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Correlation and Path Coefficient Analysis for Grain yield and its contributing traits in Rice (*Oryza sativa* L.)

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Abstract

Grain yield in rice (*Oryza sativa* L.) is a complex quantitative trait influenced by the combined action of multiple interrelated components, making it vital to understand their genetic relationships for effective selection. This investigation aimed to assess the genotypic and phenotypic correlations of grain yield per plant with its contributing traits and to separate these associations into direct and indirect effects using path coefficient analysis. Thirty diverse rice genotypes sourced from the Indian Agricultural Research Institute, New Delhi, were evaluated in a Randomized Block Design with three replications during the 2023 kharif season at the Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. Data were collected on twelve quantitative traits, and correlation coefficients along with path coefficients were computed, considering grain yield per plant as the dependent variable. Genotypic correlations were generally stronger than phenotypic ones, highlighting a solid genetic basis for the observed associations. Grain yield per plant showed highly significant positive correlations with biological yield per plant, harvest index, days to maturity, days to 50% flowering, and number of grains per panicle at both levels, while it was significantly and negatively correlated with internode length. Path coefficient analysis revealed that biological yield per plant and harvest index exerted the strongest positive direct effects on grain yield, followed by days to maturity, number of effective tillers per plant, internode length, and plant height. Conversely, panicle length, test weight, grains per panicle, grain length/width ratio, and days to 50% flowering had negative direct effects. The residual effect was minimal at both genotypic (0.0005) and phenotypic (0.00067) levels, confirming the adequacy of the traits studied. Based on these findings, biological yield per plant and harvest index are recommended as the most dependable selection criteria for enhancing rice yield.

Keywords: *Oryza sativa*; Grain yield; Genotypic correlation; Phenotypic correlation; Path coefficient analysis; Direct and indirect effects

Introduction

Rice (*Oryza sativa* L., $2n = 24$) is one of the world's most vital staple crops, providing the primary source of calories for much of Asia and Africa. Of the two cultivated rice species, *Oryza sativa* is widely grown across the globe, whereas *Oryza glaberrima* remains confined largely to West Africa. India accounts for the largest area under rice cultivation worldwide, yet its productivity lags behind several other rice-producing nations, underscoring the need for continued genetic improvement. As a major contributor to global dietary energy, rice will face increasing demand with the world population projected to reach nearly ten billion by midcentury, a pace that far outstrips current yield gains. Grain yield in rice is a complex quantitative trait shaped by the interaction of multiple component characters and environmental influences. Because of this complexity, direct selection based solely on yield performance is often inefficient. Effective breeding strategies require a clear understanding of how yield relates to its contributing traits, enabling breeders to identify reliable indirect selection criteria. Correlation coefficient analysis helps quantify the strength and direction of associations between yield and its component traits, but it cannot distinguish whether a trait contributes directly to yield or only appears associated through its relationship with other traits. Path coefficient analysis, first introduced by Wright (1921) ^[1] and later adapted for plant breeding by Dewey and Lu (1959) Nigeria, as well as "Ubulu" in the Eastern half, "Agbaseagbase" in Yoruba, "Tabashiya" in most parts of the north, and "molsa" in Kilba, is an evergreen multi-stem shrub that grows up to 200m height, ^[2] addresses this limitation

by partitioning correlations into direct and indirect effects, thereby clarifying the true causal role of each trait. Recognizing the importance of these analytical tools in identifying dependable selection criteria, the present study was undertaken to estimate genotypic and phenotypic correlations between grain yield per plant and its component traits, and to partition these correlations into direct and indirect effects through path coefficient analysis, using thirty diverse rice genotypes.

Materials and Methods

Experimental Site

The present study was conducted during the 2023 kharif season at the Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology (SVPUAT), Meerut, Uttar Pradesh, India. The site is situated at 29°40' N latitude, 77°42' E longitude, and 237 m above mean sea level. The region experiences a subtropical climate typical of western Uttar Pradesh. The experimental field soil was sandy loam in texture with good fertility status, providing favorable conditions for rice cultivation.

Experimental Materials and Design Used

The experimental material consisted of thirty diverse rice (*Oryza sativa* L.) genotypes obtained from the Indian Agricultural Research Institute (IARI), New Delhi. The genotypes were evaluated using a Randomized Block Design (RBD) with three replications. Seedlings, 25 days old, were transplanted as single plants per hill in rows measuring 3 m in length, with a spacing of 20 cm between rows and 15 cm between plants. Fertilization was carried out at the rate of 120 kg nitrogen, 60 kg phosphorus (P₂O₅), and 60 kg potassium (K₂O) per hectare, applied through urea, diammonium phosphate, and muriate of potash, respectively. The full dose of phosphorus and potassium, along with half of the nitrogen, was incorporated at transplanting, while the remaining nitrogen was top-dressed in two equal splits at the tillering and panicle initiation stages. All recommended agronomic and plant protection practices were uniformly followed across the experimental plots.

