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

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.247>

TRAIT INTERRELATIONSHIP AND YIELD NETWORK ANALYSIS IN ELITE RICE (*Oryza sativa* L.) CULTURES

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(Date of Receiving : 06-04-2026; Date of Revision : 26-05-2026; Date of Acceptance : 12-06-2026)

ABSTRACT

Understanding the interrelationship among yield and its contributing traits is essential for improving rice productivity under irrigated conditions. The present investigation was conducted during Rabi 2025–26 to evaluate genetic variability, trait association, and yield relationships in 22 elite rice cultures along with two checks under puddled transplanted conditions. The experiment was laid out in a randomized block design with three replications. Observations were recorded for days to 50 per cent flowering, plant height, effective bearing tillers m⁻², panicle length, filled grains panicle⁻¹, test weight, and grain yield. Analysis of variance revealed significant differences among the genotypes for all the traits, indicating the presence of substantial variability. High heritability coupled with high genetic advance was observed for effective bearing tillers m⁻², filled grains panicle⁻¹, and grain yield, suggesting the predominance of additive gene action. Correlation analysis indicated a positive association of grain yield with test weight and plant height, whereas days to 50 per cent flowering and effective bearing tillers m⁻² showed negative association with yield. Path coefficient analysis identified test weight as the most influential trait with the highest positive direct effect on grain yield. Principal component analysis showed that the first two principal components explained more than 73 per cent of the total variability among genotypes. Cluster analysis grouped the genotypes into distinct clusters, indicating considerable genetic divergence. Trait network analysis further confirmed the central role of test weight in determining grain yield and highlighted the complex interaction among agronomic characters. The study suggested that emphasis on test weight along with balanced expression of yield-related traits would be effective for selection and development of high-yielding rice cultivars under irrigated ecosystems.

Keywords : Rice, genetic variability, correlation analysis, path coefficient analysis, trait network analysis, grain yield.

Introduction

Rice (*Oryza sativa* L.) is the staple food for more than half of the global population and plays a crucial role in food and nutritional security, particularly in Asia (FAO, 2025). Recent estimates indicate that global rice production reached nearly 543 million tonnes (milled basis) during 2024/25, while India recorded about 149 million tonnes, maintaining its

position as the leading producer and exporter of rice worldwide (USDA, 2025). However, sustaining future rice productivity has become increasingly difficult due to shrinking agricultural land, irregular rainfall patterns, water scarcity, and changing climatic conditions (Kumar *et al.*, 2024). In this context, the development of high-yielding and stable rice cultivars continues to be a major priority in rice breeding programmes (Prasad *et al.*, 2025).

Grain yield in rice is a complex quantitative trait influenced by several component characters and environmental interactions (Falconer and Mackay, 1996). Therefore, improvement in yield largely depends on understanding the extent of variability present among breeding materials and identifying traits with greater contribution towards productivity. Advanced varietal trials provide an effective platform for evaluating elite rice cultures for yield performance and associated agronomic traits under field conditions (Singh and Chaudhary, 1985). Estimation of genetic variability parameters such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance helps breeders to assess the effectiveness of selection and the possibility of genetic improvement in different traits (Burton and DeVane, 1953; Johnson *et al.*, 1955).

Correlation and path coefficient analyses are important statistical tools widely used for studying the relationship among yield and its contributing traits in rice. Correlation analysis provides information on the degree and direction of association between characters, whereas path analysis separates these associations into direct and indirect effects, thereby identifying traits with true contribution towards grain yield (Dewey and Lu, 1959). Several studies have reported significant positive associations of productive tillers, panicle length, filled grains per panicle, test weight, and biological yield with grain yield in rice genotypes (Saran *et al.*, 2023; Venkatraman *et al.*, 2023; Islam *et al.*, 2025). Such information is highly useful in formulating efficient selection strategies in rice improvement programmes.

In recent years, trait network analysis has emerged as a powerful approach for understanding the complex interrelationships among agronomic characters (Mitra *et al.*, 2019). Unlike conventional pairwise association studies, network analysis enables visualization of multidimensional interactions among traits and assists in identifying key traits that occupy central positions within the yield architecture. The integration of network-based analytical approaches with traditional biometrical methods has improved the understanding of trait dependency and selection efficiency in crop improvement studies (Raza *et al.*, 2024; Khan *et al.*, 2024). Principal component analysis and cluster analysis have also been widely employed to identify key traits contributing to genetic divergence and to classify rice genotypes into distinct groups for effective parent selection in breeding programmes (Islam *et al.*, 2024; Chandraker *et al.*, 2024).

