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GENETIC VARIABILITY AND MULTIVARIATE ANALYSIS OF YIELD AND GRAIN QUALITY TRAITS IN F₃ RICE (*Oryza sativa* L.) SEGREGANTS DERIVED FROM KPR-1 × BPT-5204

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ABSTRACT

The present study was carried out to evaluate genetic variability and multivariate divergence among rice genotypes for grain yield and related traits in the F₃ generation of the cross KPR-1 × BPT-5204. One hundred segregating F₃ lines along with six checks were evaluated in an augmented design during *Kharif* 2025 at AHRS, Kathalagere. Observations were recorded for phenological, plant architectural, yield and grain quality traits. Estimates of genetic parameters showed high GCV and PCV for number of tillers per plant (21.68% and 27.14%, respectively). Grain yield per plant, number of grains per panicle and number of productive tillers per plant exhibited moderate variability. High heritability coupled with high genetic advance as per cent of mean was observed for number of tillers per plant and protein content, indicating the predominance of additive gene action and effectiveness of direct selection for these traits. Principal component analysis revealed that the first five components with eigenvalue greater than 1 explained 68.44 per cent of the total variation, with major contributions from plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per panicle and grain yield per plant. Among the evaluated material, F₃ entries E-46, E-43, E-55, E-36 and E-45 emerged as the promising segregants based on superior grain yield per plant and desirable yield-contributing traits.

Key words: Rice, F₃ segregating population, Genetic variability, Heritability, Principal Component Analysis (PCA).

Introduction

Rice (*Oryza sativa* L.) remains the principal staple cereal for more than half of the world's population, with the majority of production and consumption concentrated in Asia. Rice provides nearly 20% of the world's dietary energy. It is mainly composed of starch (78–79%) and is also a valuable source of protein, vitamins and essential minerals such as iron, phosphorus and magnesium along with B vitamins including thiamine and niacin (Ali *et al.*, 2026). In India, rice occupies a central place in both the cropping system and the national diet. Continued gain in productivity is essential to meet the food demands of a growing population against a backdrop of shrinking

cultivable land and increasing pressure from biotic and abiotic stresses. Meeting this demand calls for a steady supply of improved varieties combining high yield potential with desirable grain quality. The development of such varieties largely depends on the genetic variability and diversity available to the breeder.

Genetic variability is the raw material of any crop improvement programme. Without adequate heritable genetic variation for grain yield and its component traits, even carefully practiced selection cannot bring about meaningful genetic gain. Breeders therefore continually seek to generate, characterize and exploit variability through hybridization between genetically diverse parents,

followed by selection in the segregating generations that follow. Among the segregating generations, the F_3 generation occupies a particularly important position. At this stage, the variability generated through recombination in the F_2 generation becomes more clearly expressed and partially stabilized. This provides breeders with an opportunity to identify superior segregants and estimate genetic parameters such as heritability and genetic advance with greater precision (Venkatesan *et al.*, 2019). Parameters such as genotypic and phenotypic coefficients of variation, heritability in the broad sense and genetic advance as a percentage of mean together indicate not only how much variation exists but also how effectively it can be fixed through selection. Traits governed largely by additive gene action, reflected in high heritability coupled with high genetic advance, are particularly amenable to improvement through simple selection methods. Whereas traits under strong non-additive or environmental influence require more elaborate breeding strategies (Johnson *et al.*, 1955; Falconer and Mackay, 1996).

Beyond estimating variability for individual traits, it is equally important to understand how the traits that make up yield are structured in relation to one another and which of them account for the greatest share of the total variation present in a population. Genetic diversity is commonly assessed using multivariate statistical techniques, which analyse several traits simultaneously to classify genotypes based on their overall variation. Multivariate statistical methods such as Principal Component Analysis (PCA), cluster analysis, and discriminant function analysis facilitate the classification of genotypes by simultaneously evaluating variation in agro-morphological and quality traits. Among these methods, Principal Component Analysis (PCA) is widely used to reduce the complexity of multivariate data by transforming correlated traits into a few principal components that explain most of the variation. Traits with higher component loadings contribute more to genotype differentiation. Therefore, PCA provides an efficient approach for identifying the major traits responsible for genetic diversity and selecting diverse genotypes for crop improvement (Sao *et al.*, 2020). In the present study, PCA was employed to evaluate agro-morphological and quality traits in rice, with the aim of identifying diverse genotypes that can be utilized in future breeding programmes. Accordingly, this study was conducted to evaluate genetic variation, heritability and diversity for yield and related traits, with the objective of identifying promising genotypes and key characters for rice breeding programmes.

