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RESEARCH ARTICLE

# Multivariate analysis for improving selection of yield and related traits in rice (*Oryza sativa* L.)

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## Abstract

Rice (*Oryza sativa* L.) serves as a staple food for nearly half of the world population, with yield being critical traits for both consumers and food security. In this study, 45 diverse rice genotypes, including standard checks, were evaluated for yield and related agronomic traits over the 2023 and 2024 growing seasons. The experiment was carried out at lovely professional university, Jalandhar, Punjab, using a randomized complete block design (RCBD) with three replications. Rice genotypes such as Goyadi (G35), Kalamati (G39), AAU DR-1 (G16), IR 167 1662 (G40) and Mala Gauri (G26) showed the maximum potential for achieving superior seed yield per plant (SYP). These genotypes consistently exhibited robust average results in various traits related to yield. In terms of specific traits, IR 82635-B-B-75-2 (G41), G39, CO-51 (G42) and Kanchan (G14) were identified for earliest Days to 50 % flowering (DFF), while IR 167 1662 (G40), Khajur (G25), Asamiya Dhan (G15), CO-51 (G42) and IR 82635-B-B-75-2 (G41) were the earliest to reach maturity. For reduced Plant height (PH), genotypes Fara Dhan (G37), Kani Dhan (G36), Tama Koni (G34), Khajur (G25) and Bhushu (G11) stood out. The promising performance of these genotypes across multiple yield-contributing traits suggests they can serve as valuable male parents in hybridization programs. High estimates of phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) coefficients of variation remained observed for both Harvest index (HI) and Seed yield per plant (SYP), indicating significant genetic variability with minimal environmental influence. Cluster analysis revealed that Cluster II had the minimum intra-cluster distance (ICD), suggesting greater homogeneity among its genotypes, whereas Cluster IV ICD. The maximum genetic divergence was found among Clusters IV and VII, while the least was between Clusters IV and VI. Traits such as PH and grains/panicle (GPP) contributed most to the total genetic divergence. Principal Component Analysis showed that PC1 was largely influenced by traits like 1000 seeds weight (TSW), SYP and DFF, while PC2, PC3 and PC4 contributed significantly to yield enhancement, supporting their use in selection for yield improvement.

**Keywords:** correlation and path analysis; genetic variability; genetic divergence; principal component analysis; superior rice seed yield

## Introduction

The objective of this research was to advance breeding strategies for the selection of yield and yield-contributing characters in rice (*Oryza sativa* L.) through the application of multivariate analysis. Multivariate approaches have been proven to be successful in elucidating intricate relationships between traits. The present research contributes to that effort by determining significant agronomic characters with high contribution to yield and thus facilitating the creation of high-yielding rice genotypes (1-3).

Rice is an essential food staple for the populations of Asia, Africa and the Americas and Over the past decade, global rice production has reached approximately 800 million tonnes (Top Rice Producing Countries in the World (2025 Rankings) (4). Roughly 30 % of the land utilized for grain crops is used for rice production, which occupies 11 % of all croplands worldwide and world's population is predicted to increase by 12 %, which will increase demand for rice, additional 500 million metric tons of rice must be produced, or at least 13 % more, to meet this need (5).

Rice covers more than 11 % of the earth's farmable land, which amounts to roughly 165.03 million hectares. The total worldwide output is around 776.46 million metric tons, resulting in an average yield of 4.7 tons per hectare. Asia is the leading region for rice farming, accounting for nearly 90 % of the total global output and consumption. In India, rice is cultivated across 47.8 million hectares, making it the largest rice-growing area on the planet. With a production of 45 million metric tons and a yield of 4.32 tons per hectare, India stands as the second-largest rice producer globally (FAOSTAT, 2023). To include advantageous features and accomplish desired modifications and germplasm's diversity is crucial and can play remarkable role in crop improvement (6). A thorough grasp of the genetic variability that currently exists is essential for successful breeding and agricultural improvements (7). Genetic variability is crucial to the success of plant breeding since it facilitates the choice of high-yielding and adapted varieties. Moreover, the connection between introduced lowland rice varieties and yield characters in the study region is not yet well researched. Genetic variability in yield and its components should be understood for choosing appropriate rice varieties for breeding (8). Correlation analysis is a useful statistical method for studying relationships between traits, allowing for the formulation of selection strategies that improve favorable traits without harming others. Through measuring the strength and direction of variable relationships, correlation analysis allows for the identification of positive or negative relationships, thus giving insights into trait interactions that lead to efficient yield improvement (9).

