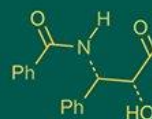


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(4): 878-883
www.biochemjournal.com
Received: 13-01-2026
Accepted: 16-02-2026

Rajkamal Gour
Ph.D. Scholar, Department of
Genetics and Plant Breeding,
CoA, IGKV, Raipur,
Chhattisgarh, India

Suyash Prasad
Ph.D. Scholar, Department of
Genetics and Plant Breeding,
CoA, IGKV, Raipur,
Chhattisgarh, India

Apurva Verma
Ph.D. Scholar, Department of
Genetics and Plant Breeding,
CoA, IGKV, Raipur,
Chhattisgarh, India

Prakash
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
RMD CARS, IGKV,
Chhattisgarh, India

Vivek Kumar Sandilya
SMS (Subject Matter
Specialist), KVK, IGKV,
Chhattisgarh, India

Jyoti Sahu
Guest Scientist, CARS
Raigarh, Department of
Genetics and Plant Breeding,
IGKV, Raigarh, Chhattisgarh,
India

Sunil Kumar Nair
Principal Scientist,
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Corresponding Author:
Rajkamal Gour
Ph.D. Scholar, Department of
Genetics and Plant Breeding,
CoA, IGKV, Raipur,
Chhattisgarh, India

Elucidating trait associations and key determinants of grain yield through correlation and path coefficient analysis in rice (*Oryza sativa* L.)

Rajkamal Gour, Suyash Prasad, Apurva Verma, Prakash, Vivek Kumar Sandilya, Jyoti Sahu and Sunil Kumar Nair

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i4Sk.8233>

Abstract

The present investigation was undertaken to assess the association among grain yield and its contributing characters and to determine the direct and indirect effects of component traits on yield. The experiment was conducted during kharif-2023 at the Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.). The experimental material comprised 36 rice genotypes along with four checks namely IR 64, MTU-1010, IGKV-R1 and IGKV-R2. The genotypes were evaluated in a randomized block design with two replications for eleven quantitative traits. Correlation analysis revealed that grain yield per plot exhibited strong positive and significant association with biological yield, harvest index, test weight and number of filled grains per panicle. Positive but non-significant association was also observed with plant height, panicle length and effective tillers. Path coefficient analysis indicated that biological yield and harvest index exerted the highest positive direct effects on grain yield at both genotypic and phenotypic levels, followed by test weight and number of filled grains per panicle, indicating their major contribution toward yield improvement. Traits such as days to maturity and unfilled grains showed negative direct effects, suggesting limited usefulness as direct selection criteria. Based on overall performance, the genotypes IGKV R2, IGKV R1 and R2761-39-1 were identified as promising entries for higher yield and desirable component traits, indicating their potential utilization in future rice breeding programmes.

Keywords: Rice, correlation analysis, path coefficient analysis, grain yield and yield attributing traits

Introduction

Rice (*Oryza sativa* L.) is a cornerstone of India's agriculture and food security, serving as the staple diet for nearly two-thirds of the population and contributing a large share of daily caloric intake (FAO, 2023) [5]. India is one of the world's largest rice producers, with the crop occupying a substantial portion of the gross cropped area and total food grain output (Ministry of Agriculture & Farmers Welfare, 2023) [7]. Beyond its nutritional role, rice cultivation supports rural livelihoods, generates employment, and contributes significantly to agricultural income and GDP, especially in the eastern and central rice belts (FAO, 2023; ICAR, 2025) [5, 6].

Given the pressures of population growth, climatic variability and diminishing natural resources, plant breeding has become critical for enhancing rice productivity, resilience and nutritional quality. Recent advances in breeding, including the development of high-yielding, climate-resilient and biofortified varieties, reflect a paradigm shift in rice improvement strategies. Novel varieties such as genome-edited lines with increased yield potential and stress tolerance demonstrate the potential of modern breeding approaches (EconomicTimes, 2025) [4].