Materials and Methods

The present investigation was carried out during Kharif 2025 at the Agricultural and Horticultural Research Station (AHRS), Kathalagere, under the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. The experimental material comprised 100 F_3 breeding lines derived from the cross KPR-1 $\times$ BPT-5204, along with six check varieties, evaluated using an augmented design. Entries were transplanted 21 days after sowing at a spacing of 20 $\times$ 15 cm. Observations were recorded for quantitative traits viz., days to 50 per cent flowering, days to maturity, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, spikelet fertility, test weight, L/B ratio, grain yield per plant and quality traits namely carbohydrate and protein content. Adjusted mean data were subjected to Analysis of Variance as per the procedure applicable to Augmented Design, and genetic variability parameters viz., phenotypic and genotypic coefficients of variation were estimated as per Burton (1952), heritability in broad sense by Burton and De Vane (1953) and genetic advance as per cent of mean by Johnson *et al.*, (1955). Diversity analysis was carried out through Principal Component Analysis (PCA), wherein eigenvalues and eigenvectors were computed to identify the principal components contributing to total variability. The genotypes were plotted on a two-dimensional scatter diagram based on the scores of the first two principal components (PC1 and PC2) using R software (R 4.6.0).

Results and Discussion

Assessment of Genetic Variability Parameters

The analysis of genetic variability revealed the presence of considerable variation among the F_3 rice genotypes for all the characters studied (Table 1). In the present investigation, the phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits, indicating the influence of environmental factors on expression of these characters. However, the relatively narrow difference between PCV and GCV observed for traits such as length–breadth ratio, carbohydrate content and protein content suggested that these characters were less influenced by the environment and were predominantly governed by genetic factors. Similar findings were observed by Mahesh *et al.*, (2022) and Roy *et al.*, (2021).

High GCV and PCV were observed for number of tillers per plant (21.68% and 27.14%, respectively), indicating the presence of substantial genetic variability

Table 1: Estimates of Variability Parameters in F₃ generation of rice.

Trait	Mean	Range		GCV (%)	PCV (%)	h ² BS (%)	Class	GA	GAM (%)	Class
		Min	Max							
DDF	114.09	109.00	120.75	0.79	1.68	22.16	Low	0.87	0.77	Low
DM	146.92	139.50	155.00	1.31	1.66	62.09	High	3.12	2.12	Low
PH	85.10	72.06	106.84	4.91	6.20	62.66	High	6.82	8.02	Low
PL	19.58	13.15	25.93	8.52	11.73	52.80	Medium	2.50	12.78	Medium
NT	12.90	5.48	23.93	21.68	27.14	63.83	High	4.61	35.74	High
NPT	9.91	5.18	16.07	19.11	25.61	55.72	Medium	2.92	29.43	High
NG	201.08	139.19	328.02	11.98	16.05	55.68	Medium	37.07	18.43	Medium
SF	84.55	65.51	92.94	1.89	5.28	12.87	Low	1.18	1.40	Low
TW	20.35	15.89	29.83	5.18	9.65	28.86	Low	1.17	5.74	Low
LBR	3.20	2.55	4.33	7.68	8.26	86.30	High	0.47	14.71	Medium
CHO	71.88	49.76	78.87	4.83	5.54	75.96	High	6.24	8.68	Low
PRO	8.56	6.34	10.86	9.98	10.22	95.32	High	1.72	20.10	High
GY	26.82	18.87	40.39	11.79	14.76	63.82	High	5.21	19.43	Medium

DDF – Days to 50 per cent flowering; DM – Days to maturity; PH – Plant height (cm); PL – Panicle length (cm); NT – Number of tillers per plant; NPT – Number of productive tillers per plant; NG – Number of grains per panicle; SF – Spikelet fertility (%); TW – Test weight (g); LBR – Length to breadth ratio; PRO – Protein content (g per 100 g); CHO – Carbohydrate content (g per 100 g); GY – Grain yield per plant (g)

