



Correlation and Path Coefficient Analysis of Yield Attributing Traits on Grain Yield in Rice (*Oryza sativa* L.) Genotypes

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Abstract

The present investigation was conducted to study the associations and path coefficients analysis of yield attributing traits for grain yield in nine rice genotypes. The study was carried out at five locations for two consecutive Kharif seasons in the years 2022 and 2023. The pooled data were subjected to association analysis and path coefficient analysis for morphological traits. Correlation analysis revealed that panicle length, number of filled spikelets per panicle, spikelet fertility percent, grain yield per ha, harvest index, and test weight showed highly significant positive associations with grain yield per plant at the phenotypic level. Among them, only panicle length and harvest index showed highly significant positive associations at genotypic levels. This indicates that panicle length and harvest index improvement could enhance grain yield. Genotypic correlations for panicle length were higher than phenotypic correlations, suggesting a strong genetic basis for the observed associations. Path coefficient analysis indicated that panicle length, days to 50% flowering, number of effective tillers per plant, number of panicles per plant, harvest index, and test weight exerted positive direct effects on grain yield per plant. Though except panicle length and harvest index all other characters showed negative correlation which is due to negative indirect effects exerted by the associated attributing characters.

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Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops cultivated worldwide and constitutes the principal staple food for more than half of the global population (Bellon *et al.*, 1998) ^[2]. Rice is generally believed to have originated in Southeast Asia, from where it subsequently spread to different parts of the world. Owing to its widespread cultivation and fundamental contribution to human nutrition, rice occupies a central position in global food and livelihood security. The available research documents demonstrate that rice grain yield is governed by a complex network of attributing traits whose relative contributions may vary across genetic backgrounds and production environments. These findings emphasize the importance of evaluating both trait associations and causal relationships before establishing reliable selection indices for breeding programs (Li *et al.*, 2019; Saleh *et al.*, 2020; Faysal *et al.*, 2022) ^[17, 5]. Understanding trait interplay through correlation studies in rice genotypes plays a critical role in establishing selection criteria (Nirmodh *et al.*, 2009) ^[11], while advanced genetic parameters such as combining ability analysis are pivotal for commercializing aromatic rice hybrids (Tirkey *et al.*, 2014) ^[20].

India is one of the world's leading producers and exporters of rice and, therefore, plays a vital role in ensuring global food security. During 2025–26, the country's rice production was estimated at a record 154.024 million tonnes, and India was reported to have surpassed China as the world's largest rice-producing nation (Press Information Bureau, 2026) ^[14]. Chhattisgarh is popularly known as the Rice Bowl of India. Rice is grown on 68.8 percent (32.85 lakh hectares in Kharif and in addition to this, approx. 0.5 lakh hectares is sown as summer paddy during December to May) of the total 47.75 lakh hectares of agricultural

land in the state. The agricultural land constitutes 34 percent of the state's total geographical area. Similar yield and trait variability assessments under the specific agro-climatic conditions of the Chhattisgarh Plains have proven essential for selecting resilient genotypes in other major staple crops such as bread wheat (Joshi *et al.*, 2026)^[6].

Rice is grown under diverse soil and climatic conditions ranging from water deficit to waterlogging conditions. The distinct rice germplasms facilitate optimal growth under varying environmental conditions. The world population is projected to reach a peak of 10.4 billion by the 2080s, with approximately 9.7 billion people anticipated by 2050 (Norman *et al.*, 2022)^[12]. This poses a significant challenge in feeding the world's population within ecological boundaries (Rockström *et al.*, 2020)^[15]. Multi-environment evaluations have shown that grain yield and several major yield-component traits, including the number of panicles, panicle length, spikelet number, and grain weight, are highly responsive to genotype $\times$ environment interactions. Such multi-location variability patterns and genetic diversity evaluations are well-documented across cereal and forage germplasm accessions to dissect genotype-by-environment dynamics (Toppo *et al.*, 2022; Belsariya *et al.*, 2024)^[21, 3].

