



Path and PCA for Trait Selection in Advanced Generation Aromatic Rice Genotypes with the Goal of Increasing Grain Yield

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ABSTRACT

The study was conducted during *kharif* (June–November, 2024) at the Agriculture Farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, Birbhum, West Bengal, India to select suitable traits with high PC scores by Path and Principal Component Analysis (PCA) in thirty-five advance generation aromatic rice genotypes for enhanced grain yield. Thirty-day old single seedling per hill was transplanted in randomized complete block design (RCBD) with three replications. According to path analysis plant height, flag leaf breadth, panicle length, number of secondary branches panicle⁻¹ and test weight have positive relation with grain yield plant⁻¹ and could be directly selected. In terms of principal component analysis, maximum variability was found in PC1 (35.2%) and four PCs had eigen value greater than one. In PC1 the traits grain yield plant⁻¹, number of primary branches panicle⁻¹, Spikelet fertility percentage, test weight and number of secondary branches panicle⁻¹ contributed most towards variability. Days to 50% flowering which made the most contribution to the total diversity, followed by flag leaf length, grain yield plant⁻¹, number of panicles plant⁻¹, number of primary branches panicle⁻¹, plant height, Spikelet fertility percentage and test weight displayed the longest vector length. On the basis of biplot analysis genotypes, namely 6(MED×PST-5-6), 18(MED×Pakbas-2), 19 (MED×Pakbas-3), 21 (MED×T-Basmati), 22 (Baskota×Gopalbhog-1) and 29 (Baskota×Gobindobhog) identified as the most divergent types for the yield-attributing traits of aromatic rice. Hence these genotypes can be utilized for trait improvement in breeding programs for the traits contributing for major variation.

KEYWORDS: Aromatic rice, path analysis, PCA, PC scores, biplot

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1. INTRODUCTION

Among the cereals, rice (*Oryza sativa* L.) is one of the most vital crops because around 3.5 billion people worldwide rely on it for sustenance, making it a vital food and nutrition source for a sizable portion of the human population (Alam et al., 2024) and it is the most carbohydrate rich product crops in the Asian countries (Suliartini et al., 2020). In order to meet the food demand of the rising population country has to produce about 137.29 mt of rice by 2030–31 with an annual incremental rate of 2.15% (Bhatt et al., 2023). The ever increasing population of the country is forcing the planners to produce more and more with ever shrinking natural resources (Bharose et al., 2023). The rich rice biodiversity of the old alluvial region evolved over time and was sustained through continuous interaction with the environment and ecosystem (Sen et al., 2023). *Oryza sativa*, also known as Asian rice, or, less frequently, *Oryza glaberrima*, sometimes known as African rice, are grass species that produce 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 is a nature's gift to Indian sub-continent. Epicureans acclaimed its delightful fragrance, taste and texture which makes it the best among the aromatic rice of the world (Mohammad et al., 2016). Chen et al. (2008) demonstrated that mutation in *Badh2* accumulates 2-acetyl-1-pyrroline (2-AP), a potent flavour compound in aromatic cultivars. The aroma of aromatic rice varieties is present in all parts of the crop except the roots and almost all stages of the crop, especially at the seedling, booting, and flowering stage of the plant. 2-AP has been identified as the primary aromatic compound in aromatic varieties especially basmati (Buttery et al., 1988), black rice (Yang et al., 2008), brown rice (Jezussek et al., 2002) and Thai jasmine rice KDML105. The foundation of every breeding program is genetic variability; hence breeding efforts may be improved by choosing parents with greater diversity for various yield and quality characteristics. Genetic diversity can directly provide information on germplasm richness and the extent of their genetic amelioration (Burman et al., 2023). The path coefficient, a common partial regression coefficient, quantifies the relative importance of each variable and describes the cause-and-effect relationship (Tiwari et al., 2025). Path coefficient analysis quantifies the direct impact of one variable on another using a standardized regression coefficient. The trait with a strong genetic progress and a high association with grain yield would be more suited for selection. To determine the relationship and measure of one character on another either directly or indirectly, correlation of traits with yield in conjunction with path coefficient analysis will be a crucial tool (Jangala et al., 2022; Kumar et al., 2025). PCA

