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PATH AND PRINCIPAL COMPONENT ANALYSIS BASED TRAIT SELECTION FOR ENHANCING YIELD OF AROMATIC RICE IN F_6 GENERATION

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ABSTRACT

Path analysis was conducted on 10 quantitative characters of F_6 generation of aromatic rice to evaluate their direct and indirect impact on grain yield plant^{-1}. Principal component analysis was done to study the variability in characters. Days to 50% flowering, plant height (cm), flag leaf length (cm), panicle length (cm), number of panicles plant^{-1}, number of primary branches panicle^{-1}, number of secondary branches panicle^{-1}, number of spikelets panicle^{-1}, spikelet fertility%, test weight (g) and grain yield plant^{-1} (g) were studied in this experiment. A low residual effect (0.0181) in the genotypic path coefficient analysis indicated that 98.19% of variability was attributed to the 10 independent characters studied. By four (PC1, 2, 3 and 4) of the eleven PC that were calculated in the analysis had eigen values larger than one. Together, PC1 PC2, PC3 and PC4 accounted for around 77.2% of the variance.

Key words : Path analysis, Principal component analysis, Aromatic rice, Residual effect, Eigen value.

Introduction

In the World Rice is used as the oldest staple food. It occupies 23.3 % of gross cropped area of India. It is a monocot, annual, short day and C3 plant having chromosome 2n = 2x = 24 belonging to family Poaceae (Gramineae). 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*., 2025). 2-Acetyl-1-pyrroline (2AP), a principal aroma compound has been detected in all aerial plant parts of aromatic rice (Yoshihashi *et al*., 2002 and Fayaz *et al*., 2024). The nature of the relationship between yield and other characteristics was ascertained by path coefficient analysis, which was also used to examine the direct and indirect effects of various characteristics on grain yield. A mathematical method called principal component analysis (PCA) is used to divide a large number of variables into their major components and evaluate how each one contributes to the overall variation. PCA is a well-known multivariate statistical technique that is used to rank genotypes based on PC scores and determine the smallest number of components that can explain the greatest amount of variability out of the total variability Path coefficient analysis has been used in paddy by Balakrishnan *et al*. (2025), Salunkhe *et al*. (2024), Harshraj *et al*. (2024), Yadav *et al*. (2024), Kole *et al*. (2024), Bhutta *et al*. (2019) and principal component analysis by Beena *et al*. (2021), Chandraker *et al*. (2024) Ghosh *et al*. (2025), Sheeba *et al*. (2025).

Materials and Methods

Path coefficient analysis was performed in accordance with Dewey and Lu's (1959) recommendations. A standardized partial regression coefficient called the path coefficient quantifies the direct impact of one independent variable on a dependent variable as well as indirect impacts via other variables. Path coefficient analysis was performed using yield as the dependent variable and other yield-attributing variables as independent variables.

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.

Experimental procedure

In 2024, during the kharif season (June–December), the F_6 families were raised alongside their parents in a duplicated study. The 40 unique F_6 families 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.

Statistical analysis

Path coefficient analysis was performed in accordance with Dewey and Lu's (1959) recommendations with the help of R studio and Principal component analysis was performed by Agri analyze.

Results and Discussion

The goal of the current study was to identify the direct and indirect effects of different traits on grain yield, as well as to evaluate the pattern of character variations, separate the traits, and identify the various parental accessions.

Path analysis

The current study examines the impact of ten additional characteristics on grain yield plant^{-1}. Genotypic and Phenotypic correlation coefficients were separated using path analysis and the findings of the genotypic and phenotypic path analysis are shown in Tables 1 and 2, respectively.

Genotypic path analysis

Test weight (0.7766), spikelet fertility % (0.6606), secondary branches panicle^{-1} (0.3457), panicle length (0.1020) and spikelet panicle^{-1} had positive direct effect on grain yield plant^{-1}. Test weight had positive direct effect (0.7766) on grain yield plant^{-1}. It exhibited positive indirect effect through spikelet fertility %. It had significant positive correlation with grain yield plant^{-1} (0.75755). Therefore, it can be utilized for selection for grain yield. spikelet fertility % had positive direct effect (0.6606) on grain yield plant^{-1}. It exhibited indirect effect through test weight, secondary branches panicle^{-1}, and spikelet panicle^{-1} which compensated the indirect negative effect. It had significant positive correlation with grain yield plant^{-1}(0.6285). Secondary branches panicle^{-1} had positive direct effect (0.3257) on grain yield plant^{-1} and it exhibited positive indirect effect through spikelet fertility %, spikelet panicle^{-1}, and panicle length. It had significant positive correlation with grain yield plant^{-1} (0.36346). Panicle length displayed positive direct effect, countered by negative indirect effect of most of traits except plant height, secondary branches panicle^{-1}, spikelet panicle^{-1} and test weight leading to a positive significant correlation with grain yield plant^{-1}. Spikelet panicle^{-1} had positive direct effect with negative indirect effect of days to 50% flowering, number of panicle

