



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.076>

YIELD TRAIT ANALYSIS IN RICE (*ORYZA SATIVA* L.) RESTORER LINES THROUGH GENETIC VARIABILITY, CORRELATION AND PATH COEFFICIENT STUDIES

Teena Patel^{1*}, S.K. Singh¹, Kumar Jai Anand¹ and Nagesh Bichewar²

¹Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), 482004, India

²Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, 500030, India

*Corresponding author Email: teenapateljbp@gmail.com

(Date of Receiving : 11-08-2024; Date of Acceptance : 03-10-2024)

ABSTRACT

Tasar silkworm *Antheraea mylitta* (D.) wild sericigenous insect which produces tropical tasar silk. It reared outside in wild conditions which attracts lots of pests and predators and among them, predatory wasps have become more significant over the past 3-4 years and have been observed in major tasar growing areas like Bankura and Patel Nagar (Suri) in West Bengal, Kathikund, Dumka, and Kharsawan in Jharkhand, as well as Baripada region in Odisha. The major predatory wasps of tasar silkworm are *Polistes olivaceus*, *P. stigma*, and *P. strigosus*. They are among the commonly observed species in the tasar ecosystem, and they pose a substantial threat to the well-being of the tasar silkworm if left uncontrolled. The *Polistes* wasps are social insects that reside in colonies comprising drones, workers, and egg-laying queens. They construct paper nests using wood fibers or coarse, papery materials and communicate through the use of pheromones. *Polistes* wasps exhibit remarkable efficiency and intelligence as versatile predators, covering long distances to find prey and employing a combination of hovering and walking on plants to locate their quarry. They are attracted to plants emitting frass odours and those that have been subjected to herbivore-induced damage. The article provides an overview of the management and challenges associated with controlling predatory wasps in tasar sericulture and it is concluded by emphasizing the need for further research to develop effective management strategies for controlling predatory wasps in tasar sericulture.

Keywords: Tasar silkworm, Predatory wasps, Behaviour and Hibernation

Introduction

Rice is the most crucial crop globally, with half of the world's population consuming it daily. In some Asian nations, rice accounts for over 70% of the calorie intake (Rahman and Zhang, 2022). Additionally, rice is a fundamental staple for Asia and Africa's poorest and most undernourished populations, who often cannot afford or access more nutritious foods. Therefore, rice is a vital commodity worldwide, closely tied to global food security, economic growth, employment, social stability, and regional peace (Yadev and Kumar, 2018).

In 2022-23, global rice production reached 514 million tons, with India contributing 135.75 million

tons (Foreign Agricultural Services, 2024). By 2025, 758 million tonnes of rice is required to meet global demand (Nakano *et al.*, 2019). To address the rising global demand, it is crucial to boost production by emphasizing the promotion and cultivation of hybrid varieties. This approach is essential for narrowing the yield gap, rather than solely concentrating on low-yielding cultivars (Rout, 2020). Large-scale adoption of hybrid rice in India is a feasible solution for food security issues (Pranathi *et al.*, 2016; Kavya *et al.*, 2023). The improvement of parental lines should be prioritized to explore heterosis in hybrid rice, as finding appropriate parental lines for effective heterotic pairings is one of the most challenging aspects of hybrid breeding.

A successful plant breeding program depends on genetic variability and the breeder's ability to select desired traits. High variability within a population is a key for identifying and developing improved varieties, particularly for quantitative traits (Adhikari *et al.*, 2018). Other important selection criteria include heritability and genetic advance. Estimates of heritability and genetic advance must be addressed when predicting gain under selection and selecting superior varieties (Ali *et al.*, 2002).

Correlation coefficient analysis assesses the relationships between plant traits to find attributes for genetic improvement (Karim *et al.*, 2014). Rice grain yield is a complex, polygenic trait impacted by various factors. Direct selection for yield can be misleading; thus, it is critical to understand the relationships between yield and its component traits (Sarker *et al.*, 2020).

Yield and its component traits are intricate, involving multiple interrelated factors (Ikeda *et al.*, 2013; Zhou *et al.*, 2018). Therefore, path analysis, which separates the correlation coefficient into its direct and indirect effect components, is essential. Singh *et al.* (1985) noted that path analysis helps distinguish these effects (Saleh *et al.*, 2020).

In this context, the current study aims to identify the most critical traits for breeding programs by examining genetic variability parameters, heritability, genetic advance as a percentage of the mean, correlation coefficients and path analysis in restorer lines of rice.

Materials and Methods

The experiment was conducted during *kharif* 2020 under the Rice Improvement Project at Seed Breeding Farm, JNKVV, Jabalpur (MP). The experimental material included 80 rice fertility restorer lines (Table 1) planted in a randomized complete block design with three replications. Each genotype was planted with one seedling per hill in three rows, each five meters long, with a 15×20 cm spacing. Observations were carefully documented for five plants randomly selected from each replication. Standard agronomic practices were applied to ensure a healthy crop. Data were recorded on 13 yield attributing traits: Days to maturity (DTM), Number of tillers per plant (NOT), Number of effective tillers per plant (NOET), Plant height (PH), Stem thickness (ST), Flag leaf length (FLL), Flag leaf width (FLW), Panicle length (PL), Panicle weight (PW), Total spikelets per panicle (TSPP), Fertile spikelets per panicle (FSPP), Thousand seed weight (1000 SW) and Grain yield per plant (GYPP). The mean values of the randomly selected plants from all replications were used to compile the experimental data.