and greater scope for improvement through selection. Higher GCV and PCV were earlier reported by Debsharma *et al.*, (2022). Moderate GCV and high PCV were recorded for number of productive tillers per plant (19.11% and 25.61%, respectively) whereas number of grains per panicle (11.98% and 16.05%, respectively) and grain yield per plant (11.79% and 14.76%, respectively) exhibited moderate GCV and PCV suggesting the existence of moderate variability for these traits, which were similar to the findings of Divya *et al.*, (2018). Low GCV and PCV were observed for days to 50% flowering, days to maturity, plant height, spikelet fertility, L/B ratio, test weight and carbohydrate content, indicating limited genetic variability for these traits and a greater influence of environmental factors on their expression. Similar observations have been reported in rice by Ghosh and Sharma (2012) and Sravani *et al.*, (2022). The low estimates of GCV indicate limited genetic variability and comparatively greater environmental influence on the expression of these traits.

Heritability estimates ranged from 12.87% for spikelet fertility to 95.32% for protein content. High heritability (>60%) was observed for protein content (95.32%), length to breadth ratio (86.30%), carbohydrate content (75.96%), number of tillers per plant (63.83%), grain yield per plant (63.82%), plant height (62.66%) and days to maturity (62.09%), indicating that a major proportion of the observed variation for these traits was genetic in nature. High heritability for these characters was reported by Ghosh and Sharma (2012), Roy *et al.*, (2015), Anis *et al.*, (2016), Singh *et al.*, (2022) and

Sravani *et al.*, (2022). Moderate heritability was recorded for panicle length (52.80%), number of productive tillers per plant (55.72%) and number of grains per panicle (55.68%). Whereas days to 50% flowering, spikelet fertility and test weight exhibited low heritability, indicating a greater influence of environmental factors on these traits.

Heritability estimates alone are not sufficient for predicting the effectiveness of selection and should be considered along with genetic advance as per cent of mean (GAM). High heritability coupled with high GAM was observed for number of tillers per plant (63.83% and 35.74%, respectively) and protein content (95.32% and 20.10%), indicating the predominance of additive gene action and suggesting that direct selection for these traits would be highly effective. Similar findings were reported by Debsharma *et al.*, (2023), Niharika *et al.*, (2022) and Umamaheswar *et al.*, (2024). Number of productive

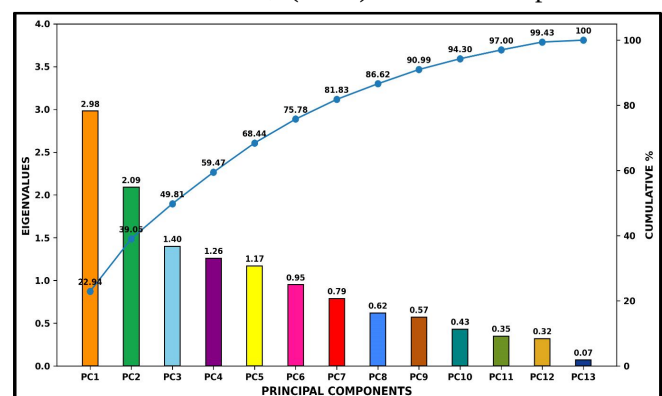
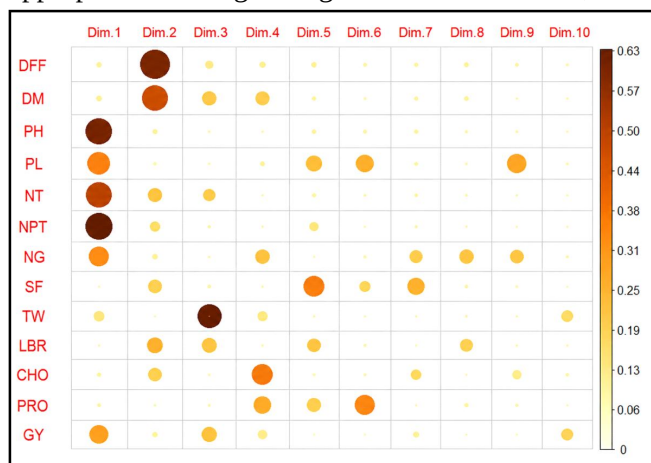
**Fig. 1:** Scree Plot showing Eigenvalues of Principal Components.