Grain yield is a complex polygenic trait determined by the combined and interactive effects of several interrelated characters. Accordingly, a clear understanding of the relationships between grain yield and its attributing traits is essential for developing efficient selection strategies in rice-breeding programs. Correlation analysis is consequently a valuable tool for formulating effective selection criteria, identifying promising yield-related characters, and selecting suitable parental combinations for crop improvement (Saketh *et al.*, 2023)^[16]. Furthermore, because direct selection for grain yield alone may obscure compensatory or antagonistic relationships among component traits, the combined evaluation of correlation magnitude, trait inheritance, and direct effects can improve the biological interpretation of potential selection targets (Saleh *et al.*, 2020; Faysal *et al.*, 2022; Ata-Ul-Karim *et al.*, 2022)^[17, 1, 5]. Similar frequency distribution analyses and assessments of genetic variability parameters in yield attributing traits have provided critical directions for trait-based selection in crop species (Toppo and Sahu, 2022)^[21, 22].

Although correlation analysis provides useful information regarding the direction and magnitude of associations among traits, it does not differentiate the direct contribution of an individual character from its indirect influence through other correlated traits. Path coefficient analysis addresses this limitation by partitioning correlation coefficients into direct and indirect effects. It therefore facilitates the identification of characters that exert a substantial direct influence on grain yield, as well as traits whose associations with yield arise mainly through their relationships with other variables. The combined application of correlation and path coefficient analyses can thus provide a comprehensive understanding of yield determination and enable breeders to formulate effective selection strategies for simultaneous yield improvement (Kahani and Hittalmani, 2015)^[7].

Materials and Methods

The field experiment was conducted in two consecutive Kharif seasons during 2022 and 2023 at five different locations. The locations were College of Agriculture, IGKV, Raipur; KVK Dhamtari; KVK Bhatapara; KVK Balod; and

KVK Kanker. The experimental material comprised nine genotypes of rice laid out in a Randomized Complete Block Design (RCBD) with four replications. The plot size was $2\text{ m} \times 5\text{ m}$. A spacing of $20\text{ cm} \times 15\text{ cm}$ between rows and plants was maintained throughout the experiment. Recommended agronomic and plant-protection practices were applied uniformly to all experimental plots during the crop-growth period to minimize non-experimental variation and ensure a uniform crop stand.

Observations were recorded on five randomly selected plants per replication for thirteen morphological traits, namely: days to 50 percent flowering, plant height (cm), total number of tillers per plant, number of effective tillers per plant, number of panicles per plant, panicle length (cm), total number of spikelets per panicle, number of fertile spikelets per panicle, spikelet fertility percent, grain yield per plant (g), grain yield per ha on plot basis (q), harvest index (%), and test weight (g). The data were pooled over five locations in each Kharif season (Kharif 2022 and Kharif 2023). The pooled data of individual seasons were then again pooled over the two seasons for correlation and path analysis.

Genotypic and phenotypic correlation coefficients among the studied traits were estimated following the procedure proposed by Miller *et al.* (1958)^[10]. Path coefficient analysis was performed according to the method described by Dewey and Lu (1959)^[4] to partition the correlation coefficients into direct and indirect effects of the component traits on grain yield. Statistical computations were carried out using Windostat Version 9.50 (Indostat Services).

Results and Discussion

The correlation analysis revealed that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for characters like days to 50% flowering, plant height (cm), and panicle length (cm), possibly because environmental effects modified the associations among characters at the phenotypic level (Table 1). The wider genotypic than phenotypic correlations observed here are consistent with reports in which genetic associations among rice traits exceeded their phenotypic counterparts, although the magnitude and direction of individual relationships varied with germplasm and environment (Ata-Ul-Karim *et al.*, 2022; Faysal *et al.*, 2022; Singh *et al.*, 2023)^[1, 5, 19]. This pattern of genetic relationships overriding phenotypic noise aligns with trait correlation dynamics reported in rice genotypes by Nirmodh *et al.* (2009)^[11].

