Agriculture Association of Textile Chemical and Critical Reviews Journal (2025) 218-227

AATCC Review

06 June 2025: Received
24 July 2025: Revised
02 August 2025: Accepted
01 September 2025: Available Online

https://aatcc.peerjournals.net/

Original Research Article

Open Access

Multivariate and quantitative genetic analyses of yield traits in advanced lines of rice (*Oryza sativa* L.)

Ramya Rathod*[1], **B. Soundharya**[2], **A. Krishna Chaitanya**[3], **Sai Charan M**[4], **Akula Dinesh**[5], **G. Rakesh**[1] and **B. Balaji Naik**[6]

[1]*Department of Genetics and Plant Breeding, PJTAU - Regional Sugarcane and Rice Research Station, Rudrur– 503 188, Telangana, India*
[2]*Department of Genetics and Plant Breeding, PJTAU- Regional Agricultural Research Station, Warangal– 506 007, Telangana, India*
[3]*Department of Soil Science and Agriculture Chemistry, PJTAU - Regional Sugarcane and Rice Research Station, Rudrur– 503 188, Telangana, India*
[4]*Department of Entomology, PJTAU - Regional Sugarcane and Rice Research Station, Rudrur– 503 188, Telangana, India*
[5]*Department of Genetics and Plant Breeding, PJTAU - Agricultural Research Station, Mudhole – 504 102, Telangana, India*
[6]*Department of Agronomy, PJTAU - Centre for Digital Agriculture, Rajendranagar – 500 030, Telangana, India*

ABSTRACT

*Rice yield is a complex quantitative trait influenced by multiple interacting components. According to variance analysis, all traits had highly significant differences, indicating enough variability for selection. The largest mean squares were seen in grain yield (F = 245.50***), days to 50% flowering (F = 66.56***), and plant height (F = 37.47***), indicating their significant contribution to overall variation. Grain yield (h2 = 99.60%, GAM = 28.13%) and filled grains per panicle (h2 = 96.40%, GAM = 28.21%) were both strongly controlled by additive control, indicating high heritability across traits and a high potential for direct selection. The influence of non-additive gene action was evident in the low GAM but high panicle length and tiller number heritability. Days until 50% flowering and panicle length were found to be significant positive direct contributors to yield by correlation and path analyses. At the same time, test weight and filled grain number primarily acted indirectly. The tillering ability, filled grain number, flowering duration, and panicle architecture were the main contributors to 61.51% of the total variation in the first three PCs captured by principal component analysis. Three groups of genotypes were created using hierarchical clustering, and each group had its own distinct yield strategy: Cluster I prioritized heavier grains and tillering, Cluster II had longer panicles and higher test weight, and Cluster III had panicle density and grain number. Several high-yielding outliers were found to be promising donor parents (>8.8 t ha^{-1}). This integrated method offers reliable selection indices and useful donor identification by combining genetic parameters, correlation, path, PCA, and clustering. The results directly apply to rice improvement initiatives by ICAR and AICRIP that focus on resilient and high-yielding cultivars for irrigated environments.*

Keywords: *Irrigated Rice; Grain Yield; Heritability; Genetic Advance; Path & correlation Analysis; Principal Component Analysis; Genetic Diversity.*

1. Introduction

Over half of the world's population depends on rice (*Oryza sativa* L.), making it the most significant cereal crop globally [45]. The anticipated 535.8 million tons of milled rice production in 2024–2025 will come primarily from Asia, with India overtaking China as the largest producer and top exporter with almost 147 million tons [47]. A staple of India's food and nutritional security, rice is grown on about 45 million hectares and yields an average of 4.1 t/ha. Grain quality, panicle architecture, flowering time, and tillering ability are all polygenic traits heavily influenced by environmental factors, making it challenging to increase yield [7, 13]. Genetic variability, as measured by heritability, genotypic/phenotypic coefficients of variation (GCV, PCV), and genetic advance as a percentage of mean (GAM), is essential for practical breeding [5, 26]. While traits with high heritability but low GAM suggest non-additive action, necessitating hybridization or recombination breeding, high heritability and GAM generally indicate additive gene control, favoring direct selection [40, 48]. Features controlled mainly by additive means, like test weight, panicle density, and the number of grains per panicle, continue to be excellent choices for selection [14, 12].

Gaining insight into the interactions between traits is essential to increasing yield. Panicle length, test weight, and filled grain number typically have strong positive direct effects on yield, according to correlation and path analyses, whereas excessive tillering frequently lowers panicle productivity [55, 28]. By distinguishing between direct and indirect effects, path analysis improves trait dissection. For example, it demonstrates that plant height has little direct influence but can indirectly contribute through panicle traits [46]. Variability studies are strengthened by complementary multivariate tools: hierarchical clustering divides genotypes into groups that help identify heterotic parents, whereas PCA highlights important diversity axes, such as panicle architecture, grain number, and

---

Corresponding Author: **Ramya Rathod*

DOI: https://doi.org/10.21276/AATCCReview.2025.13.04.218

© 2025 by the authors. The license of AATCC Review. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).

tillering ability [35, 39]. Combined, these strategies improve the resolution of trait associations and provide breeders with robust selection criteria.

Integrating conventional variability estimates with contemporary tools has become crucial as sustainability and climate resilience gain more attention. Precise capture of trait expression is now possible thanks to developments in high-throughput phenotyping, such as digital panicle analysis and 3D imaging [56]. However, limited environments, analytical scope, or traits limited most studies between 2020 and 2025 [9, 42]. In order to fill this gap, the current study uses a single framework that combines ANOVA, genetic parameters, correlation, path analysis, PCA, and clustering to evaluate a diverse irrigated rice panel that represents major Indian ecologies. It finds high-yielding outliers (>8.8 t/ha) as possible donor parents for heterosis breeding, QTL pyramiding, selection index development, and defining effective selection indices. This work offers practical insights for ICAR and AICRIP programs by connecting variability estimates with useful donor identification. It speeds up creating resilient, high-yielding cultivars appropriate for irrigated environments.

2. MATERIALS AND METHODS

Plant Material and Experimental Site

Twenty-nine advanced rice genotypes developed by the Rice Breeding Section of RS & RRS, Rudrur, PJTAU, Telangana, India, were used in the study. The trial was carried out in Kharif 2024 at RS & RRS, Rudrur (18°46′N, 77°53′E; 391 m above msl) under irrigated transplanted conditions.

Experimental Design and Crop Management

A Randomized Block Design (RBD) with three replications was used to assess the genotypes. Every entry was elevated in plots of 12 m^2, spaced 20 × 15 cm apart. To reduce non-genetic variance, puddled transplanted rice was grown using recommended agronomic techniques, such as land preparation, nutrient management, irrigation, and plant protection.

Data Collection

Observations were recorded on days to 50% flowering (DFF), plant height (PH, cm), number of tillers per plant (NT), panicles per m^2 (NP), panicle length (PL, cm), filled grains per panicle (NFG/P), test weight (TW, g), and grain yield (GY, kg ha^{-1}). Data were recorded from 10 randomly selected competitive plants per replication, NP on a unit area basis, and GY at the plot level (converted to ha^{-1}). Border plants were excluded.