is a multivariate technique for compressing, transforming, and reducing data. The present investigation was carried out to estimate the relative contribution of various traits for total genetic variability present in aromatic landraces by Principal Component Analysis (Burman et al., 2021). The goal of PCA is to extract useful information and represent it as new variables called principal components that show patterns of similarity in parameters and observations, like map points. "Eigenvalues" assess each component's importance and relevance to the overall variance, and each vector coefficient indicates the extent to which each original variable contributed to each principal component (Mondal et al., 2024). Accordingly, PCA was carried out to determine the relationship among traits and find the traits which varied together, thus segregating the traits to distinguish advanced lines for rice improvement.

2. MATERIALS AND METHODS

2.1. Experimental site

The study was conducted during *Kharif* (June–November, 2024) at the Agriculture Farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, Birbhum, West Bengal, India. The summer temperatures ranged from 25.5°C to 41.5°C, and they were hot and dry. The average rainfall ranges from 1300 to 1600 mm prevailing sub-tropical humid climatic condition. The elevation was roughly 58.9 m above mean sea level.

2.2. Experimental soil

Soil was distinguished by lateritic formations and a sandy loam texture. The contents of phosphate and organic carbon were low to medium, whereas the potash amount was medium to high. The soil had an initial pH of 5.6, electrical conductivity of 0.11 dS m⁻¹. It had 0.61% organic carbon, 223.3 kg ha⁻¹ available N, 16.2 kg ha⁻¹ available P, and 171.5 kg ha⁻¹ available K. The fertilizer was supplied at the rate of 40:40:40 kg ha⁻¹ N: P₂O₅: K₂O, respectively for the basal dose following which N dose was applied to 20 kg N ha⁻¹ each for two top dressing.

2.3. Experimental material

The thirty-five families developed from 10 cross combinations with 13 different parents (Table 1) belonging Basmati type, Non-basmati type and Mutant type were used in the experiment. Families were grown separately during the *Kharif* season of 2024 from the seeds of distinct plants from the F₅ families.

2.4. Experimental procedure

On June 28th, 2024, the seeds from selected 35 individual F₅ plants were planted separately in a nursery bed (Table 2). On July 28th, 2024, thirty-day-old seedlings were moved to the main field in RCBD with three replications, with a

Table 1: 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.	PusaSugandh 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

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 and measures were observed to ensure a good harvest. Ten plants were randomly chosen from the middle rows of each plot to record the following parameters: plant height, number of panicles, panicle length, number of primary and secondary branches, flag leaf length, and flag leaf breadth, number of spikelet, grain yield, test weight and spikelet fertility. Days to 50% flowering were recorded on basis of entire plot.

2.5. Characters studied

For each of the three replications, the growth data of the 35 genotypes were obtained from all ten plants. The twelve traits that were examined included days to 50% flowering, plant height, flag leaf length, flag leaf breadth, number of panicles plant⁻¹, panicle length, number of primary branches panicle⁻¹, number of secondary branches panicle⁻¹, number of spikelet panicle⁻¹, spikelet fertility %, test weight and grain yield plant⁻¹.

2.6. Statistical analysis

The best gain traits for selecting and breeding aromatic rice were evaluated according to path analysis and principal component analysis. Path Coefficient analysis was carried out as suggested by Dewey and Lu (1959). PCA was performed by using R studio (Rathod et al., 2023) and Agri analyze website.

