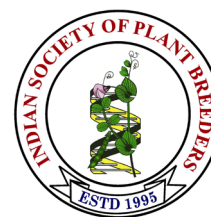


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Research Note

Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.) for yield and its component traits

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Abstract

The present study was conducted to evaluate genetic variability, heritability, and interrelationships among twelve agronomic traits in 27 paddy genotypes under irrigated conditions. The experiment was laid out in a randomized block design (RBD) with three replications during *Kharif* 2024 at the research farm of AKS University, Satna, Madhya Pradesh. Highly significant differences among genotypes were observed for all traits. High heritability coupled with high genetic advance was noticed for number of productive tillers per plant, number of spikelets per plant and biological yield per plant, indicating the role of additive gene action and potential for selection. High GCV and PCV values were recorded for number of productive tillers per plant, harvest index, and number of spikelets per panicle suggesting substantial genetic variability and potential for selection. Genotypic and phenotypic correlation analyses revealed that strong positive associations on seed yield with biological yield, harvest index, number of productive tillers per plant and harvest index. Path coefficient analysis showed that biological yield exerted highest positive direct effect on seed yield followed by harvest index and biological yield per plant. This study suggests that these traits are crucial for yield improvement in rice and can be targeted in breeding programs.

Keywords: Rice, Genetic Variability, Correlation, Path Analysis

Rice (*Oryza sativa* L.), a self-pollinated cereal, belonging to the Poaceae family ($2n=2x=24$), is a staple food for over half of the global population, particularly in Asia (Khush, 2005; FAO, 2023). It holds immense significance for millions of individuals globally, especially in developing nations, and serves as the foundation of nourishment in the Asia-Pacific Region. The crop thrives in hot, humid climates with average temperatures ranging from 20°C to 37°C throughout its life cycle (IRRI, 2013; Singh *et al.*, 2021). In India, rice is predominantly cultivated during the *Kharif* season and is commonly grown in regions that receive substantial rainfall annually. In areas with limited rainfall, it is also cultivated using irrigation methods (GOI, 2024; FAO, 2023).

India is the world's second-largest producer of rice, contributing significantly to global production. In the 2023–24 crop year, India's rice production reached an estimated 137.82 million metric tons from 47.83 million hectares (Maps for UPSC, 2024), with an average yield

of 2,882 kilograms per hectare. Madhya Pradesh is a key contributor to India's rice production, with a production of 70,20,000 metric tons in 2023, marking an increase from the previous year's production of 48,10,000 metric tons (CEIC Data, 2024).

Enhancing rice yield and its component traits is imperative to meet the escalating global demand. Genetic variability within rice genotypes plays a pivotal role in this enhancement, offering avenues for improvement in traits such as grain size, plant height, and resistance to biotic and abiotic stresses. Understanding the relationships among these traits through correlation and path analysis is essential for effective breeding programs aimed at yield improvement (Nagaraju *et al.*, 2023; Kishore *et al.*, 2015). This research paper focuses on the genetic variability, correlation, and path analysis for yield and its component traits in rice genotypes. By examining these genetic parameters, the study aims to identify key traits influencing yield, providing valuable insights for breeders

and agronomists striving to develop high-yielding, resilient rice varieties. The findings are anticipated to contribute significantly to the advancement of rice breeding strategies, aligning with the global objective of ensuring food security through sustainable agricultural practices.

The present study was conducted at the Research Farm of the Department of Genetics and Plant Breeding, AKS University, Satna, Madhya Pradesh, India, during *Kharif*, 2024 season. The experiment was laid out in a Randomized Block Design (RBD) with three replications. The experimental plot was maintained at a row spacing of 25 cm and plant-to-plant spacing of 15 cm. Geographically, Satna is situated at 24.34°N latitude and 80.49°E longitude, located in the Vindhya region of Madhya Pradesh.

