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## ASSESSMENT OF VARIABILITY AND TRAITS ASSOCIATION IN RICE (*Oryza sativa* L.) GENOTYPES THROUGH CORRELATION AND PRINCIPAL COMPONENT ANALYSIS

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### ABSTRACT

Rice (*Oryza sativa* L.), a member of the Poaceae family, is among the most widely cultivated and consumed cereal crops worldwide, serving as the primary food source for over half of the global population. The crop is believed to have originated in Asia, particularly in India and China, and is grown extensively under a wide range of tropical and subtropical environments. Rice is a self-pollinated annual species with a chromosome number of  $2n = 24$  and possesses a high degree of adaptability to diverse ecological conditions. The present study was carried out during the *Kharif* season of 2022 at the Agricultural Research Farm, Hirapuri Colony, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur. The experiment involved the evaluation of 13 promising rice germplasm lines. The experiment was undertaken to estimate correlation and principal components analysis among the rice genotypes to identifying traits contributing to grain yield improvement. The correlation coefficients at phenotypic level, the trait grain yield per plant showed a significant positive correlation with panicle length and grains per panicle, while at genotypic level, panicle length, grains per panicle and grain breadth. In PCA analysis, first two principal components, PC1 and PC2, accounted for 33.8% and 27.2% of the total variation. PC1 showed positive correlation with the trait's effective tillers per plant and grain breadth and PC2 found positive correlation with the traits plant height followed by 1000 grain weight, effective tillers per plant, panicle length, grains per panicle, grain length, grain breadth and grain yield per plant.

**Keywords:** Rice, Variability, Genotypic Correlation, Phenotypic Correlation, PCA

### Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and serves as the primary staple food for more than half of the global population (Asma *et al.*, 2023; Darko *et al.*, 2025). Rice is a self-pollinated annual herbaceous plant with a diploid chromosome number of  $2n=24$  (Mohapatra and Sahu, 2022). Today, rice is cultivated in more than 100 countries, with Asia accounting for nearly 90% of global production and consumption (Glauber and Mamun, 2025). Countries such as India, China, Indonesia, Bangladesh, Vietnam and Thailand are among the leading rice production and consumption.

India occupies a prominent position in global rice cultivation, possessing the largest area under rice and contributing substantially to world production (Sahu *et al.*, 2025; Yamini *et al.*, 2025). Rice cultivation plays a crucial role in ensuring food security, generating employment opportunities and supporting the livelihoods of millions of farming households (Patra *et al.*, 2025; Amandaria *et al.*, 2025).

Rice is grown under a wide range of production systems, including irrigated, rainfed lowland, upland, deep-water and coastal ecosystems. The crop requires warm temperatures, adequate water supply and fertile soils for optimum growth and development (Mahdavi

*et al.*, 2025; Sawant *et al.*, 2025). Advances in breeding, agronomic management, irrigation practices and crop protection technologies have significantly increased rice productivity over the past several decades (Singh and Solanki, 2026). Rice is not only a major source of carbohydrates but also provides essential proteins, vitamins, minerals and dietary energy to billions of people. Globally rice contributes nearly 20% of the dietary energy supply for humans. Beyond its nutritional significance, rice has substantial economic importance through domestic trade, export earnings and industrial utilization.

The success of rice breeding programs largely depends on the effective exploitation of genetic variability and the identification of traits associated with grain yield. Grain yield is a complex quantitative trait controlled by several component characters and strongly influenced by environmental conditions. Understanding the relationships among these traits is essential for developing efficient selection strategies. Correlation analysis is one of the most widely used statistical tools in plant breeding for determining the degree and direction of association among different traits. It enables breeders to identify characters that contribute directly or indirectly to grain yield and therefore serve as useful selection criteria. Several studies in rice have reported significant positive associations of grain yield with several traits. Such information facilitates simultaneous improvement of multiple traits and increases the efficiency of breeding programs.