3. RESULTS AND DISCUSSION

3.1. Path coefficient analysis

The significant positively correlated characters which exhibited high and positive direct effects (Table 3) of 0.4871, 0.5578, 0.3526, 0.3945, 0.6926, 0.4449, 0.605, 0.6729 and 0.7051 on grain yield plant⁻¹ were plant height, flag leaf breadth, number of panicles plant⁻¹, Panicle length, number of secondary branches panicle⁻¹, and test weight, respectively, indicating a true relationship among these characters. Therefore, a direct selection through these traits might also be more effective. Flag leaf length (0.5578) and number of spikelet panicle⁻¹ (0.605) showed a positive correlation with

Table 2: List of genotypes under different cross combination used in the experiment

Number of genotypes	Cross combination	Genotypes within cross combination	Number of genotypes	Cross combination	Genotypes within cross combination
1.	MED×PST-5	1	21.	MED×T-Basmati	
2.		2	22.	Baskota×Gopalbhog	1
3.		3	23.		2
4.		4	24.		3
5.		5	25.	Baskota×Tulaipanji	1
6.		6	26.		2
7.		7	27.	Baskota×Dehradunpahari	1
8.		8	28.		2
9.		9	29.	Baskota×Gobindobhog	
10.	MED×Basmati	1	30.	PB-1×BM-24	1
11.		2	31.		2
12.		3	32.		3
13.		4	33.	MSD-1×PST-5	1
14.		5	34.		2
15.		6	35.		3
16.		7			
17.	MED×Pakbas	1			
18.		2			
19.		3			
20.		4			

grain yield but had a negative or negligible direct effect; it suggested that the observed correlation was largely due to indirect effects. In such cases, the contributing indirect traits should be considered collectively during selection. Number

Table 3: Genotypic path coefficient analysis of 12 quantitative characters on grain yield In F_6 families of rice

Characters	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	No. of panicles plant ⁻¹	Panicle length (cm)
Days to 50% flowering	0.5960	-0.0222	0.0844	0.0352	-0.5769	0.1374
Plant height (cm)	-0.0204	0.6491	-0.2204	0.0998	-0.1638	0.2708
Flag leaf length (cm)	-0.1530	0.4351	-0.3288	0.1904	0.1819	0.1590
Flag leaf breadth (cm)	0.0349	0.1077	-0.1041	0.6015	-0.2876	0.1713
Number of panicles plant ⁻¹	-0.3632	-0.1123	-0.0632	-0.1828	0.9466	-0.2593
Panicle length (cm)	0.1212	0.2601	-0.0774	0.1525	-0.3633	0.6757
Number of primary branches panicle ⁻¹	0.1837	0.2440	-0.0703	0.1579	-0.1603	0.4145
Number of secondary branches panicle ⁻¹	0.1595	0.1431	-0.0860	-0.0142	-0.1553	0.2752
Number of spikelet panicle ⁻¹	0.1619	0.2637	-0.1319	0.2716	-0.2686	0.1110
Spikelet fertility %	0.3302	0.1469	-0.0724	0.1639	-0.1907	0.1469
Test weight (g)	0.1042	0.1319	-0.0719	0.0893	-0.1743	0.0696

Table 3: Continue...

Characters	No. of primary branches panicle ⁻¹	No. of secondary branches panicle ⁻¹	No. of spikelet panicle ⁻¹	Spikelet fertility (%)	Test weight (g)	Correlation with grain yield plant ⁻¹
Days to 50% flowering	-0.3196	0.1091	-0.0327	0.0200	0.1829	0.2137
Plant height (cm)	-0.3898	0.0899	-0.0488	0.0082	0.2126	0.4871**
Flag leaf length (cm)	-0.2219	0.1067	-0.0482	0.0080	0.2287	0.5578**
Flag leaf breadth (cm)	-0.2723	-0.0096	-0.0543	0.0098	0.1552	0.3526*
Number of panicles plant ⁻¹	0.1756	-0.0669	0.0341	-0.0073	-0.1926	-0.0912
Panicle length (cm)	-0.6362	0.1661	-0.0197	0.0079	0.1077	0.3945*
Number of primary branches panicle ⁻¹	-1.0371	0.3488	-0.0137	0.0218	0.6034	0.6926**
Number of secondary branches panicle ⁻¹	-0.8872	0.4078	-0.0035	0.0216	0.5839	0.4449**
Number of spikelet panicle ⁻¹	-0.1180	0.0118	-0.1202	0.0110	0.4127	0.605**
Spikelet fertility %	-0.6264	0.2438	-0.0368	0.0361	0.5313	0.6729**
Test weight (g)	-0.5983	0.2276	-0.0474	0.0183	0.9561	0.7051**