A total of 27 rice genotypes exhibiting a wide range of agronomic and morphological variability were used in the investigation. Observations were recorded from five randomly selected plants per genotype, per replication, and the mean values were used for statistical analysis (IRRI, 1980). The 12 traits evaluated included: days to 50% flowering (DF), plant height (cm) (PH), number of productive tillers per plant (NPTPP), panicle length (cm) (PL), flag leaf length (cm) (FLL), flag leaf width (cm) (FLW), number of spikelets per panicle (NSPP), days to maturity (DM), Test weight (g) (TW), biological yield per plant (g) (BYPP), harvest index (%) (HI), and seed yield per plant (g) (SYPP). Analysis of variance (ANOVA) was performed for all traits following the procedure described by Panse and Sukhatme (1967) to estimate genotypic and phenotypic variance components. Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated as described by Burton (1952) to assess the extent of variability among the genotypes. The phenotypic correlation coefficients (r) among traits were computed using the formula proposed by Burton and DeVane (1953). Path coefficient analysis was performed according to Dewey and Lu (1959) to partition correlation coefficients into direct and indirect effects. The statistical analysis was done by using Agri Analyze Software <https://www.agrianalyze.com>

This methodological framework enabled the precise quantification of genetic variability, correlation, and causal relationships among yield and its component traits, providing a scientific basis for selection and breeding strategies in rice genotypes

The ANOVA indicated that the mean sum of squares due to genotypes were highly significant for all the traits viz., days to 50% flowering, plant height, number of productive tillers per plant, flag leaf length, flag leaf width, days of maturity, panicle length, number of seeds per panicle, test weight, harvest index, biological yield per plant, seed yield per plant. The mean sum of squares due to replication showed non-significant differences for all the traits under study indicating homogeneity among replications. Mean

sum of square from analysis of variance for various traits are given in Table 2. The findings were quite similar to as reported by Gautam *et al.* (2017) for days to 50% flowering, days to maturity, grain yield per plant; Kumar *et al.* (2018) for plant height, seed yield per plant; Rani *et al.* (2023); Yadav *et al.* (2018) for biological yield per plant and harvest index.

The mean values, ranges, and measures of variability for all genotypes across traits are presented in **Table 1**. The data reveal considerable genetic variation for all traits, as evidenced by significant critical differences and moderate to low coefficients of variation, indicating reliable experimental precision.

The overall mean DF was 52.07 days, with a range from 38.00 to 68.00 days. Early-flowering genotypes such as *Siddha Sonnalu* (G7) and *RDR 1140* (G9) may be better suited for short-duration cropping systems or regions with restricted growing windows. Conversely, late-flowering genotypes (e.g., *Bonhit*, *Swarna*) may leverage longer vegetative growth if the season permits. The significant CD ensures that the observed differences in flowering time are not due to experimental error. PH averaged 96.68 cm, varying from 47.6 cm to 120.4 cm. Tall genotypes such as *Nagri Dubraj* (G27) may contribute to greater biomass accumulation, but also pose risk of lodging under high fertility or wind. Dwarf to semi-dwarf types (e.g., *Bonhit* (G3)) may offer structural stability. Because height is correlated with yield via biomass and harvest index, the observed variation offers useful selection scope. The mean NPTPP count was 25.1, with extremes of 14.2 to 50.8. Genotype *CG Dhan 1919* (G24) exhibited the highest tiller count (50.8), implying strong tillering ability a trait often positively correlated with yield. However, excess tillers might increase competition, so balance with panicle fertility is essential. PH varied between 18.66 to 31.4 cm, with a mean of 24.49 cm. *Dihula* (G5) recorded the longest panicles. Longer panicles generally accommodate more spikelets, thus offering yield advantage, assuming adequate grain filling. Mean FLL was 33.66 cm (range 24.0 to 47.2 cm), while FLW ranged from 1.80 to 2.08 cm (mean 1.90 cm). Genotypes with long and broad flag leaves (e.g., *Masura* (G2)) may possess higher photosynthetic area, enhancing source strength during grain filling. The mean NSPP stood at 222, with variation from 130.6 to 340.4 spikelets. *Dihula* (G5) again stood out for its high spikelet number, aligning with its long panicles. This trait is a direct contributor to yield potential, provided grain filling is adequate. DM duration ranged from 86.0 to 138.0 days, mean 114 days. *Masura* (G2) was longest in maturity, whereas *Dihula* (G5) matured earlier, which can be advantageous in double-cropping or constrained rainfall environments. TW ranged from 13.0 to 28.0 g with mean 21.24 g. *Masura* (G2) recorded the highest test weight, indicating bold, dense grains, a desirable quality trait. BYPP averaged 304.0 g, varying between 175.8 g and 398.0 g. *Dubraj* (G22) produced the highest biomass, evidencing strong vegetative performance. HI (the ratio