The application of principal component analysis in rice breeding provides valuable insights into the genetic structure of germplasm collections and facilitates the identification of superior genotypes possessing desirable trait combinations. Furthermore, PCA-based biplot analysis enables visualization of relationships among genotypes and traits, thereby improving the interpretation of complex datasets and assisting breeders in making informed selection decisions. The combined use of correlation analysis and PCA provides a comprehensive framework for evaluating rice germplasm, identifying key yield determinants and designing effective breeding strategies for crop improvement.

Therefore, the present study was undertaken to Assess variability and traits association in rice (*Oryza sativa* L.) genotypes through correlation and principal component analysis. The findings are expected to facilitate the identification of superior genotypes and key selection criteria for enhancing grain yield and accelerating the development of improved rice cultivars.

## Materials and Methods

The present study was carried out during the Kharif season of 2022 at the Agricultural Research Farm, Hirapuri Colony, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur. The experiment involved the evaluation of 13 promising rice germplasm lines. Nursery sowing of all genotypes was completed on 22 June 2022, and seedlings were transplanted to the main field on 4 July 2022. Each genotype was grown in 1.5 m long rows with three replications. A spacing of 20 cm × 15 cm was maintained to ensure proper crop growth and facilitate the assessment of various genetic parameters. Standard agronomic practices recommended for rice cultivation were followed throughout the crop season. The experiment was undertaken to estimate correlation and principal components analysis among the rice genotypes to identifying traits contributing to grain yield improvement.

**Table 1:** List of rice genotypes used in present study.

| Sr. No. | Accession Genotypes   | Location        |
|---------|-----------------------|-----------------|
| 1.      | Pooja                 | NRRI, Cuttack   |
| 2.      | Chintu                | BHU, Varanasi   |
| 3.      | Badshah Bhog          | BHU, Varanasi   |
| 4.      | Swarna Sub-1          | NRRI, Cuttack   |
| 5.      | Sarju-52              | ANDUAT, Ayodhya |
| 6.      | Damini                | NRRI, Cuttack   |
| 7.      | Varsha Dhan           | NRRI, Cuttack   |
| 8.      | Swarna                | NRRI, Cuttack   |
| 9.      | CR Dhan 501           | NRRI, Cuttack   |
| 10.     | CR Dhan 1009          | NRRI, Cuttack   |
| 11.     | Dhanrekha             | BHU, Varanasi   |
| 12.     | CR Dhan 503(Jalamani) | NRRI, Cuttack   |
| 13.     | CR Dhan 511           | NRRI, Cuttack   |

## Results and Discussions

### Box plot Analysis

The box plots (Fig. 1) demonstrated substantial variation among the rice genotypes for 11 traits evaluated. Days to 50% flowering and days to maturity varied from approximately 103 to 136 days and 133 to 162 days, respectively, indicating the existence of both early and late maturing genotypes within the population. Plant height showed a broad range of variation (98-152 cm), suggesting considerable genetic diversity for this trait. In contrast, 1000-grain weight exhibited comparatively lower variability, with most genotypes concentrated around the median value, although one genotype was identified with a distinctly lower grain weight. Moderate variation was observed for effective tillers per plant and panicle length, reflecting differences in tillering ability and panicle

architecture among the genotypes. The number of grains per panicle displayed a wide range, highlighting significant potential for selecting superior genotypes with enhanced yield attributes. Similarly, grain length, grain breadth and grain length-breadth ratio exhibited moderate variability, indicating diversity in grain dimensions and shape. Grain yield per plant ranged from approximately 21.5 to 27.5g.

### Correlation analysis

Correlation analysis is a valuable statistical approach used to determine the degree and nature of association between different traits. It provides insight into how changes in one character influence another, helping researchers identify traits that contribute significantly to important attributes such as yield. By understanding these relationships, breeders can select desirable traits more effectively and improve breeding efficiency. Thus, correlation analysis is an essential tool for genetic evaluation, crop improvement, and informed selection strategies.