Table 1 : Genotypic path coefficient analysis of 10 quantitative characters on grain yield in F_6 families of rice.

Characters	DFF	PH (cm)	FLL (cm)	NPP	PL (cm)	PB	SB	SPP	SFP	TW (g)	Correlation with GYP
DFF	**-0.060**	0.023	0.195	0.025	0.037	-0.036	0.114	0.013	0.000	-0.255	0.056
PH (cm)	-0.003	**0.434**	-0.220	0.003	0.060	-0.015	0.112	0.010	-0.259	-0.029	0.093
FLL (cm)	0.023	0.191	**-0.501**	0.026	0.011	-0.012	0.034	-0.005	0.144	0.352	0.263
NPP	-0.008	0.006	-0.068	**0.196**	-0.040	0.078	-0.202	-0.017	-0.017	0.101	0.029
PL (cm)	-0.022	0.257	-0.053	-0.078	**0.102**	-0.067	0.249	0.020	-0.003	0.019	0.42544**
PB	-0.011	0.033	-0.032	-0.080	0.036	**-0.193**	0.244	0.021	0.353	0.217	0.58853**
SB	-0.020	0.141	-0.049	-0.114	0.074	-0.136	**0.346**	0.027	0.109	-0.013	0.36346*
SPP	-0.022	0.123	0.077	-0.097	0.058	-0.115	0.269	**0.035**	0.207	-0.194	0.34086*
SFP	0.000	-0.170	-0.109	-0.005	-0.001	-0.103	0.057	0.011	**0.661**	0.288	0.6285**
TW (g)	0.020	-0.016	-0.227	0.025	0.003	-0.054	-0.006	-0.009	0.245	**0.777**	0.75755**

Residual effect = 0.0181 *, **, significant at 5% and 1% level respectively Bold figure indicate direct effect.

Table 2 : Phenotypic path coefficient analysis of 10 quantitative characters on grain yield in F_6 families of rice.

Characters	DFF	PH (cm)	FLL (cm)	NPP	PL (cm)	PB	SB	SPP	SFP	TW (g)	Correlation with GYP
DFF	**0.022**	0.005	-0.009	-0.038	0.010	0.002	-0.003	0.112	0.008	-0.074	0.0336
PH (cm)	-0.001	**-0.168**	0.008	0.005	0.084	0.006	-0.014	0.158	-0.006	0.018	0.0906
FLL (cm)	-0.005	-0.039	**0.035**	0.035	0.011	0.002	-0.001	-0.025	0.009	0.138	0.1583
NPP	-0.002	-0.002	0.002	**0.495**	-0.027	-0.010	0.013	-0.133	0.001	0.054	0.39299**
PL (cm)	0.001	-0.076	0.002	-0.071	**0.185**	0.018	-0.035	0.274	-0.002	0.019	0.3157**
PB	0.001	-0.021	0.002	-0.104	0.074	**0.046**	-0.037	0.302	0.016	0.162	0.44089**
SB	0.001	-0.045	0.001	-0.128	0.127	0.034	**-0.050**	0.375	0.007	0.021	0.34221**
SPP	0.004	-0.048	-0.002	-0.121	0.093	0.026	-0.035	**0.546**	0.016	-0.102	0.37821**
SFP	0.003	0.021	0.006	0.013	-0.008	0.014	-0.007	0.173	**0.052**	0.223	0.49139**
TW (g)	-0.002	-0.005	0.007	0.042	0.005	0.012	-0.002	-0.086	0.018	**0.644**	0.6329**

Residual effect = 0.1137 *, **, significant at 5% and 1% level respectively Bold figure indicate direct effect.