Table 1 : List of 80 rice restorer lines used in the study programme

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	Mahamaya	28.	Laxmi-144	55.	JNPT-81
2.	R-548	29.	IR09N26	56.	JNPT-782
3.	R-650	30.	IR-79854-38-2-4	57.	NPT14-12
4.	R-704	31.	IR-79854-48-2-1	58.	JNPT767
5.	Abhya	32.	AD02207	59.	JR-81
6.	R-321	33.	PAU-3832-79-4-3-1	60.	NPT-3803
7.	R-296	34.	RP5219-9-6-7-3-2-1-1	61.	NPT-3804
8.	R-712	35.	MTU1153	62.	NPT-3805
9.	R-710	36.	UPR2628-9-1-1	63.	NPT-3806
10.	R-304	37.	MTU11320-41-2-1	64.	NPT-3810
11.	JR -503	38.	P-3123	65.	NPT-3817
12.	Sugandha-3	39.	MC-13	66.	NPT-3820
13.	NPT-10	40.	TRC2013-2	67.	NPT-3821
14.	NPT-13-01	41.	VNR-212	68.	E-TP-1001
15.	NPT-15	42.	CR3424-2-2-5	69.	E-TP-1008
16.	NPT-29	43.	HRI-183	70.	E-TP-1014
17.	NPT-35-01	44.	NP-9165	71.	E-TP-1018
18.	NPT-37	45.	CR3703-11-1	72.	E-TP-1019
19.	NPT-65	46.	RP5911-52-13-3-2-2-1	73.	E-TP-1021
20.	NPT-70	47.	CR2829-PLN-32	74.	E-TP-1023
21.	NPT(S) 81	48.	CANP-318	75.	E-TP-1054
22.	JNPT809	49.	ANP-526	76.	E-TP-1062
23.	NP-72	50.	ANP-553	77.	E-TP-1064
24.	NP-1024	51.	Johar	78.	IME-1101
25.	NP-8421	52.	PR35766-B-24-3-18	79.	E-TP-1124
26.	PSP-456	53.	IR838614-678-8	80.	1E-TP-2
27.	Gemini	54.	HRT-181		

An analysis of variance (ANOVA) was executed for the randomized complete block design using the approach described by Panse and Sukhatme in 1985. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to Burton's method (1952). Variation ranges were classified as high (> 20%), moderate (10-20%), or low (< 10%) following the classification by Sivasubramanian and Madhavamenon (1973). Broad-sense heritability (h^2 (bs)) was estimated as the ratio of genotypic variance to total variance based on the method suggested by Hanson (1956) and categorized as high (> 60%), moderate (30-60%), or low (< 30%) as suggested by Robinson *et al.* (1949). Genetic advance was calculated and categorized as high (> 20%), moderate (10-20%), or low (< 10%) following the guidelines of Johnson *et al.* (1955). For all combinations of quantitative characters, correlation coefficients were calculated using the formula

suggested by Miller *et al.* (1958). The direct and indirect contributions of diverse characters to yield were assessed through path coefficient analysis as suggested by Wright (1921) and further elaborated by Dewey and Lu (1959).

Results and Discussion

The analysis of variance displayed significant variability among the genotypes for the studied traits, as indicated by the significant mean sum of squares due to genotypes for all the examined traits (Table 2). Understanding the consequence of environmental factors on different attributes requires considering the genetic and phenotypic coefficients of variation (GCV and PCV) (Akinwale *et al.*, 2011). The slightly higher phenotypic coefficient of variation compared to the genotypic coefficient of variation (Fig. 1) suggests minimal impact of environmental factors on these traits.

Table 2 : ANOVA for yield attributing traits in fertility restorer lines

Source of variation	d.f.	Mean sum of squares						
		DTM	NOT	NOET	PH	ST	FLL	FLW
Replication	2	26.22	0.1157	0.2136	5104.55	1.09	6.30	0.00
Genotype	79	128.14**	5.2915 **	5.3401 **	5375.57**	2.74**	170.32**	0.23**
Error	159	21.25	0.4192	0.4248	4863.62	0.16	2.14	0.01
	d.f.	Mean sum of squares						
		PL	PW	TSPP	FSPP	1000 SW	GYPP	
Replication	2	0.14	0.16	19.06	32.60	0.16	2.397	
Genotype	79	12.97**	78.32* *	14104.72**	10382.48**	57.46**	69.728**	
Error	159	1.09	0.41	105.94	78.92	0.37	1.419	

*Significant at 5% level, ** Significant at 1% level

DTM-days to maturity, NOT-Number of tillers per plant, NOET-Number of effective tillers per plant, PH-Plant height, ST-Stem thickness, FLL-Flag leaf length, FLW- Flag leaf width, PL-Panicle length, PW-Panicle weight, TSPP-Total spikelets per panicle, FSPP-fertile spikelets per panicle, 1000 SW- Thousand seed weight, GYPP -Grain yield per plant

Table 3 : Genetic parameter of variability for yield and its components traits

Traits	Mean	Range		H^2 (bs) (%)	GA as % of mean	GCV%	PCV%
		MIN	MAX				
DTM	124.37	111.33	143.00	62.60	7.83	4.80	6.06
NOT	9.46	5.6	13.40	79.48	24.73	13.46	15.10
NOET	7.55	4.20	12.60	79.41	30.08	16.38	18.39
PH	120.50	94.93	153.80	96.05	4.11	9.313	9.503
ST	4.67	3.13	7.33	84.60	37.64	19.87	21.60
FLL	38.55	23.10	56.43	96.30	39.26	19.42	19.79
FLW	1.30	0.63	2.23	92.40	42.05	21.24	22.10
PL	26.35	20.60	33.17	78.50	13.78	7.55	8.53
PW	26.94	13.90	36.90	98.50	38.67	18.92	19.07
TSPP	206.94	51.67	405.33	97.80	67.24	33.01	33.38
FSPP	173.88	42.00	352.33	97.80	68.65	33.71	34.09
1000 SW	22.12	13.50	33.57	98.10	40.23	19.72	19.91
GYPP	21.99	11.70	33.17	94.10	43.37	21.70	22.37