### Estimates of correlation coefficients at phenotypic level:

The character days to 50% flowering found significance positive correlation with the traits days to maturity (0.905), plant height (0.757) and grain length (0.432) (Table-2). Trait plant height (0.735) found positive significance correlation with the trait days to maturity. The plant height showed significance positive correlation with 1000 grain weight (0.477), panicle length (0.484) and grain length (0.666). The traits panicle length, grain length and grain breadth found positive significance correlation with the trait 1000 grain weight with the values (0.367), (0.645) and (0.566). Panicle length showed significant positive correlation with the traits grain length, grain length-breadth ratio and grain yield per plant with values (0.565), (0.319) and (0.327). Trait grains per panicle found positive significance correlation with the trait grain yield per plant (0.743). Grain length showed significance positive correlation with grain length-breadth ratio with value 0.437.

### Estimates of correlation coefficients at genotypic level

The days to 50% flowering showed significant positive correlation with the traits days to maturity (0.942), plant height (0.769) and grain length (0.479) (Table-3). Traits plant height, grain length and grain breadth ratio found positive significant correlation with days to maturity with the values 0.742, 0.348 and 0.324. Plant height was found significant positive correlation with the traits 1000 grain weight (0.479), panicle length (0.485) and grain length (0.743). The

traits 1000 grain weight found with the traits panicle length (0.368), grain length (0.726) and grain breadth (0.727). The trait effective tillers per plant was not show significant positive correlation with any trait. The traits grain length (0.634), grain length and breadth ratio (0.335), and grain yield per plant were found positive significance correlation with the trait panicle length. Trait grain per panicle was showed positive correlation with grain breadth (0.508) and grain yield per plant (0.813). Grain length significance positive correlated with the trait grain length breadth ratio (0.475). The trait grain breadth found significant correlation with the trait grain yield per plant (0.317).

The final output of numerous component qualities, grain yield is a crucial characteristic. When selecting for grain yield, a few component qualities that are positively correlated with grain yield are significant. Grain yield per plant is strongly and positively connected with spikelets per panicle, grains per panicle, and fertility percentage, according to a correlation study that looked at both phenotypic and genotypic levels. Therefore, the features with which yield is positively connected should be prioritized in order to increase yield. Previous researchers Russinga *et al.*, 2020; Singh *et al.*, 2020; Bhargava *et al.*, 2021; Kumar *et al.*, 2024 and Nath and Kole, 2021; demonstrated significant relationships among grain yield and the yield-related traits evaluated in the study. The strongest positive correlation was observed between the number of filled grains per panicle and the total grain number per panicle, followed by a highly significant positive association between grain length and the grain length-to-width ratio. Correlation analysis indicated a strong positive relationship of grain yield per plant with harvest index and days to maturity. In contrast, significant negative associations were observed between grain yield and days to 50% flowering, flag leaf area, biological yield, and 1000-grain weight. Path coefficient analysis further demonstrated that harvest index exerted a substantial positive direct effect on grain yield per plant, whereas days to 50% flowering showed a pronounced negative direct effect, highlighting its adverse influence on yield performance.