Path analysis (PA) applies regression methods to analyze more than one variable at a time and it is thus a powerful tool to study intricate multi-factorial relationships and the relationships between various traits. PA-assists in ascertaining both direct/ indirect influences of variables on desired traits, hence gaining a better understanding of their role in improving yield (10). Cluster analysis (CA) is an important hybrid rice breeding approach to screen of genetically diverse parental lines to obtain high heterosis. It groups individuals according to genetic differences and identifies the best parents, which improves hybrid vigor, yield and resistance. It enhances breeding efficiency, leading to increased productivity and agricultural sustainability (11). In this research, genetic diversity among germplasm lines was evaluated using Mahalanobis $D^2$ analysis to assess genetic divergence among genotyped rice lines. The main aim was to improve productivity using varied fertility restorer lines for hybridization and the selection of elite genotypes with better agronomic characteristics (12).

Principal Component Analysis (PCA) is a unique multivariate approach applied to big datasets for simpler analysis, visualization, or compression and it usually comprises mean-centering the data and then applying eigenvalue decomposition to the covariance matrix or singular value decomposition. PCA assists in determining the lowest number of components responsible for remarkable variation and can be employed to rank genotypes according to principal component scores (13).

Keeping this point in view the present investigation has been undertaken with following, to evaluate yield-related traits among different rice genotypes, to perform multivariate analysis to assess the relationships among yield traits, to analyze the direct and indirect effects of selected traits, including genetic divergence, on rice yield performance.

## Materials and Methods

### Experimental site and material

The experiment was carried out at the agriculture farm, Lovely professional university (LPU), Jalandhar, Punjab located 225 meters above mean sea level at latitude of 31.15 N and longitude of 75.69E. The trial was conducted during the *kharif* season of 2023-2024. Forty-five genotypes of rice germplasms (Table 1) were collected from Kapurthala district and stored at division of genetics and plant breeding (GPB), LPU, Punjab. Germplasms nursery was sown on 4th of June 2023 and transplanted on 2nd of July 2023

### Nursery raising and transplanting

The field trial involving diverse rice cultivars was conducted during the Kharif seasons of 2023 and 2024 at the research fields of Lovely Professional University. Uniform seedlings were raised in a well-managed nursery, with sowing on June 6, 2023 and June 4, 2024, followed by transplanting on July 2, 2023 and June 30, 2024, respectively. The field layout followed standard agronomic practices, maintaining 15 × 20 cm spacing. Nutrient application followed the recommended dose of 120:60:60 kg/ha (N:P:K), with nitrogen applied in three splits before transplanting, post-first weeding and at flowering to support optimal growth and yield.

### Morphological data collection

Morphological data were taken from five randomly chosen representative plants per genotype in each replication. The observations were noted for every trait according to the Standard Evaluation System (14). Eleven quantitative traits were measured: days to 50 % flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, grains per panicle, biological yield per plant, harvest index, 1000-seed weight and seed yield per plant. Morphological data were recorded at the time of physiological maturity and during plant harvest. Harvesting of plants was carried out in November and December of both 2023 and 2024.

### Statistics analysis of data

The data were subjected to analysis of variance (ANOVA) by the general linear model (GLM) procedure for randomized complete block design (RCBD) in SAS version 9.2 to determine the genotypic effects and their interactions (15). For characteristics whose mean squares are homogeneous, the variance components were estimated, after which combined analysis of variance followed. The formulas presented by (16, 17) were utilized for the computation of phenotypic and genotypic variances, their associated coefficients, broad-sense heritability and genetic advancement. To evaluate the genetic diversity between 45 genotypes and 4 check landraces, a dendrogram was created using Windostat 9.3 software.