*Classes of Heritability (%): High >60%, Moderate 30-60%, Low <30%

*Classes of GA as % of mean at 5%: high >20%, Moderate 10-20%, Low <10%

*Classes of PCV (%), and GCV (%): high >20, Moderate 10-20, Low <10

The high GCV and PCV were found for the traits flag leaf width, total spikelets per panicle, fertile spikelets per panicle and grain yield per plant (Table 3), which indicates a high degree of variability in these traits, making direct selection effective for crop improvement. Results are in concurrence with Saha *et al.* (2019) and Konate *et al.* (2016) for fertile spikelets per panicle, Basavaraja *et al.* (2013) for total spikelets per panicle, Barde *et al.* (2021) for grain yield per plant and Nath *et al.* (2021) for flag leaf width. Medium GCV and PCV were found for traits such as number of tillers per plant, number of effective tillers per plant, stem thickness, flag leaf length, panicle weight, and thousand seed weight. Similar findings were obtained by Nithya *et al.* (2020) for the number of tillers per plant; Girma *et al.* (2018) for the number of effective tillers per plant; Keerthiraj and Biju (2020) for stem thickness, flag leaf length, panicle weight and thousand seed weight. The low value of GCV and PCV was found for plant height traits, panicle length and days to maturity. These traits exhibited less variability, suggesting that selection based on them may not be fruitful. Rashid *et al.* (2017) found similar results for days to maturity and panicle length, Bhargava *et al.* (2021) for panicle length and Adhikari *et al.* (2018) for plant height.

An attempt was made to estimate the broad sense heritability in the present investigation. All the traits under investigation expressed high heritability (>60%). Earlier researchers, Demeke *et al.* (2023) and Kavaya *et al.* (2023) found similar results. High heritability

indicates that the selection for such traits would be less tedious because the genotype and phenotype coincide closely due to the environment's minimal impact on the phenotype. Heritability alone is insufficient for selecting the best individual due to its inclusion of both additive and non-additive gene effects (Dey *et al.*, 2021). Fig. 2 depicts the magnitudes of broad sense heritability (h^2) and genetic advance as per cent of mean for different traits.

High genetic advance primarily results from additive gene action. Thus, combining heritability with genetic advance is more effective for selection (Kishor *et al.*, 2008). In this study, high heritability accompanied with high genetic advance as percentage of mean showed by the number of tillers per plant, number of effective tillers per plant, stem thickness, flag leaf length, flag leaf width, panicle weight, total spikelets per panicle, fertile spikelets per panicle, thousand seed weight and grain yield per plant. Daula *et al.* (2020) reported similar findings for the number of tillers per plant; Kavaya *et al.* (2021) for number of effective tillers per plant and grain yield per plant; Keerthiraj and Biju (2020) for flag leaf length, flag leaf width, thousand seed weight and stem thickness; Kulsum *et al.* (2022) for panicle weight, Nath *et al.* (2021) for total spikelets per panicle; Aditya and Bhartiya (2013) for fertile spikelets per panicle. High heritability with moderate genetic advance was also found for panicle length. Kavaya *et al.* (2023) obtained a similar result.

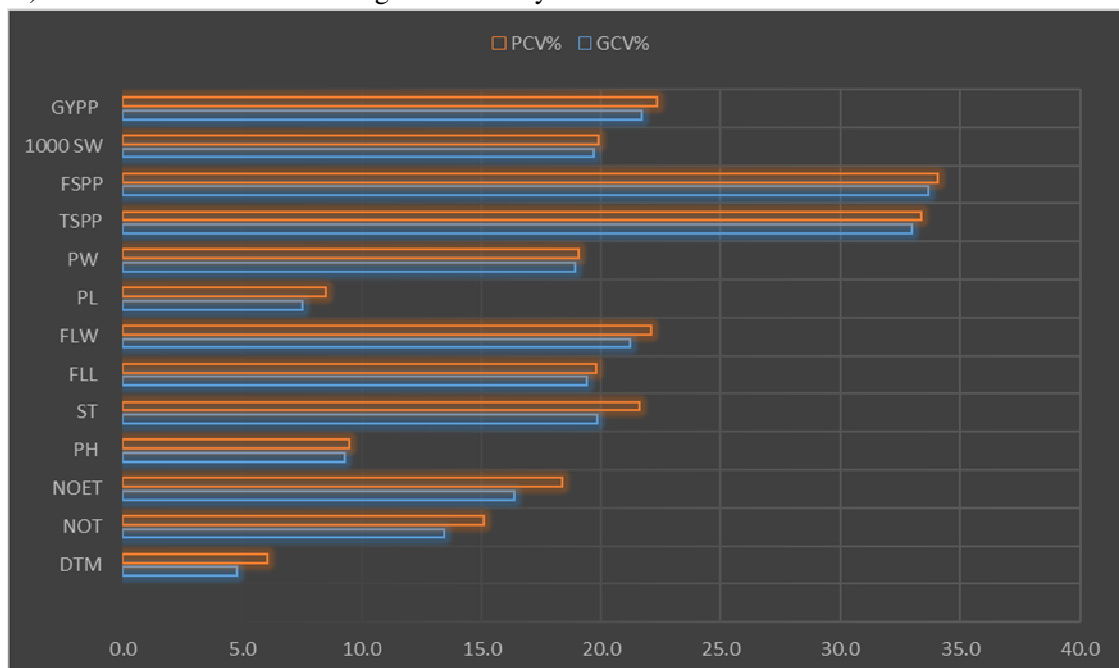


Fig. 1 : Clustered bar diagram comparing the values of Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation

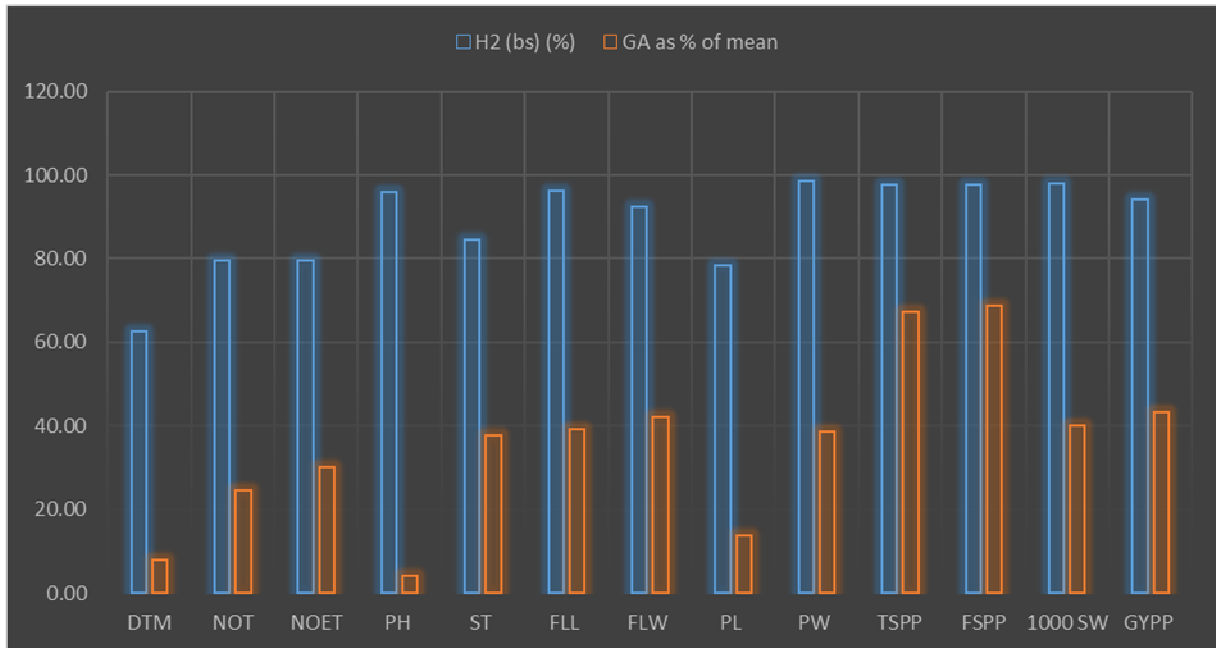


Fig. 2 : Column chart representing the magnitude of broad-sense heritability (h^2) and genetic advance as percentage of mean for various traits.

The correlations between thirteen yields and their related traits were calculated in the present study by considering grain yield per plant as the dependent variable (Table 3). Fig. 3 provides a visual representation of the correlations among the traits. Grain yield per plant revealed a significant and positive

association with panicle weight followed by fertile spikelets per panicle, total spikelets per panicle, number of tillers per plant, number of effective tillers per plant, flag leaf width and flag leaf length, which suggests that improving these traits could ultimately lead to increased yield.

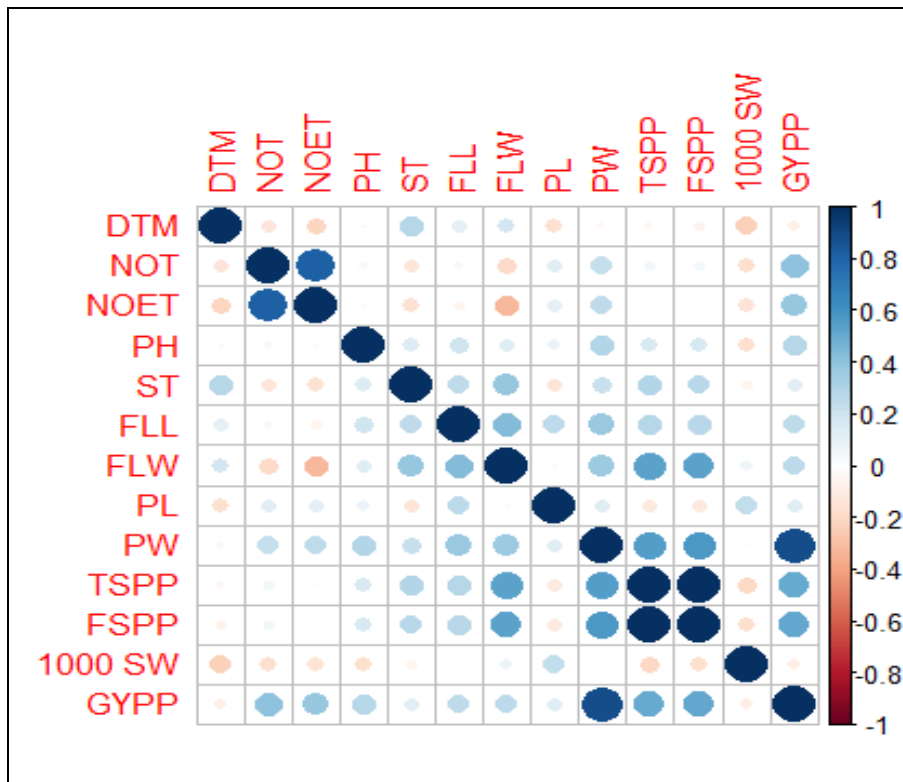


Fig. 3 : Depiction of phenotypic correlation coefficients between the traits

The findings were in consonance with Sharma *et al.* (2021) for panicle weight, Nath *et al.* (2021) for fertile spikelets per panicle and total spikelets per panicle, Ranawake *et al.* (2014) for number of tillers per plant; Bhargava *et al.* (2021) for number of effective tillers per plant, Aditya and Bhartiya (2013) for flag leaf length and flag leaf width.