Table 1. Mean performance for 12 characters in rice germplasm

S. No.	Varieties	DFF	PH	NPTTP	PL (cm)	FLL (cm)	FLW (cm)	NSPP	DM	TW (g)	BYPP (g)	HI (%)	SYPP (g)
1	Biranj (G1)	52.33	89.13	17.47	24.47	32.13	1.91	279.60	90.33	21.73	396.00	10.52	41.67
2	Masura (G2)	45.00	110.00	25.07	18.66	47.2	1.85	168.60	138.	28.0	177.93	33.15	55.67
3	Bonhit (G3)	65.00	48.27	39.03	27.36	36.21	1.82	130.6	96.33	14.13	283.93	18.43	52.33
4	Jeera Shankar (G4)	45.00	110.00	25.07	21.80	24.0	1.85	168.60	92.33	13.0	175.8	31.28	55.67
5	Dihula (G5)	45.00	110.00	25.01	31.4	27.40	1.85	340.4	86.0	21.00	177.93	7.56	25.0
6	Sujala (G6)	54.33	97.13	15.20	24.05	37.41	1.90	199.80	105.33	19.93	320.27	17.28	88.0
7	Siddha Sonnalu (G7)	41.33	86.40	35.40	25.40	31.39	1.94	182.00	110.33	24.33	279.27	18.50	51.67
8	JGL 24423 (G8)	56.67	106.00	19.40	25.37	35.17	1.88	199.20	117.33	21.03	260.27	20.49	53.33
9	RDR 1140 (G9)	41.67	87.40	24.67	26.00	27.93	1.84	291.53	119.33	19.00	310.27	16.76	52.00
10	MTU 1075 (G10)	49.33	106.07	30.20	24.67	36.70	1.92	184.60	107.33	19.23	330.27	16.25	53.67
11	RNR 15098 (G11)	44.67	89.07	15.40	24.73	34.93	1.91	163.00	109.33	22.00	350.27	13.61	47.67
12	WGL 18833 (G12)	46.67	80.73	49.80	19.99	37.99	1.96	181.80	105.33	19.67	290.27	11.37	33.00
13	KNM 118 (G13)	50.33	102.53	41.80	20.40	31.53	1.99	253.20	109.33	22.57	280.27	17.71	49.67
14	NP 124-8 (G14)	58.33	93.33	38.20	23.00	43.49	1.91	262.00	108.33	26.30	320.27	15.41	49.33
15	MTU 1075 (G15)	52.33	103.00	17.40	21.00	32.80	2.06	173.20	112.33	23.67	300.27	18.11	54.33
16	MTU 1032 (G16)	45.33	110.33	15.60	23.50	35.77	1.99	286.60	113.33	18.27	350.27	19.32	67.67
17	Dhan Madhu Raj 55 (G17)	47.67	88.93	16.40	24.00	32.47	1.8	257.60	116.33	21.47	370.27	13.05	48.33
18	MTU 1001 (G18)	51.33	82.27	24.20	20.60	26.00	2.08	150.80	117.33	17.77	280.27	18.20	51.00
19	MTU 1010 (G19)	56.33	89.93	15.20	24.60	27.60	1.86	225.60	115.33	16.40	300.27	16.38	49.17
20	Devbhog (G20)	58.33	92.20	17.40	29.00	40.07	1.91	318.00	129.33	22.80	340.27	16.46	56.00
21	Swarna (G21)	60.33	98.73	19.60	25.32	31.36	1.88	338.40	131.33	20.33	370.27	14.31	53.00
22	Dubraj (G22)	59.33	112.27	21.40	23.52	32.67	1.82	265.00	132.33	21.53	398.0	13.12	43.33
23	HMT (G23)	57.33	107.93	23.00	25.40	32.33	1.90	217.00	135.33	23.37	290.27	10.79	31.33
24	CG Dhan 1919 (G24)	52.33	79.67	50.8	23.20	24.13	1.93	168.87	130.33	16.97	280.27	16.05	45.00
25	Vikram TCR (G25)	53.33	102.87	16.40	29.00	27.47	1.97	269.00	133.33	24.13	216.60	23.39	50.67
26	Zinc Rice (G26)	60.33	92.93	17.80	22.60	33.60	1.88	198.40	134.33	25.27	384.47	13.96	53.67
27	Nagri Dubraj (G27)	52.33	120.40	19.13	30.40	35.87	1.85	276.47	130.33	22.07	179.40	29.00	52.00
1	Mean	52.07	96.68	25.1	24.49	33.66	1.9	222	114.	21.24	304.	17.1	50.0
2	Max	68.00	120.40	50.8	31.4	47.2	2.08	340.4	138.	28.0	398.0	33.15	88.0
3	Min	38.00	47.6	14.2	18.66	24.0	1.8	130.6	86.0	13.0	175.8	7.56	25.0
4	SEm	0.85	0.65	0.30	0.14	0.39	0.079	0.37	0.06	0.26	0.29	1.18	52.0
5	SEd	1.20	0.92	0.42	0.20	0.55	0.01	0.53	0.09	0.37	0.41	1.68	5.42
6	CD at 5%	2.42	1.85	0.86	0.42	1.11	0.02	1.07	0.182	0.74	0.42	3.66	10.8
7	CD at 1%	3.2	2.47	1.14	0.55	1.48	0.03	1.42	0.24	0.99	1.11	4.49	14.49
8	C.V.%	2.84	1.17	2.09	1.04	2.01	0.71	0.29	0.09	2.15	0.16	12.04	13.26