## Results

### Analysis of variance (ANOVA) for yield and quality traits

The ANOVA showed significant differences ($p \leq 0.05$) in all the traits evaluated, including DFF, DM, PH, TT, PT, PL, GPP, BY, HI, TSW and SYP. This strong variability highlights considerable genetic differences among the genotypes (Table 2). Such diversity provides an encouraging basis for making informed selections aimed at specific breeding goals. The significant F-values for all traits were further supported by the calculation of the critical difference (C.D.) at the 5 % level as shown in Table 2.

### Mean performance of genotypes for various traits

Fig. 1 shows the general mean, range, standard error and critical difference (CD) of eleven quantitative traits in rice. The total time until DM ranged from 121.33 to 146.67 days, with an average of about 130.06 days. On the other hand, the period until the first flowering showed a wider fluctuation, varying from 86.67 to 117.00 days and had an average of 97.68 days. The height of the plants varied from 98.94 cm to 171.57 cm, with an average of 121.03 cm. Meanwhile, the TT showed a range from 11.63 cm to 29.43 cm, averaging at 20.61 cm. One of the main goals in improving crops is to boost the PT. The PL showed an average of 10.73 cm, with values fluctuating between 7.63 cm and 15.47 cm, while the length varied from 16.68 cm to 27.79 cm, averaging at 23.41 cm.

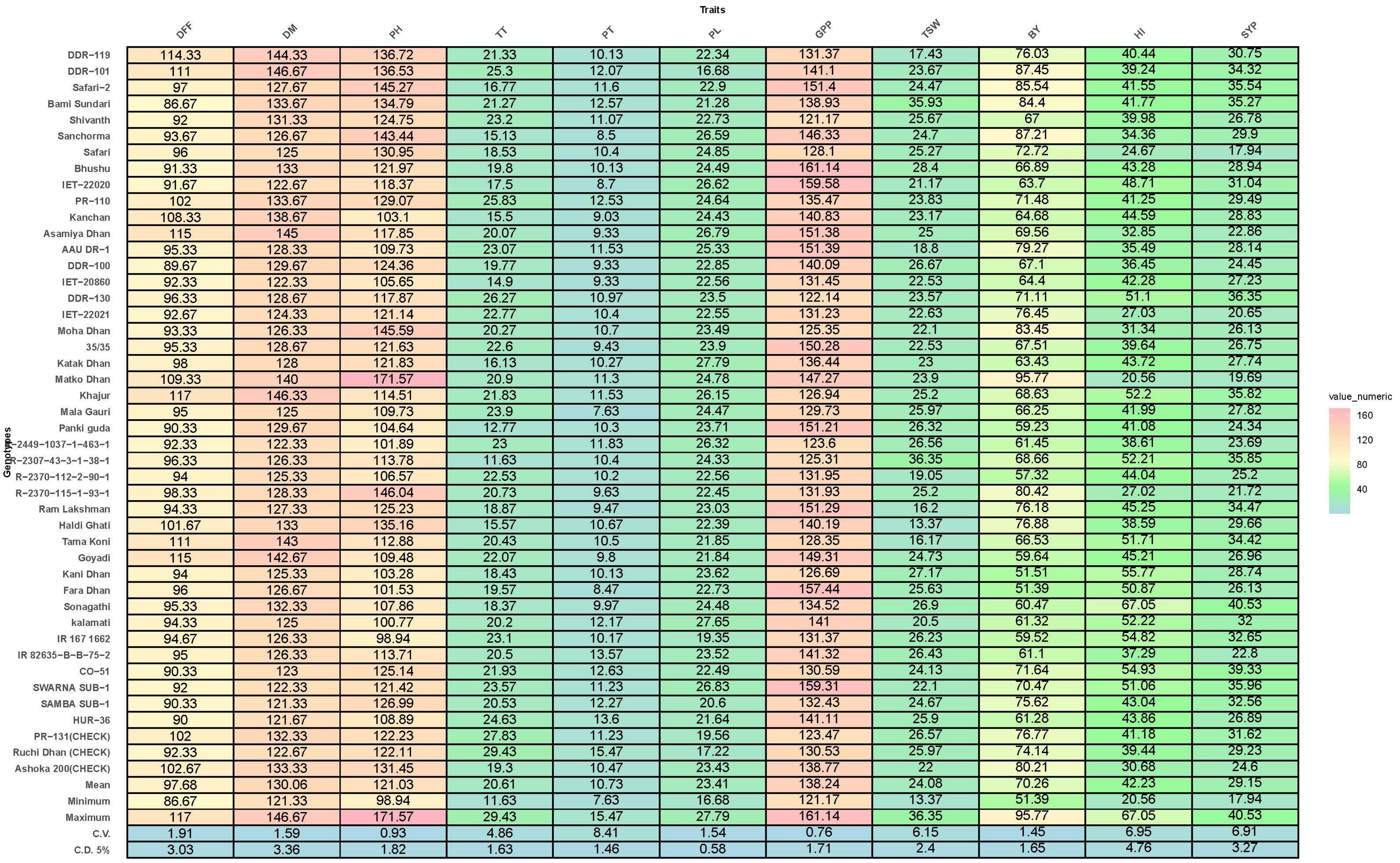
**Table 1.** Description of the genotypes used in the investigation