In the regional context of Chhattisgarh, rice plays an outsized role in both agricultural production and socio-economic development. The state contributes significantly to India's *kharif* rice output with multi-million tonne production and record paddy procurement reflecting its importance in the national food procurement system (BigMint Bureau, 2025; Oneindia Staff, 2026) [1, 8]. Consequently, improving rice through both conventional and modern breeding techniques remains central to sustainable agricultural intensification in India and in key rice-producing states like Chhattisgarh.

Continued integration of advanced genetic tools with region-specific breeding objectives will be crucial for addressing future challenges related to food security, climate resilience and farmer welfare.

Path coefficient analysis serves as an effective approach to separate genetic influences from environmental effects in trait relationships by breaking down correlations into direct and indirect contributions, thereby offering a clearer picture of how different characters influence yield. Such information is essential for identifying key traits that can be targeted in the selection of high-yielding genotypes (Babu *et al.*, 2012) ^[9]. In crop improvement, particularly for complex quantitative traits like grain yield, selection based only on yield performance is often not sufficient; a deeper understanding of genetic parameters and the interactions among yield-related traits is necessary to support efficient breeding strategies (Nikhil *et al.*, 2014) ^[10]. Correlation and path coefficient analyses together help in assessing the strength and nature of associations among traits, while also clarifying their individual contributions through direct and indirect effects. This combined approach enhances the precision of selection and aids breeders in formulating effective strategies for yield improvement in rice (Yadav *et al.*, 2018) ^[11].

Materials and Methods

The present investigation was conducted at the Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.), Raipur, Chhattisgarh. The investigation was established in a randomized block design involving two replications during *kharif*-2023. The study adopted 36 rice lines as well as four IR 64, MTU-1010, IGKV-R1 and IGKV-R2 strains are used as checks.

Observations Plant height, Panicle length, Number of effective tillers per plant, Number of filled grains per panicle, Number of unfilled grains per panicle, Harvest index and 100 seed weight were recorded on randomly selected five plants of each pot, apart from the days to 50% flowering, Days to maturity, biological and grain yield observations, which were obtained on a plot basis at the ideal stage of plant growth from each line in both replications. Thus, morphological and agronomical data were collected for 11 quantitative characters at appropriate growth stage of rice plant.

Correlation coefficients were calculated using the approach of Falconer and Mackay (1964). Genotypic and phenotypic correlation coefficients for all the possible comparisons were computed as per the formulae suggested by Miller *et al.*, (1958) ^[3]. while path coefficient analysis followed the method of Dewey and Lu (1959) ^[2]. Path coefficient analysis is a powerful tool for quantifying the degree of interaction one variable has on the other. It is just a standardized partial regression coefficient that separates the correlation coefficient into direct and indirect impact measurements. The partitioning of genotypic correlation coefficient of traits into direct and indirect effects was carried out using the procedure suggested by Dewey and Lu (1959) ^[2]. Yield per plot was treated as the dependent variable and the remaining eleven traits as independent variables, with simultaneous equations used to estimate their direct and indirect contributions to yield.

Table 1: List of experimental material.

S. No.	Genotype	S. No.	Genotype
1	R 2483-RP5525-B-DRR-SPS-285-1	21	R 2404-151-1-72-1
2	R 2404-362-1-178-1	22	R 2754-11-1
3	R 2773-C8-2-4	23	R 2755-50-1
4	R 2462-RP5530-DRR-SPS-47-1	24	R 2748-4-1
5	R 2418-489-1-304-1	25	R 2742-117-1
6	R 2299-146-1-120-1	26	R 2743-93-1
7	R 2420-1418-1-743-1	27	R 2740-62-1
8	R 2442-C1-11-445-1	28	R 2754-51-1
9	R 2551-C10-6-510-1	29	R 2761-39-1
10	R 2697-41-1	30	R 2754-12-1
11	R 2699-4-1	31	R 2733-50-1
12	R 2405-169-1-93-1	32	R 2741-21-1
13	R 2404-151-2-73-1	33	R 2756-2-1
14	R 2404-158-2-82-1	34	R 2749-35-1
15	R 2404-166-1-90-1	35	R 2737-38-1
16	R 2555-C16-5-551-1	36	R 2740-98-1
17	R 2405-173-1-96-1	37	IR 64 (Check)
18	R 2404-1531-76-1	38	MTU1010 (Check)
19	R 2547-C6-1-477-1	39	IGKV R1 (Check)
20	R 2698-101-1	40	IGKV R2 (Check)