Table 2: Principal component analysis and vector loadings for grain yield and related traits in F_3 generation of rice

PCs	PC 1	PC 2	PC 3	PC 4	PC 5
Eigen Value	2.98	2.10	1.40	1.26	1.17
Percentage of Variance (%)	22.94	16.12	10.76	9.66	8.97
Cumulative Percentage (%)	22.94	39.05	49.81	59.47	68.44
Eigen vectors					
Days to 50% flowering	-0.14	0.77	-0.03	0.28	0.23
Days to maturity	-0.18	0.67	0.26	0.39	0.22
Plant height (cm)	0.77	-0.22	-0.02	-0.01	0.20
Panicle length (cm)	0.58	-0.05	0.01	0.22	0.32
No. of tillers	0.72	0.41	-0.37	-0.04	-0.23
No. of Productive tillers per plant	0.79	0.35	-0.25	-0.05	-0.30
No. of grains per panicle	0.58	-0.22	-0.04	0.43	0.02
Spikelet fertility (%)	-0.06	-0.42	0.23	0.13	-0.58
Test weight (g)	0.32	-0.01	0.78	-0.21	0.17
Length to breadth ratio	0.08	-0.51	-0.43	-0.10	0.47
Carbohydrate content (%)	-0.21	-0.43	-0.11	0.60	0.21
Protein content (%)	-0.27	-0.04	-0.20	0.52	-0.37
Grain yield per plant (g)	0.54	-0.19	0.48	0.31	-0.12

tillers per plant showed moderate heritability (55.72%) coupled with high GAM (25.61%), indicating the possibility of improvement through selection despite moderate genetic control.

High heritability associated with moderate GAM was observed for length to breadth ratio (86.30% and 14.71%, respectively) and grain yield per plant (63.82% and 19.43%, respectively), while number of grains per panicle exhibited moderate heritability with moderate GAM. These combinations suggest the involvement of both additive and non-additive gene effects, and improvement in these traits through selection may be possible with appropriate breeding strategies. On the other hand, traits

**Fig. 2:** Correlation plot depicting contribution of yield related traits to principal components in F_3 generation of rice.

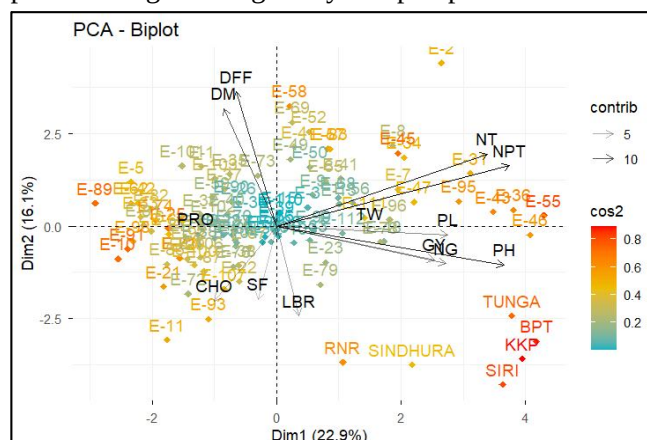
such as days to maturity, plant height and carbohydrate content exhibited high heritability coupled with low GAM, whereas days to 50% flowering, spikelet fertility and test weight showed low heritability with low GAM. These results indicate the predominance of non-additive gene action and/or greater environmental influence, suggesting that direct selection for these traits may be less effective in early generations.

Overall, the results indicate that number of tillers per plant, protein content and grain yield per plant possess substantial genetic variability and favourable genetic parameters, making them promising selection criteria for the genetic improvement of rice.

Principal Component Analysis

Principal component analysis (PCA) was performed to assess the pattern of genetic diversity and to identify the major traits contributing to the total variation among the F_3 rice genotypes. Thirteen quantitative characters were reduced into thirteen principal components, of which the first five principal components (PCs) possessed eigenvalues greater than one and together explained 68.44% of the total phenotypic variation. The first principal component (PC1) accounted for 22.94% of the total variation, followed by PC2 (16.12%), PC3 (10.76%), PC4 (9.66%) and PC5 (8.97%). The scree plot (Fig. 1) showed a sharp decline in eigenvalues after the fifth principal component, indicating that the first five principal components adequately explained most of the variability present among the genotypes. Similar method of principal component analysis in rice was done by Srivastava *et al.*, (2017), Sudeepthi *et al.*, (2020), Thakur *et al.*, (2023) and Reddy *et al.*, (2019).