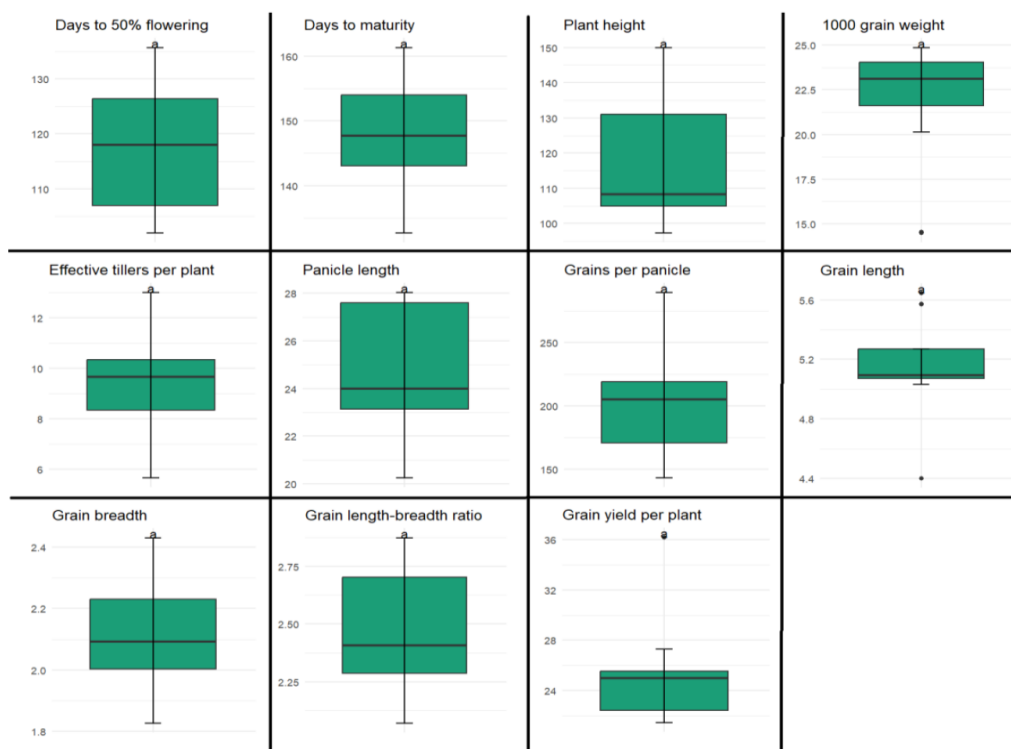
### Principal Components Analysis

Principal Component Analysis (PCA) is an effective statistical method used to summarize complex datasets by reducing the number of variables while preserving most of the original information. It helps identify the traits that contribute most to genetic variation and provides a clear understanding of the relationships among different characters. PCA is also useful for classifying genotypes based on their

similarities and differences, facilitating the identification of important traits for selection. Consequently, it serves as a valuable tool in plant breeding and genetic improvement programs for efficient data analysis and decision-making. In the present study (Table-4), the PCA analysis was studied among the traits and their contribution to the total genetic variation. The first four principal components, PC1 (33.79%), PC2 (27.18%), PC3 (14.63%) and PC4 (10.58%) of the total variation, respectively, explaining 86.18% of the overall variability. PC1 showed positive correlation with the trait's effective tillers per plant (0.20) and grain breadth (0.07) while traits days to 50% flowering (-0.85), days to maturity (-0.78), plant height (-0.89), 1000 grain weight (-0.45), panicle length (-0.53), grain length (-0.81) and grain length-breadth ratio (-0.53). PC2 found positive correlation with the traits plant height followed by 1000 grain weight, effective tillers per plant, panicle length, grains per panicle, grain length, grain breadth and grain yield per plant with values (0.28, 0.69, 0.31, 0.34, 0.77, 0.28, 0.84 and 0.68) but traits days to 50% flowering (-0.05), days to maturity (-0.21) and grain length-breadth ratio (-0.58) found negative correlation. The traits panicle length (0.63), grains per panicle (0.14), grain length (0.25), grain length-breadth ratio (0.52) and grain yield per plant (0.50) showed positive correlation with PC3, while the traits days to 50% flowering (-0.36), days to maturity (-0.44), plant height (-0.04), 1000 grain weight (-0.11), effective tillers per plant (-0.37) and

grain breadth (-0.38) found negative correlation. In PC4 the traits 1000 grain weight (0.46), grain length (0.30) and grain breadth (0.29) were showing positive correlation, but the traits days to flowering (-0.23), days to maturity (-0.36), plant height (-0.20), effective tillers per plant (-0.45), panicle length (-0.01), grains per panicle (-0.43), grain length breadth ratio (-0.12) and grain yield per plant (-0.39) showed negative correlation.