Statistical Analysis

The Randomized Block Design (RBD) model was used to perform analysis of variance (ANOVA) to determine whether genotype differences were significant [42]. In accordance with [5, 16], the following genetic variability parameters were estimated: broad-sense heritability (h^2b), genetic advance as a percentage of mean (GAM), and genotypic and phenotypic coefficients of variation (GCV, PCV). Path coefficient analysis was used to separate these associations into direct and indirect effects on grain yield in accordance with [51, 59], while genotypic and phenotypic correlation coefficients were calculated in accordance with [60]. Hierarchical clustering was based on Ward's minimum variance method using Euclidean distance [49], and principal component analysis (PCA) was carried out in accordance with [18, 17].

Software and Packages

R v4.5.1 was used for all analyses [32]. Base R, correlation and path analyses with agricolae and lavaan, PCA with FactoMineR and factoextra, and clustering with statistics were used to calculate genetic variability. ggplot2 was used to create visualizations such as histograms, boxplots, dendrograms, and PCA biplots [50].

RESULTS AND DISCUSSION

2. ANOVA

Table 1. Analysis of variance (ANOVA) for yield and yield-contributing traits

Trait	df	Mean Square	F value
Test weight (gm)	28	3.31	30.27***
Plant height (cm)	28	134.17	37.47***
Panicle length (cm)	28	3.01	5.61***
Number of tillers per plant	28	0.52	2.80**
Number of filled grains/panicle	28	5361.71	27.50***
Days to 50% flowering	28	18.68	66.56***
Number of panicles/m^2	28	1030.89	4.46***
Grain yield (kg/ha)	28	2480371.19	245.50***

For all traits examined, the ANOVA results showed highly significant differences between the genotypes (Table 1), indicating substantial genetic variability in the experimental material. Grain yield and days to 50% flowering had the highest mean square values (F = 245.50* and F = 66.56*), suggesting that genetic factors were the primary source of variation, making these traits highly suitable for selection in breeding programs. Significant differences in flowering and yield characteristics and their importance for productivity and adaptation have also been documented in previous studies on cereals [46, 7].

Along with the number of spikelets and grains produced, there were significant changes in plant height (F = 37.47*) and panicle length (F = 5.61*), both critical for biomass production. Test weight (F = 30.27*) and the number of filled grains per panicle (F = 27.50*) showed notable variability, highlighting their importance for final yield determination. The number of tillers per plant (F = 2.80) contributes significantly to the bulk density of the panicle but shows limited genetic variability, reflecting stronger environmental influence. These findings are consistent with earlier research that emphasized spike weight and grain number as key determinants of yield variability in rice and wheat [31, 42].

Most traits did not exhibit significant replication effects, which indicates that the observed differences were genetic rather than environmental. Their importance for breeding is highlighted by the high variability observed for days to 50% flowering, plant height, panicle length, number of filled grains per panicle, test weight, and number of panicles per m^2. The most crucial selection factor is still grain yield, which is polygenic and highly variable. Similar results were found in multi-environment trials, where the component traits contributed directly and indirectly to yield variation [9, 4]. These findings suggest that the examined germplasm possesses sufficient variability to serve as a valuable resource for developing high-yielding cultivars.

2.1. GENETIC PARAMETERS OF VARIABILITY

Days to 50% flowering (DFF)

The average number of days to 50% flowering was 94.59, ranging from 88 to 100 days (Table 2). A narrow genetic base was suggested by the slight difference between GCV (2.62%) and PCV (2.64%).

© 2025 AATCC Review. All Rights Reserved.

Genetics played a significant role in the trait's high heritability (98.50%) and low GAM (5.35%), but the scope of improvement was constrained by its limited variability. Fixation of alleles or non-additive gene action frequently causes high heritability with low GAM [26, 5]. Similar findings in rice were reported in [43, 21].

Table 2. Genetic Variability Estimates for Yield and Yield-Related Traits in Rice Genotypes.

Trait	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	GAM (%)
DFF	94.59	88	100	2.62	2.64	98.50	5.35
PH	117.78	105	138	5.60	5.68	97.30	11.38
NT/Pl.	8.67	8	10	3.88	4.82	64.90	6.44
NP/m^2	352.87	272	398	4.66	5.25	78.80	8.53
PL	24.01	21	26	3.78	4.17	82.30	7.07
NFG/P	297.49	181	396	13.95	14.21	96.40	28.21
TW	13.64	11	16	7.59	7.70	97.20	15.42
GY	6633.94	4527	8889	13.68	13.71	99.60	28.13

Plant height (PH)

Plant height (PH) ranged from 105 to 138 cm, averaging 117.78 cm (Table 2). It displayed high heritability (97.30%), moderate GAM (11.38%), and moderate PCV (5.68%) and GCV (5.60%). According to these findings, selection is effective even though genetic gain may be small because additive control predominates. Similar results were reported in [11, 2].

Number of tillers per plant (NT/pl)

The average number of tillers per plant (NT/Pl) was 8.67, ranging from 8 to 10 (Table 2). It showed low GAM (6.44%), moderate heritability (64.90%), lower GCV (3.88%), and moderate PCV (4.82%). This suggests a significant impact of the environment, which diminishes the efficacy of early-generation selection. Similar findings were reported in [54, 10].

Number of panicles per m^2 (NP/m^2)

The average number of panicles per m^2 (NP/m^2) was 352.87, ranging from 272 to 398 (Table 2). It showed moderate GAM (8.53%), PCV (5.25%), heritability (78.80%), and GCV (4.66%). Recurrent selection is helpful because, despite the apparent effects of the environment, selection can be somewhat successful under partial additive control. Similar findings were reported in [34, 30].

Panicle length (PL)

Panicle length (PL) had a low GCV (3.78%), PCV (4.17%), GAM (7.07%), and high heritability (82.30%), with an average of 24.01 cm and a range of 21–26 (Table 2). Limited variability prevents direct selection from improving despite high heritability, indicating non-additive control and the necessity of hybridization. Similar findings were reported in [41, 8].