of grain to biological yield) averaged 17.1%, with a range 7.56% to 33.15%. *Masura* (G2) exhibited the highest harvest index (33.15%), showing superior partitioning of assimilates to grains. SYPP was 50.0 g, spanning 25.0 to 88.0 g. The highest yielding genotype was *Sujala* (G6) (88.0 g), while *Dihula* (G5) recorded the lowest. The wide variation in seed yield underlines the potential for genetic improvement *via* selection. The significant differences among genotypes for all traits (as per CD and

1% significance) confirm that genetic effects predominate over environmental error, enabling reliable selection decisions. Moderate to low CV values across traits further substantiate experimental precision. findings were quite similar to as reported for days to 50% flowering, days to maturity, grain yield per plant by Gautam *et al.* (2017), Selvaraj *et al.* (2011) for plant height, grain panicle length and Kumar *et al.* (2018)), for biological yield per plant and harvest index.

High GCV and PCV values were recorded for number of productive tillers per plant (40.74 to 40.79), harvest index (27.08 to 29.64) and number of spikelets per panicle (25.64) (**Table 2**), suggesting substantial genetic variability and potential for selection. It is important to note that the PCV values were consistently greater than the GCV values, suggesting a significant environmental impact on the traits. These findings are consistent with those observed in earlier studies by Acharya *et al.* (2018), Nagaraju *et al.* (2023), and Tiwari and Singh (2024). Number of spikelets per panicle (99.9) exhibited the highest heritability, followed closely by number of effective tillers per plant (99.7) and biological yield per plant (99.9). The highest genetic advance as percentage of the mean was observed for number of effective tillers per plant (83.82), number of spikelets per panicle (52.82) and harvest index (50.97) followed by biological yield per plant

(36.70), plant height (32.07) and flag leaf length (31.52), while flag leaf width (6.69) showed low value (**Table 2**). High heritability and high genetic advance as percentage of mean indicate the predominant role of additive gene effects and hence better effectiveness for selection. Comparable findings were reported in the studies by Kumar *et al.* (2024). Chaubey and Singh (2023).