Studies on the inter-relationships between yield component traits revealed a significant and positive correlation of Days to maturity with stem thickness (Rahangdale *et al.*, 2019) ; number of tillers per plant with number of effective tillers per plant and panicle weight (Ranawake *et al.*, 2014); plant height with panicle weight (Ranawake *et al.*, 2014); stem thickness with flag leaf length, panicle length, total spikelets per panicle, fertile spikelets per panicle (Panika *et al.*, 2022) and flag leaf width (Surjaye *et al.*, 2022); flag leaf length with flag leaf width, panicle length, panicle weight, total spikelets per panicle and fertile spikelets per panicle (Aditya and Bhartiya (2013); flag leaf width with panicle weight, total spikelets per panicle, fertile spikelets per panicle (Aditya and Bhartiya, 2013) and panicle weight (Surjaye *et al.*, 2022); panicle length with 1000SW (Daula *et al.*, 2020); panicle weight with total spikelets per panicle and fertile spikelets per panicle (Panika *et al.*, 2022); total spikelets per with fertile spikelets per panicle (Ranawake *et al.*, 2014).

Table 4 : Phenotypic correlation coefficient between the traits

	DTM	NOT	NOET	PH	ST	FLL	FLW	PL	PW	TSPP	FSPP	1000SW	GYPP
DTM	1.0000	-0.1281*	-0.2255**	0.0356	0.2438**	0.1044	0.1545*	-0.1661**	-0.0569	-0.0439	-0.0543	-0.2019**	-0.1033
NOT	-0.1281*	1.0000	0.7885**	-0.0027	-0.1213	0.0689	-0.1537*	0.0857	0.2255**	0.0405	0.0411	0.3490**	0.3740**
NOET	-0.2255**	0.7885**	1.0000	-0.0537	-0.1443*	-0.0358	-0.2717**	0.0888	0.2420**	-0.0226	-0.0113	0.1160	0.3598**
PH	0.0350	-0.0027	-0.0537	1.0000	0.0802	0.1389*	0.0973	0.0456	0.1805**	0.1024	0.1047	-0.1018	0.1644*
ST	0.2438**	-0.1213	-0.1443*	0.0802	1.0000	0.2480**	0.3437**	-0.1397*	0.2043**	0.2842**	0.2666**	-0.0477	0.1101
FLL	0.1044	0.0689	-0.0358	0.1389*	0.2480**	1.0000	0.4085**	0.2318**	0.3582**	0.2881**	0.2840**	-0.0039	0.2624**
FLW	0.1545*	-0.1537*	-0.2717**	0.0973	0.3437**	0.4085**	1.0000	0.0161	0.3490**	0.5237**	0.5203**	0.0613	0.272**
PL	-0.1661**	0.0857	0.0888	0.0456	-0.1397*	0.2318**	0.0161	1.0000	0.1236	-0.1123	-0.1121	0.2213**	0.1186
PW	-0.0569	0.2255**	0.2420**	0.1805**	0.2043**	0.3582**	0.3490**	0.1236	1.0000	0.5460**	0.5603**	-0.0228	0.8895**
TSPP	-0.0439	0.0405	-0.0226	0.1024	0.2842**	0.2881**	0.5237**	-0.1123	0.5460**	1.0000	0.9896**	-0.1917**	0.4975**
FSPP	-0.0543	0.0411	-0.0113	0.1047	0.2666**	0.2840**	0.5203**	-0.1121	0.5603**	0.9896**	1.0000	-0.1654*	0.5091**
1000 SW	-0.2019**	0.0973	0.1160	-0.1018	-0.0477	-0.0039	0.0613	0.2213**	-0.0228	-0.1917**	-0.1654*	1.0000	-0.0774
GYPP	-0.1033	0.3740**	0.3598**	0.1644*	0.1101	0.2624**	0.2720**	0.1186	0.8895**	0.4975**	0.5091**	-0.0774	1.0000

*Significant at probability level of 0.05 and **Significant at probability level 0.01

DTM-days to maturity, NOT-Number of tillers per plant, NOET-Number of effective tillers per plant, PH -Plant height, ST -Stem thickness, FLL -Flag leaf length, FLW - Flag leaf width, PL -Panicle length, PW-Panicle weight, TSPP-Total spikelets per panicle, FSPP-fertile spikelets per panicle, 1000 SW- Thousand seed weight, GYPP -Grain yield per plant.

Table 5 : Genotypic path coefficient analysis representing direct and indirect effects on single plant yield

	DTM	NOT	NOET	PH	ST	FLL	FLW	PL	PW	TSPP	FSPP	1000 SW	GYPP
DTM	-0.0681	0.0121	0.0172	-0.0056	-0.0226	-0.0094	-0.0139	0.0128	0.0033	0.0025	0.0034	0.0163	-0.1111
NOT	-0.0353	0.1998	0.1618	0.0291	-0.0295	0.0173	-0.0383	0.0311	0.0505	0.0087	0.0090	-0.0324	0.3926
NOET	0.0244	-0.0784	-0.0968	-0.0026	0.0167	0.0032	0.0327	-0.0135	-0.0260	0.0030	0.0018	0.0136	0.3757
PH	-0.0125	-0.0219	-0.0041	-0.1505	-0.0766	-0.0910	-0.0606	-0.0459	-0.1449	-0.0826	-0.0852	0.0787	0.9462
ST	0.0091	-0.0040	-0.0047	0.0139	0.0273	0.0073	0.0110	-0.0041	0.0060	0.0083	0.0078	-0.0017	0.1255
FLL	-0.0068	-0.0042	0.0016	-0.0295	-0.0131	-0.0489	-0.0210	-0.0131	-0.0183	-0.0147	-0.0145	-0.0001	0.2828
FLW	0.0050	-0.0047	-0.0083	0.0100	0.0100	0.0107	0.0247	0.0007	0.0092	0.0137	0.0136	0.0017	0.2952
PL	-0.0133	0.0110	0.0099	0.0215	-0.0107	0.0190	0.0020	0.0707	0.0106	-0.0086	-0.0085	0.0179	0.1529
PW	-0.0500	0.2570	0.2733	0.9794	0.2226	0.3800	0.3788	0.1532	1.0177	0.5524	0.5669	-0.0215	0.9068
TSPP	0.0084	-0.0101	0.0072	-0.1265	-0.0704	-0.0692	-0.1275	0.0281	-0.1251	-0.2305	-0.2283	0.0448	0.4977
FSPP	-0.0109	0.0097	-0.0041	0.1222	0.0618	0.0640	0.1188	-0.0260	0.1203	0.2138	0.2159	-0.0362	0.5092
1000 SW	0.0390	0.0264	0.0228	0.0850	0.0100	-0.0003	-0.0114	-0.0411	0.0034	0.0316	0.0272	-0.1626	-0.0814