Results and Discussion

Correlation Analysis

Days to 50% flowering (DFF) exhibited a positive and significant association with days to maturity (0.932**) and test weight (0.255*). Positive but non-significant relationships were also observed with UFG, HI, ET and GYP. Negative but non-significant correlations were noticed with PL, PH, BY and FG. These findings indicate that late flowering genotypes generally required longer duration and tended to produce bolder grains. Similar positive association of flowering time with maturity duration was reported in rice by Saleh *et al.* (2020) ^[14], Saketh *et al.* (2023) ^[15] and Saran *et al.* (2023) ^[16].

Days to maturity showed significant positive correlation with DFF (0.932**) and TW (0.283*), while other positive associations were non-significant. Negative but non-significant relationships were observed with BY, PH, PL and FG. This suggests that late maturing genotypes may possess comparatively heavier grains and extended grain filling period. Similar results were reported by Akter *et al.* (2020) ^[12] and Islam *et al.* (2025) ^[13].

Plant height expressed significant positive correlation with panicle length (0.566**), biological yield (0.248*) and test weight (0.227*). Positive but non-significant association with grain yield was also observed. These findings indicate that taller plants tend to accumulate more biomass and support longer panicles. Comparable observations were reported by Saketh *et al.* (2023) ^[15], Saleh *et al.* (2020) ^[14] and Saran *et al.* (2023) ^[16].

Panicle length had significant positive association with plant height (0.566**) and unfilled grains (0.249*), while positive but non-significant relationships were observed with FG, HI, TW and GYP. Longer panicles generally provide greater spikelet-bearing surface and may improve sink size. Positive association of panicle length with yield traits has been widely reported by Tiwari *et al.* (2025) ^[18], Saleh *et al.* (2020) ^[14] and Saketh *et al.* (2023) ^[15].

Table 2: Correlation among yield and studied yield components in rice genotypes.

Variable	DFF	DM	PH	PL	ET	FG	UFG	GYP	BY	HI	TW
DFF	1.0 **	0.932 **	-0.09	-0.106	0.067	-0.036	0.175	0.027	-0.065	0.12	0.255 *
DM	0.932 **	1.0 **	-0.065	-0.047	0.036	-0.045	0.18	0.003	-0.096	0.131	0.283 *
PH	-0.09	-0.065	1.0 **	0.566 **	-0.202	0.184	-0.055	0.182	0.248 *	-0.105	0.227 *
PL	-0.106	-0.047	0.566 **	1.0 **	-0.098	0.165	0.249 *	0.042	-0.075	0.133	0.062
ET	0.067	0.036	-0.202	-0.098	1.0 **	0.004	0.084	0.132	0.033	0.134	-0.166
FG	-0.036	-0.045	0.184	0.165	0.004	1.0 **	-0.039	0.23 *	0.241 *	-0.034	-0.273 *
UFG	0.175	0.18	-0.055	0.249 *	0.084	-0.039	1.0 **	0.053	-0.099	0.196	-0.066
GYP	0.027	0.003	0.182	0.042	0.132	0.23 *	0.053	1.0 **	0.694 **	0.316 **	0.295 **
BY	-0.065	-0.096	0.248 *	-0.075	0.033	0.241 *	-0.099	0.694 **	1.0 **	-0.458 **	0.251 *
HI	0.12	0.131	-0.105	0.133	0.134	-0.034	0.196	0.316 **	-0.458 **	1.0 **	0.003
TW	0.255 *	0.283 *	0.227 *	0.062	-0.166	-0.273 *	-0.066	0.295 **	0.251 *	0.003	1.0 **

** Significant at 1%, * Significant at 5%.

DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers; FG = Number of filled grains per panicle; UFG = Number of unfilled grains per panicle BY = Biological yield/plot (kg); HI = harvest index; TW = Test weight (g); GYP = Grain yield per plot (kg).