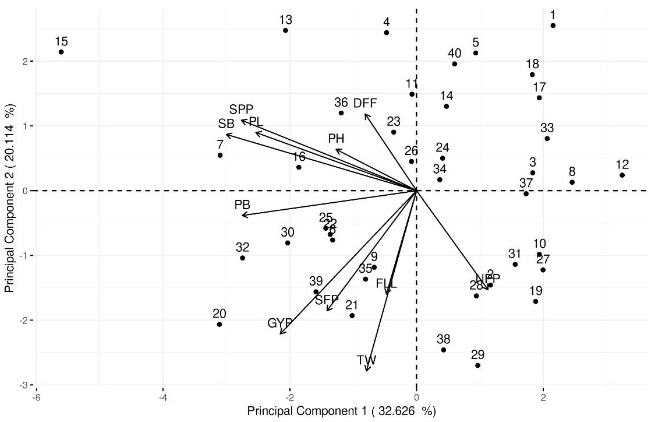

Fig. 1 : Biplot.

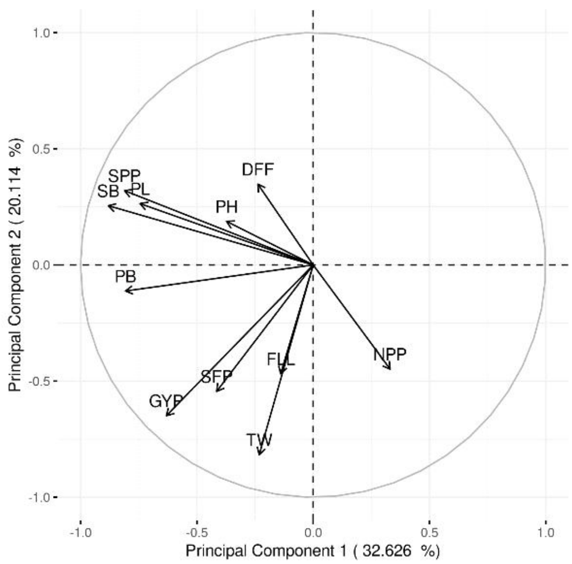

Fig. 2 : Correlation circle.

plant^{-1}, primary branches panicle^{-1}and test weight but overall positive significant correlation with grain yield plant^{-1}. number of panicle plant^{-1} had positive direct effect with positive indirect effect of plant height, primary branches panicle^{-1}and test weight. Overall there is a low positive non-significant correlation with grain yield plant^{-1}. Primary branches panicle^{-1} had negative direct effect but with positive indirect effect of plant height, PL, secondary branches panicle^{-1}, spikelet panicle^{-1}, spikelet fertility %, and test weight. Overall positive significant correlation with grain yield plant^{-1}.

Similar result of direct effect was also found by Kumar *et al*. (2025), Harshraj *et al*. (2024), Yadav *et al*. (2024), Balakrishnan *et al*. (2025), Alshugeairy *et al*. (2023), Jangala *et al*. (2022), Renuprasath *et al*. (2023), Faysal *et al*. (2022), Santhipriya *et al*. (2017).

A low residual effect (0.0181) in the genotypic path coefficient analysis indicated that 98.19% of variability was attributed to the 10 independent characters studied. This indicated that sufficient characters were used for path analysis. Overall, test weight, spikelet fertility %, and spikelet panicle^{-1} emerge as the most critical traits for enhancing grain yield and should be prioritized in breeding programs aimed at yield improvement in rice.

Phenotypic path analysis

Results of phenotypic path analysis disclosed that test weight (0.6437) had highest positive direct effect on grain yield plant^{-1}. Spikelet panicle^{-1} (0.5460) and number of panicle plant^{-1} (0.4948) also had high positive direct effect on grain yield plant^{-1}. Test weight (0.6437) had highest positive direct effect on grain yield plant^{-1} and correlation coefficient with grain yield plant^{-1} was 0.6329. It exhibited indirect positive effect through flag leaf length, number of panicle plant^{-1}, PL, primary branches panicle^{-1} and spikelet fertility % which are negligible. The indirect effect of this character through days to 50% flowering, plant height, secondary branches panicle^{-1} and spikelet panicle^{-1} were negative and small. Spikelet panicle^{-1} had a positive direct effect (0.5460) and low positive indirect effect with days to 50% flowering, PL, primary branches

Table 3 : Eigen value standard deviation, variance proportion, and cumulative proportion.