*Significant at probability level of 0.05 and **Significant at probability level 0.01

DTM-days to maturity, NOT-Number of tillers per plant, NOET-Number of effective tillers per plant, PH-Plant height, ST-Stem thickness, FLL-Flag leaf length, FLW - Flag leaf width, PL-Panicle length, PW-Panicle weight, TSPP-Total spikelets per panicle, FSPP-fertile spikelets per panicle, 1000 SW- Thousand seed weight, GYPP-Grain yield per plant

While correlation evaluates the relationship between two variables, path coefficient analysis determines the cause of the relationship between them, considering all possible simple correlations and assuming linearity and additivity (Sarker, 2020). The diagonals of the table depict the direct effects, while

the rest of the values report the indirect effect of different traits on each other (Table 5). The selection of traits with a direct and significant effect on yield can be improved in collaboration to enhance rice productivity. The genotypic path diagram for grain yield is shown in Fig. 4.

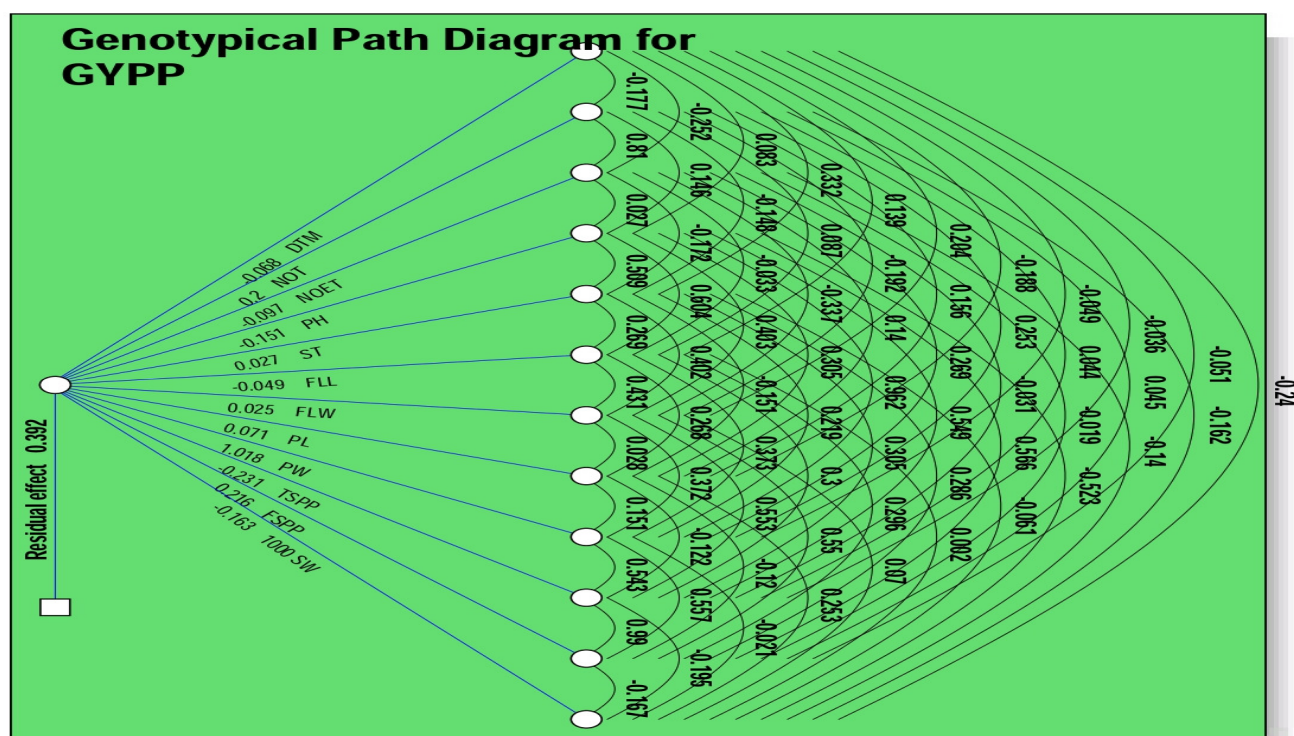


Fig. 4 : Genotypical path diagram

Trait panicle weight exerted maximum positive direct effect followed by fertile spikelets per panicle, number of tillers per plant, panicle length, stem thickness and flag leaf width. This strong correlation indicates that yield improvement is directly linked to these traits. The findings were in propinquity with Guru *et al.* (2016) for panicle weight, Kishore *et al.* (2015) for fertile spikelets per panicle, Seyoum *et al.* (2012) for the number of tillers per plant, Saha *et al.* (2019) for panicle length, Panika *et al.* 2022 for stem thickness, Aditya and Bhartiya (2013) for flag leaf width.

The residual effect at the phenotypic level was 0.392. The trait panicle weight showed the highest positive direct effect among all the yield-contributing traits. Hence, it can be regarded as a significant contributor to plant yield.

Conclusion

Traits like fertile spikelets per panicle, total spikelets per panicle, grain yield per plant, and flag leaf width have high estimates of PCV and GCV, along

with high genetic advance as a percentage of the mean and high heritability. Direct selection of these traits, driven by additive gene action, could effectively enhance genetic improvement. Correlation and path coefficient analysis identified panicle weight and number of fertile spikelets per panicle as the most critical yield-related traits due to their strong association and direct effects on grain yield. Therefore, selecting these traits is essential for isolating superior plant types to enhance grain yield. Moreover, this analysis can guide breeders in designing selection strategies aimed at improving grain yield in future.