Materials and Methods

Experimental Site and Plant Material

The present investigation was carried out during Rabi 2025 at the experimental farm of the concerned research station under irrigated puddled transplanted conditions. The experimental material comprised 22 elite rice entries along with two widely cultivated check varieties, namely RDR 1162 and KNM 1638. The entries were evaluated to study variability, trait association, and yield relationships among important agronomic and yield-attributing characters.

Nursery Raising and Crop Establishment

Seeds of all the entries and checks were raised in a well-prepared nursery, and 35-day-old healthy seedlings were transplanted to the main field. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was transplanted in uniform plots by maintaining a spacing of 15 cm × 15 cm between rows and plants.

The field was puddled thoroughly before transplanting to ensure proper establishment of seedlings. Recommended agronomic practices for irrigated rice cultivation were followed uniformly throughout the crop growth period. Fertilizers were applied as per standard recommendations in split doses. Irrigation was provided at regular intervals to maintain adequate soil moisture conditions. Necessary intercultural operations, weed management practices, and plant protection measures were undertaken as and when required to maintain a healthy crop stand.

Recording of Observations

Observations were recorded on days to 50 per cent flowering, plant height (cm), number of panicles m⁻², panicle length (cm), number of filled grains per panicle, 1000-grain weight (g) and grain yield (kg ha⁻¹). Data were recorded from ten randomly selected competitive plants in each replication excluding border plants, whereas observations on days to 50 per cent flowering, number of panicles m⁻² and grain yield per plot were recorded on a plot basis following standard evaluation procedures.

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) as suggested by Panse and Sukhatme (1985) to determine the significance of differences among the genotypes. Genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense, and genetic advance as per cent of mean were estimated following standard

biometrical methods proposed by Burton and DeVane (1953) and Johnson *et al.* (1955).

Correlation coefficients were computed to assess the magnitude and direction of association among different characters. Path coefficient analysis was carried out according to the method suggested by Dewey and Lu (1959) to partition the correlation coefficients into direct and indirect effects of component traits on grain yield. Trait network analysis was performed to visualize and interpret the complex interrelationships among yield and yield-attributing traits. All statistical analyses and graphical visualizations were performed using R software version 4.6.0. The packages ‘agricolae’ were used for analysis of variance and mean comparisons, ‘lavaan’ for path coefficient analysis, ‘corrplot’ and ‘PerformanceAnalytics’ for correlation analysis, and ‘qgraph’ and ‘igraph’ packages were employed for construction and visualization of trait networks.

Results and Discussion

Analysis of Variance

The analysis of variance revealed highly significant differences among the advanced rice

genotypes for all the characters studied (Table 1). Significant variation was observed for days to 50 per cent flowering, plant height, effective bearing tillers m^{-2} , panicle length, number of filled grains panicle $^{-1}$, test weight and grain yield. This indicated the presence of considerable variability among the genotypes evaluated under Rabi conditions. Availability of variability among breeding materials is essential for effective selection and crop improvement.

Among the different characters, number of filled grains panicle $^{-1}$ recorded the highest F-value followed by grain yield and days to 50 per cent flowering (Table 1). This indicated the existence of wider variability for these traits among the tested genotypes. The observed differences among the entries may be due to their diverse genetic background and differential response to environmental conditions.

Similar results were earlier reported by Saran *et al.* (2023), Kumar *et al.* (2024), and Islam *et al.* (2025), who observed significant differences among rice genotypes for yield and yield-related traits.

Table 1 : Analysis of Variance for Different Traits in Advanced Rice Genotypes under Rabi Conditions

Trait	Genotype Mean Square	Error Mean Square	F value
Days to 50% flowering	29.837	0.182	164.016***
Plant height (cm)	88.992	4.577	19.442***
Effective bearing tillers m^{-2}	7688.964	83.381	92.215***
Panicle length (cm)	1.301	0.124	10.476***
Number of filled grains panicle $^{-1}$	4425.994	9.317	475.066***
Test weight (g)	2.403	0.056	42.808***
Grain yield (kg ha^{-1})	1478757.075	8696.367	170.043***

Note: *** Significant at $P \leq 0.001$

Genetic Variability

The estimates of phenotypic coefficient of variation were slightly higher than the corresponding genotypic coefficient of variation for all the characters studied (Table 2). The narrow difference between PCV and GCV indicated that environmental influence on these traits was relatively low and most of the variation was genetic in nature.

High GCV and PCV values were recorded for number of filled grains panicle $^{-1}$ and effective bearing tillers m^{-2} (Table 2). Grain yield also exhibited comparatively high variability. These findings suggested the presence of substantial variation for these traits and indicated greater scope for improvement through selection. On the other hand, lower variability was observed for days to 50 per cent

flowering and panicle length, indicating comparatively narrow variation for these traits.