of panicles plant⁻¹ which had negative correlation with yield (-0.0912) but had positive and very high direct effect (0.9466), (Table 3) under these circumstances, a restricted simultaneous model is to be followed i.e. restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect (Singh and Kakkar, 1977). Path coefficient analysis (Dewey and Lu, 1959) showed the direct and indirect effect of independent variables on the dependent variable (grain yield⁻¹ plant). Similar outcomes were also reported by earlier workers i.e. Jungala et al. (2022), Mondal et al. (2024), Sadhu et al. (2025) for days to 50% flowering; Mondal et al. (2024), Sadhu et al. (2025), Balakrishnan et al. (2025) for plant height; Alshugeairy et al. (2023) for indirect effect of flag leaf length and Hossain et al. (2022) for direct effect of flag leaf length; Hossain et al. (2022) for flag leaf breadth; Jangala et al. (2022), Renuprasath et al. (2023), Mondal et al. (2024) for number of panicles plant⁻¹; Mondal et al. (2024), Sadhu et al. (2025), Balakrishnan et al. (2025) for Panicle length; Kole and Deo (2024) for indirect effect and Faysal et al. (2022) for direct effect for number of primary branches panicle⁻¹; Nath and Kole (2021), Faysal et al. (2022) for secondary branches panicle⁻¹; Sadhu et al. (2025), Balakrishnan et al. (2025) for direct effect of number of spikelet panicle⁻¹; Mondal et al. (2024), Balakrishnan et al. (2025), Bhogal et al. (2025) for Spikelet fertility percentage; Acharjee et al. (2021), Salunkhe et al. (2024), Mondal et al. (2024), Sadhu et al. (2025), Balakrishnan et al. (2025) for test weight.

The residual effect determined how best the causal factors account for the variability of the dependent factor, the yield in this case. Here a low residual effect (0.101) showed that the variables under study could explain 89.9% of the yield-variability.

3.2. Principal component analysis

PCA reduced the dimensionality of the data and helped highlight the most influential traits. Components were considered primary if they explained a variance more than four and had eigen values exceeding one (Brejda et al., 2000; Abimbola et al., 2016). Principal Component Analysis (PCA) was conducted using 12 morphological traits to assess phenotypic diversity among 35 aromatic rice germplasm. The analysis utilized the singular value decomposition method, generating a total of 12 principal components (Table 4). According to Kaiser's rule-which considered components with eigen values 1 as significant-only four components were retained for further interpretation. The

Table 4: Eigen values, proportion of variance and cumulative proportion of variance

Principal component	Eigen values	Proportion of variance	Cumulative proportion
PC-1	4.2	35.203	35.203
PC-2	1.8	15.365	50.568
PC-3	1.5	12.68	63.247
PC-4	1.2	10.27	73.517
PC-5	0.8	6.653	80.17
PC-6	0.7	5.496	85.666
PC-7	0.6	4.892	90.558
PC-8	0.4	2.977	93.535
PC-9	0.3	2.898	96.433
PC-10	0.2	1.962	98.395
PC-11	0.1	1.128	99.523
PC-12	0.1	0.477	100

findings presented a summary of the principal component analysis, listing each principal component along with its corresponding eigenvalue, percentage contribution to the total variance (Table 4), and the key traits that contributed most significantly to each component.

