Basmati (2) respectively. 5 Out of 6 solitary cluster one of parent was MED and 3 cluster had same parent MED × Basmati and 2 cluster had MED × T-Basmati. All six solitary cluster had one mutant parent which was MSD-1 and MED. Similar type of findings were reported by Chakraborty and Bhattachraya (2018). The formation of solitary clusters may be due to the total isolation, preventing the gene flow or intensive selection pressure for diverse adaptive complexes. Distribution of 40 genotypes into various cluster were given in Table 6.

Average intra and inter cluster distance values

Among the eleven clusters, Cluster V showed the maximum intra-cluster distance (25.86) Cluster VI, VII, VIII, IX, X, and XI did not show any intra-cluster diversity due to the presence of solitary genotypes. Minimum average inter-cluster distance was observed between cluster I and VIII (28.49) and maximum inter-cluster distance was found between cluster IV and X (160.46).

Selecting various parents within a single group is best done when there is high intra-cluster diversity, as in Cluster V. When trying to maximize genetic diversity and combine extremely dissimilar qualities, a high inter-cluster distance (such as between IV and X) is ideal.

For every character, none of the clusters shows the highest mean. Clusters that were reasonably far apart were used to spread the highest and lowest mean values. There is a significant degree of variety within the duster, as indicated by the intra-cluster distance of 25.86 within cluster V. Therefore, in order to maximize the potential variety inside the cluster, individuals from each family from this cluster can be passed on to the following generation. Highest inter-cluster distance was found between cluster IV and Cluster 10. Cluster IV had highest number of primary branches per panicle, number of secondary branches per panicle and spikelet fertility. It had also 2nd highest yield and number of spikelet per panicle. While cluster X is a solitary cluster. It had lowest mean value of flag leaf length, 2nd lowest Secondary branches per panicle and 3rd lowest test weight. Families from cluster IV and cluster X can be crossed for improving family of cluster X.

Based on finding from this research panicle length, number of primary branches per panicle, test weight, number of spikelet per panicle and number of secondary branches per panicle are most contributing character toward grain yield per plant. Days 50% flowering and plant height does not have significant effect regarding grain yield per plant. If plants are late maturing variety it had more incidence biotic and abiotic stresses. If plant height is more then it had lodging problem. Families from cluster I, II and IV were found to be best performing. Cluster III and V were found to be poor performing.

Table 2 : Analysis of variance (Mean square) for eleven quantitative characters in F6 families of Aromatic rice

Source	df	DFF	PH (cm)	FLL (cm)	NPP	PL (cm)	PB	SB	NSP	SFP	TW (g)	GYP (g)
Replication	2	0.975	117.35	151.651	11.5566	0.177	0.5055	2.293	508.3	31.664	2.7322	11.661
Genotypes	39	26.3***	597.4***	59.923**	12.181**	11.52***	4.29***	46.06***	6379.3***	57.21***	25.4***	41.9***
Error	78	9.5989	137.25	31.041	5.6908	0.9954	0.4939	7.168	1115	23.884	4.047	17.939

*, **, *** significant at 5%, 1% and 0.1% level respectively

(DFF- Days to 50% flowering, PH- Plant height, FLL - Flag leaf length, NPP - Number of panicle per plant, PL - Panicle length, SB - Secondary branches per panicle, PB- Primary branches per panicle, SPP - Spikelet per panicle, SFP - Spikelet fertility percentage, TW - Test weight, GYP - Grain Yield per plant)

Table 3 : Mean performance of 40 F_6 families for eleven quantitative characters.