Number of filled grains per panicle (NFG/P)

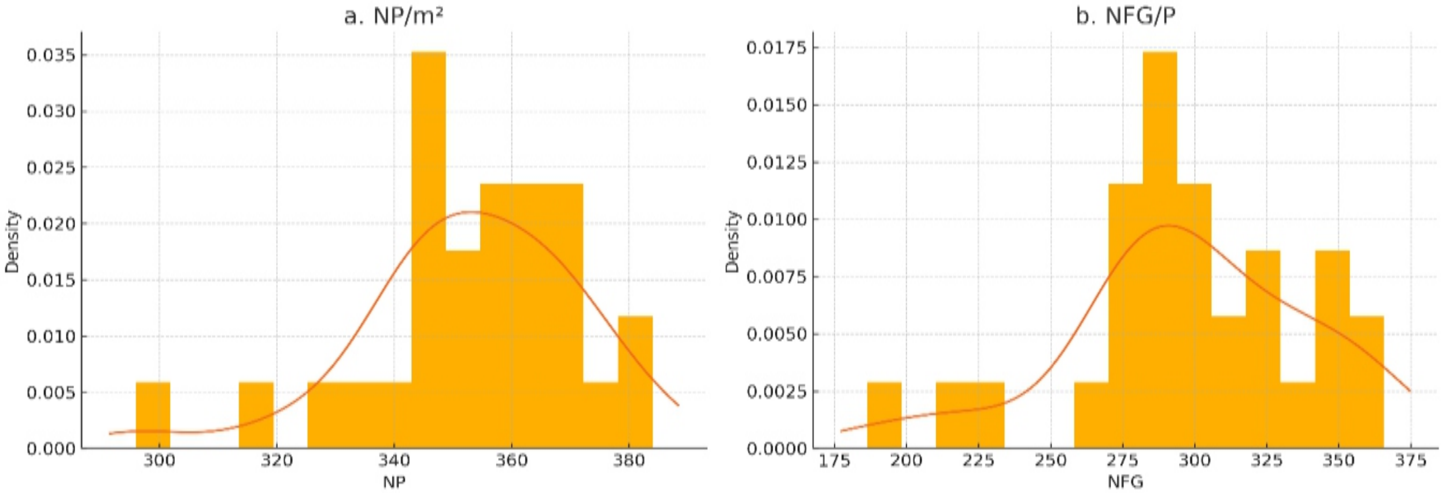
The average number of filled grains per panicle (NFG/P) was 297.49, ranging from 181 to 396 (Table 2). It showed very high heritability (96.40%), high GCV (13.95%), PCV (14.21%), and GAM (28.21%). These results indicate strong additive control, making grain number selection highly effective. Similar findings were reported in [48, 36].

Test weight (TW)

Test weight (TW) ranged from 11 to 16 g, averaging 13.64 g (Table 2). It showed moderate GCV (7.59%) and PCV (7.70%), very high heritability (97.20%), and moderate GAM (15.42%). The close alignment of GCV and PCV suggests little environmental influence, while high heritability coupled with moderate GAM confirms its potential for steady improvement through direct selection. Similar observations were reported in [10, 37].

Grain yield (GY):

The average grain yield (GY) was 6633.94 kg/ha, ranging from 4527 to 8889 kg/ha (Table 2). It showed high GAM (28.13%), very high heritability (99.60%), and high GCV (13.68%) and PCV (13.71%). These values demonstrate that yield is the most reliable trait for direct selection because it is strongly heritable and predominantly governed by additive gene action. The combination of high heritability and GAM ensures strong prospects for genetic gain across environments. Similar findings were reported in [40, 38].



© *2025 AATCC Review.* All Rights Reserved.

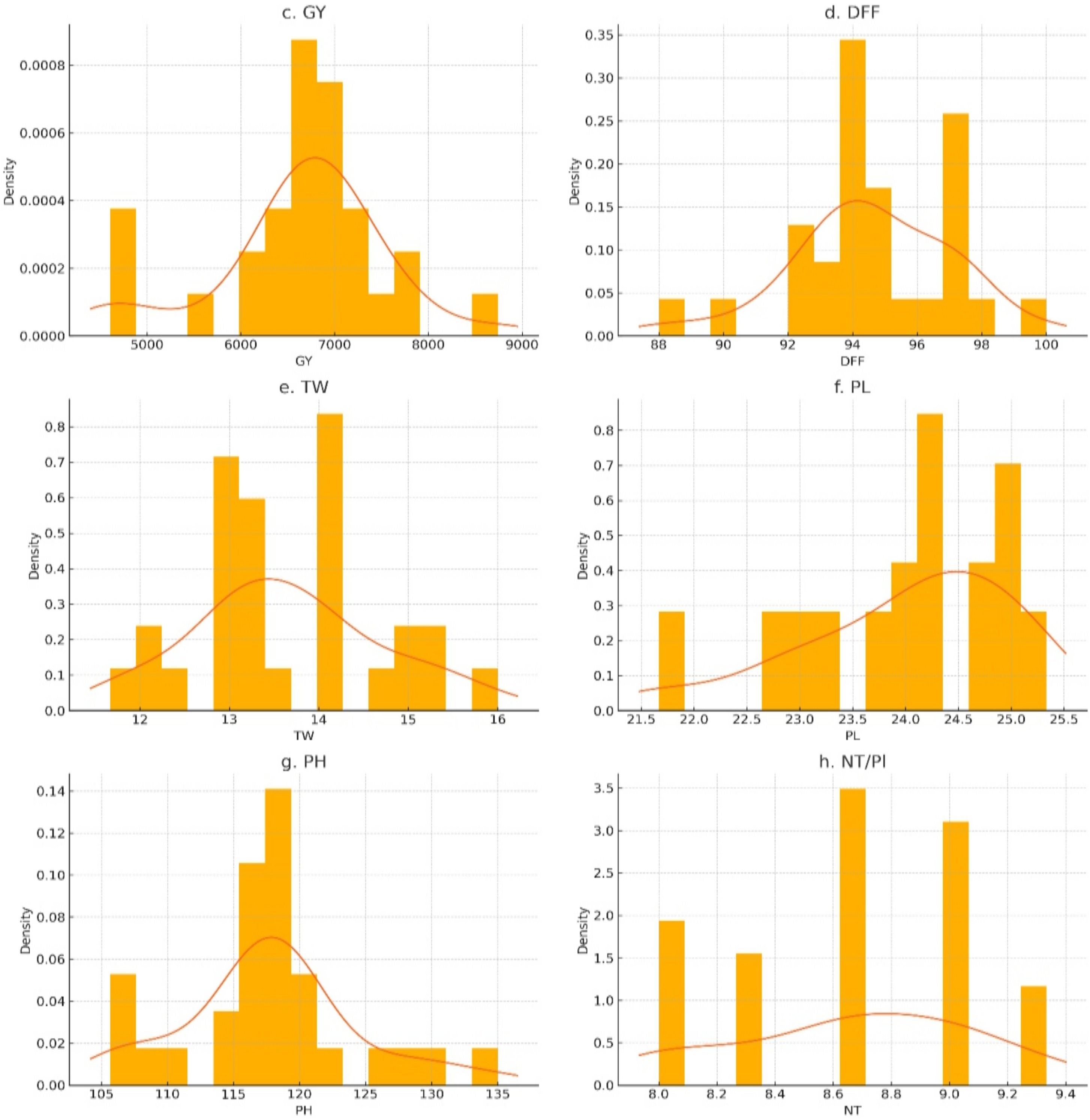


Figure 1. The frequency distribution of 29 rice genotypes for yield and yield-related characteristics. (a) NP/m^2: number of panicles per square meter; (b) NFG/P: number of filled grains per panicle; (c) GY: grain yield (kg/ha); (d) DFF: days to 50% flowering; (e) TW: test weight (g); (f) PL: panicle length (cm); (g) PH: plant height (cm); and (h) NT/Pl: number of tillers per plant.