Ear-bearing tillers showed positive but non-significant correlation with HI, GYP, UFG, DFF, DM, BY and FG. Although associations were weak, productive tillers are biologically important contributors to final yield. Positive relationship of productive tillers with grain yield was earlier reported by Saran *et al.* (2023)^[16], Salunkhe *et al.* (2025)^[17] and Tiwari *et al.* (2025)^[18].

Filled grains exhibited significant positive correlation with BY (0.241*) and GYP (0.230*), whereas a significant negative association was observed with TW (-0.273*). These results suggest that increased grain filling contributes directly to grain yield, though competition among grains may reduce grain weight. Similar findings were reported by Saleh *et al.* (2020)^[14], Saran *et al.* (2023)^[16] and Akter *et al.* (2020)^[12].

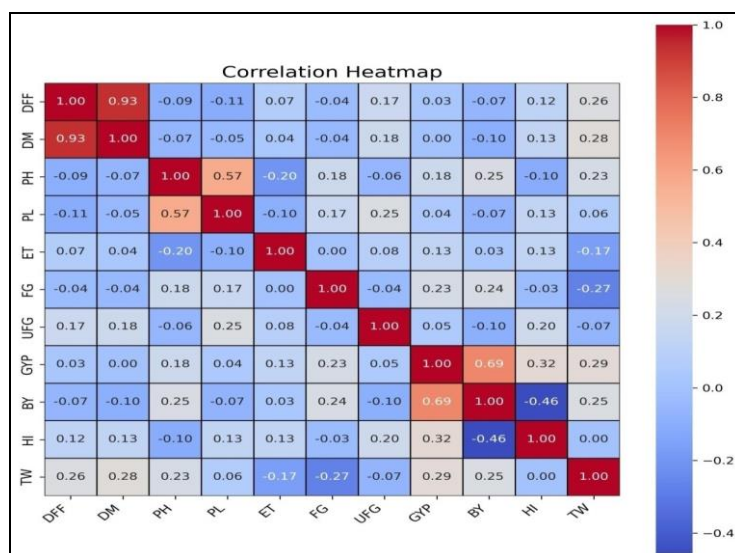
Unfilled grains showed significant positive correlation with PL (0.249*) and positive but non-significant association with several other traits. Negative correlations with BY, TW, PH and FG were non-significant. This indicates that unfilled grains had limited usefulness as a selection criterion for yield improvement. Similar observations regarding undesirable effect of sterile or unfilled grains were reported by Saleh *et al.* (2020)^[14] and Islam *et al.* (2025)^[13].

Grain yield per plant exhibited strong positive and significant correlation with BY (0.694**), HI (0.316**), TW (0.295**) and FG (0.230*). These findings indicate that biomass production, efficient assimilate partitioning, bold

grains and grain filling are major determinants of grain yield. Similar results were reported by Saleh *et al.* (2020), Saran *et al.* (2023)^[16], Saketh *et al.* (2023)^[15] and Tiwari *et al.* (2025)^[18].

Biological yield showed significant positive association with GYP (0.694**), TW (0.251*), PH (0.248*) and FG (0.241*), whereas a significant negative association was observed with HI (-0.458**). This suggests that greater dry matter production enhances grain yield, although excessive vegetative growth may reduce partitioning efficiency. Similar findings were reported by Saran *et al.* (2023)^[16], Saleh *et al.* (2020)^[14] and Akter *et al.* (2020)^[12].

Harvest index exhibited significant positive correlation with GYP (0.316**) and significant negative association with BY (-0.458**). This indicates that genotypes with better translocation efficiency from biomass to grains tend to realize higher productivity. Similar positive association of harvest index with grain yield was reported by Saran *et al.* (2023)^[16], Tiwari *et al.* (2025)^[18] and Islam *et al.* (2025)^[13]. Test weight recorded significant positive correlation with GYP (0.295**), DM (0.283*), DFF (0.255*), BY (0.251*) and PH (0.227*), while it showed significant negative correlation with FG (-0.273*). These findings suggest that bold grains positively contribute to yield and are often associated with longer crop duration. Similar results were documented by Saleh *et al.* (2020)^[14], Saran *et al.* (2023)^[16] and Salunkhe *et al.* (2025)^[17].