Acknowledgement

The authors express their sincere thanks to the Indian Council of Agricultural Research (ICAR) for funding the Coordinated Research Project on Hybrid Technology in Rice, which significantly aided in carrying out this research. The authors also wish to acknowledge Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, for their invaluable support and the facilities provided.

References

- Abebe, T., Alamerew S. and Tulu L. (2017). Genetic variability, heritability, and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, *Ethiopia. Adv. Crop Sci. Tech.*, **1**(5), 1-8.
- Adhikari, B.N., Joshi B.P., Shrestha J. and Bhatta N.R. (2018). Genetic variability, heritability, genetic advance, and correlation among yield and yield components of rice (*Oryza sativa* L.). *J. Agric. Nat. Resour.*, **1**(1), 149-160.
- Aditya, J.P. and Bhartiya A. (2013). Genetic variability, correlation, and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills. *J. Rice Res.*, **6**(2), 24-34.
- Akinwale, M.G., Gregorio G., Nwilene F., Akinyele B.O., Ogunbayo S.A. and Odiyi A.C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr. J. Plant Sci.*, **5**(3), 207-212.
- Ali, A., Khan A.S. and Asad M.A. (2002). Drought tolerance in wheat: genetic variation and heritability for growth and ion relations. *Asian J. Plant Sci. Res.*, **1**, 420-422.
- Barde, M.A., Mohammed M.S., Oyekunle M., Usman I.S. and Shaahu A. (2021). Estimation of genetic variability, heritability, and genetic advance in rice (*Oryza sativa* L.) genotypes. *Int. J. Res. Innov. Appl. Sci.*, **4**(1), 40-47.
- Basavaraja, T.A., Mallikarjun M. and Gangaprasad S.K. (2013). Variability, heritability, and genetic advance for yield and yield attributing characters in different local rice (*Oryza sativa* L.) cultivars. *Asian J. Bio Sci.*, **8**(1), 60-62.
- Bhargava, K., Shivani D., Pushpavalli S.N.C.V.L., Sundaram R.M., Beulah P. and Senguttuvel P. (2021). Genetic variability, correlation, and path coefficient analysis in segregating population of rice. *Electron. J. Plant Breed.*, **12**(2), 549-555.
- Burton, G.W. (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Congr.*, **1**, 227-232.
- Demeke, B., Dejene T. and Abebe D. (2023). Genetic variability, heritability, and genetic advance of morphological, yield-related, and quality traits in upland rice (*Oryza sativa* L.) genotypes at Pawe, northwestern Ethiopia. *Cogent Food Agric.*, **9**(1), 2157099.
- Dewey, J.R. and Lu K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51**, 515-518.
- Dey, S., Kumar R., Battan K.R., Chhabra A.K. and Reddy A.L. (2021). Study of coefficient of variation, heritability, and genetic advance for different traits of rice genotypes grown under aerobic conditions. *Int. J. Bio-resour. Stress Manag.*, **12**(5), 426-430.
- Foreign Agricultural Services. (2024). US Department of Agriculture. Country Summary: India - Rice. Available from: <https://ipad.fas.usda.gov/countrysummary/Default.aspx?id=INandcrop=Rice>.
- Girma, B.T., Kital M.A., Banje D.G., Biru H.M. and Serbessa T.B. (2018). Genetic variability study of yield and yield-related traits in rice (*Oryza sativa* L.) genotypes. *Adv. Crop Sci. Tech.*, **6**(4), 381.
- Govintharaj, P., Manonmani S. and Robin S. (2018). Character association and path analysis in bacterial blight resistance genes pyramided segregating population of rice (*Oryza sativa* L.). *Genetika*, **50**(1), 11-20.
- Guru, T., Padma V., Reddy D.V.V., Rao P.R. and Rao D.S. (2016). Correlation and path coefficient analysis for grain yield and other component traits in rice genotypes. *Int. J. Agric. Sci. Res.*, **6**(5), 363-370.
- Hanson, C.H., Robinson H.F. and Comstock R.E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.*, **48**(6), 268-272.
- Ikeda, M., Miura K., Aya K., Kitano H. and Matsuoka M. (2013). Genes offering the potential for designing yield-related traits in rice. *Curr. Opin. Plant Biol.*, **16**, 213-220.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J.*, **47**, 477-482.
- Karim, D., Siddique M.N.A., Sarker U., Hasnat J. and Sultana J. (2014). Phenotypic and genotypic correlation coefficient of quantitative characters and character association of aromatic rice. *J. Biosci. Agric. Res.*, **1**, 34-46.
- Kavya, G., Senguttuvel P., Shivani D. and Barbadikar K.M. (2023). Estimation of variability, correlation coefficient, and path analysis in improved restorer lines of rice (*Oryza sativa* L.). *Int. J. Environ. Clim. Change*, **13**(11), 2853-2862.
- Keerthiraj, B. and Biju S. (2020). Genetic variability, heritability, and genetic advance of yield and lodging-related traits in rice (*Oryza sativa* L.). *Electron. J. Plant Breed.*, **11**(4), 1093-1098.
- Kishor, C., Prasad Y., Haider Z.A., Kumar R. and Kumar K. (2008). Quantitative analysis of upland rice. *Oryza*, **45**(4), 268-272.
- Kishore, N.S., Srinivas T., Nagabhushanam U., Pallavi M. and Sameera S.K. (2015). Genetic variability, correlation, and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. *SAARC J. Agric.*, **13**(1), 99-108.
- Konate, A.K., Zongo A., Kam H., Sanni A. and Audebert A. (2016). Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agromorphological traits. *Afr. J. Agric. Res.*, **11**(35), 3340-3346.
- Kulsum, U., Sarker U. and Rasul M.G. (2022). Genetic variability, heritability, and interrelationship in salt-tolerant lines of T. Aman rice. *Genetika*, **54**(2), 761-776.
- Miller, D.A., Williams J.C., Robinson H.F. and Comstock K.B. (1958). Estimates of genotypic and environmental variances and covariances in plant cotton and their implication in selection. *Agron. J.*, **50**, 126-131.
- Nakano, H., Takai T. and Kondo M. (2019). Identification of quantitative trait loci for panicle structure and grain filling using a cross between indica and japonica type high-yielding rice cultivars. *Plant Prod. Sci.*, **22**(4), 443-455.
- Nath, S. and Kole P.C. (2021). Genetic variability and yield analysis in rice. *Electron. J. Plant Breed.*, **12**(1), 253-258.
- Nithya, N., Beena R., Stephen R., Abida P.S., Jayalekshmi V.G., Viji M.M. and Manju R.V. (2020). Genetic variability, heritability, correlation coefficient, and path analysis of morphophysiological and yield-related traits of rice under drought stress. *Chem. Sci. Rev. Lett.*, **9**(33), 48-54.
- Panika, N., Singh Y., Singh S.K., Rahangdale S. and Shukla R.S. (2022). Genetic variability, correlation, and path coefficient study of indigenous rice (*Oryza sativa* L.)