3.2.1. Scree plot

The first four of the twelve PCs, PC1, PC2, PC3, and PC4, had eigen values of 4.2, 1.8, 1.5, and 1.2, respectively (eigen value > 1) aligning with the observations reported by Sadhu et al. (2025), and the eigen values of the other PCs gradually decreased (eigen value < 1). This pattern demonstrated that the majority of variance was recorded by the first four PCs, with the other PCs contributing very little to the variation that was observed (Figure 1). Following the fourth PC, the

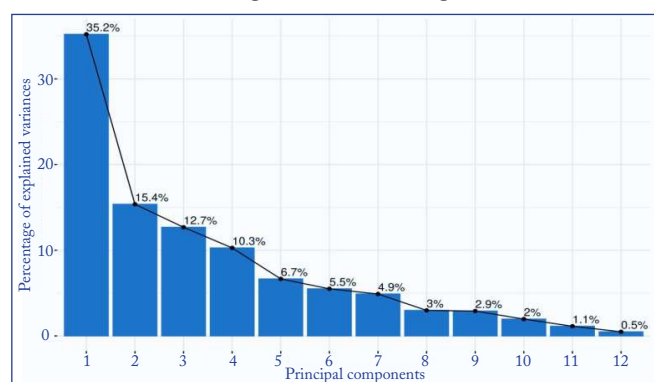


Figure 1: Percentage of explained variances of principal components

plot progressively levels off in an "elbow" pattern (Gour et al., 2021). The percentage of overall variation in the data linked to each derived main component was shown by the scree plot, which was a straightforward line segment. Y-axis, showed the percentage of explained variation, and an X-axis,

showed the principal component numbers, were used to graphically depict the percentage of variation attributable to each principal component. Principal component 1 showed 35.2% variability with an eigen value of 4.2, which gradually decreased. Umadevi et al. (2019) also reported the highest variability in PC1 with an eigenvalue exceeding 1.0. As shown in Figure 1, main component 1 showed the greatest amount of variation.

3.2.2. PC loadings

The eigenvalues obtained from PCA represented the amount of variation explained by each principal component and helped to determine the number of components to retain. PCs with higher eigenvalues, along with variables showing high factor loadings, were considered strong indicators of the underlying characteristics of the system. Table 5, which displayed the factor loading scores for the variables, mentioned the PCA results. The variables that have a stronger correlation with each component were represented by PC loadings. In PC1 the traits grain yield plant⁻¹, number of primary branches panicle⁻¹, Spikelet fertility percentage, test weight and, number of secondary branches panicle⁻¹ contributed most towards variability. The genotypes showed presence under this PC will be potent for transfer of yield traits after hybridization for the transfer of dominated traits in the deficient lines for the development of high yielding rice lines. These findings were in agreement with the findings of Tiruneh et al. (2019), Lalhruaitluangi et al. (2025). In PC2 days to 50% flowering, flag leaf length, number of panicles plant⁻¹ and plant height primarily contributed to the variability. In PC3 number of panicles plant⁻¹, number of spikelet panicle⁻¹, flag leaf breadth, number of primary branches panicle⁻¹ and number of secondary branches panicle⁻¹ most significantly

Table 5: Principal component loadings for different characters for yield and contributing traits

Traits	PC-1	PC-2	PC-3	PC-4
Days to 50% flowering (DFF)	-0.1858	-0.5217	-0.2762	0.0463
Plant height (PH)	-0.2737	0.3516	-0.0671	-0.3546
Flag leaf length (FLL)	-0.2212	0.5142	-0.0258	-0.1149
Flag leaf breadth (FLB)	-0.1936	0.1489	-0.4228	0.0125
No. of panicles plant ⁻¹ (NP)	0.1055	0.3876	0.4648	0.3029
Panicle length (PL)	-0.2689	-0.0536	0.0161	-0.5994
No. of primary branches panicle ⁻¹ (PB)	-0.3634	-0.1481	0.3361	-0.201
No. of secondary branches panicle ⁻¹ (SB)	-0.3272	-0.2069	0.4277	-0.0853
No. of spikelet panicle ⁻¹ (SPP)	-0.2757	0.1789	-0.46	0.2195
Spikelet fertility % (SFP)	-0.3465	-0.1947	0.0261	0.29
Test weight (TW)	-0.3376	-0.047	0.1153	0.3942
Grain yield plant ⁻¹ (GYP)	-0.4141	0.1664	0.0453	0.2691

influenced the variability. In PC4 Panicle length, test weight, plant height and number of panicles plant⁻¹ most significantly influenced the variability.