Table 2 and Correlation plot (Fig. 2) revealed that number of tillers per plant, number of productive tillers per plant, plant height, number of grains per panicle, panicle length and grain yield per plant contributed

**Fig. 3:** PCA biplot illustrating diversity for grain yield and related traits in F_3 generation of rice.

positively towards PC1, indicating that these traits were the major contributors to the observed genetic variability. In contrast, days to 50% flowering, days to maturity, protein content and carbohydrate content exhibited negative loadings on PC1. On PC2, days to 50% flowering, days to maturity, number of tillers per plant and number of productive tillers per plant showed positive contributions, whereas length to breadth ratio, spikelet fertility, carbohydrate content and grain yield per plant contributed negatively.

The PCA biplot (Fig. 3) provided an integrated representation of the relationships among the F₃ rice genotypes and the measured quantitative traits. The first two principal components explained 22.9% (PC1) and 16.1% (PC2) of the total phenotypic variation, accounting for 39.0% of the overall variability. This distribution indicates that the first two components effectively summarized the major sources of variation present in the segregating population.

The arrangement of trait vectors in the biplot showed that plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, test weight and grain yield per plant were oriented in a similar direction, indicating a positive association among these characters. Their close proximity suggests that these traits contributed jointly to the variation represented by PC1 and collectively influenced grain yield. The observed relationship implies that selection for these attributes may simultaneously improve yield performance in the breeding population.

In contrast, days to 50% flowering (DFF) and days to maturity (DM) occupied a different region of the biplot, indicating that these phenological traits contributed to variation independently of the major yield-related characters. Their distinct orientation suggests that differences in flowering and maturity duration were governed by a separate source of variation, largely represented by the second principal component.

The distribution of genotypes across the biplot revealed substantial genetic variability within the F₃ population. Several promising entries, including E-46, E-43, E-55, E-36 and E-45 were positioned in the positive direction of PC1, close to the vectors representing grain yield and its associated traits. Their location indicates superior performance for important yield-contributing characters and highlights their potential for further advancement in subsequent generations.

Conversely, genotypes positioned on the negative side of PC1 were located away from the major yield-associated vectors, suggesting comparatively lower

expression of these desirable traits. Many entries clustered near the origin, reflecting average performance and a relatively smaller contribution to the total genetic divergence observed among the segregating lines.

The check varieties (KKP-5, BPT-5204, Tunga, Sahyadri Sindhura, Sahyadri Siri and RNR-15048) were clearly separated from most of the F₃ progenies, indicating considerable divergence between the checks and the derived segregating population. This separation demonstrates the effectiveness of hybridization and recombination in generating broad genetic variability.

Overall, the PCA biplot identified plant height, number of tillers, number of productive tillers, panicle length, number of grains per panicle, test weight and grain yield per plant as the major traits responsible for the observed genetic variation among the F₃ lines. The association of superior genotypes with these trait vectors indicates their usefulness in identifying promising segregants for selection. Therefore, the PCA biplot proved to be an effective multivariate approach for visualizing trait relationships, assessing genetic diversity, and selecting desirable genotypes for future rice improvement programmes.

Conclusion

The present investigation demonstrated the existence of substantial genetic variability among the F₃ segregating lines of rice derived from the cross KPR-1 × BPT-5204, indicating considerable scope for genetic improvement through selection. Estimates of genetic parameters revealed high genotypic and phenotypic coefficients of variation for number of tillers per plant, while high heritability coupled with high genetic advance was observed for number of tillers per plant and protein content, suggesting the predominance of additive gene action and the effectiveness of direct selection for these traits. Grain yield per plant, number of productive tillers per plant, and number of grains per panicle also exhibited favourable variability and can be considered important selection criteria in early segregating generations. Principal Component Analysis identified five principal components with eigenvalues greater than one, accounting for 68.44% of the total phenotypic variation. Traits such as plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, and grain yield per plant were the major contributors to genetic divergence among the F₃ lines. The PCA biplot further identified promising segregants, particularly E-46, E-43, E-55, E-36 and E-45, which were closely associated with desirable yield contributing traits and therefore represent valuable

breeding materials for further evaluation and advancement. Overall, the combined use of genetic variability parameters and principal component analysis was found to be effective in identifying superior genotypes and key yield-related traits. These findings provide a reliable basis for selection in subsequent generations and will facilitate the development of high-yielding rice varieties with improved agronomic performance and grain quality.

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Declaration of Competing Interest

The authors confirm that there are no known financial or personal conflicts of interest that may have influenced the outcomes or interpretation of this research.

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