- accessions for different yield and quality contributing traits. *Environ. Ecol.*, **40**(4), 2777-2786.
- Panse, V.G. and Sukhatme P.V. (1985). Statistical Methods for Agricultural Workers. Indian Council Agric. Res. Publ., 87-89.
- Pranathi, K., Viraktamath B.C., Neeraja C.N., Balachandran S.M., Hari Prasad A.S., Koteswara Rao P., Revathi P., Senguttuvel P., Hajira S.K., Balachiranjeevi C.H., Bhaskar Naik S., Abhilash V., Praveen M., Parimala K., Kulkarni S.R., Anila M., Rekha G., Koushik M.B.V.N., Kemparaju B., Madhav M.S., Mangrauthia S.K., Harika G., Dilip T., Kale R.R., Vishnu Prasanth V., Ravindra Babu V. and Sundaram R.M. (2016). Development and validation of candidate gene-specific markers for the major fertility restorer genes, Rf4 and Rf3 in rice. *Mol. Breed.*, **36**(145), 1-14.
- Rahangdale, S., Singh Y., Koutu G.K. and Tiwari S. (2019). Genetic variability, correlation, and path coefficient studied for yield and quality traits in JNPT lines of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. Appl. Sci.*, **8**(10), 1025-1037.
- Ranawake, A.L. and Amarasinghe U.G.S. (2014). Relationship of yield and yield-related traits of some traditional rice cultivars in Sri Lanka as described by correlation analysis. *J. Sci. Res. Rep.*, **3**(18), 2395-2403.
- Rashid, M., Nuruzzaman M., Hassan L. and Begum S. (2017). Genetic variability analysis for various yield attributing traits in rice genotypes. *J. Bangladesh Agric. Univ.*, **15**(1), 15-19.
- Robinson, F.A., Comstock R.E. and Harvey P.H. (1949). Estimation of heritability and degree of dominance in corn. *Agron. J.*, **41**, 353-359.
- Rout, D., Jena D., Singh V., Kumar M., Arsode P., Singh P., Katara J.L., Samantaray S. and Verma R.L. (2020). Hybrid rice research: Current status and prospects. *Intech. Open*, 23-45.
- Saha, S., Hassan L., Haque M., Islam M. and Rasel M. (2019). Genetic variability, heritability, correlation, and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *J. Bangladesh Agric. Univ.*, **17**(1), 26-32.
- Saleh, M.M., Salem K.F. and Elabd A.B. (2020). Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. *Bull. Natl. Res. Cent.*, **44**, 1-6.
- Sarker, U. (2020). Variability, heritability, character association, and path coefficient analysis in advanced breeding lines of rice (*Oryza sativa* L.). *Genetika*, **52**(2), 711-726.
- Seyoum, M., Alamerew S. and Bantte K. (2012). Genetic variability, heritability, correlation coefficient, and path analysis for yield and yield-related traits in upland rice (*Oryza sativa* L.). *J. Plant Sci.*, **7**(1), 13-22.
- Sharma, M., Singh A.K., Salgotra R.K., Sharma B.K., Gangurde S.S., Bakshi P., Raina M. and Kumar B. (2021). Assessment of genetic advance and correlation coefficient for yield and yield attributed traits of RIL population in basmati rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **10**(1), 328-330.
- Singh, R.K. and Chaudhary B.D. (1977). Biometrical methods in quantitative genetics analysis. *Kalyani Publ.*
- Sivasubramanian, S. and Madhavamenon P. (1973). Genetic analysis of quantitative characters in rice through diallel crosses. *Madras Agric. J.*, **60**, 1097-1098.
- Surjaye, N., Singh Y., Singh S.K., Rahangdale S. and Mehta A.K. (2022). Genetic variability, correlation, and path coefficient study for various yield and quality traits in NPT lines of rice (*Oryza sativa* L.). *Environ. Ecol.*, **40**(1), 115-122.
- Wright, S. (1921). Correlation and causation. *J. Agric. Res.*, **20**, 557-585.
- Yadev, S. and Kumar V. (2018). Feeding the world while caring for the planet. *Direct Seeded Rice Consort.*, **1**(2), 1-18.
- Zhou, Y., Tao Y., Yuan Y., Zhang Y., Miao J., Zhang R., Yi C., Gong Z., Yang Z. and Liang G. (2018). Characterization of a novel quantitative trait locus, GN4-1, for grain number and yield in rice (*Oryza sativa* L.). *Theor. Appl. Genet.*, **131**(3), 637-648.