No. of Genotype	Family	Genotype within family	DFF	PH (cm)	FLL (cm)	NPP	PL	PB	SB	SPP	SFP	TW (g)	GYP (g)
1	MED × Basmati	1	98.67	111.60	23.73	11.80	21.75	6.96	19.87	174.07	72.61	15.80	10.04
2		2	100.67	91.00	23.87	14.00	20.27	7.40	14.58	200.67	93.26	19.63	16.92
3		3	94.33	117.23	25.33	13.40	19.09	6.93	16.58	221.60	87.32	14.69	12.85
4		4	99.67	127.40	28.13	10.07	26.42	6.20	21.33	239.13	80.56	16.22	12.22
5		5	101.67	115.60	24.07	13.67	23.80	6.49	16.31	242.27	83.85	12.79	12.43
6		6	102.00	89.40	25.80	13.80	21.91	8.67	22.56	258.27	92.19	18.17	19.83
7		7	104.00	90.07	28.17	10.40	23.42	9.59	27.74	292.80	93.55	17.63	16.85
8		8	96.67	107.87	30.80	13.53	21.06	5.44	15.07	194.40	87.42	15.08	11.47
9		9	103.33	98.67	27.07	12.33	21.14	7.89	18.87	242.07	91.98	21.53	18.69
10		10	99.00	99.87	28.53	15.47	20.34	6.87	16.04	183.93	84.99	18.94	14.98
11		11	98.33	111.07	28.23	14.47	22.21	7.18	24.84	261.20	86.10	12.99	12.14
12		12	98.67	94.93	32.13	12.67	20.13	5.36	15.60	152.87	86.16	15.63	10.08
13	Baskota × Gobindobhogh	1	97.33	126.27	29.00	11.80	23.82	9.22	23.11	341.60	88.18	10.79	11.92
14		2	99.33	95.27	25.27	12.13	20.62	7.89	20.47	255.40	86.38	13.87	12.90
15		3	101.67	139.40	25.67	10.27	26.43	10.62	31.51	367.60	89.56	16.59	17.77
16	MED × PST-5	1	101.33	125.27	26.85	11.80	24.61	7.96	23.67	237.00	90.82	18.88	16.31
17		2	98.67	102.67	19.93	13.20	21.78	6.91	17.87	177.33	85.24	14.49	10.90
18		3	103.67	92.07	24.67	15.40	19.20	6.98	20.18	235.93	89.25	11.21	10.31
19	MED × Pakbas	1	94.00	82.40	30.00	14.00	19.74	7.16	17.89	184.73	88.25	19.30	14.67
20		2	98.00	127.33	41.07	14.20	25.36	8.93	25.64	238.87	91.56	19.87	22.06
21	MSD-1 × Baskota		100.33	113.53	27.33	16.33	21.40	9.20	20.60	224.20	91.83	20.71	19.76
22	Baskota × Dehradunpahari	1	94.67	103.87	32.13	12.27	21.30	9.80	24.13	256.07	85.92	18.12	17.37
23		2	98.00	107.20	25.53	9.80	21.36	7.58	20.07	277.20	87.51	17.29	14.28
24		3	98.67	116.73	25.53	11.40	20.74	7.64	19.36	226.27	85.13	18.73	13.43
25		4	97.67	116.43	35.20	9.30	21.08	8.10	22.54	272.72	89.13	20.62	15.98
26		5	103.33	100.00	29.53	12.00	19.82	9.18	18.51	237.87	92.70	14.32	12.84
27	PB-1 × BM-24	1	97.67	124.60	31.53	14.73	20.00	7.62	16.18	136.73	83.79	21.17	11.93
28		2	96.00	117.60	34.40	13.07	19.77	7.84	16.76	196.93	89.87	20.64	12.91
29		3	95.33	114.53	32.20	15.40	19.48	8.00	14.91	195.53	91.35	20.40	18.02
30	PB-1 × Gopalbhogh	1	97.67	125.20	36.80	13.00	25.57	9.11	23.62	214.40	88.13	19.64	16.19
31		2	95.67	92.53	26.93	12.67	20.30	7.47	16.82	178.87	91.17	19.02	13.22
32	Baskota × BM-24	1	94.67	91.80	24.00	10.80	23.90	9.78	26.36	266.53	93.02	21.20	19.57
33		2	98.33	107.60	30.80	14.13	21.09	7.49	18.80	164.47	78.13	15.93	10.44
34	MSD-1 × PST-5	1	102.00	101.87	23.67	12.40	21.37	7.93	18.16	209.67	90.44	17.76	14.20
35		2	99.33	97.13	26.83	13.13	22.72	8.44	19.36	227.67	91.73	20.51	18.91
36		3	103.00	98.00	19.22	12.00	22.61	9.78	23.16	235.67	83.74	17.93	16.37
37	MED × T- Basmati	1	92.33	82.67	23.07	11.20	20.35	8.02	17.44	198.00	86.77	17.20	11.91
38		2	97.67	91.73	33.60	14.53	21.19	7.44	16.18	218.73	92.48	19.72	19.39
39	Baskota × Gopalbhogh		94.33	108.73	31.13	11.80	22.83	8.96	24.27	223.00	91.22	21.34	17.68
40	MED × Kailkasha		98.33	89.07	30.33	5.60	20.33	8.98	20.87	199.40	90.18	14.53	10.76
	Range(Max)		104.00	139.40	41.07	16.33	26.43	10.62	31.51	367.60	93.55	21.53	22.06
	Range(Min)		92.33	82.40	19.22	5.60	19.09	5.36	14.58	136.73	72.61	10.79	10.04
	Grand Mean		98.65	106.16	28.20	12.60	21.76	7.98	20.19	226.54	88.09	17.52	14.76
	Coefficient of Variance		3.00	13.29	15.85	15.99	9.01	15.00	19.40	20.36	4.96	16.62	21.74
	Standard Error of Mean		1.79	6.76	3.22	1.38	0.58	0.41	1.55	19.28	2.82	1.16	2.45
	Critical Difference at 5%		5.04	19.04	9.06	3.88	1.62	1.14	4.35	54.28	7.94	3.27	6.88
	Critical difference at 1%		6.68	25.26	12.01	5.14	2.15	1.52	5.77	71.99	10.54	4.34	9.13