The PCA biplot (Fig. 3) illustrates the association among the studied traits and their contribution to the total genetic variation. The first two principal components, PC1 and PC2, accounted for 33.8% and 27.2% of the total variation, respectively, explaining 61.0% of the overall variability. Traits such as grains per panicle, grain yield per plant (GY/P), effective tillers per plant (ETPP) and grain breadth (GB) were grouped together on the positive side of the axes, indicating a strong positive relationship among them. This suggests that higher grain yield is closely associated with an increased number of grains per panicle and effective tillers. Conversely, plant height (PH), cluster number (CL), days to 50% flowering (DFF), days to maturity (DM), leaf breadth (LB), panicle length (PL), and 1000-grain weight (1000 GW) were located on the negative side of PC1, indicating an inverse relationship with yield-related traits. Similar results were also found by the previous works Charistina *et al.*, 2021; Kumari *et al.*, 2021; Tiwari *et al.*, 2022 and Krishna *et al.*, 2022.



**Fig. 1 :** Boxplot analysis for variability in field condition

**Table 2 :** Estimates of correlation coefficients at phenotypic level:

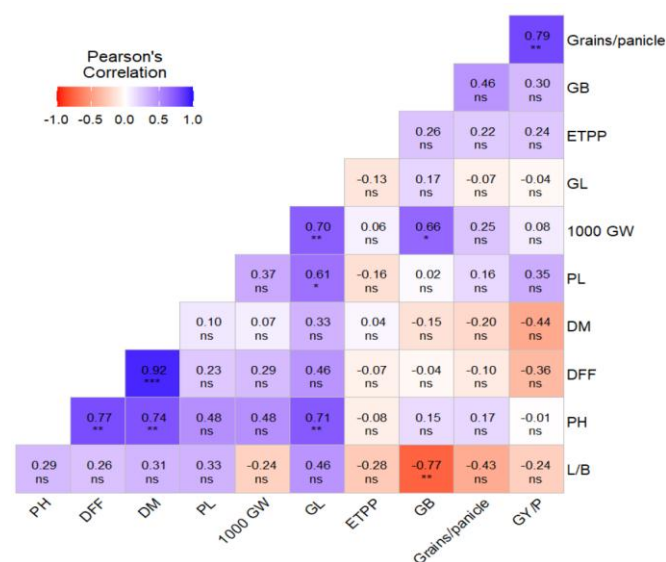
| Characters     | DFF   | DM      | PH (cm) | 1000 GW (g) | ETPP   | PL (cm) | Grains/panicle | GL[L] (mm) | GB[B] (mm) | L/B      | GY/P(g)  |
|----------------|-------|---------|---------|-------------|--------|---------|----------------|------------|------------|----------|----------|
| DFF            | 1.000 | 0.905** | 0.757** | 0.285       | -0.074 | 0.232   | -0.104         | 0.432**    | -0.037     | 0.247    | -0.335*  |
| DM             |       |         | 0.735** | 0.072       | 0.040  | 0.102   | -0.200         | 0.295      | -0.120     | 0.293    | -0.424** |
| PH(cm)         |       |         |         | 0.477**     | -0.082 | 0.484** | 0.166          | 0.666**    | 0.129      | 0.286    | -0.007   |
| 1000 GW(g)     |       |         |         |             | 0.055  | 0.367*  | 0.248          | 0.645**    | 0.566**    | -0.226   | 0.082    |
| ETPP           |       |         |         |             |        | -0.151  | 0.210          | -0.110     | 0.262      | -0.264   | 0.217    |
| PL(cm)         |       |         |         |             |        |         | 0.163          | 0.565**    | 0.014      | 0.319*   | 0.327*   |
| Grains/panicle |       |         |         |             |        |         |                | -0.064     | 0.388*     | -0.417** | 0.743**  |
| GL[L](mm)      |       |         |         |             |        |         |                |            | 0.103      | 0.437**  | -0.075   |
| GB[B](mm)      |       |         |         |             |        |         |                |            |            | -0.718** | 0.280    |
| L/B            |       |         |         |             |        |         |                |            |            |          | -0.233   |
| GY/P(g)        |       |         |         |             |        |         |                |            |            |          | 1.000    |