Seed yield per plant (SYPP) showed strong positive correlation with harvest index (0.487) and number of productive tillers per plant (0.432). Plant height (0.184) and spikelet per panicle (0.159) were also positively correlated. Negative correlations were observed between SYPP with days to 50% flowering (-0.106) and test weight (-0.112) at genotypic level (Table3). SYPP maintained positive correlations with HI (0.595**), spikelets per panicle (0.105), and panicle length (0.122). Negative

Table 2. Estimates of genetic parameter for 12 characters in Rice germplasm

S. No.	Characters	Range		Grand Mean	Heritability (h ²)	GCV	PCV	GA	GA % of mean
		Min.	Max.						
1	Days To 50% Flowering	38.00	68.00	52.074	94.9%	12.27	12.60	12.83	24.63
2	Plant Height (cm)	47.6	120.6	96.686	99.4%	15.61	15.65	31.01	32.07
3	No. of Productive tillers/Plant	14.20	50.80	25.154	99.7%	40.74	40.79	21.08	83.82
4	Panicle Length (cm)	18.66	31.4	24.499	99.0%	10.92	10.97	5.48	22.40
5	Flag Leaf Length(cm)	24.0	47.2	33.667	98.3%	15.43	15.56	10.61	31.52
6	Flag Leaf Width	1.8	2.08	1.9138	95.5%	3.32	3.40	0.12	6.69
7	No.of Spikelets Per Panicle	130.6	340.4	222.358	99.9%	25.64	25.64	117.45	52.82
8	Days to Maturity	114.469	138.0	138.000	99.9%	12.31	12.31	29.04	25.37
9	Test Weight (g)	13.0	28.0	21.245	97.6%	13.76	13.93	5.95	28.01
10	Biological Yield/Plant (g)	175.8	398.0	304.775	99.9%	17.82	17.82	111.88	36.70
11	Harvest Index (%)	7.56	33.15	17.103	83.4%	27.08	29.64	8.71	50.97
12	Seed Yield Per Plant (g)	25.0	88.0	50.080	43.8%	11.72	17.70	8.01	16.00

Table 3. Genotypic correlation for yield and yield contributing characters

S.No.	DFF	PH	NPTPP	PL	FLL	FLW	SPP	DM	TW	BY	HI	SYPP
DFF	1	-0.223	-0.142	0.092	0.152	-0.294	0.206	0.339	-0.121	0.096	-0.147	-0.106
PH		1	0.345	0.126	0.204	0.053	0.265	0.117	0.534 **	0.174	0.294	0.184
ETPP			1	-0.27	0.079	-0.011	0.380*	0.256 *	-0.109	-0.197	-0.119	0.432 *
PL				1	0.135*	-0.425*	0.267	0.253	0.093	0.138	0.231	0.171
FLL					1	-0.203	0.071*	-0.359	-0.363	-0.237	0.181*	0.095
FLW						1	0.054	0.062	0.116	0.100	-0.116	-0.061
SPP							1	0.391 *	-0.163**	-0.0216**	-0.053**	0.159
DM								1	0.095	-0.019*	-0.061	0.116
TW									1	0.075	-0.056	-0.112
BY										1	-0.843 **	0.016
HI											1	0.487**
SYPP												1

DF=Days to 50% flowering, PH=Plant height (cm), NPTPP=No. of productive tillers per plant, PL=Panicle Length (cm), FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), NSPP=No. of spikelet per panicle, DM=Days to maturity, TW=Test weight (g), BYPP=Biologic yield / plant (g), HI=Harvest index (%), SYPP=Seed yield per plant (g)

Table 4. Phenotypic correlation for yield and yield contributing characters

S.No.	DFF	PH	NPTPP	PL	FLL	FLW	SPP	DM	TW	BY	HI	SYPP
DFF	1	0.214	0.140	-0.093*	0.155	-0.278 *	0.201	0.329 **	-0.108*	0.093	0.117	-0.050*
PH		1	0.343 **	0.125	0.205	0.052	0.264 *	0.117	0.524 **	-0.174	-0.270	-0.126
ETPP			1	-0.275	0.079	-0.010	-0.380 **	-0.255 *	-0.108	-0.197	-0.106	-0.281
PL				1	0.137	-0.416 **	0.266	0.252 *	0.094	0.138	-0.216	0.122
FLL					1	0.190	0.071	0.357	-0.360	-0.2354	-0.154	0.079
FLW						1	0.053	0.061	0.129	0.098	-0.084	-0.071
SPP							1	0.391 **	-0.162*	-0.216*	-0.048*	0.105
DM								1	-0.094	-0.019	-0.056	-0.077
TW									1	0.075	0.048	0.071
BY										1	-0.770 **	-0.010
HI											1	0.595**
SYPP												1