High heritability coupled with high genetic advance as per cent of mean was observed for number of filled grains panicle $^{-1}$, effective bearing tillers m^{-2} and grain yield (Table 2). This suggested the predominance of additive gene action and indicated that direct phenotypic selection for these traits would be effective. Plant height and test weight showed high heritability with moderate genetic advance, suggesting the involvement of both additive and non-additive gene effects.

The present findings are in close agreement with earlier reports of Venkatraman *et al.* (2023), Prasad *et al.* (2025), and Raza *et al.* (2024), who also observed high heritability and genetic advance for major yield-

attributing traits in rice. Similar observations on the existence of substantial genetic variability and scope for effective selection among rice genotypes were reported by Rezk *et al.* (2024).

Table 2 : Genetic Variability Parameters for Different Traits in Advanced Rice Genotypes under Rabi Conditions

Trait	Mean	GCV (%)	PCV (%)	Heritability (%)	GA	GAM (%)
Days to 50% flowering	108.17	2.91	2.93	98.19	6.42	5.93
Plant height (cm)	90.87	5.84	6.29	86.01	10.13	11.15
Effective bearing tillers m ⁻²	314.91	15.99	16.25	96.82	102.06	32.41
Panicle length (cm)	23.85	2.63	3.01	75.95	1.12	4.71
Number of filled grains panicle ⁻¹	228.20	16.81	16.87	99.37	78.79	34.53
Test weight (g)	14.32	6.17	6.40	93.16	1.76	12.28
Grain yield (kg ha ⁻¹)	5401.78	12.96	13.07	98.26	1429.40	26.46

Note: GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance and GAM = Genetic advance as per cent of mean

Correlation Analysis

Correlation analysis revealed different levels of association among the studied traits (Figure 1). Grain yield showed positive association with test weight and plant height. Among these traits, test weight exhibited a stronger positive relationship with grain yield, indicating its important contribution towards productivity. This suggested that genotypes possessing bolder grains had better yield potential under the present conditions.

Days to 50 per cent flowering exhibited a negative association with grain yield (Figure 1). This indicated that delayed flowering genotypes tended to produce lower grain yield. Effective bearing tillers m⁻² also showed a negative association with grain yield, suggesting that increased tillering alone may not necessarily improve yield performance. Excessive tillering may result in competition among tillers for assimilates, thereby affecting grain development.

Positive association was observed between panicle length and test weight, while days to 50 per cent flowering showed positive association with plant height and number of filled grains panicle⁻¹. These relationships indicated the interconnected nature of yield and its contributing traits. The correlogram clearly illustrated the magnitude and direction of positive and negative associations among the studied characters.

Similar positive association between test weight and grain yield was reported by Kumar *et al.* (2024) and Islam *et al.* (2025). Negative association of excessive tillering with yield was also observed by Saran *et al.* (2023) in irrigated rice genotypes.

Principal Component Analysis

Principal component analysis revealed that the first principal component contributed the maximum proportion of total variability among the evaluated rice genotypes (Table 3). The first two principal components together accounted for more than 73 per cent of the total variation, indicating that a major portion of the variability present among the genotypes was governed by a limited number of important agronomic and yield-related traits.

Table 3 : Principal Component Analysis of Different Traits in Advanced Rice Genotypes under Rabi Conditions

Principal Component	Eigen Value	Variability Explained (%)	Cumulative Variability (%)
PC1	3.42	48.86	48.86
PC2	1.71	24.41	73.27
PC3	0.88	12.57	85.84
PC4	0.46	6.57	92.41
PC5	0.29	4.14	96.55
PC6	0.17	2.43	98.98
PC7	0.07	1.02	100.00

Note: PC = Principal component

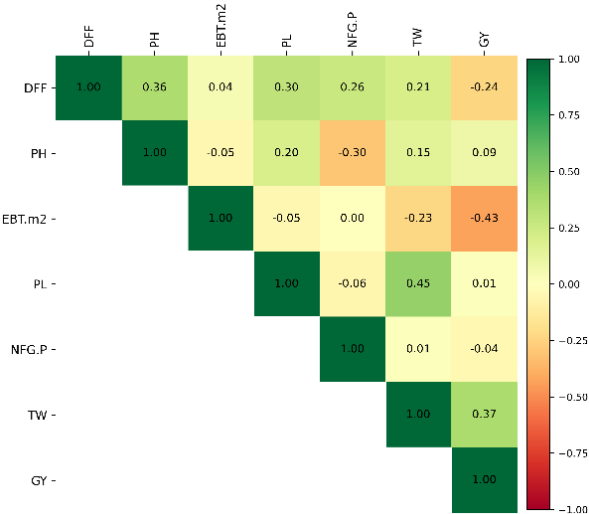


Fig. 1 : Correlogram showing correlation among yield and yield-attributing traits in advanced rice genotypes under Rabi conditions.