Traits Recorded

For recording observations, five competitive plants were randomly selected from each genotype in every replication, except for the traits days to 50% flowering and days to maturity, which were assessed on a whole-plot basis. Data were collected on twelve quantitative traits: days to 50% flowering, days to maturity, plant height (cm), number of effective tillers per plant, panicle length (cm), number of grains per panicle, internode length (cm), grain length/width ratio, biological yield per plant (g), harvest index (%), test weight (g), and grain yield per plant (g). The harvest index was calculated as the ratio of grain yield to biological yield per plant, expressed as a percentage.

Statistical Analysis

For statistical analysis, the mean values from three replications were used for each of the twelve traits. Genotypic and phenotypic correlation coefficients between grain yield per plant and its eleven component traits, as well as among the component traits themselves, were estimated from the variance-covariance components following the procedure outlined by Searle (1961) [3]. The significance of correlation coefficients was tested using the tabulated t-values at (n-2) degrees of freedom.

$$r_{xy}(g) = \frac{Cov_{xy}(g)}{\sqrt{Var_x(g) \times Var_y(g)}}$$

Where,

r_{xy}	=	Correlation between characters x and y.
Cov_{xy}	=	Covariance for characters x and y.
V_x	=	Variance for character x.
V_y	=	Variance for character y.

Path coefficient analysis was carried out following the approach first introduced by Wright (1921) [1] and later refined for plant breeding applications by Dewey and Lu (1959) [2]. In this study, grain yield per plant was considered the dependent variable, while the remaining eleven traits were treated as independent (causal) variables. Genotypic and phenotypic correlation coefficients were partitioned into direct and indirect effects by solving the simultaneous equations linking correlation and path coefficients through matrix inversion. The residual effect, representing the contribution of factors not included in the analysis, was estimated using the standard formula:

$$R = 1 - (\sum P_{iy}r_{iy})^{1/2}.$$

Software used: All statistical analyses, including correlation and path coefficient computations, were performed using the R statistical programming language.

Correlation Analysis

The genotypic and phenotypic correlation coefficients among the twelve quantitative traits are summarized in Table 1. In nearly all trait combinations, genotypic correlations were slightly stronger than their phenotypic counterparts, although the direction of association remained consistent across both levels. This pattern suggests that the observed relationships are primarily governed by genetic factors, with environmental influences exerting only a minor modifying effect.

Grain yield per plant showed highly significant positive genotypic correlations with biological yield per plant (0.795), harvest index (0.727), days to maturity (0.627), days to 50% flowering (0.577) and grains per panicle (0.553). A significant positive correlation was also observed with panicle length (0.259). Non-significant positive associations were recorded with plant height (0.131), grain length/width ratio (0.125) and test weight (0.018). Conversely, internode length exhibited a highly significant negative correlation (−0.672), while number of effective tillers per plant showed a non-significant negative correlation (−0.197). The phenotypic correlations closely mirrored the genotypic trends, with highly significant positive associations with biological yield per plant (0.787), harvest index (0.725), days to maturity (0.621), days to 50% flowering (0.569) and grains per panicle (0.547). Panicle length was significantly and positively correlated (0.256), whereas internode length displayed a highly significant negative correlation (−0.666). Among the component traits, days to 50% flowering showed a strong positive association with days to maturity (0.876 genotypic, 0.871 phenotypic) and grains per panicle (0.532, 0.525), but was negatively correlated with internode length (−0.528, −0.526) and effective tillers per plant (−0.296, −0.294). Days to maturity was positively associated with grains per panicle (0.627, 0.621) and biological yield per plant (0.554, 0.549), while negatively associated with internode length (−0.528, −0.523) and effective tillers per plant

(-0.349, -0.341). Plant height was strongly and positively linked with panicle length (0.623, 0.609), though its association with yield was weak. Effective tillers per plant showed negative correlations with panicle length (-0.292, -0.288) and biological yield per plant (-0.261, -0.255). Panicle length was positively associated with grains per panicle (0.308, 0.301) and negatively with internode length (-0.266, -0.265). Grains per panicle exhibited strong positive correlations with harvest index (0.623, 0.607) and grain yield, but strong negative correlations with internode length (-0.607, -0.601) and test weight (-0.225, -0.224). Internode length showed highly significant negative correlations with biological yield per plant (-0.451, -0.448) and harvest index (-0.594, -0.580), in addition to its negative association with yield. Traits such as grain length/width ratio and test weight displayed generally weak, non-significant associations with most traits, including yield. Interestingly, biological yield per plant and harvest index were only weakly correlated with each other (0.162, 0.147), yet each maintained a very strong independent correlation with grain yield per plant.