DF=Days to 50% flowering, PH=Plant height (cm), NPTPP=No. of productive tillers per plant, PL=Panicle Length (cm), FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), NSPP=No. of spikelet per panicle, DM=Days to maturity, TW=Test weight (g), BYPP=Biologic yield / plant (g), HI=Harvest index (%), SYPP=Seed yield per plant (g)

phenotypic correlation was recorded with days to 50% flowering (-0.050*) and number of productive tillers per plant (-0.281) at phenotypic level and the results are presented in Table 4. Overall, traits associated with reproductive efficiency showed a stronger association with yield than those related to vegetative growth. Singh *et. al.* (2021), Akter *et.al.*,(2016), Khalequzzaman *et.al.*, (2022) in their study revealed that a positive and significant association was observed for filled grains per panicle, days to flowering, days to maturity, grain length and decorticated grain length breadth ratio with yield/hill at both genotypic and phenotypic levels.

The direct and indirect impacts of different traits on SYPP are presented in Table 5 & 6. Biological yield per plant (1.405) and Harvest index (1.726) showed highest direct positive effect on seed yield per plant, and panicle length (0.015), plant height (0.003) also had positive direct effects (Table 5). Spikelets per panicle (-0.082) and days to 50% flowering (-0.050) had negative direct effects at genotypic level, although their indirect contributions through traits like HI and BYPP were substantial. Harvest index (1.553) and biological yield (1.180) exhibited the highest direct positive effects at phenotypic level. Traits like test weight (-0.158) and spikelet per panicle (-0.082) had negative direct effects but contributed positively

Table 5. Genotypic path matrix of direct and indirect effects of different traits on grain yield per plant

trait	DFF	PH	NPTPP	PL	FLL	FLW	SPP	DM	TW	BY	HI	'r'
DFF	-0.050	-0.001	-0.002	0.001	0.043	-0.054	-0.017	0.061	0.031	0.135	-0.254	-0.107
PH	0.011	0.003	-0.004	0.002	0.057	-0.010	-0.022	0.021	-0.137	-0.245	0.507	0.185
ETPP	0.007	-0.001	0.011	-0.004	0.022	0.002	0.031	-0.046	0.028	-0.277	-0.207	-0.432 *
PL	-0.005	0.000	-0.003	0.015	0.038	-0.079	-0.022	0.045	-0.024	-0.195	0.400	0.172
FLL	-0.008	0.001	0.001	0.002	0.280	-0.038	-0.006	-0.065	-0.093	0.334	-0.313	0.096
FLW	0.015	0.000	0.000	-0.006	-0.057	0.185	0.004	0.011	-0.030	0.141	-0.202	0.061
SPP	-0.010	0.001	-0.004	0.004	0.020	-0.010	-0.082	0.070	-0.042	0.305	-0.092	0.159
DM	-0.017	0.000	-0.003	0.004	-0.101	0.011	-0.032	0.180	-0.025	-0.028	-0.107	-0.116
TW	0.006	0.002	-0.001	0.001	0.102	0.021	-0.013	0.017	-0.257	0.106	-0.097	-0.112
BY	-0.005	-0.001	-0.002	-0.002	0.067	0.019	-0.018	-0.004	-0.019	1.405	-1.456	-0.016
HI	0.007	0.001	-0.001	0.003	-0.051	-0.022	0.004	-0.011	0.014	-1.185	1.726	0.487 **