The higher contribution of PC1 suggested that yield and major yield-attributing traits played a significant role in differentiating the genotypes. The cumulative variability explained by the first three principal components exceeded 85 per cent, demonstrating the effectiveness of PCA in summarizing the overall variability among the breeding materials into a few major components.

The PCA biplot further illustrated the distribution and grouping pattern of genotypes based on their trait expression (Figure 2). Genotypes located far from the origin exhibited greater divergence, indicating substantial variability among the evaluated entries. The wide dispersion of several genotypes across different quadrants suggested the existence of considerable genetic diversity, which could be effectively utilized in hybridization and selection programmes. In contrast, closely grouped genotypes indicated similarity in agronomic performance and genetic background.

The PCA results clearly demonstrated the usefulness of multivariate analysis in identifying important traits contributing towards genetic divergence and yield improvement in rice. Similar observations regarding the effectiveness of PCA in rice genetic diversity studies were also reported by Khan *et al.* (2024) and Raza *et al.* (2024). The usefulness of principal component analysis in identifying superior rice genotypes and major sources of variation was further demonstrated by Khatun *et al.* (2023) and Islam *et al.* (2024).



Fig. 2 : Principal component analysis (PCA) biplot showing the distribution and genetic divergence of advanced rice genotypes based on agronomic and yield-related traits under Rabi conditions

Cluster Analysis

Cluster analysis grouped the advanced rice genotypes into distinct clusters based on similarity among agronomic traits (Figure 3). The dendrogram indicated the presence of substantial genetic divergence among the evaluated genotypes. Genotypes grouped in distant clusters may possess diverse genetic backgrounds and can be utilized as potential parents in hybridization programmes to generate wider variability and superior segregants.

The clustering pattern also suggested that grouping of genotypes was mainly based on trait performance rather than geographical origin. Genotypes with similar agronomic expression were grouped together despite differences in their background. The observed divergence among clusters provides useful information for selection of suitable parents in breeding programmes.

Similar clustering behaviour among rice genotypes was reported by Prasad *et al.* (2025) and Venkatraman *et al.* (2023). Chandraker *et al.* (2024) and Singh *et al.* (2024) also reported the effectiveness of cluster analysis in identifying genetically diverse parents for hybridization and selection programmes in rice.

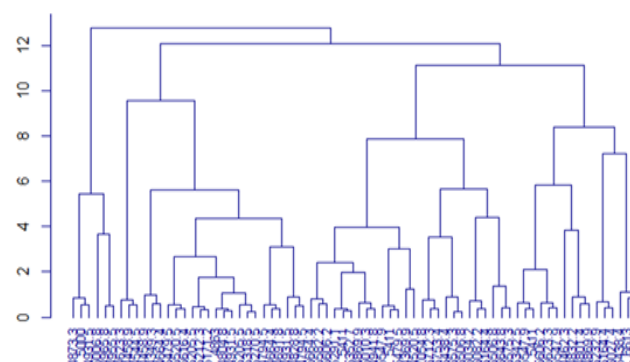


Fig. 3 : Dendrogram showing cluster analysis of advanced rice genotypes based on agronomic traits, indicating genetic divergence and grouping pattern among the evaluated genotypes.

Path Coefficient Analysis

Path coefficient analysis revealed that test weight exerted the highest positive direct effect on grain yield (Table 4). This indicated that grain weight contributed directly towards increased productivity and could serve as an effective selection criterion for yield improvement in rice.

Table 4 : Path Coefficient Analysis Showing Direct Effects of Different Traits on Grain Yield in Advanced Rice Genotypes under Rabi Conditions

Trait	Direct Effect (Estimate)	Standardized Direct Effect (Std. all)	z-value	P-value
Days to 50% flowering (DFF)	-85.161	-0.382	-3.356	0.001**
Plant height (PH)	24.343	0.197	1.778	0.075
Effective bearing tillers m ⁻² (EBT.m ²)	-4.520	-0.323	-3.375	0.001**
Panicle length (PL)	-96.571	-0.099	-0.913	0.361
Number of filled grains panicle ⁻¹ (NFG.P)	1.992	0.106	0.991	0.322
Test weight (TW)	304.943	0.396	3.679	0.000***

Residual Effect

Parameter	Value
Residual variance of grain yield	295233.533
Standardized residual effect	0.609

Note: Std. all = Standardized direct effect, ** Significant at $P \leq 0.01$, *** Significant at $P \leq 0.001$

Residual effect indicates the proportion of variation not explained by the traits included in the path analysis

Plant height and number of filled grains panicle⁻¹ also exhibited positive direct effects on grain yield, although their magnitude was comparatively lower. In contrast, days to 50 per cent flowering and effective bearing tillers m⁻² recorded significant negative direct effects on grain yield (Table 5). These findings indicated that delayed flowering and excessive tillering may adversely affect grain yield under the present experimental conditions.