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

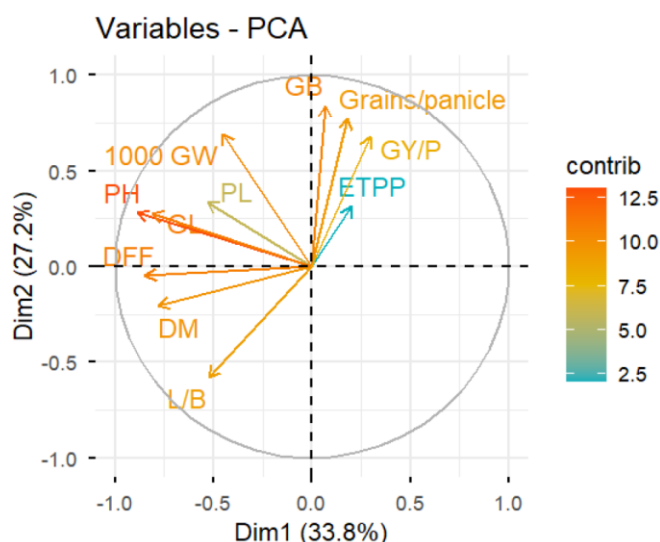
**Table 3 :** Estimates of correlation coefficients at genotypic level:

| Characters     | DFF   | DM      | PH (cm) | 1000 GW (g) | ETPP   | PL (cm) | Grains/panicle | GL[L] (mm) | GB[B] (mm) | L/B      | GY/P(g)  |
|----------------|-------|---------|---------|-------------|--------|---------|----------------|------------|------------|----------|----------|
| DFF            | 1.000 | 0.924** | 0.769** | 0.290       | -0.066 | 0.235   | -0.104         | 0.479**    | -0.038     | 0.267    | -0.372*  |
| DM             |       |         | 0.742** | 0.074       | 0.041  | 0.103   | -0.201         | 0.348*     | -0.175     | 0.324*   | -0.455** |
| PH(cm)         |       |         |         | 0.479**     | -0.086 | 0.485** | 0.168          | 0.743**    | 0.173      | 0.298    | -0.009   |
| 1000 GW(g)     |       |         |         |             | 0.059  | 0.368*  | 0.249          | 0.726**    | 0.727**    | -0.241   | 0.084    |
| ETPP           |       |         |         |             |        | -0.170  | 0.228          | -0.145     | 0.257      | -0.283   | 0.246    |
| PL(cm)         |       |         |         |             |        |         | 0.164          | 0.634**    | 0.024      | 0.335*   | 0.363*   |
| Grains/panicle |       |         |         |             |        |         |                | -0.078     | 0.508**    | -0.439** | 0.813**  |
| GL[L](mm)      |       |         |         |             |        |         |                |            | 0.227      | 0.475**  | -0.016   |
| GB[B](mm)      |       |         |         |             |        |         |                |            |            | -0.807** | 0.317*   |
| L/B            |       |         |         |             |        |         |                |            |            |          | -0.250   |
| GY/P(g)        |       |         |         |             |        |         |                |            |            |          | 1.000    |

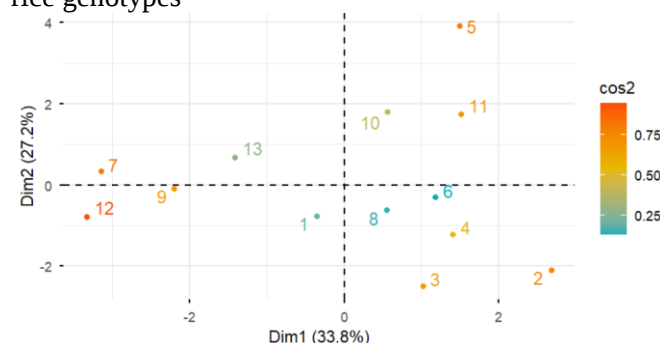
\*, \*\* significant at 5% and 1% level, respectively