Genotypic Residual effect = 0.457

Bold values indicate direct effect

DF=Days to 50% flowering, PH=Plant height (cm), NPTPP=No. of productive tillers per plant, PL=Panicle Length (cm), FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), NSPP=No. of spikelet per panicle, DM=Days to maturity, TW=Test weight (g), BYPP=Biologic yield / plant (g), HI=Harvest index (%), SYPP=Seed yield per plant (g)

Table 6. Phenotypic path matrix of direct and indirect effects of different traits on grain yield per plant

trait	DFF	PH	NPTTP	PL	FLL	FLW	SPP	DM	TW	BY	HI	'r'
DFF	-0.021	0.002	-0.012	-0.001	0.029	-0.033	-0.016	0.057	0.017	0.110	-0.182	-0.050
PH	0.005	-0.010	-0.030	-0.001	0.039	-0.006	-0.022	0.020	-0.083	-0.205	0.420	0.126
ETPP	0.003	0.003	0.087	0.002	0.015	0.001	0.031	-0.044	0.017	-0.232	-0.165	-0.281 *
PL	-0.002	-0.001	-0.024	-0.007	0.026	-0.049	-0.022	0.044	-0.015	-0.163	0.337	0.123
FLL	-0.003	-0.002	0.007	-0.001	0.188	-0.022	-0.006	-0.062	-0.057	0.278	-0.240	0.080
FLW	0.006	0.001	0.001	0.003	-0.036	0.118	0.004	0.011	-0.020	0.116	-0.132	0.071
SPP	-0.004	-0.003	-0.033	-0.002	0.013	-0.006	-0.082	0.068	-0.026	0.256	-0.076	0.106
DM	-0.007	-0.001	-0.022	-0.002	-0.067	0.007	-0.032	0.172	-0.015	-0.023	-0.088	-0.078
TW	0.002	-0.005	-0.009	-0.001	0.068	0.015	-0.013	0.016	-0.158	0.088	-0.075	-0.071
BY	-0.002	0.002	-0.017	0.001	0.044	0.012	-0.018	-0.003	-0.012	1.180	-1.196	-0.011
HI	0.002	-0.003	-0.009	-0.002	-0.029	-0.010	0.004	-0.010	0.008	-0.909	1.553	0.595 **

Phenotypic Residual effect= 0.1005

Bold values indicate direct effect

D 50%F=Days to 50% flowering, PH=Plant height (cm), NPTTP=No. of productive tillers per plant, PL=Panicle Length (cm), FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), NSPP=No. of spikelet per panicle, DM=Days to maturity, TW=Test weight (g), BYPP=Biologic yield / plant (g), HI=Harvest index (%), SYPP=Seed yield per plant (g)

through indirect effects on Harvest index and Biological yield per plant. These results emphasized that selection for higher biological yield and improved harvest index can significantly enhance seed yield. The indirect effects of these traits were less pronounced, indicating their direct contribution to grain yield.

The findings corroborate previous reports by Kumar *et al.* (2024) and Gautam *et al.* (2017), Pathak *et al.* (2024), Tiwari and Singh (2024). Emphasizing the importance of traits like biological yield and harvest index in rice breeding. The significant variability and strong associations of these traits with seed yield affirm their role in enhancing productivity.

The present investigation revealed that substantial genetic variation existed among the 27 rice genotypes. Traits such as biological yield, harvest index and number of productive tillers are strongly associated with seed yield and exhibit high heritability and genetic advance, indicating their suitability for selection in breeding programs. Path coefficient analysis further confirmed their direct contribution to yield. These genotypes offer valuable genetic resources for developing high-yielding rice varieties and can be effectively utilized in hybridization programs aimed at yield enhancement. Correlation and path analysis further validated the interdependence of traits, highlighting the value of focusing on reproductive traits like harvest index and spikelets per panicle, architecture, and partitioning efficiency (HI) over merely vegetative growth. Genotypes such as Sujala, Masura, and MTU 1032 demonstrated promising potential for yield enhancement and could serve as parents in breeding programs. Future breeding efforts should prioritize traits with high direct effects on seed yield and incorporate stable genotypes across environments. This strategic

selection, supported by thorough variability analysis, will lead to sustainable improvement in rice productivity.

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