Panicle length showed a low negative direct effect on grain yield. The residual effect indicated that a major proportion of yield variation was explained by the traits included in the analysis. The present findings highlighted the importance of test weight as a reliable yield-contributing character in advanced rice genotypes.

Similar positive direct effects of test weight on grain yield were reported by Saran *et al.* (2023), Kumar *et al.* (2024), and Islam *et al.* (2025).

Trait Network Analysis

Trait network analysis provided better understanding of the complex interactions among yield and yield-related traits (Figure 4). The network structure revealed a strong positive connection between test weight and grain yield. This indicated the central role of test weight in determining productivity among the studied genotypes.

Positive interaction was also observed between panicle length and test weight, suggesting that improvement in panicle architecture may indirectly contribute towards better grain development. In contrast, effective bearing tillers m⁻² showed a strong negative association with

grain yield. This suggested that excessive tillering may reduce efficient assimilate partitioning towards grain formation.

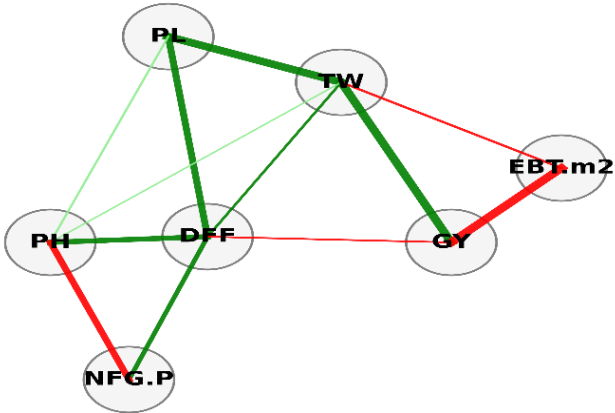


Fig. 4 : Trait network analysis showing the positive and negative interactions among grain yield and yield-attributing traits in advanced rice genotypes under Rabi conditions.

Days to 50 per cent flowering also exhibited negative association with grain yield, indicating the advantage of relatively early flowering genotypes under the tested conditions. The network analysis further demonstrated that grain yield is governed by the collective interaction of several interconnected traits rather than a single character.

Recent studies by Mitra *et al.* (2019), Raza *et al.* (2024), and Khan *et al.* (2024) also emphasized the usefulness of network-based approaches in understanding trait interactions and identifying key selection criteria in crop improvement programmes.

Conclusion

The study demonstrated the presence of considerable variability among the advanced rice genotypes evaluated under Rabi irrigated puddled conditions, indicating good potential for effective

selection and crop improvement. Traits such as effective bearing tillers m^{-2} , number of filled grains panicle $^{-1}$ and grain yield exhibited high heritability along with high genetic advance, suggesting the importance of additive gene effects and the usefulness of direct selection for these characters. Correlation and path analyses revealed that test weight had the strongest positive influence on grain yield, making it an important trait for improving productivity. In contrast, delayed flowering and excessive tillering showed negative effects on yield under the present conditions. Multivariate analyses including PCA and cluster analysis confirmed the existence of substantial genetic divergence among the genotypes, which can be effectively utilized in future breeding programmes. Trait network analysis further highlighted the interconnected nature of yield and its contributing characters, with test weight occupying a central role in the yield network. Overall, the findings suggest that selection based on test weight along with balanced expression of other yield-related traits would be beneficial for developing high-yielding rice cultivars.

Acknowledgements

The authors sincerely acknowledge Professor Jayashankar Telangana Agricultural University for providing financial support for this research. The authors also thank the technical staff and field assistants at the Regional Sugarcane and Rice Research Station, Rudrur for their assistance in field experimentation and data collection.

Authors' Contributions

RR designed the experiment and conducted the field trials. AKC, SC, RR and JC assisted in data collection. RR, AKC and SC performed the statistical analysis. KPC supervised the study and RR & KPC revised the manuscript. All authors read and approved the final manuscript.

Conflict of interest:

Authors do not have any conflict of interests to declare.

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