Correlation analysis revealed that grain yield per plant exhibited highly significant positive associations with panicle length, number of filled spikelets per panicle, spikelet fertility percent, grain yield per ha on plot basis, harvest index, and test weight at the phenotypic level. Significant positive correlation at the phenotypic level was found for traits like total tillers per plant and number of panicles per plant, while positive but non-significant correlation was observed for number of effective tillers per plant and total number of spikelets per panicle. At the genotypic level, panicle length had the strongest highly significant positive correlation with grain yield per plant, followed by days to 50% flowering, plant height, and harvest index (%). These findings are consistent with those reported by Meena *et al.* (2020)^[9], Phom and Chaturvedi (2022)^[13], and Saran *et al.* (2023)^[18]. Furthermore, the estimation of genetic variability parameters

and trait associations reported by Toppo and Sahu (2022)^[21, 22] and Joshi *et al.* (2026)^[6] supports targeting morphological components with high direct genetic correlation.

The concordant positive associations of panicle length and harvest index with grain yield per plant indicate coordinated contributions of sink size and plant biomass. Similar studies have identified panicle length as a useful yield-selection variable while emphasizing that their relative importance is population-dependent (Li *et al.*, 2019; Saleh *et al.*, 2020; Ata-Ul-Karim *et al.*, 2022)^[17, 1]. The significant correlations of days to 50% flowering have also been reported by Faysal *et al.* (2022)^[5], Ata-Ul-Karim *et al.* (2022)^[1], and Singh *et al.* (2023)^[19]. Combining ability studies in hybrid breeding programs have further highlighted the contribution of specific yield traits toward superiority in aromatic rice (Tirkey *et al.*, 2014)^[20].

The genotypic correlation coefficients for most characters were generally lower than the corresponding phenotypic correlation coefficients, indicating that the observed associations were governed by genetic factors having significant environmental influence. Therefore, improvement in grain yield may be achieved through simultaneous selection for panicle length and harvest index in which environmental influence is lower. This stability of key yield traits across environments reinforces findings from multi-location variability studies in crop germplasms (Toppo *et al.*, 2022; Belsariya *et al.*, 2024)^[21, 3].

The results of the path coefficient analysis are presented in Table 2 and Fig. 1. The analysis revealed that panicle length exerted the highest positive direct effect on grain yield per plant, followed by days to 50% flowering, number of effective tillers per plant, number of panicles per plant, harvest index, total tillers per plant, and test weight. These results agree with Kahani and Hittalmani (2015)^[7], Faysal *et*

al. (2022)^[5], and Saleh *et al.* (2020)^[17], who reported direct influences of these yield components.

The positive direct effects recorded for total tillers per plant, number of effective tillers per plant, number of panicles per plant, and test weight, when considered alongside their negative total correlations with grain yield, suggest that their positive direct contributions were substantially counterbalanced by negative indirect effects operating through other traits. Consequently, these traits should not be prioritized as independent selection criteria solely on the basis of their diagonal path coefficients. Their usefulness in yield-oriented selection programs should be validated across independent populations and production environments (Li *et al.*, 2019; Faysal *et al.*, 2022; Ata-Ul-Karim *et al.*, 2022)^[1, 5].

Conclusion

The correlation analysis identified days to 50% flowering, panicle length, and harvest index as the traits most consistently associated with grain yield per plant at the genotypic level. Path coefficient analysis further showed that days to 50% flowering, panicle length, and harvest index had large positive direct effects. Although total tillers per plant, effective tillers per plant, panicle length, and test weight exerted direct positive effects on grain yield per plant, their negative total correlations suggested that negative indirect effects offset their direct contributions. In contrast, days to 50% flowering, panicle length, and harvest index combined favorable correlations with direct and indirect effects, providing a coherent basis for selection. Integrating findings from broader variability studies across environments and crops (Belsariya *et al.*, 2024; Toppo and Sahu, 2022; Joshi *et al.*, 2026)^[3, 21, 6] confirms that morphological traits exhibiting strong direct effects and genotypic stability are the most reliable targets for systematic crop improvement.