**Fig 1:** Correlation matrix for yield and yield component traits

Path Analysis

The genotypic and phenotypic path coefficient analyses enabled partitioning of correlation coefficients into direct and indirect effects, thereby clarifying the relative importance of different traits in determining grain yield per plant. In general, genotypic effects were of higher magnitude than phenotypic ones, indicating the influence of environmental factors on trait expression.

Days to 50% flowering exhibited a positive association with grain yield at both genotypic ($r = 0.3058$) and phenotypic ($r = 0.0243$) levels, with positive direct effects of 0.54226 and 0.01599, respectively. The higher genotypic direct effect indicates its inherent genetic contribution, while positive

indirect effects via harvest index, test weight, and plant height further strengthened its role. However, negative indirect effects through biological yield, unfilled grains, and days to maturity suggest the need for cautious selection.

Days to maturity also showed a positive correlation with yield at genotypic ($r = 0.3667$) and phenotypic ($r = 0.0088$) levels, despite exhibiting negative direct effects (-0.5655 and -0.02676, respectively). This clearly indicates that its apparent association with yield is largely indirect, mainly mediated through traits such as harvest index and test weight, thereby limiting its effectiveness as a direct selection criterion.

Table 3: Genotypic direct and indirect effects of 10 studied traits on grain yield in rice genotypes

Trait	DFF	DM	PH	PL	ET	FG	UFG	BY	HI	TW	GYP
DFF	0.542258	-0.56249	0.000635	-0.00445	-0.0004	4.82E-06	-0.001	-0.07138	0.36823	0.034355	0.3058 NS
DM	0.539368	-0.5655	0.000523	-0.00114	0.000204	-0.00064	-0.00112	-0.15421	0.513241	0.035979	0.3667 *
PH	-0.04165	0.035807	-0.00826	0.025114	-0.00619	0.002418	0.000135	0.582742	-0.21147	0.020909	0.3996 *
PL	-0.05733	0.015308	-0.00493	0.042065	-0.0029	0.002416	-0.00147	-0.21624	0.200376	0.003933	-0.0188 NS
ET	-0.00845	-0.0045	0.001992	-0.00475	0.02565	0.000141	-0.00034	0.036191	0.192939	-0.01828	0.2206 NS
FG	0.000255	0.035327	-0.00195	0.009917	0.000352	0.010249	-0.00019	0.232662	0.07032	-0.04402	0.3129 *
UFG	0.125983	-0.14678	0.000259	0.01439	0.001997	0.000461	-0.00431	-0.1561	0.386735	-0.00642	0.2162 NS
BY	-0.02779	0.062601	-0.00346	-0.00653	0.000666	0.001712	0.000483	1.39302	-0.81764	0.026818	0.6299 **
HI	0.172644	-0.25095	0.001511	0.007288	0.004279	0.000623	-0.00144	-0.9848	1.156573	-0.00172	0.104 NS
TW	0.222065	-0.24253	-0.00206	0.001972	-0.00559	-0.00538	0.00033	0.445321	-0.02378	0.08389	0.4742 **
Residual effect : 0.02											
*Direct effects on main diagonal, DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers; FG = Number of filled grains per panicle; UFG = Number of unfilled grains per panicle BY = Biological yield/plot (kg); HI = harvest index; TW = Test weight (g); GYP = Grain yield per plot (kg).											

Plant height recorded positive correlations with yield at genotypic ($r = 0.3996$) and phenotypic ($r = 0.195$) levels, but its direct effects were negligible and negative (-0.00826 and -0.0205, respectively). This suggests that plant height contributes to yield indirectly, primarily through biological yield, panicle length, and filled grains, rather than through a direct influence.