Most genotypes clustered between 340 and 365, indicating a unimodal distribution of panicles per square meter (NP/m^2). There were donors with larger sink sizes, as evidenced by the concentration of filled grains per panicle (NFG/P) between 285 and 315, and a subset of genotypes exceeding 330. The distribution of grain yield (GY) was comparatively wider, with most entries falling between 6.4 and 7.3 t ha^{-1}. However, a few genotypes showed exceptionally high performance (>8.5 t ha^{-1}), indicating that there is still plenty of room for yield improvement.

© *2025 AATCC Review.* All Rights Reserved.

Days to 50% flowering (DFF) showed a narrow distribution (92–96 days) with a few early- and late-flowering outliers, offering opportunities for phenological diversification. Test weight (TW) was moderately variable (13–15 g), with distinct low (~11–12 g) and high (~16 g) classes, while panicle length (PL) showed limited variability (23–25 cm). Plant height (PH) exhibited a bimodal tendency, with peaks around 116–121 cm and minor groups at the extremes, providing useful variability for stature ideotypes. Tillers per plant (NT) displayed the least variation, tightly concentrated around 8.5–9.0, indicating that tillering is under more stabilizing selection than other traits.

b. CORRELATION ANALYSIS

Table 3. Genotypic (rg) and Phenotypic (rp) Correlation Coefficients for Yield and Yield-Related Traits in Rice Genotypes

Trait	DFF	PH (cm)	NT/Pl.	NP/m^2	PL (cm)	NFG/P	TW (gm)	GY (kg/ha)
DFF	**1.00 (1.00)**	0.49*** (0.51**)	0.01 (−0.00)	0.17 (0.25)	−0.07 (−0.07)	0.09 (0.10)	0.07 (0.07)	0.22* (0.22)
PH (cm)		**1.00 (1.00)**	0.00 (0.01)	−0.04 (−0.04)	0.15 (0.16)	0.18 (0.17)	−0.14 (−0.15)	−0.12 (−0.12)
NT/Pl.			**1.00 (1.00)**	0.23* (0.36)	−0.23* (−0.29)	−0.33** (−0.42*)	0.01 (0.01)	0.09 (0.11)
NP/m^2				**1.00 (1.00)**	−0.04 (0.02)	−0.05 (−0.04)	0.05 (0.13)	0.10 (0.16)
PL (cm)					**1.00 (1.00)**	0.11 (0.13)	0.35*** (0.40*)	0.02 (0.02)
NFG/P						**1.00 (1.00)**	−0.37*** (−0.40*)	−0.04 (−0.04)
TW (gm)							**1.00 (1.00)**	−0.02 (−0.03)

Note: DFF = Days to 50% Flowering; PH = Plant Height; NT/Pl. = Number of Tillers per Plant; NP/m^2 = Number of Panicles per m^2; PL = Panicle Length; NFG/P = Number of Filled Grains per Panicle; TW = Test Weight; GY = Grain Yield. Values outside parentheses are phenotypic correlations (rp), and inside are genotypic correlations (rg). Significance levels: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Plant height and days to 50% flowering were significantly positively correlated at both the genotypic and phenotypic levels, showing that taller plants tended to flower later (Table 3). Similar observations have been reported in aerobic and irrigated rice, where flowering duration was positively associated with plant vigor [58, 46].

Grain filling and density depend heavily on panicle structure, as shown by the positive correlation between test weight and panicle length. These findings confirm that a larger sink size and better resource distribution directly improve grain weight and quality (Table 3) [13].

The number of filled grains per panicle and the number of tillers per plant were negatively correlated at both the genotypic and phenotypic levels. This indicates a trade-off between panicle fertility and tiller production. Similar observations were reported in [52, 29], where excessive tillering was found to reduce grain set and sink efficiency.

Grain yield showed moderately positive correlations with both days to 50% flowering and test weight. This indicates that genotypes with superior grain filling capacity and slightly longer growth duration achieved higher yields under the experimental conditions (Table 3). Comparable results have been reported in other evaluations of rice germplasm [46, 13].

	DFF	PH	NT/Pl	NP/m2	PL	NFG/P	TW	GY
DFF	1.00	0.51	0.00	0.25	-0.07	0.10	0.07	0.22
PH	0.51	1.00	0.01	-0.04	0.16	0.17	-0.15	-0.12
NT/Pl	0.00	0.01	1.00	0.36	-0.29	-0.42	0.01	0.11
NP/m2	0.25	-0.04	0.36	1.00	0.02	-0.04	0.13	0.16
PL	-0.07	0.16	-0.29	0.02	1.00	0.13	0.40	0.02
NFG/P	0.10	0.17	-0.42	-0.04	0.13	1.00	-0.40	-0.04
TW	0.07	-0.15	0.01	0.13	0.40	-0.40	1.00	-0.03
GY	0.22	-0.12	0.11	0.16	0.02	-0.04	-0.03	1.00

Figure 2: A heatmap displaying the correlations between yield and yield-related traits in rice genotypes, both genotypically (rg) and phenotypically (rp). Green and red represent positive and negative associations, with color intensity signifying the degree of correlation.

Also, the correlation heatmap (Figure 2) gives a graphical summary of how strong and what type of associations there are. DFF's strong positive correlation with PH and PL's with TW are examples of strong positive correlations (green), which are easily recognized, and strong negative correlations (red) like NT/Pl. with NFG/P also show possible trade-offs. The stronger genotypic correlations emphasize the predominance of additive gene action in these associations, which is advantageous in rice breeding because it allows more reliable selection of yield and yield-related traits.

c. PATH ANALYSIS

The path coefficient analysis revealed different traits' direct and indirect effects on grain yield at the phenotypic and genotypic levels Table 4.

© 2025 AATCC Review. All Rights Reserved.

Table 4. Phenotypic (P) and Genotypic (G) Path Coefficients of Grain Yield and Yield-Related Traits in Rice Genotypes

Trait	DFF	PH (cm)	NT/Pl.	NP/m^2	PL (cm)	NFG/P	TW (gm)	GY (kg/ha)
DFF (G)	0.5344	-0.3099	0.0000	-0.0072	-0.0231	-0.0119	-0.0227	0.2245
DFF (P)	0.4399	-0.2221	0.0011	0.0008	-0.0151	-0.0065	-0.0148	0.2178
PH (G)	0.2725	-0.4811	0.0017	0.0011	0.0529	-0.0202	0.0486	-0.1238
PH (P)	0.2156	-0.3829	0.0000	-0.0002	0.0324	-0.0130	0.0297	-0.1185
NT/Pl. (G)	0.0000	-0.0048	0.1722	-0.0103	-0.0958	0.0499	-0.0032	0.1068
NT/Pl. (P)	0.0044	-0.0000	0.1122	0.0012	-0.0497	0.0239	-0.0021	0.0875
NP/m^2 (G)	0.1336	0.0192	0.0620	-0.0287	0.0066	0.0048	-0.0421	0.1561
NP/m^2 (P)	0.0748	0.0153	0.0258	0.0050	-0.0086	0.0036	-0.0106	0.1033
PL (G)	-0.0374	-0.0770	-0.0499	-0.0006	0.3304	-0.0155	-0.1296	0.0163
PL (P)	-0.0308	-0.0574	-0.0258	-0.0002	0.2160	-0.0080	-0.0742	0.0178
NFG/P (G)	0.0534	-0.0818	-0.0723	0.0011	0.0430	-0.1189	0.1296	-0.0449
NFG/P (P)	0.0396	-0.0689	-0.0370	-0.0002	0.0238	-0.0725	0.0785	-0.0362
TW (G)	0.0374	0.0722	0.0017	-0.0037	0.1322	0.0476	-0.3240	-0.0347
TW (P)	0.0308	0.0536	0.0011	0.0002	0.0756	0.0268	-0.2121	-0.0238

Residual effect: Genotypic = 0.6085 & Phenotypic = 0.6919

Note: DFF = Days to 50% Flowering; PH = Plant Height; NT/Pl. = Number of Tillers per Plant; NP/m^2 = Number of Panicles per m^2; PL = Panicle Length; NFG/P = Number of Filled Grains per Panicle; TW = Test Weight; GY = Grain Yield. Bold values are direct effects; other values are indirect effects.