3.2.3. Correlation circle

A useful tool in a breeding program, the correlation circle (Figure 2) showed the length of the vector and relation between traits based on the angle. Each trait's vector length revealed how it contributed to overall diversity; days to 50% flowering displayed the longest vector length, followed by flag leaf length and grain yield plant⁻¹. According to this, days to 50% flowering made the most contribution to the total diversity, followed by flag leaf length, grain yield plant⁻¹, number of panicles plant⁻¹, number of primary branches panicle⁻¹, plant height, Spikelet fertility percentage and test weight. The vectors' angles revealed the correlations between traits: straight angles (90°) suggested no correlation, obtuse angles (>90°) indicated negative links, and acute angles (<90°) indicated positive relationships (Sadhu et al. 2025).

According to this from Figure 2, number of spikelet panicle⁻¹, number of secondary branches panicle⁻¹, Spikelet fertility percentage, number of primary branches panicle⁻¹, panicle length, test weight, flag leaf length, flag leaf breadth, and plant height were positively correlated with grain yield plant⁻¹. Days to 50% flowering, numbers of primary branches panicle⁻¹, number of secondary branches panicle⁻¹, Spikelet fertility percentage, Panicle length and test weight were negatively correlated with number of panicles plant⁻¹.

The Figure 3 showed the distribution of genotypes based on first two PCs serving as a valuable tool for the breeding programme. According to Acharjee et al. (2021) and Behera et al. (2023) genotypes that were situated in proximity on a biplot were seen as similar when graded on specified traits. The diversity of genotypes would increase with increase in the distance between the genotype and the

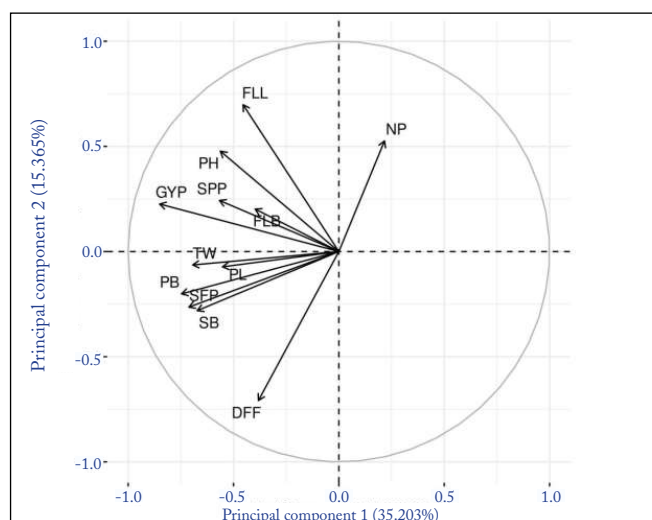


Figure 2: Correlation circle

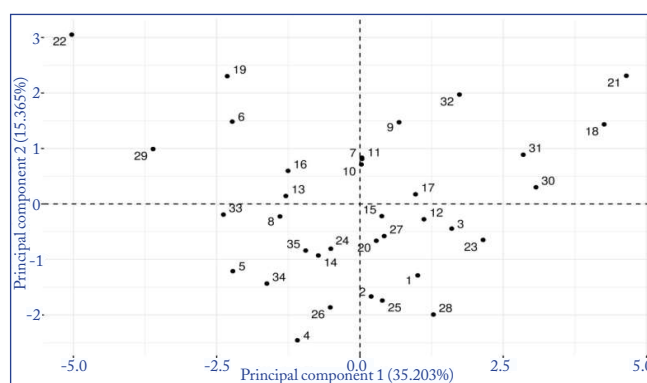


Figure 3: Distribution of genotypes; (Genotypes were numbered from 1–35 as per the serial number in Table 3)

place of origin. Maximum genetic diversity was shown by the genotypes 6(MED×PST-5-6), 18(MED×Pakbas-2), 19 (MED×Pakbas-3), 21 (MED×T-Basmati), 22 (Baskota×Gopalbhog-1) and 29 (Baskota×Gobindobhog) being situated far from the biplot origin. These genotypes might be useful for upcoming breeding initiatives aimed at improving grain yield for aromatic rice and associated characteristics.