Panicle length showed a weak association with yield at genotypic ($r = -0.0188$) and phenotypic ($r = 0.0866$) levels, although it exerted positive direct effects (0.04206 and 0.01749, respectively). Its contribution appears to be conditional, with positive indirect effects via harvest index and filled grains, but offset by negative influences through biological yield and unfilled grains.

Effective tillers exhibited positive correlations with yield at genotypic ($r = 0.2206$) and phenotypic ($r = 0.1245$) levels. The direct effect was positive at the genotypic level (0.02565) but negative at the phenotypic level (-0.00473), reflecting environmental sensitivity. Nevertheless, its indirect contributions via biological yield and harvest index underline its supportive role in yield determination.

Filled grains showed consistent positive associations with yield at genotypic ($r = 0.3129$) and phenotypic ($r = 0.2188$) levels, along with positive direct effects (0.01025 and 0.01516, respectively). This stability across both levels indicates that filled grains is a reliable component trait, contributing both directly and indirectly through biological yield and other associated traits.

Unfilled grains exhibited weak positive correlations with yield at genotypic ($r = 0.2162$) and phenotypic ($r = 0.0555$) levels, but its direct effects were negative (-0.00431 and -0.00017, respectively), confirming its detrimental influence. The positive correlation appears to be an outcome of

indirect effects rather than a true causal relationship.

Biological yield emerged as the most influential trait, showing strong positive correlations with grain yield at genotypic ($r = 0.6299$) and phenotypic ($r = 0.69$) levels, along with the highest direct effects (1.39302 and 1.06951, respectively). Its substantial contribution, both directly and indirectly through traits such as test weight and filled grains, highlights its central role in yield improvement.

Harvest index also exhibited a positive association with yield at genotypic ($r = 0.104$) and phenotypic ($r = 0.301$) levels, with high direct effects of 1.15657 and 0.81104, respectively. This indicates its efficiency in partitioning assimilates toward economic yield, making it a key selection criterion despite some negative indirect effects via biological yield and test weight.

Test weight showed a positive and significant association with grain yield at genotypic ($r = 0.4742$) and phenotypic ($r = 0.2952$) levels, supported by positive direct effects (0.08389 and 0.04002, respectively). Its contribution was further enhanced by favorable indirect effects through biological yield and days to 50% flowering, confirming its importance in yield improvement.

Overall, the findings clearly indicate that biological yield and harvest index exert the strongest direct influence on grain yield at both genotypic and phenotypic levels, followed by supportive contributions from filled grains and test weight. In contrast, traits such as days to maturity and unfilled grains showed negative direct effects, suggesting that their apparent associations with yield are largely indirect. Therefore, emphasis should be placed on traits with strong direct effects in selection programmes, as also advocated by Dewey and Lu (1959) [2].

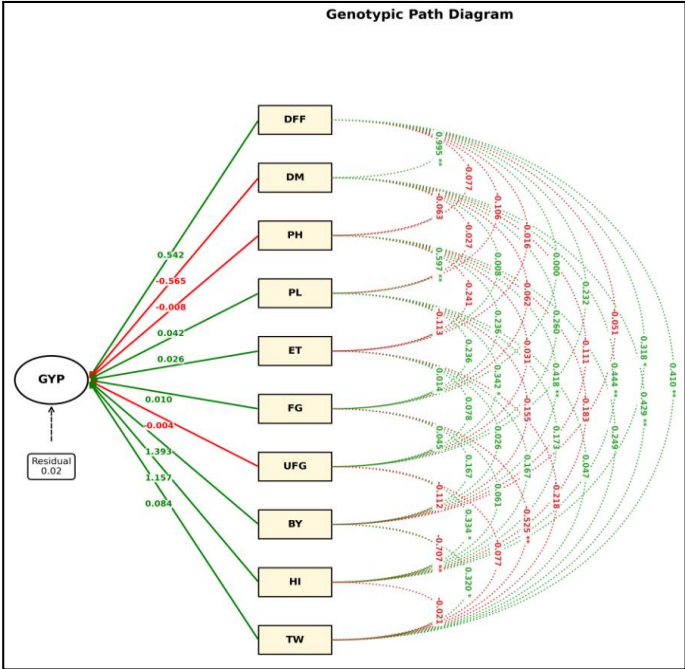


Fig 2: Genotypic path diagram for yield and its contributing traits

Table 4: Phenotypic direct and indirect effects of 10 studied traits on grain yield in rice genotypes