Path Coefficient Analysis

The genotypic and phenotypic correlation coefficients of grain yield per plant with its component traits were partitioned into direct and indirect effects, as shown in Table 2. In these tables, the diagonal (bold) entries represent the direct effects of each trait on grain yield per plant, while the off-diagonal values in the same row indicate the indirect effects mediated through other traits. The final column provides the overall correlation coefficient of each trait with grain yield per plant.

- **Direct effects:** At the genotypic level, the strongest positive direct effect on grain yield per plant was contributed by biological yield per plant (0.6937), followed by harvest index (0.6183). Smaller positive direct effects were observed for days to maturity (0.0291), number of effective tillers per plant (0.0113), internode length (0.0069), and plant height (0.0064). In contrast, negative direct effects were recorded for panicle length (-0.0245), test weight (-0.0089), grains per panicle (-0.0083), grain length/width ratio (-0.0046) and days to 50% flowering (-0.0030). The phenotypic path analysis closely reflected this pattern. Biological yield per plant (0.6947) and harvest index (0.6261) again exerted the highest positive direct effects, followed by days to maturity (0.0244), effective tillers per plant (0.0110), internode length (0.0073) and plant height (0.0056). Negative direct effects were observed for panicle length (-0.0234), test weight (-0.0086), grains per panicle (-0.0064), grain length/width ratio (-0.0030) and days to 50% flowering (-0.0005).
- **Indirect effects:** At the genotypic level, biological yield per plant not only exerted the strongest direct effect on grain yield but also contributed positively through several indirect pathways. Its largest positive indirect effects were mediated via days to maturity (0.3843 genotypic, 0.3813 phenotypic), days to 50% flowering (0.3488, 0.3454), grains per panicle (0.1716, 0.1697), panicle length (0.1431, 0.1435) and harvest index (0.1123, 0.1022). Conversely, it contributed negatively through internode length (-0.3129, -0.3109) and effective tillers per plant (-0.1808, -0.1768). Similarly, harvest index exerted strong positive indirect effects via grains per panicle (0.3853, 0.3800), days to maturity (0.2414, 0.2377) and days to 50% flowering (0.2289, 0.2244), while its largest negative indirect effect was mediated through internode length (-

0.3672, -0.3629). Although days to maturity and days to 50% flowering had relatively small direct effects, they contributed substantially to grain yield through strong positive indirect effects, primarily channeled via biological yield per plant and harvest index. Internode length, despite its small positive direct effect (0.0069 genotypic, 0.0073 phenotypic), showed strongly negative indirect effects through biological yield per plant and harvest index. These negative pathways explain its overall strong negative correlation with grain yield.

- **Residual effect:** The residual effect was found to be very low in both genotypic (0.0005) and phenotypic (0.00067) path analyses. This indicates that the twelve traits studied collectively explained nearly all of the variation in grain yield per plant, leaving only a negligible proportion attributable to factors outside the scope of the investigation.

Discussion

This investigation provided a detailed understanding of the associations between grain yield and its component traits through correlation and path coefficient analyses in thirty diverse rice genotypes. Overall, genotypic correlation coefficients were consistently higher in magnitude than the corresponding phenotypic coefficients, while the direction of association remained nearly identical at both levels. Such close agreement between genotypic and phenotypic estimates suggests that the expression of these traits is predominantly governed by genetic factors, with environmental influences playing only a minor role. Comparable findings have been reported by Lohiteswararao *et al.* (2021) [4], Sadhana *et al.* (2022) [5], and Saketh *et al.* (2023) [6], who also observed stronger genotypic than phenotypic correlations for grain yield and its component traits in rice. These consistent results reinforce the conclusion that genotypic correlations provide a more dependable basis for selection in rice breeding programmes. Grain yield per plant was found to be highly and positively associated with biological yield per plant, harvest index, days to maturity, days to 50% flowering, and grains per panicle at both genotypic and phenotypic levels. Among these, biological yield per plant and harvest index exhibited the strongest correlations with grain yield, underscoring the importance of efficient biomass production coupled with effective assimilate partitioning in determining productivity.