3.2.4. Bi-plot

A useful tool in a breeding program, the biplot (Figure 4) showed interactions between genotypes and the traits based on the first two PCs or it was the combination of both Figure 2 and 3. As a visual aid, the biplot diagram made it easy to see how traits related to one another and allowed for the identification of genotypes that excelled in particular aspect. The most important results were highlighted by the biplot, which focused on grouping accessions into four groups according to both PCs. Genotypes located near the trait vectors in the same quadrant were anticipated to show favourable performance for those specific traits. The purpose

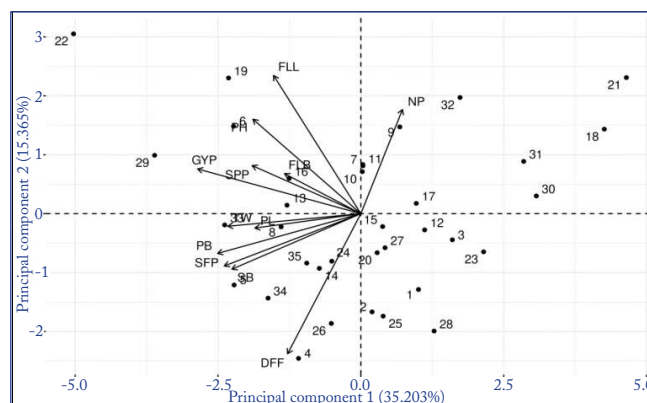


Figure 4: Biplot of principal components analysis (PCA) for twelve yield attributing traits of 35 rice genotypes, representing the relationships between traits and genotypes along with first two principal components (PC1 and PC2), with vector lengths representing trait contribution to diversity

Table 6: Principal component scores of 35 aromatic rice families

Number of genotypes	Family	Genotypes within families	PC-1	PC-2	PC-3	PC-4
1.	MED×PST-5	1	1.0084	-1.2875	0.6511	0.9457
2.		2	0.1957	-1.6676	0.198	-0.0365
3.		3	1.6012	-0.4445	-0.0527	0.5463
4.		4	-1.0911	-2.457	2.5417	-3.6494
5.		5	-2.2183	-1.2113	-0.8401	-0.1722
6.		6	-2.228	1.4833	0.193	0.0069
7.		7	0.0331	0.8341	0.3173	0.5291
8.		8	-1.3954	-0.2248	-2.7563	0.3641
9.		9	0.6821	1.4722	-2.3646	-0.5899
10.	MED×Basmati	1	0.025	0.7125	1.7779	1.5123
11.		2	0.0359	0.812	0.7849	1.4449
12.		3	1.1167	-0.2762	0.0502	0.6892
13.		4	-1.2929	0.1434	0.4537	0.765
14.		5	-0.7263	-0.9285	0.9416	0.6222
15.		6	0.3811	-0.2191	1.2859	1.1188
16.		7	-1.2549	0.5968	-0.0296	0.8914
17.	MED×Pakbas	1	0.9694	0.1741	1.531	0.6922
18.		2	4.2605	1.4343	0.1175	-1.4251
19.		3	-2.3155	2.3031	1.5903	1.2969
20.		4	0.2854	-0.6633	-1.3504	1.4213
21.	MED×T-Basmati		4.6476	2.3098	-1.6748	-1.1334
22.	Baskota×Gopalbhog	1	-5.0289	3.052	-0.637	-2.0485
23.		2	2.1483	-0.6482	0.3719	-0.3373
24.		3	-0.5089	-0.807	1.2196	-0.2561
25.	Baskota×Tulaipanji	1	0.3902	-1.7404	0.5325	-1.9975
26.		2	-0.5175	-1.8638	-0.7282	0.1106
27.	Baskota×Dehradunpahari	1	0.4228	-0.579	-1.2483	0.1451
28.		2	1.2817	-1.9926	-2.0961	0.0082
29.	Baskota×Gobindobhog		-3.6098	0.9899	-0.0349	-1.1273
30.	PB-1×BM-24	1	3.0715	0.3008	0.5996	0.0048
31.		2	2.8494	0.8873	0.724	-0.3353
32.		3	1.7357	1.9715	0.2708	-0.9483
33.	MSD-1×PST-5	1	-2.3827	-0.1923	0.0072	0.1615
34.		2	-1.6244	-1.4344	-2.2277	0.0573
35.		3	-0.947	-0.8397	-0.1192	0.7231