At the phenotypic level, days to 50% flowering had a strong positive direct effect (0.4399*), emphasizing its importance in determining yield. This result is consistent with [7], who reported the significant impact of flowering time on wheat grain yield. Plant height had a negative direct effect (–0.3829*), but its indirect positive effects through other traits reduced the overall negative impact. This suggests that although taller plants may not always be advantageous, their association with yield-related traits can mitigate the direct negative contribution.

Number of tillers per plant had a moderate positive direct effect (0.1122), while number of panicles per square metre contributed only marginally (0.0050), indicating limited contributions to yield under the present conditions. Test weight and number of filled grains per panicle showed negative direct effects (–0.2121 and –0.0725), but their indirect effects partly compensated, showing that their influence operates through other traits. Panicle length exerted a strong positive direct effect (0.216 at phenotypic level; 0.3304 at genotypic level*), establishing its importance as a yield-related trait.

At the genotypic level, direct effects were generally stronger, indicating greater stability and less environmental interference. For example, days to 50% flowering had a strong positive direct effect (0.5344), while plant height contributed negatively (–0.4811). Indirect contributions were also higher at this level, particularly for test weight (0.2893) and plant height (0.3573), showing that these traits acted as important mediators. Notably, the residual effects were lower at the genotypic level (0.6085) than the phenotypic level (0.6919), confirming that genotypic path analysis explained a greater proportion of yield variation.

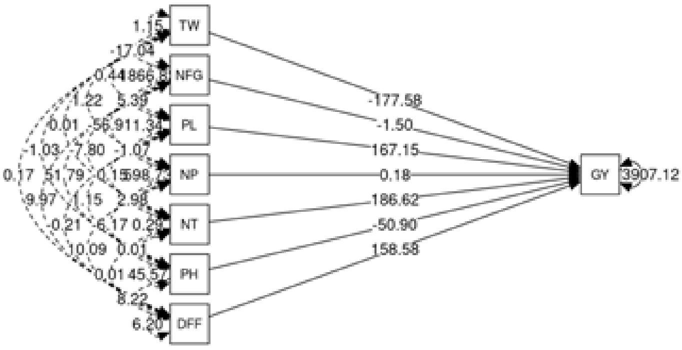


Figure 3. Path diagram showing direct and indirect effects of yield-related traits on grain yield in rice. The thickness and direction of arrows represent the magnitude and sign of effects.

The path coefficient matrix (Table 4) and the path diagram (Figure 3) illustrate these relationships, with arrows representing the magnitude and direction of effects. Overall, days to 50% flowering and panicle length emerged as the most reliable direct contributors to grain yield. In contrast, plant height, test weight, and number of tillers per plant contributed mainly through indirect pathways. These results are consistent with previous research identifying flowering duration and panicle traits as reliable selection criteria for improving yield [9, 7]. The stronger direct and indirect effects at the genotypic level confirm that these traits are under strong genetic control and can be effectively targeted in breeding programs.

d. PRINCIPAL COMPONENT ANALYSIS

Principal component analysis (PCA) was performed to evaluate the contribution of yield and yield-related traits to overall genetic variability among genotypes. The first three principal components (PCs) explained 61.51% of the total variation (Table 6). PC1 accounted for 22.58% of the variance, PC2 for 20.40%, and PC3 for 18.53%. Each additional component explained less than 14% of the variation, showing that the first three PCs sufficiently captured the main differences among traits. Similar trends in rice were reported in [19, 35].

Table 5. Trait contributions (%) to the first three principal components in rice genotypes

Trait	PC1 Contribution (%)	PC2 Contribution (%)	PC3 Contribution (%)
Days to 50% Flowering	0.11	45.38	1.56
Plant Height (cm)	7.55	28.09	0.98
Number of Tillers per Plant	31.10	3.19	5.32
Number of Panicles per m^2	13.38	13.10	0.92
Panicle Length (cm)	3.70	0.25	46.07
Number of Filled Grains/ Panicle	31.91	2.35	1.19
Test Weight (gm)	8.55	1.43	43.95
Grain Yield (kg/ha)	3.71	6.22	0.00

© *2025 AATCC Review.* All Rights Reserved.

Table 6. Eigenvalues, variance explained, and cumulative variance explained by principal components

Principal Component	Eigenvalue	Variance Explained (%)	Cumulative Variance (%)
PC1	1.81	22.58	22.58
PC2	1.63	20.40	42.98
PC3	1.48	18.53	61.51
PC4	1.07	13.39	74.90
PC5	0.85	10.67	85.57
PC6	0.66	8.25	93.83
PC7	0.32	4.01	97.84
PC8	0.17	2.16	100.00

The number of tillers per plant (31.10%) and the number of filled grains per panicle (31.91%) contributed the most to PC1, followed by the number of panicles per m^2 (13.38%) and test weight (8.55%) (Table 5). This shows that tillering ability and grain number were the primary sources of variability among genotypes in PC1. Similar importance of these traits was reported in [24, 22]. Plant height (28.09%) and days to 50% flowering (45.38%) contributed the most to PC2, along with the number of panicles per m^2 (13.10%), showing that maturity and plant stature essentially explained variation along this axis. Comparable findings were reported in [53].
PC3 was mainly explained by test weight (43.95%) and panicle length (46.07%), while the number of tillers per plant contributed less (5.32%). This axis reflected variation associated with panicle structure and grain size. Comparable results were reported in [33]. In breeding terms, these results show that PC1 was dominated by fertility and tillering traits, PC2 by maturity duration and plant height, and PC3 by panicle and grain traits. Selecting parents from contrasting PCs increases the probability of generating superior recombinants, as also suggested in [38, 15]. The PCA biplot (Figure 4) further illustrates these associations, where vectors indicate trait contributions and genotype positions reflect variability patterns across PC1 & Pc2.