Principal Component	Eigen value	Standard deviation	Proportion of Variance	Cumulative Proportion
PC1	3.6	1.8945	32.63	32.63
PC2	2.2	1.4874	20.112	52.742
PC3	1.5	1.2449	14.088	66.83
PC4	1.1	1.0693	10.395	77.225
PC5	0.7	0.8648	6.8	84.025
PC6	0.6	0.7696	5.384	89.409
PC7	0.4	0.6539	3.887	93.296
PC8	0.4	0.6111	3.395	96.69
PC9	0.2	0.4576	1.903	98.594
PC10	0.1	0.3494	1.11	99.704
PC11	0.0	0.1804	0.296	100

panicle^{-1}, and spikelet fertility %. negative indirect effect with plant height, flag leaf length, number of panicle plant^{-1}, secondary branches panicle^{-1} and test weight. Spikelet panicle^{-1} had significant positive correlation with grain yield plant^{-1} (0.37821). Number of panicle plant^{-1} had a positive direct effect (0.4948) and low positive indirect effect with flag leaf length, secondary branches panicle^{-1}, spikelet fertility % and test weight. It had negative indirect effect with days to 50% flowering, plant height, PL, primary branches panicle^{-1}, spikelet panicle^{-1}. Number of panicle plant^{-1} had significant positive correlation with grain yield plant^{-1} (0.3929). Panicle length and primary branches panicle^{-1} had low positive direct effect but it had significant positive correlation with grain yield plant^{-1}. The secondary branches panicle^{-1} had a strong indirect positive correlation with grain yield plant^{-1} but a negligible negative direct impact on grain yield plant^{-1}. Because of spikelet fertility %, it had an indirect low positive effect. Therefore, secondary branches panicle^{-1} cannot be considered for indirect selection of grain yield.

These ten characteristics accounted for 88.63% of the variability in grain yield plant^{-1}, according to the residual value of 0.1137 for phenotypic path analysis. This implies that sufficient characters have been considered for path analysis research. In summary, test weight, spikelet fertility %, spikelet panicle^{-1} and number of panicle plant^{-1} are the most influential traits for improving grain yield plant^{-1} at the phenotypic level and should be prioritized in rice breeding programs.

Principal component analysis

Eleven characteristics were included in the Principal Component Analysis. Analysis was done using the singular value decomposition approach. With an eigen value of 1.89, PC1 accounted for the largest variation

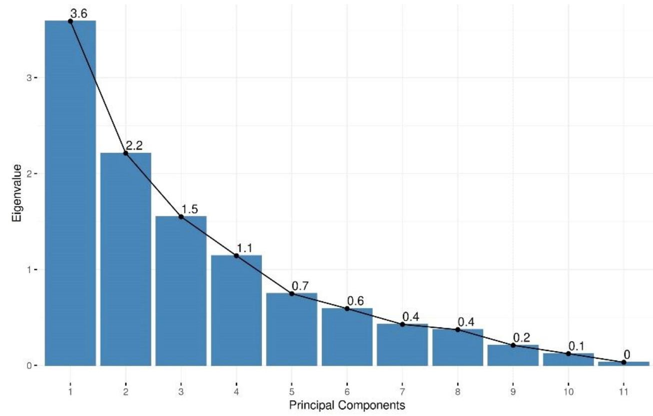

Fig. 3 : Eigenvalue graph.

(32.63%) (Figs. 1 and 2). Variations of 20.11%, 14.09%, and 10.39% were explained by the major components PC2, PC3 and PC4, respectively. Four (PC1, 2, 3 and 4) of the eleven PC that were calculated in the analysis had eigen values larger than one (Kaiser's rule states that primary components larger than one should be considered for additional analysis). Together, PC1 PC2, PC3 and PC4 accounted for around 77.2% of the variance. PC5, PC6, PC7, PC8, PC9, PC10 and PC11 contribute little variance (Table 3, Fig. 3).

The original variables or characteristics are shown by arrows on the biplot. An arrow's length represents how strongly a feature contributes to the primary components; longer arrows indicate more influence. An arrow's direction indicates the degree of correlation between features: traits at roughly 90 degrees are mainly uncorrelated, traits that have arrows pointing in the same direction are positively correlated, and traits pointing in opposite directions are negatively correlated. It is also possible to figure out the relationship between individuals and traits: individuals, who are oriented in the direction of an arrow for a trait typically have higher values for that trait, whereas individuals, who are oriented in the opposite direction have lower values. In general, individuals close to the plot's center (origin) display average values for all traits (Acharjee *et al*., 2021).