**Fig. 2 :** Pearson's correlation matrix illustrating the strength and direction of relationships among different traits of rice genotypes**Table 4 :** Principal component analysis showing the relative proportion of variance and trait contributions in the rice genotypes

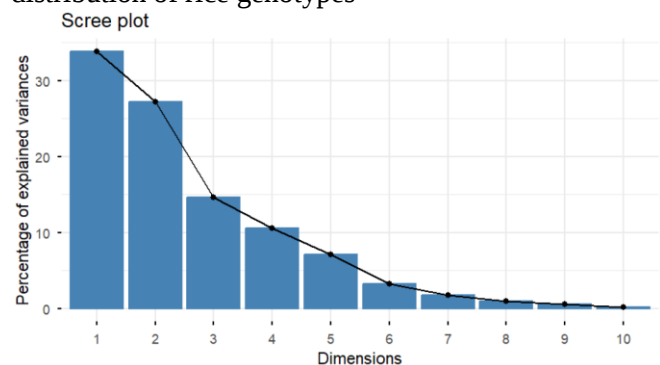
|                             | PC1          | PC2          | PC3          | PC4          |
|-----------------------------|--------------|--------------|--------------|--------------|
| <b>Eigenvalue</b>           | <b>3.72</b>  | <b>2.99</b>  | <b>1.61</b>  | <b>1.16</b>  |
| <b>Variance%</b>            | <b>33.79</b> | <b>27.18</b> | <b>14.63</b> | <b>10.58</b> |
| <b>Cumulative variance%</b> | <b>33.79</b> | <b>60.96</b> | <b>75.60</b> | <b>86.18</b> |
| DFF                         | -0.85        | -0.05        | -0.36        | -0.23        |
| DM                          | -0.78        | -0.21        | -0.44        | -0.36        |
| PH                          | -0.89        | 0.28         | -0.04        | -0.20        |
| 1000 GW                     | -0.45        | 0.69         | -0.11        | 0.46         |
| ETPP                        | 0.20         | 0.31         | -0.37        | -0.45        |
| PL                          | -0.53        | 0.34         | 0.63         | -0.01        |
| Grains/panicle              | 0.18         | 0.77         | 0.14         | -0.43        |
| GL                          | -0.81        | 0.28         | 0.25         | 0.30         |
| GB                          | 0.07         | 0.84         | -0.38        | 0.29         |
| L/B                         | -0.53        | -0.58        | 0.52         | -0.12        |
| GY/P                        | 0.30         | 0.68         | 0.50         | -0.39        |



**Fig. 3 :** PCA biplot analysis showing the relative proportion of variance and trait contributions in the rice genotypes



**Fig. 4 :** Individuals-PCA plot analysis showing the distribution of rice genotypes



**Fig. 5 :** PCA scree plot showing the relative proportion of variance and trait contributions in the rice genotypes

## Conclusion

Considerable variability was observed among the rice genotypes for all the traits evaluated in the study. The correlation coefficients at phenotypic level, the trait grain yield per plant showed a significant positive correlation with panicle length and grains per panicle, while at genotypic level, panicle length, grains per panicle and grain breadth. In PCA analysis, first two principal components, PC1 and PC2, accounted for

33.8% and 27.2% of the total variation. PC1 showed positive correlation with the trait's effective tillers per plant and grain breadth and PC2 found positive correlation with the traits plant height followed by 1000 grain weight, effective tillers per plant, panicle length, grains per panicle, grain length, grain breadth and grain yield per plant. Correlation analysis and principal component analysis (PCA) revealed substantial variation among the traits and highlighted their usefulness as indirect selection criteria.

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