The positive correlation between grain yield and biological yield reflects the capacity of genotypes to accumulate greater dry matter during crop growth, while the association with harvest index highlights superior translocation of photosynthates from vegetative tissues to developing grains. These findings align with earlier reports by Rai *et al.* (2014) [7], Kumar *et al.* (2018) [8], Singh and Verma (2018) [9], Kiran *et al.* (2023) [10], and Kujur *et al.* (2023) [11], who also identified biological yield and harvest index as the most decisive traits influencing grain yield in rice. The highly significant positive association of grain yield with days to maturity and days to 50% flowering indicates that genotypes with comparatively longer crop duration were able to accumulate greater biomass, sustain photosynthetic activity for an extended period, and ultimately produce higher grain yield. A longer growth duration generally ensures adequate vegetative development prior to the reproductive phase, thereby enhancing assimilate production and improving grain filling. Similar findings have been reported by Lakshmi *et al.* (2014) [12], Sarker *et al.* (2014) [13], Tummuri *et al.* (2016) [14], Nayak *et al.* (2016) [15] and Saha *et al.* (2019) [16], who also

observed significant positive relationships between flowering duration, maturity period, and grain yield in rice. Grains per panicle exhibited a strong positive correlation with grain yield, highlighting the importance of increased sink size in yield improvement. Genotypes producing a greater number of grains per panicle are able to utilize assimilates more efficiently during the grain-filling stage, thereby enhancing grain production. Similarly, panicle length showed a significant positive association with grain yield, suggesting that longer panicles generally accommodate more spikelets and thus contribute indirectly to higher grain productivity. These findings are consistent with earlier reports by Sivasankar *et al.* (2018) ^[17], Budhlakoti *et al.* (2019) ^[18] and Saketh *et al.* (2023) ^[6], who emphasized the role of panicle architecture and grain number as key determinants of rice yield. Plant height showed only a weak positive association with grain yield, suggesting that while taller plants may contribute to greater biomass accumulation, their direct role in grain production is relatively limited. Similarly, grain length/width ratio and test weight exhibited weak and non-significant associations with grain yield, indicating that these quality-related traits exert comparatively little influence on productivity in the present set of genotypes. Comparable findings were reported by Kumar *et al.* (2018) ^[8] and Singh *et al.* (2018) ^[19], who also observed that grain quality traits generally contribute less to yield improvement compared to biomass-related characters.

Internode length exhibited a highly significant negative correlation with grain yield, biological yield, and harvest index at both genotypic and phenotypic levels. This suggests that excessive internode elongation may promote vegetative growth without proportionately enhancing reproductive efficiency, thereby reducing assimilate allocation to grain development. Consequently, genotypes with comparatively shorter internodes, coupled with higher biological yield and harvest index, are expected to achieve superior grain productivity. Similar observations were reported by Al-Musawi and Al-Anbari (2019) ^[20] and Lohiteswararao *et al.* (2021) ^[4], who also found that excessive vegetative elongation adversely affected grain yield through inefficient assimilate partitioning.

While correlation analysis provides valuable insights into the magnitude and direction of associations among traits, it cannot distinguish whether these relationships are direct or mediated indirectly through other traits. Therefore, path coefficient analysis was employed to partition the observed correlations into direct and indirect effects, enabling identification of the actual contribution of individual traits to grain yield.

The path coefficient analysis clearly demonstrated that biological yield per plant exerted the strongest positive direct effect on grain yield at both genotypic and phenotypic levels, followed by harvest index. These two traits therefore emerge as the principal determinants of grain yield and represent the most dependable selection criteria for improving productivity. Their strong positive correlations, coupled with high direct effects, confirm that improvement in these traits would