able 4 : Phenotypic and Genotypic Coefficients of Variation, heritability, and genetic advance foe eleven quantitative characters in F_6 Families of rice

Characters	Grand Mean	Range		Coefficient of Variation (%)		Heritability (%)	Genetic advance	Genetic advance as percent of mean
		Min	Max	GCV	PCV			
DFF	98.65	92.33	104.00	2.39	3.95	36.67	2.94	2.98
PH (cm)	106.16	82.40	139.40	11.67	16.05	52.78	18.53	17.46
FLL(cm)	28.20	19.22	41.07	11.00	22.61	23.67	3.11	11.03
NPP	12.60	5.60	16.33	11.67	22.24	27.54	1.59	12.62
PL(cm)	21.76	19.09	26.43	8.61	9.75	77.89	3.41	15.65
PB	7.98	5.36	10.62	14.11	16.63	71.94	1.97	24.65
SB	20.19	14.58	31.51	17.83	22.22	64.40	5.95	29.47
SPP	226.54	136.73	367.60	18.49	23.65	61.15	67.48	29.79
SFP	88.09	72.61	93.55	3.78	6.72	31.74	3.87	4.39
TW(g)	17.52	10.79	21.53	15.24	19.08	63.80	4.39	25.08
GYP(g)	14.51	4.76	22.06	19.46	35.08	30.78	3.23	22.24

Table 5 : Genotypic and Phenotypic correlation for eleven characters in F_6 families of rice.

Characters		PH (cm)	FLL (cm)	NPP	PL (cm)	PB	SB	SPP	SFP	TW (g)	GYP (g)
DFF	G	0.052	-0.389 *	0.129	0.362 *	0.186	0.330 *	0.362 *	-0.001	-0.328 *	0.056
	P	-0.027	-0.253 **	-0.078	0.054	0.033	0.061	0.206 *	0.162	-0.116	0.034
PH(cm)	G		0.440 **	0.013	0.593 **	0.077	0.324 *	0.282	-0.392 *	-0.037	0.093
	P		0.234 *	0.011	0.454 **	0.124	0.271 **	0.289 **	-0.125	0.028	0.091
FLL(cm)	G			0.135	0.105	0.065	0.098	-0.155	0.219	0.454 **	0.263
	P			0.071	0.060	0.043	0.027	-0.045	0.171	0.214 *	0.158
NPP	G				-0.396 *	-0.407**	-0.583 **	-0.497 **	-0.026	0.130	0.029
	P				-0.144	-0.210 *	-0.260 **	-0.244 **	0.026	0.085	0.393 **
PL(cm)	G					0.350 *	0.721 **	0.573 **	-0.005	0.025	0.425 **
	P					0.399 **	0.688 **	0.502 **	-0.041	0.029	0.316 **
PB	G						0.707 **	0.595 **	0.535 **	0.279	0.589 **
	P						0.733 **	0.554 **	0.304 **	0.252 **	0.441 **
SB	G							0.778 **	0.165	-0.017	0.363 *
	P							0.688 **	0.132	0.033	0.342 **
SPP	G								0.313 *	-0.250	0.341 *
	P								0.317 **	-0.158	0.378 **
SFP	G									0.371 *	0.629 **
	P									0.347**	0.491 **
TW (g)	G										0.758 **
	P										0.633 **