of the biplot was to emphasized the most significant findings by grouping accessions into four categories according to both PCs. Accession groups in Quadrant II and III were distinguished by their high potential output. Days to 50%

flowering, numbers of primary branches panicle⁻¹, number of secondary branches panicle⁻¹, Spikelet fertility percentage, test weight and plant height were all highest for genotypes in quadrant II. Plant height, flag leaf length, flag leaf breadth,

Table 7: Genotypes showing Top 5 PC scores

Sl. No.	PC-1	PC-2	PC-3	PC-4
1.	MED×T-Basmati (4.6476)	Baskota×Gopalbhog-1(2.4566)	MED×PST-5-4 (2.5417)	MED×Basmati-1 (1.5123)
2.	MED×Pakbas-2 (4.2605)	MED×T-Basmati (2.3098)	MED×Basmati-1 (1.7779)	MED×Basmati-2 (1.4449)
3.	PB-1×BM-24-1 (3.0715)	MED×Pakbas-3 (2.3031)	MED×Pakbas-3 (1.5903)	MED×Pakbas-4 (1.4213)
4.	PB-1×BM-24-2 (2.8494)	PB-1×BM-24-3 (1.9715)	MED×Pakbas-1 (1.531)	MED×Pakbas-3 (1.2969)
5.	Baskota×Gopalbhog-2 (2.1483)	MED×PST-5-6 (1.4833)	MED×Basmati-6 (1.2859)	MED×Basmati-6 (1.1188)

number of spikelet panicle⁻¹, grain yield plant⁻¹ traits and genotypes were gathered in Quadrant III. Quadrant IV comprises genotypes that were distinguished by number of panicles plant⁻¹ character, while quadrant I had nothing. The loading plot depicted that almost all the genotypes and variables had shown high degree of variation and similar results were observed by Christina et al. (2021), Behera et al. (2022), Choudhary et al. (2022), Roy et al. (2024). Principal component scores of 35 aromatic rice families were presented in Table 6.

The highest contribution to yield-attributing features was shown by individuals with high PC scores (Patel et al., 2022). PCA helped pinpoint the five genotypes that had the highest PC scores (Table 7), suggesting they make the most significant contribution to traits linked to yield. These top-performing genotypes, as presented in Table 7, include-MED×T-Basmati, PB-1×BM-24-1,2 and3, Baskota×Gopalbhog-1 and 2, MED×PST-5-4 and 6, MED×Basmati-1, 2 and 6, MED×Pakbas-1, 2, 3 and 4. The contribution of trait specific elements of the genotypes is recognised based on the highest PC scores reported in each PC. The genotypes with the highest PC scores will be used as a donor for the transfer of desired traits given by the genotype's traits. Selection of the best recombinants in segregating generations after hybridization could be beneficial for the development of high yielding rice lines. Similar results were reported by Talekar et al. (2022), Tiwari et al. (2022), Al-Khayri et al. (2023), Lalhrualtuangi et al. (2025).

4. CONCLUSION

Important characters such as Number of primary branches panicle⁻¹, Spikelet fertility percentage, test weight and, number of secondary branches panicle⁻¹ were identified as key principal components which directly or indirectly have influenced grain yield plant⁻¹. In the biplot accession groups of Quadrant II and III were distinguished by their high

potential output and got knowledge regarding the good performance of specific genotypes for specific traits which may be employed as parents for breeding elite varieties of aromatic rice.

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