directly enhance grain yield. Similar conclusions were reported by Rai *et al.* (2014) ^[7], Kumar *et al.* (2018) ^[8], Sadhana *et al.* (2022) ^[5], Kiran *et al.* (2023) ^[10] and Saketh *et al.* (2023) ^[6], who also identified biological yield and harvest index as the most influential direct contributors to rice yield. Other traits such as days to maturity, effective tillers per plant, plant height, and internode length also recorded positive direct effects, though their magnitudes were considerably lower. Notably, days to maturity contributed substantially to grain yield through strong positive indirect effects, primarily mediated via biological yield and harvest index. This indicates that the influence of maturity duration on yield is expressed mainly through enhanced biomass accumulation and improved assimilate partitioning rather than through an independent direct contribution. Comparable findings have been reported by Sarker *et al.* (2014) ^[13], Saha *et al.* (2019) ^[16] and Kiran *et al.* (2023) ^[10]. Interestingly, panicle length, grains per panicle, grain length/width ratio, test weight, and days to 50% flowering exhibited negative direct effects on grain yield, despite showing positive simple correlations. This indicates that their apparent favorable associations with yield were largely due to indirect effects mediated through biological yield and harvest index, rather than their own independent contributions. Such discrepancies are common in complex quantitative traits, where reliance on simple correlation alone may lead to misleading conclusions about the actual importance of a character. Similar observations were reported by Solomon and Wegary (2016) ^[21], Devi *et al.* (2017) ^[22] and Bhujel *et al.* (2018) ^[23], who also documented positive correlations accompanied by negative direct effects for several yield components in rice. The residual effects were very low in both genotypic (0.0005) and phenotypic (0.00067) path analyses, confirming that the twelve traits included in the present investigation collectively explained almost the entire variability in grain yield. This demonstrates the adequacy of the selected traits for explaining yield variation and validates the reliability of the estimated direct and indirect effects. Comparable low residual effects have been reported by Nanda *et al.* (2019) ^[24] and Kujur *et al.* (2023) ^[11], indicating that the major yield-determining traits were effectively represented in the path model.

Overall, the results of correlation and path coefficient analyses complemented each other and clearly established that biological yield per plant and harvest index are the most important and dependable selection criteria for improving grain yield in rice. Their strong positive associations with grain yield, coupled with the highest positive direct effects, confirm that simultaneous improvement of these traits will directly enhance productivity. In addition, traits such as days to maturity and grains per panicle exerted substantial positive indirect effects, primarily mediated through biological yield and harvest index. This highlights the importance of optimum maturity duration and larger sink size in supporting biomass accumulation and efficient assimilate partitioning.

Table 1: Estimation of genotypic correlations among the different characters in rice

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers per plant	Panicle length	Grains per panicle	Internode length	Grain length/width ratio	Test weight	Biological yield per plant	Harvest index	Grain yield per plant
Days to 50% flowering	1.000	0.876**	0.192	-0.296**	0.373**	0.532**	-0.528**	0.257*	0.288**	0.503**	0.370**	0.577**
Days to maturity			0.256*	-0.349**	0.405**	0.627**	-0.528**	0.420**	0.196	0.554**	0.390**	0.627**
Plant height				-0.252*	0.623**	0.122	0.089	-0.109	0.062	0.146	0.057	0.131
No. of effective tillers per plant					-0.292**	-0.177	0.166	-0.093	0.180	-0.261*	-0.041	-0.197
Panicle length						0.308**	-0.266*	-0.122	0.189	0.206	0.217*	0.259*
Grains per panicle							-0.607**	0.243*	-0.225*	0.247*	0.623**	0.553**
Internode length								-0.179	-0.053	-0.451**	0.594**	-0.672**
Grain length/width ratio									-0.129	0.023	0.167	0.125
Test weight										0.145	-0.126	0.018
Biological yield per plant											0.162	0.795**
Harvest index												0.727**
Grain yield per plant												1.000

*, ** significant at 5% and 1% level, respectively

Table 2: Estimation of phenotypic correlations among the different characters in rice

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers per plant	Panicle length	Grains per panicle	Internode length	Grain length/width ratio	Test weight	Biological yield per plant	Harvest index	Grain yield per plant
Days to 50% flowering	1.000	0.871**	0.183	-0.294**	0.368**	0.525**	-0.526**	0.248*	0.287**	0.497**	0.358**	0.569**
Days to maturity			0.251*	-0.341**	0.398**	0.621**	-0.523**	0.389**	0.195	0.549**	0.380**	0.621**
Plant height				-0.239*	0.609**	0.120	0.084	-0.105	0.060	0.144	0.055	0.129
No. of effective tillers per plant					-0.288**	-0.174	0.161	-0.075	0.177	-0.255*	-0.036	-0.190
Panicle length						0.301**	-0.265*	-0.105	0.186	0.207	0.209*	0.256*
Grains per panicle							-0.601**	0.223*	-0.224*	0.244*	0.607**	0.547**
Internode length								-0.172	-0.053	-0.448**	-0.580**	-0.666**
Grain length/width ratio									-0.118	0.027	0.147	0.116
Test weight										0.144	-0.121	0.019
Biological yield per plant											0.147	0.787**
Harvest index												0.725**
Grain yield per plant												1.000

*, ** significant at 5% and 1% level, respectively

Table 3: Genotypic direct (bold) and indirect (unbold) effect of yield components as partitioned by path analysis