Trait	DFF	DM	PH	PL	ET	FG	UFG	BY	HI	TW	GYP
DFF	0.015992	-0.02495	0.001823	-0.00182	-0.00031	-0.00057	-2.90E-05	-0.07262	0.096594	0.010206	0.0243 NS
DM	0.014915	-0.02676	0.00137	-0.00094	-0.00018	-0.00064	-2.99E-05	-0.10011	0.109814	0.011358	0.0088 NS
PH	-0.00142	0.001787	-0.0205	0.009957	0.000948	0.002858	9.22E-06	0.273474	-0.08127	0.009157	0.195 NS
PL	-0.00167	0.001445	-0.01167	0.017489	0.000425	0.002834	-4.19E-05	-0.05583	0.13082	0.002798	0.0866 NS
ET	0.001059	-0.001	0.004109	-0.00157	-0.00473	0	-1.40E-05	0.028556	0.104786	-0.00669	0.1245 NS
FG	-0.0006	0.001137	-0.00386	0.003269	0	0.015163	6.42E-06	0.250372	-0.0356	-0.01107	0.2188 NS
UFG	0.002797	-0.00482	0.00114	0.004421	-0.0004	-0.00059	-0.00017	-0.10556	0.161315	-0.00265	0.0555 NS
BY	-0.00109	0.002504	-0.00524	-0.00091	-0.00013	0.00355	1.64E-05	1.06951	-0.38816	0.009949	0.69 **
HI	0.001905	-0.00362	0.002054	0.002821	-0.00061	-0.00067	-3.30E-05	-0.51187	0.811036	-1.60E-05	0.301 **
TW	0.004078	-0.00759	-0.00469	0.001222	0.000791	-0.0042	1.10E-05	0.26588	-0.00032	0.040022	0.2952 **

Residual Effect: 0.57

*Direct effects on main diagonal, DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers; FG = Number of filled grains per panicle; UFG = Number of unfilled grains per panicle BY = Biological yield/plot (kg); HI = harvest index; TW = Test weight (g); GYP = Grain yield per plot (kg).

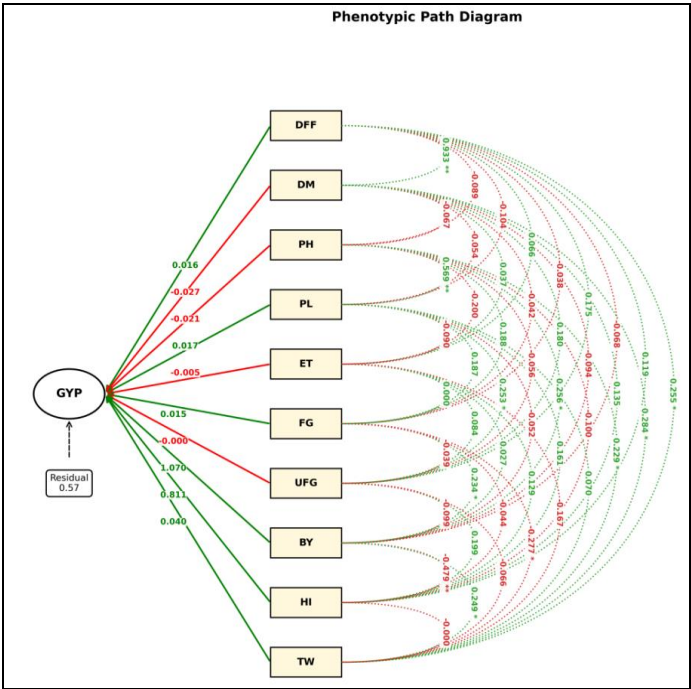


Fig 3: Phenotypic path diagram for yield and its contributing traits.