Table 1: Combined Genotypic and Phenotypic correlation coefficient of grain yield per plant with other characters in rice pooled over locations and two seasons

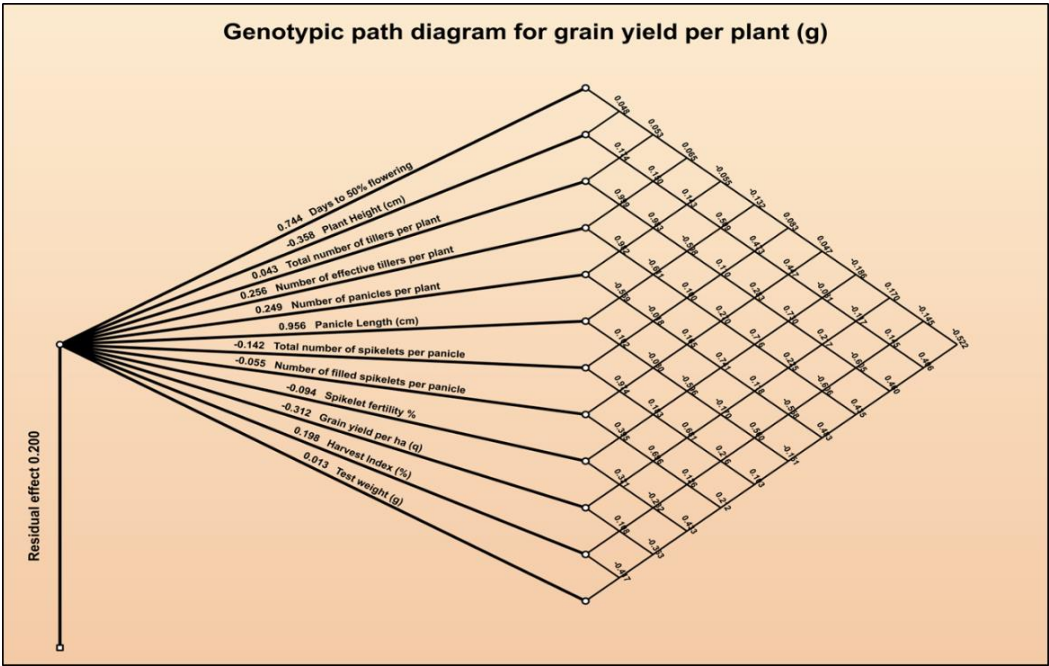
Levels	Trait	DDF	PH	TT	ET	PANPP	PANL	TNS	FS	SF	GYHA	HI	TW	GYPP
P	DDF	1.000	0.164**	-0.138**	-0.084	-0.112*	-0.008	-0.045	-0.110*	-0.179**	-0.174**	-0.113*	-0.108*	-0.101
G	DDF	1.000	0.048	0.053	0.065	-0.055	-0.132*	0.083	0.047	-0.186**	0.170**	-0.145**	-0.522**	0.525**
P	PH		1.000	0.016	0.018	-0.021	0.108*	0.065	-0.009	-0.126*	-0.179**	-0.109*	0.006	-0.193**
G	PH		1.000	0.174**	0.150**	0.143**	0.509**	0.473**	0.447**	-0.081	-0.117*	0.145**	0.406**	0.222**
P	TT			1.000	0.739**	0.676**	-0.225**	0.150**	0.204**	0.215**	0.094	-0.032	0.119*	0.105*
G	TT			1.000	0.999**	0.983**	-0.598**	0.110*	0.283**	0.730**	0.217**	-0.605**	0.460**	-0.325**
P	ET				1.000	0.520**	-0.175**	0.156**	0.234**	0.257**	0.084	0.022	0.140**	0.032
G	ET				1.000	0.982**	-0.611**	0.100	0.270**	0.716**	0.225**	-0.606**	0.435**	-0.316**
P	PANPP					1.000	-0.218**	0.111*	0.183**	0.252**	0.049	-0.005	0.148**	0.114*
G	PANPP					1.000	-0.559**	-0.018	0.165**	0.741**	0.118*	-0.558**	0.483**	-0.291**
P	PANL						1.000	0.084	0.121*	-0.034	-0.076	0.262**	0.005	0.289**
G	PANL						1.000	0.102	-0.030	-0.596**	-0.170**	0.560**	-0.151**	0.568**
P	TNS							1.000	0.718**	0.055	0.276**	0.176**	0.088	0.090
G	TNS							1.000	0.974**	0.183**	0.681**	0.216**	0.103	-0.361**
P	FS								1.000	0.467**	0.326**	0.252**	0.105*	0.194**
G	FS								1.000	0.395**	0.696**	0.126*	0.212**	-0.443**
P	SF									1.000	0.149**	0.092	0.182**	0.149**
G	SF									1.000	0.321**	-0.232**	0.433**	-0.553**
P	GYHA										1.000	0.188**	0.084	0.159**
G	GYHA										1.000	0.108*	-0.363**	-0.357**
P	HI											1.000	-0.119*	0.242**
G	HI											1.000	-0.417**	0.199**
P	TW												1.000	0.153**
G	TW												1.000	-0.440**
P	GYPP													1.000
G	GYPP													1.000