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers per plant	Panicle length	Grains per panicle	Internode length	Grain length/width ratio	Test weight	Biological yield per plant	Harvest index	Grain yield per plant
Days to 50% flowering	-0.0030	0.0255	0.0012	-0.0034	-0.0091	-0.0044	-0.0036	-0.0012	-0.0026	0.3488	0.2289	0.577**
Days to maturity	-0.0026	0.0291	0.0017	-0.0040	-0.0099	-0.0052	-0.0036	-0.0020	-0.0017	0.3843	0.2414	0.627**
Plant height	-0.0006	0.0074	0.0064	-0.0029	-0.0153	-0.0010	0.0006	0.0005	-0.0006	0.1012	0.0354	0.131
No. of effective tillers per plant	0.0009	-0.0101	-0.0016	0.0113	0.0071	0.0015	0.0011	0.0004	-0.0016	-0.1808	-0.0254	-0.197
Panicle length	-0.0011	0.0118	0.0040	-0.0033	-0.0245	-0.0026	-0.0018	0.0006	-0.0017	0.1431	0.1341	0.259*
Grains per panicle	-0.0016	0.0182	0.0008	-0.0020	-0.0075	-0.0083	-0.0042	-0.0011	0.0020	0.1716	0.3853	0.553**
Internode length	0.0016	-0.0154	0.0006	0.0019	0.0065	0.0051	0.0069	0.0008	0.0005	-0.3129	-0.3672	-0.672**
Grain length/width ratio	-0.0008	0.0122	-0.0007	-0.0011	0.0030	-0.0020	-0.0012	-0.0046	0.0011	0.0161	0.1031	0.125
Test weight (g)	-0.0009	0.0057	0.0004	0.0020	-0.0046	0.0019	-0.0004	0.0006	-0.0089	0.1003	-0.0777	0.018
Biological yield per plant	-0.0015	0.0161	0.0009	-0.0030	-0.0051	-0.0021	-0.0031	-0.0001	-0.0013	0.6937	0.1001	0.795**
Harvest index	-0.0011	0.0113	0.0004	-0.0005	-0.0053	-0.0052	-0.0041	-0.0008	0.0011	0.1123	0.6183	0.727**

Resi = 0.0005*, ** significant at 5% and 1% level, respectively

Table 4: Phenotypic direct (bold) and indirect (unbold) effect of yield components as partitioned by path analysis

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of effective tillers per plant	Panicle length	Grains per panicle	Internode length	Grain length/width ratio	Test weight	Biological yield per plant	Harvest index	Grain yield per plant
Days to 50% flowering	-0.0005	0.0213	0.0010	-0.0032	-0.0086	-0.0033	-0.0038	-0.0008	-0.0025	0.3454	0.2244	0.569**
Days to maturity	-0.0004	0.0244	0.0014	-0.0038	-0.0093	-0.0040	-0.0038	-0.0012	-0.0017	0.3813	0.2377	0.621**
Plant height	-0.0001	0.0061	0.0056	-0.0026	-0.0142	-0.0008	0.0006	0.0003	-0.0005	0.0998	0.0345	0.129
No. of effective tillers per plant	0.0001	-0.0083	-0.0013	0.0110	0.0067	0.0011	0.0012	0.0002	-0.0015	-0.1768	-0.0228	-0.190
Panicle length	-0.0002	0.0097	0.0034	-0.0032	-0.0234	-0.0019	-0.0019	0.0003	-0.0016	0.1435	0.1309	0.256*
Grains per panicle	-0.0002	0.0151	0.0007	-0.0019	-0.0070	-0.0064	-0.0044	-0.0007	0.0019	0.1697	0.3800	0.547**
Internode length	0.0002	-0.0128	0.0005	0.0018	0.0062	0.0038	0.0073	0.0005	0.0005	-0.3109	-0.3629	-0.666**
Grain length/width ratio	-0.0001	0.0095	-0.0006	-0.0008	0.0025	-0.0014	-0.0013	-0.0030	0.0010	0.0190	0.0917	0.116
Test weight	-0.0001	0.0048	0.0003	0.0020	-0.0043	0.0014	-0.0004	0.0004	-0.0086	0.0997	-0.0761	0.019
Biological yield per plant	-0.0002	0.0134	0.0008	-0.0028	-0.0048	-0.0016	-0.0033	-0.0001	-0.0012	0.6947	0.0921	0.787**
Harvest index	-0.0002	0.0093	0.0003	-0.0004	-0.0049	-0.0039	-0.0042	-0.0004	0.0010	0.1022	0.6261	0.725**