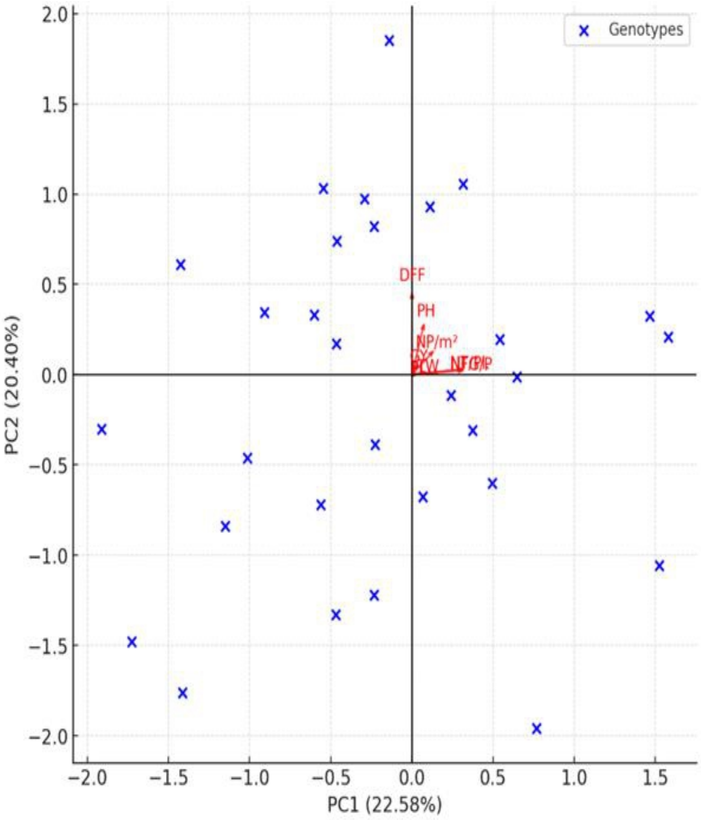


Figure 4. Illustrates the PCA biplot of the rice genotypes and the yield correlates. The first two principal components of the PCA, PC1 and PC2, respectively accounting for 22.58% and 20.40% of the variance, cumulatively account for 43% of the total variance. Figure 4 reveals that days to 50% flowering and plant height had a strong association as they clustered along PC2. The grain yield was strongly associated with the number of panicles per square metre and the number of tillers per plant, as they were clustered together in the positive axis of PC1. However, test weight and panicle length exhibited movement in opposite directions, indicating a trade-off between panicle architecture and the weight of the grain.

e. CLUSTERING

Hierarchical cluster analysis grouped the genotypes into three clusters based on yield and yield-related traits (Table 7 and Figure 5).

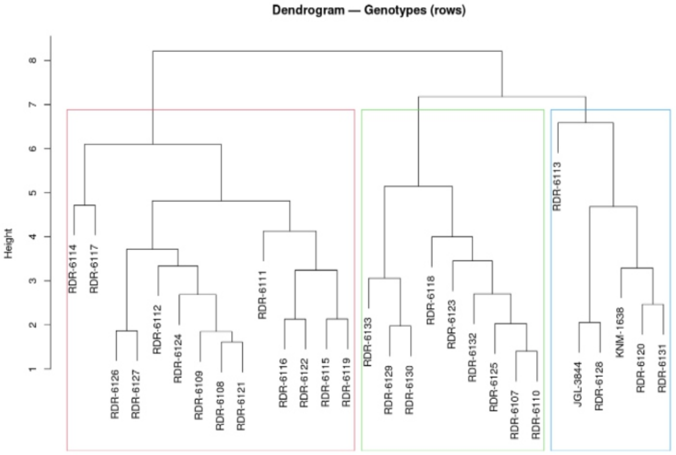


Figure 5. Dendrograms show the hierarchical clustering of rice genotypes based on yield and yield-related traits, which are grouped into three major clusters, indicating genetic diversity and trait-based similarities.

© *2025 AATCC Review.* All Rights Reserved.

Table 7. Cluster-wise mean (±SD) values of yield and yield-related traits in rice genotypes

Trait	Cluster I	Cluster II	Cluster III
Days to 50% flowering	93.50 ± 0.71	94.67 ± 0.87	94.78 ± 0.57
Plant height (cm)	121.42 ± 4.04	116.73 ± 2.36	117.32 ± 2.87
Number of tillers per plant	8.58 ± 0.33	8.80 ± 0.26	8.65 ± 0.25
Number of panicles per m^2	344.92 ± 9.54	349.33 ± 7.98	355.35 ± 6.37
Panicle length (cm)	24.42 ± 0.74	24.53 ± 0.49	23.80 ± 0.61
Number of filled grains per panicle	301.92 ± 9.24	279.53 ± 13.15	301.10 ± 7.68
Test weight (gm)	14.00 ± 0.53	14.27 ± 0.45	13.42 ± 0.52
Grain yield (kg/ha)	4843.58 ± 285.63	7796.67 ± 382.24	6701.33 ± 317.01

Cluster I contained six genotypes, including KNM-1638 and JGL-3844. This group was distinguished by early flowering, moderate plant height, and superior tillering ability. It also recorded the highest test weight and grain yield among clusters, suggesting that a combination of tillering capacity and heavier grains primarily drove yield in this group.

Cluster II included nine genotypes, such as RDR-6107 and RDR-6130. This cluster was characterized by intermediate plant height, moderate flowering, and the longest panicles among the groups. Although panicle length and grain number per panicle were relatively high, the average grain yield was lower. This demonstrates that panicle elongation alone cannot enhance productivity without complementary yield attributes.

Cluster III was the largest, with 14 genotypes including RDR-6108 and RDR-6127. This cluster consisted of taller, later-flowering genotypes that produced the highest number of panicles per unit area and more filled grains per panicle. Although its average yield was slightly lower than Cluster I, productivity in this group was clearly supported by panicle density and grain number rather than by grain size.

Finally, Cluster I relied on tillering ability and grain weight, Cluster II emphasized panicle length with limited yield efficiency, and Cluster III achieved yield through panicle density and grain number. The distinct trait combinations highlight valuable diversity, with Clusters I and III offering complementary parents for exploiting heterosis and achieving transgressive segregants in breeding programs.

Boxplots were created for each yield and yield-related trait to further show the cluster variations (Figure 6). The three groups' characteristics were clearly distinguished from one another. Despite having moderate plant height, Cluster I produced more because of its superior grain weight and tillering. The highest grain yield resulted from Cluster II's combination of the longest panicles, the most tillers per plant, and higher test weight. However, there were fewer grains per panicle, which limited this group. Cluster III achieved yield using a different approach that depended on the highest panicle density and number of grains per panicle; however, this was counterbalanced by shorter panicles and lower test weight.