Residual Effect

The residual effect was 0.02 (genotypic) and 0.571 (phenotypic), indicating that 99.98% and 99.429% of variation in grain yield was explained by the studied traits. This shows high reliability of the variables, though inclusion of additional traits may further account for remaining variation.

Conclusion

Path analysis indicated that ear-bearing tillers per m², grains per panicle, days to 50% flowering, panicle length, and test weight exerted positive direct effects on grain yield per plant. These traits can therefore be considered as key selection criteria for yield improvement. Biological yield and harvest index also showed strong direct contributions. In contrast, days to maturity and plant height exhibited negative direct effects and should be selected cautiously. The low residual values confirmed that most of the yield variation was explained by the studied traits.

References

1. BigMint Bureau. Chhattisgarh: India's rice bowl, blending volume with varietal depth [Internet]. BigMint; 2025.
2. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron J*. 1959;51(9):515-518.
3. Miller PA, Williams JC, Robinson HF, Comstock RE. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agron J*. 1958;50(3):126-131.
4. The Economic Times. India's first genome-edited rice varieties will boost rice yields by 20-30% and reduce water consumption [Internet]. 2025.
5. Food and Agriculture Organization (FAO). FAOSTAT statistical database [Internet]. FAO; 2023.
6. Indian Council of Agricultural Research (ICAR). Genome-edited rice varieties boost yields and resilience [press release]. 2025.
7. Ministry of Agriculture & Farmers Welfare. Agricultural statistics at a glance 2022. Government of India; 2023.
8. Oneindia Staff. Chhattisgarh records record rice procurement in 2025-26 [Internet]. Oneindia; 2026.
9. Babu VR, Shreya K, Dangi KS, Usharani G, Shankar AS. Correlation and path analysis studies in popular rice hybrids of India. *Int J Sci Res Publ*. 2012;2(3):1-5.
10. Nikhil B, Rangare N, Saidaiah P. Correlation and path analysis in rice (*Oryza sativa* L.). *Int J Trop Agric*. 2014;32:1-5.
11. Singh R, Yadav V, Mishra DN, Yadav A. Correlation and path analysis studies in rice (*Oryza sativa* L.). *J Pharmacogn Phytochem*. 2018;1:2084-2090.
12. Akter A, Hasan MJ, Latif MA, Kulsum MU, Biswas PL, Rahman MH, *et al*. Genetic variability, heritability, correlation and path coefficient studies for yield and yield components of some promising rice hybrids. *Bangladesh Rice J*. 2020;23(2):27-39.
13. Islam MZ, Chakrabarty T, Akter N, Khalequzzaman M, Ali MP. Genetic variability, correlation and path coefficient analysis of phenotypic traits and genetic diversity of Aman rice landraces (*Oryza sativa* L.). *Sci Rep*. 2025;15:18606-18606.
14. Saleh MM, Salem KFM, Elabd AB. Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. *Bull Natl Res Cent*. 2020;44:143-143.
15. Saketh T, Gouri Shankar V, Srinivas B, Hari Y. Correlation and path coefficient studies for grain yield and yield components in rice (*Oryza sativa* L.). *Int J Plant Soil Sci*. 2023;35(19):1549-1558.
16. Saran D, Gauraha D, Sao A, Sandilya VK, Kumar R. Correlation and path coefficient analysis for yield and yield attributing traits in rice (*Oryza sativa* L.). *Int J Plant Soil Sci*. 2023;35(18):94-101.
17. Salunkhe H, Kumar A, Janeja H, Krishna B, Talekar N, Mehandi S, *et al*. Genetic variability, correlation and path-coefficient analysis for yield and yield attributing traits in aerobic rice (*Oryza sativa* L.). *Electron J Plant Breed*. 2025;15(1):1.
18. Tiwari S. Quantitative trait analysis and path coefficient modeling for yield optimization in rice (*Oryza sativa* L.) restorer lines. *Int J Agric Ext Educ*. 2025.