Resi = 0.00067 *, ** significant at 5% and 1% level, respectively

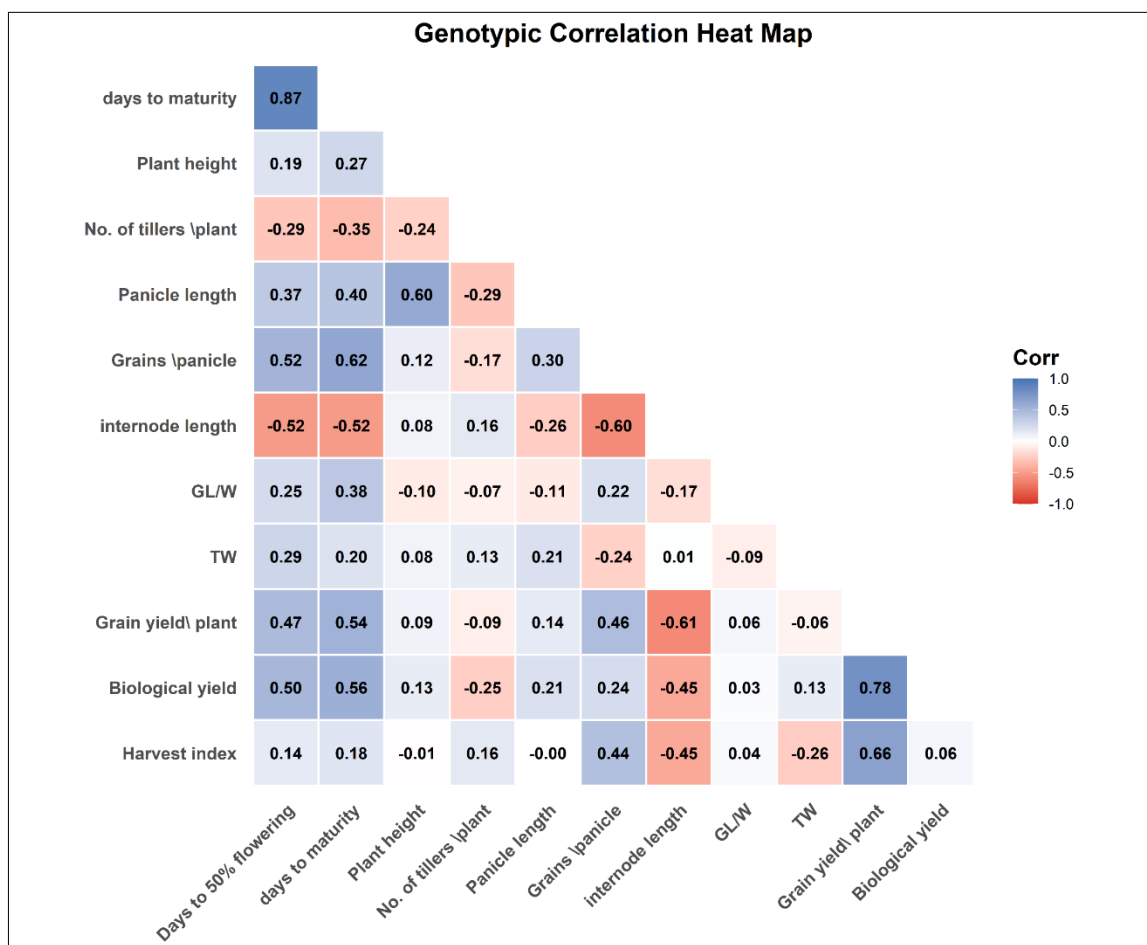
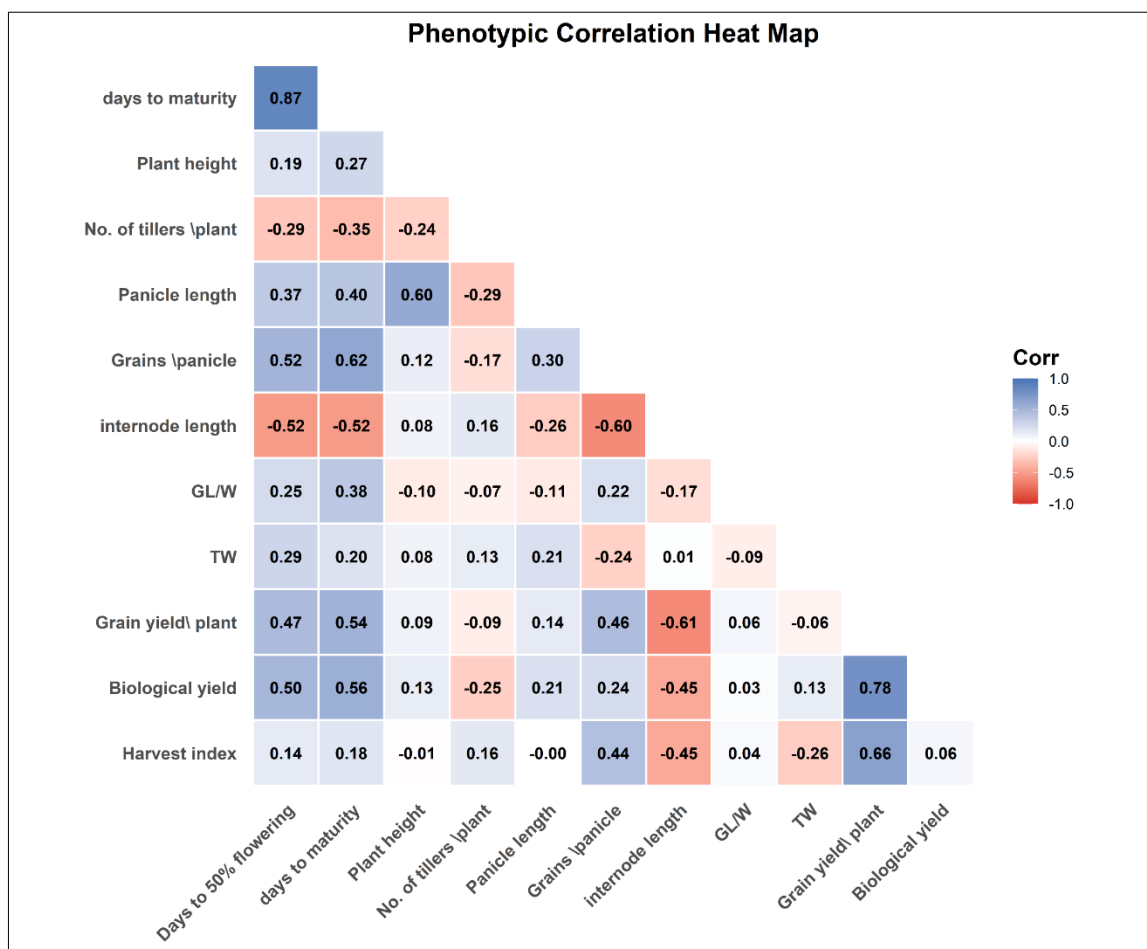
Conclusion