Using principal component analysis (PCA), the multivariate structure of the observed attributes was investigated. A total of 52.7% of the variability was explained by the first principal component (PC1), which explained 32.6% of the variation, and the second principal component (PC2), which explained 20.1%. Here genotype 13 and 15 were far away from others it means that it had unique trait combinations (Table 4). Genotype 24, 34 and 26 were very closed to the centre it had less variability. Genotypes (25, 22 and 6), (26,24 and 34), (3, 8 and 37) were very closely align it had more similarity (Fig. 4).

Table 4 : PCA score.

	Family	PC1	PC2	PC3	PC4
1	MED × Basmati	2.15	2.55	1.43	-0.01
2		1.17	-1.46	-1.84	0.94
3		1.83	0.28	0.48	-0.26
4		-0.47	2.44	2.27	0.33
5		0.93	2.13	0.43	1.81
6		-1.33	-0.76	-1.88	1.03
7		-3.10	0.55	-2.03	-0.13
8		2.46	0.13	0.98	0.17
9		-0.67	-1.18	-1.43	0.90
10		1.94	-0.98	0.19	1.06
11		-0.07	1.49	0.58	0.66
12		3.25	0.24	0.45	-0.26
13	Baskota × Gobindbhogh	-2.07	2.48	0.79	-0.27
14		0.47	1.30	-1.01	-0.15
15		-5.61	2.14	0.54	0.45
16	MED × PST	-1.86	0.36	0.53	0.84
17		1.94	1.43	-0.49	0.55
18		1.83	1.79	-1.80	1.48
19	MED × Pakbas	1.88	-1.71	-0.33	-0.95
20		-3.11	-2.06	2.44	0.64
21	MSD-2 × Baskota	-1.02	-1.93	-0.35	1.70
22	Baskota × Dehradunpahari	-1.36	-0.67	0.52	-1.29
23		-0.36	0.90	-0.38	-0.85
24		0.41	0.50	0.33	-0.18
25		-1.43	-0.58	0.88	-1.49
26		-0.08	0.45	-1.61	0.17
27	PB-1 × BM	2.00	-1.22	1.87	0.41
28		0.94	-1.63	1.19	-0.70
29		0.97	-2.70	0.71	0.31
30	PB × Gopalbhogh	-2.03	-0.81	2.32	-0.01
31		1.56	-1.14	-0.66	-0.86
32	Baskota × BM	-2.75	-1.04	-1.17	-1.48
33		2.06	0.81	1.49	0.24
34	MSD-1 × PST	0.37	0.17	-1.26	0.67
35		-0.80	-1.37	-0.86	0.43
36		-1.19	1.20	-1.59	0.76
37	MED × T- Basmati	1.73	-0.05	-0.94	-2.08
38		0.43	-2.46	-0.30	0.35
39	Baskota × Gopalbhogh	-1.59	-1.56	0.66	-1.27
40	MED × Kailasha	0.60	1.96	-1.17	-3.65

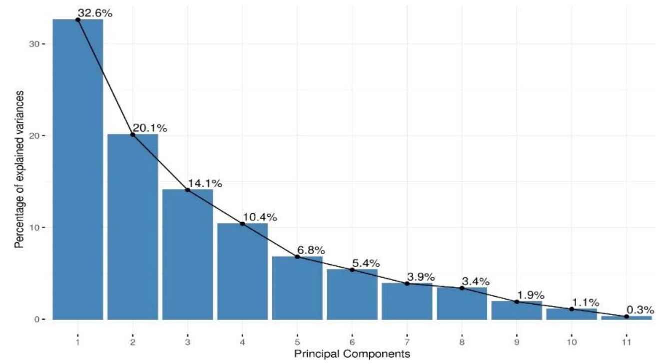

Fig. 4 : Percentage of variance.

With genotypes MED × PST-5 (3), MED × Basmati-1(1) and MED × Basmati-8 (8) standing out for their large positive contributions to the principal components linked to yield and developmental traits, the PCA scores aid in identifying genotypes with exceptional performance or distinctive trait combination.

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