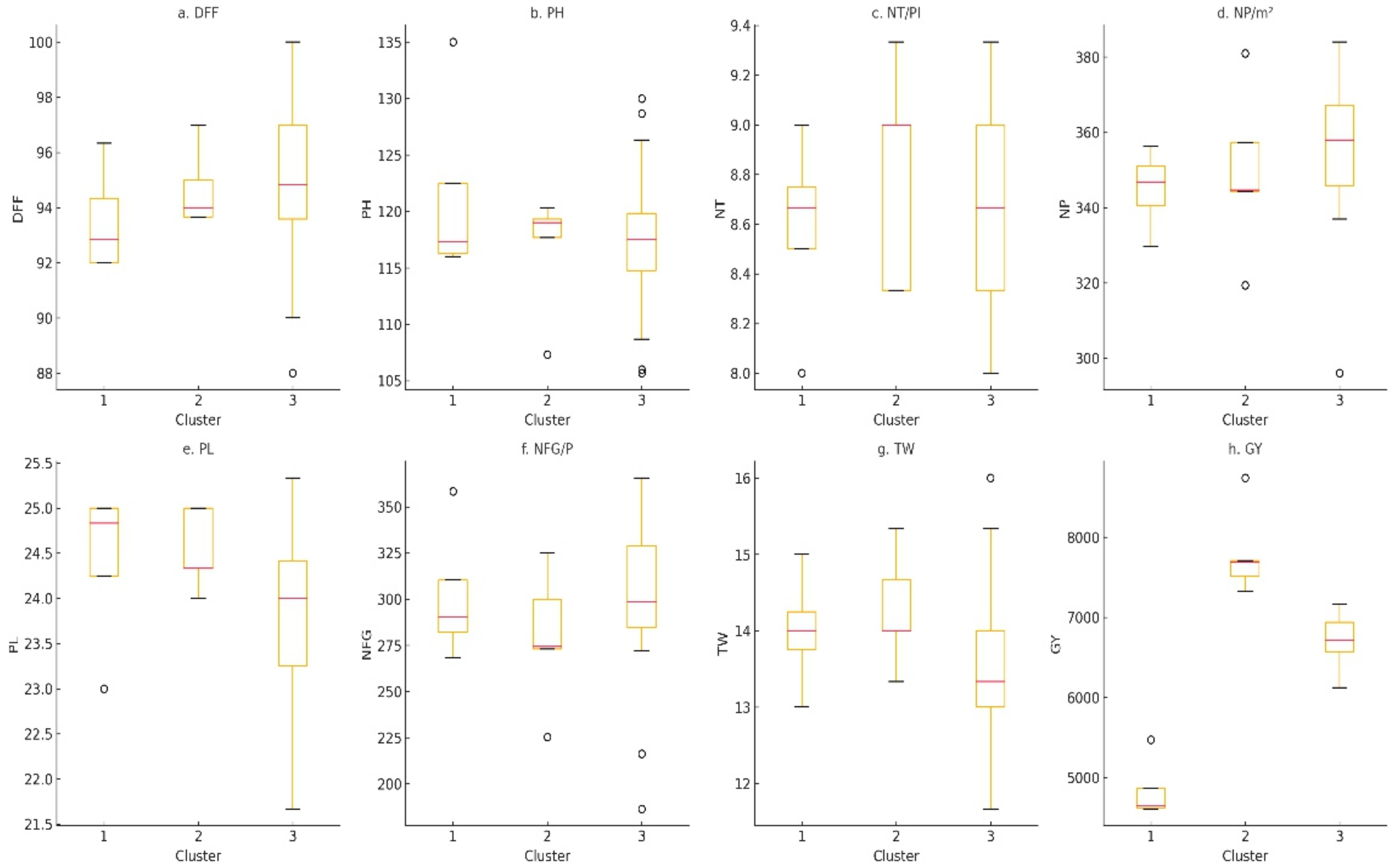


Figure 6. Boxplots showing comparative variation in yield and yield-related traits among three genotype clusters derived from hierarchical cluster analysis. Traits include: (a) DFF, days to 50% flowering; (b) PH, plant height (cm); (c) NT/Pl., number of tillers per plant; (d) NP/m^2, number of panicles per m^2; (e) PL, panicle length (cm); (f) NFG/P, number of filled grains per panicle; (g) TW, test weight (g); and (h) GY, grain yield (kg ha^{-1}).

© *2025 AATCC Review.* All Rights Reserved.

BREEDING IMPLICATIONS

The present study highlights the breeding value of key yield components such as test weight, number of filled grains per panicle, and panicle length, which contributed positively to grain yield and should form the basis of a trait-specific selection index. Correlation and path analyses confirmed that panicle number, grain number, and grain weight strongly affected yield, while PCA emphasized their collective contribution to overall variability. Cluster analysis further supported donor identification, with Cluster I genotypes excelling in grain weight, Cluster II in tillering and panicle length, and Cluster III in panicle density and grain number. These complementary trait combinations represent reservoirs of advantageous alleles that can be strategically deployed in ICAR and AICRIP breeding pipelines, while high-yielding outliers detected through boxplot analysis may serve as immediate donors in pre-breeding programs.

From a breeding strategy perspective, the most promising avenue lies in crossing divergent parents from Clusters II and III, which is expected to generate heterotic hybrids and transgressive segregants by integrating heavier grains with superior panicle density and grain number. Beyond conventional hybridization, these donors also provide scope for QTL pyramiding through marker-assisted selection, particularly for grain yield, test weight, panicle length, and filled grains per panicle that exhibited strong additive control. Coupled with modern tools such as genomic selection and high-throughput phenotyping, these approaches will accelerate the stacking of favorable alleles, enabling the development of climate-resilient, high-yielding, and widely adaptable rice cultivars.

CONCLUSION

This study demonstrated substantial genetic variability among rice genotypes for yield and its component traits, with test weight, panicle length, number of filled grains per panicle, and grain yield emerging as reliable targets for direct selection. Multivariate analyses consistently identified panicle number, grain weight, and grain number as the most influential drivers of yield variation. At the same time, clustering confirmed the presence of complementary donor pools offering contrasting trait combinations.

Conflict of Interest

The authors declare that they have no conflict of interest.

Acknowledgments

The authors gratefully acknowledge the financial support and research facilities provided by Professor Jayashankar Telangana Agricultural University (PJTAU). We also sincerely thank the Regional Sugarcane and Rice Research Station (RS & RRS), Rudrur, Rice Breeding staff for their dedicated support in experimental management, data recording, and field operations throughout the study.