The present investigation was undertaken to assess the genotypic and phenotypic correlations of grain yield per plant with its component traits and to partition these associations into direct and indirect effects through path coefficient analysis in thirty diverse rice genotypes. In general, genotypic correlation coefficients were slightly higher in magnitude than the corresponding phenotypic coefficients, indicating that the associations among the studied traits were predominantly under genetic control, with only limited modification by environmental factors. Grain yield per plant exhibited highly significant positive correlations with biological yield per plant, harvest index, days to maturity, days to 50% flowering and number of grains per panicle at both genotypic and phenotypic levels. A significant positive correlation was also observed with panicle length, while internode length showed a highly significant negative correlation with grain yield, biological yield, and harvest index.

Path coefficient analysis further clarified the causal basis of the observed associations, revealing that biological yield per plant and harvest index exerted the strongest positive direct effects on grain yield at both genotypic and phenotypic levels. These two traits therefore stand out as the most dependable selection criteria for yield improvement. They were followed, in order of magnitude, by days to maturity, number of effective tillers per plant, internode length, and plant height,

all of which recorded smaller positive direct effects. Days to maturity and days to 50% flowering, despite their modest direct effects, contributed substantially to grain yield through strong positive indirect effects transmitted via biological yield per plant and harvest index. Conversely, the negative correlation of internode length with yield was explained by its strongly negative indirect effects through these two traits, highlighting its suppressive role in productivity. The very low residual effects observed at both the genotypic (0.0005) and phenotypic (0.00067) levels confirmed that the twelve characters studied were sufficient to explain nearly all of the variation in grain yield. This demonstrates the robustness of the model and the reliability of the estimated direct and indirect effects.

On the basis of both correlation strength and the magnitude of direct effects, biological yield per plant and harvest index emerge as the most dependable and biologically meaningful selection criteria for enhancing grain yield in rice. Their consistent positive associations with yield, coupled with the highest direct contributions, confirm that emphasis on these traits during selection will be highly rewarding. In practical breeding terms, simultaneous improvement of biological yield, harvest index, optimum maturity duration, and greater grains per panicle should be prioritized during parent selection and advancement of superior segregants. This strategy will ensure the development of high-yielding rice genotypes with stable productivity across diverse environments.



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