*, **Significant at 5% and 1% level of significance, respectively; P= Phenotypic; G= Genotypic; DF = Days to 50% flowering; PH = Plant height (cm); TT= Total number of tillers per plant; ET = Number of effective tillers per plant; PANPP= Number of panicles per plant; PL = Panicle length (cm); TNS= Total number of spikelets per panicle; FS= number of filled spikelets per panicle; SF= Spikelets fertility percent; GYHA= Grain yield per ha on plot basis (q); HI= Harvest Index (%); TW= Test weight; GY= Grain yield per plant (g)

Table 2: Genotypic (G) path matrix for grain yield per plant with its attributing traits pooled over the locations and two seasons

Trait	DFF	PH	TT	ET	PANPP	PANL	TNS	FS	SF	GYHA	HI	TW	GYPP
DFF	0.7440	-0.0168	0.0022	0.0163	-0.0133	-0.1233	-0.0115	-0.0025	0.0172	-0.0520	-0.0281	-0.0067	0.5254**
PH	0.0350	-0.3575	0.0073	0.0377	0.0350	0.4770	-0.0656	-0.0239	0.0075	0.0358	0.0281	0.0052	0.2216**
TT	0.0384	-0.0611	0.0429	0.2506	0.2399	-0.5603	-0.0153	-0.0152	-0.0674	-0.0665	-0.1175	0.0059	-0.3254**
ET	0.0474	-0.0527	0.0420	0.2560	0.2396	-0.5727	-0.0139	-0.0145	-0.0661	-0.0687	-0.1177	0.0056	-0.3157**
PANP	-0.0399	-0.0502	0.0414	0.2463	0.2490	-0.5243	0.0026	-0.0088	-0.0684	-0.0362	-0.1083	0.0062	-0.2907**
PANL	-0.0960	-0.1784	-0.0252	-0.1533	-0.1365	0.9561	-0.0141	0.0016	0.0550	0.0520	0.1087	-0.0019	0.5680**
TNS	0.0602	-0.1657	0.0046	0.0251	-0.0045	0.0954	-0.1415	-0.0522	-0.0169	-0.2085	0.0419	0.0013	-0.3607**
FS	0.0341	-0.1565	0.0119	0.0678	0.0402	-0.0283	-0.1352	-0.0547	-0.0365	-0.2131	0.0244	0.0027	-0.4431**
SF	-0.1356	0.0284	0.0307	0.1797	0.1808	-0.5584	-0.0253	-0.0212	-0.0942	-0.0984	-0.0450	0.0056	-0.5528**
GYHA	0.1239	0.0410	0.0091	0.0564	0.0289	-0.1591	-0.0945	-0.0373	-0.0297	-0.3122	0.0210	-0.0047	-0.3572**
HI	-0.1057	-0.0508	-0.0255	-0.1522	-0.1362	0.5250	-0.0299	-0.0067	0.0214	-0.0332	0.1979	-0.0054	0.1988**
TW	-0.3806	-0.1423	0.0194	0.1092	0.1179	-0.1411	-0.0143	-0.0114	-0.0400	0.1112	-0.0810	0.0132	-0.4397**

Residual effects = 0.200; Bold figure in diagonal represents the direct effects*, **Significant at 5% and 1% level of significance, respectively; DF = Day to 50 percent flowering; PH = Plant height (cm); TT = Total number of tillers per plant; ET = Number of effective tillers per plant; PANPP = Number of panicles per plant; PL = Panicle length (cm); TNS = Total number of spikelets per panicle; FS = number of filled spikelets per panicle; SF = Spikelets fertility percent; GYHA = Grain yield per ha on plot basis (q); HI = Harvest Index (%); TW = Test weight; GY = Grain yield per plant (g)



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Fig 1: Genotypic path diagram showing the direct and indirect effects of component characters on grain yield

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