References

1. Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in upland cotton cross of interspecific origin. *Agron J*. 1958;50:633–636.
2. Anshuman V, Kumar P, Meena RK. Genetic variability for plant height and yield traits in rice. *J Crop Improv*. 2020;34(4):456–465.
3. Barde NK, Tiwari VK, Singh M. Trait association studies in rice. *Indian J Agric Sci*. 2024;94(4):523–529.
4. Bose LK, Singh R, Sharma A. Yield components and genetic control in irrigated rice. *Rice Sci*. 2024;31(2):95–104.
5. Burton GW. Quantitative inheritance in grasses. *Proc 6th Int Grassl Congr*. 1952;1:277–283.
6. Chakraborty S, Saha S, Roy P. Genetic variability of rice germplasm across environments. *Indian J Genet*. 2021;81(2):181–188.
7. Chaudhari PR, Singh N, Sharma R. Quantitative genetics of rice yield. *Theor Appl Genet*. 2025;138(6):1123–1135.
8. Das B, Swain D, Bastia DK. Genetic parameters of panicle length in rice. *Oryza*. 2019;56(3):223–229.
9. Friedli CJ, van Eeuwijk FA, Bustos-Korts D. Multi-environment trials and yield component contributions in cereals. *Field Crops Res*. 2025;315:109178.
10. Girish G, Prakash J, Sharma R. Heritability and variability of rice traits. *Electron J Plant Breed*. 2016;7(3):768–774.
11. Hasan MJ, Kulsum U, Akter A. Genetic variability and heritability in rice. *Bangladesh J Agril Res*. 2015;40(3):419–430.
12. Heera P, Roy A, Pradhan SK. Genetic analysis of panicle traits in rice. *Indian J Plant Genet Resour*. 2025;38(1):22–29.
13. Huang X, Zhao Y, Li J. Advances in rice genomic selection and phenotyping. *Front Plant Sci*. 2024;15:1297.
14. Islam A, Sarker M, Rahman M. Genetic variability for yield traits in rice germplasm. *Bangladesh J Agril Res*. 2025;50(1):15–26.
15. Islam MA, Rahman MA, Hossain MA. Genetic diversity and PCA in rice. *Bangladesh J Plant Breed Genet*. 2022;35(2):25–34.
16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J*. 1955;47:314–318.
17. Jolliffe IT. Principal Component Analysis. 2nd ed. Springer, New York; 2002.
18. Kaiser HF. The application of electronic computers to factor analysis. *Educ Psychol Meas*. 1960;20:141–151.
19. Kalimuthu S, Sundaram RM, Laha GS. Genetic diversity studies in rice. *Electron J Plant Breed*. 2020;11(3):795–802.
20. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol Biol*. 2005;59:1–6.
21. Kumari R, Patel SR, Choudhary AK. Genetic variability of quantitative traits in rice. *Electron J Plant Breed*. 2021;12(2):567–573.

© *2025 AATCC Review.* All Rights Reserved.

22. Kumari S, Singh PK, Sharma N. Principal component analysis for yield traits. *J Rice Res*. 2018;11(1):23–29.

23. Li ZK, Pinson SR, Park WD. Epistasis for yield traits in rice. *Genetics*. 2003;165(4):1947–1962.

24. Nandan R, Kumar P, Singh P. PCA for yield traits in rice. *Indian J Agric Sci*. 2010;80(5):423–426.

25. Ngangkham U, Parameswari C, Choudhury DR. Genetic diversity and test weight variability in rice. *Rice Sci*. 2018;25(1):11–21.

26. Panse VG, De Vane EH. Genetic variability in quantitative characters of rice. *Indian J Genet Plant Breed*. 1957;17:318–328.

27. Peng S, Khush GS, Virk P. Strategies for breeding hybrid rice for yield. *Field Crops Res*. 2008;108(1):15–29.

28. Pradhan SK, Nayak DK, Bose LK. Path analysis for yield and traits in rice. *J Genet Breed*. 2025;79(3):45–53.

29. Pradhan SK, Nayak DK, Bose LK. Trait association under irrigated rice. *Indian J Genet*. 2023;83(1):49–57.

30. Pratap A, Mehandi S, Kumar J. Genetic variability for yield and its components in rice. *J Agric Sci Technol*. 2018;20(3):615–624.

31. Puri RR, Singh A, Sharma R. Association and path coefficient analysis of rice yield. *J Crop Improv*. 2025;39(2):167–178.

32. R Core Team. R: A Language and Environment for Statistical Computing. Version 4.5.1. R Foundation for Statistical Computing, Vienna, Austria; 2025.

33. Ramesh K, Rao PR, Kumar G. Principal component analysis of rice. *Oryza*. 2017;54(4):354–360.

34. Rana JC, Sharma TR, Negi KS. Variability studies in rice germplasm. *Indian J Plant Genet Resour*. 2020;33(1):39–46.

35. Rani P, Kumari A, Rao S. Principal component analysis of rice germplasm. *Oryza*. 2021;58(2):112–118.

36. Rani P, Rao S, Prasad GSV. Genetic variability of yield traits in rice. *J Rice Res*. 2017;10(1):14–19.

37. Reddy VR, Babu VR, Ramesh MS. Heritability and genetic advance of test weight in rice. *Int J Curr Microbiol App Sci*. 2019;8(5):1029–1036.

38. Roy D, Barman H, Saha S. Genetic variability in rice under irrigated ecosystem. *J Cereal Res*. 2020;12(3):225–231.

39. Roy D, Saha S, Barman H. Cluster analysis for genetic diversity in rice. *J Cereal Res*. 2025;15(1):33–41.

40. Sarawgi AK, Rastogi NK, Soni DK. Variability and heritability in rice. *Oryza*. 2018;55(1):52–58.

41. Satheeshkumar P, Saravanan K, Senthil N. Genetic variability for panicle traits in rice. *Electron J Plant Breed*. 2017;8(1):238–244.

42. Sharma V, Patel S, Kumar A. Analysis of variance for yield-related traits in cereals. *Indian J Genet Plant Breed*. 2024;84(3):289–296.

43. Singh AK, Singh R, Singh S. Genetic parameters for yield traits in rice. *Oryza*. 2019;56(1):30–35.

44. Singh N, Sharma P, Chauhan V. Stability of flowering traits in irrigated rice. *Indian J Plant Physiol*. 2018;23(4):628–636.

45. Singh R. Rice and global food security. *Indian J Genet Plant Breed*. 2024;84(2):145–152.

46. Singh RK, Sharma P, Gupta R. Genetic variability of yield components in rice. *J Plant Biochem Biotechnol*. 2023;32(2):317–325.

47. USDA. Rice Outlook: 2024–2025. US Department of Agriculture, Economic Research Service. 2024. Available at: https://ers.usda.gov

48. Verma P, Kumari S, Singh RK. Genetic advance and heritability of yield traits in rice. *J Cereal Res*. 2022;14(1):14–21.

49. Ward JH. Hierarchical grouping to optimize an objective function. *J Am Stat Assoc*. 1963;58:236–244.

50. Wickham H. ggplot2: Elegant Graphics for Data Analysis. Springer, New York; 2016.

51. Wright S. Correlation and causation. *J Agric Res*. 1921;20:557–585

52. Yadav AK, Singh R, Verma P. Excessive tillering and yield trade-offs in rice. *Field Crops Res*. 2022;280:108963.

53. Yadav R, Chauhan B, Sharma V. Genetic diversity for yield and maturity traits in rice. *J Genet*. 2019;98:56.

54. Yadav R, Singh PK, Kumar A. Genetic variability for tillering in rice. *J Cereal Res*. 2021;13(2):145–151.

55. Yadav S, Kumar P, Singh NK. Trait association and yield components in rice. *Field Crops Res*. 2024;301:108949.

56. Yang W, Feng H, Zhang X. Advances in 3D phenotyping of rice panicle traits. *Plant Phenomics*. 2024;2024:112045.

57. Zhang Q, Li J, Xue Y. Genetics of panicle traits in rice. *Plant Sci*. 2016;242:9–18.

58. Zhao K, Tung CW, Eizenga GC. Genome-wide association mapping in rice. *Nat Genet*. 2021;53:789–798.

59.

© *2025 AATCC Review.* All Rights Reserved.