Table 6 : Distribution of 40 genotypes into various cluster

Clusters	Frequency	Name of the genotypes
1	22	MED × Basmati (1,3,5,8,11 & 12)
		MED × Pakbas (1 & 2)
		MED × PST (2 & 3)
		Baskota × Dehradunpahari (1,2,3,4 & 5)
		Baskota × Gobindbhogh (3)
		Baskota × BM (2)
		MSD-1 × PST (1,2 & 3)
		PB-1 × BM (2 & 3)
2	5	PB-1 × BM (1)
		PB-1 × Gopalbhogh (1 & 2)
		MED × Basmati (2)
		MED × Kailkasha
3	3	Baskota × Gobindbhogh (1)
		Baskota × Gopalbhogh
		Baskota × BM (1)

4	2	MED × PST (1)
		MED × Basmati (10)
5	2	Baskota × Gobindbhogh (2)
		MED × Basmati (9)
6	1	MSD-1 × Baskota
7	1	MED × T-Basmati (1)
8	1	MED × Basmati (4)
9	1	MED × Basmati (6)
10	1	MED × Basmati (7)
11	1	MED × T-Basmati (2)

Table 7 : Average intra and inter cluster $\sqrt{D^2}$ values

Cluster Number	cluster. 1	cluster. 2	cluster. 3	cluster. 4	cluster. 5	cluster. 6	cluster. 7	cluster. 8	cluster. 9	cluster. 10	cluster. 11
cluster 1	20.30	39.08	47.11	34.95	49.06	47.07	47.03	28.49	34.61	111.64	58.80
cluster 2		20.08	41.43	61.03	60.35	40.21	56.51	48.65	34.62	61.85	33.97
cluster 3			10.82	70.86	34.47	82.60	52.39	53.46	80.20	43.13	32.94
cluster 4				18.61	60.45	49.11	42.87	49.74	41.33	160.46	80.01
cluster 5					25.86	59.65	35.20	75.56	89.56	84.78	56.97
cluster 6						0.00	53.17	60.43	44.41	139.66	73.97
cluster 7							0.00	76.21	51.27	100.95	37.06
cluster 8								0.00	42.17	132.30	81.58
cluster 9									0.00	133.34	64.62
cluster 10										0.00	31.35

Table 8 : Cluster mean of 11 quantitative characters in F$_6$ Families of rice

Cluster	DFF	PH (cm)	FLL cm)	NPP	PL (cm)	PB	SB	SPP	SFP	TW (g)	GYP (g)
cluster 1	98.02	100.84	27.82	12.82	21.16	8.15	19.51	222.57	88.93	19.02	15.97
cluster 2	99.00	125.93	34.90	13.00	25.18	8.67	24.31	230.09	90.17	19.46	18.19
cluster 3	103.67	92.07	24.67	15.40	19.20	6.98	20.18	235.93	89.25	11.21	8.31
cluster 4	102.83	114.73	26.92	10.33	24.93	10.11	29.63	330.20	91.55	17.11	17.31
cluster 5	100.83	94.53	29.93	8.80	20.07	9.08	19.69	218.63	91.44	14.42	8.80
cluster 6	97.33	126.27	29.00	11.80	23.82	9.22	23.11	341.60	88.18	10.79	11.92
cluster 7	97.67	124.60	31.53	14.73	20.00	7.62	16.18	136.73	83.79	21.17	11.93
cluster 8	94.33	117.23	25.33	13.40	19.09	6.93	16.58	221.60	87.32	14.69	12.85
cluster 9	99.67	127.40	28.13	10.07	26.42	6.20	21.33	239.13	80.56	16.22	12.22
cluster 10	101.67	115.60	24.07	13.67	23.80	6.49	16.31	242.27	83.85	12.79	12.43
cluster 11	98.20	105.63	26.97	13.13	21.39	6.37	18.65	191.97	83.51	14.80	10.52

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