| Genotype code | Genotype | Origin |
|---|---|---|
| G1 | PR-131 (Check) | Punjab Agricultural University |
| G2 | Ruchi Dhan (Check) | Central Rice Research Institute, Cuttack, Odisha |
| G3 | Ashoka 200 (Check) | Anand Agricultural University, Gujarat |
| G4 | DDR-119 | Anand Agricultural University, Gujarat |
| G5 | DDR-101 | Anand Agricultural University, Gujarat |
| G6 | Safari-2 | Indian Institute of Rice Research, Hyderabad |
| G7 | Bami Sundari | Local traditional cultivar, Jalandhar |
| G8 | Shivanth | Local cultivar, Jalandhar |
| G9 | Sanchorma | Local cultivar, Jalandhar |
| G10 | Safari | Indian Institute of Rice Research, Hyderabad |
| G11 | Bhushu | Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh |
| G12 | IET-22020 | Central Rice Research Institute, Cuttack, Odisha |
| G13 | PR-110 | Punjab Agriculture university, Ludhiana |
| G14 | Kanchan | Local cultivar, Phagwara, Jalandhar |
| G15 | Asamiya Dhan | Traditional landrace, Assam |
| G16 | AAU DR-1 | Anand Agricultural University, Gujarat |
| G17 | DDR-100 | Anand Agricultural University, Gujarat |
| G18 | IET-20860 | Anand Agricultural University, Gujarat |
| G19 | DDR-130 | Anand Agricultural University, Gujarat |
| G20 | IET-22021 | Anand Agricultural University, Gujarat |
| G21 | Moha Dhan | Local cultivar, Phagwara, Jalandhar |
| G22 | URG-1 | Banaras Hindu University |
| G23 | Katak Dhan | Landrace, Cuttack, Odisha |
| G24 | Matko Dhan | Local cultivar, Ludhiana |
| G25 | Khajur | Local cultivar, Jalandhar |
| G26 | Mala Gauri | Local cultivar, Jalandhar |
| G27 | Panki guda | Local cultivar, Phagwara, Jalandhar |
| G28 | R-2449-1037-1-463-1 | Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh |
| G29 | R-2307-43-3-1-38-1 | Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh |
| G30 | R-2370-112-2-90-1 | Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh |
| G31 | R-2370-115-1-93-1 | Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh |
| G32 | Ram Lakshman | Local cultivar, Ludhiana |
| G33 | Haldi Ghati | Local cultivar, Jalandhar |
| G34 | Tama Koni | Local cultivar, Jalandhar |
| G35 | Goyadi | Local cultivar, Jalandhar |
| G36 | Kani Dhan | Local cultivar, Jalandhar |
| G37 | Fara Dhan | Local cultivar, Jalandhar |
| G38 | Sonagathi | Local cultivar, Jalandhar |
| G39 | kalamati | Local cultivar, Jalandhar |
| G40 | IR 167 1662 | International rice research institute |
| G41 | IR 82635-B-B-75-2 | International rice research institute |
| G42 | CO-51 | Tamil Nadu Rice Research Institute |
| G43 | SWARNA SUB-1 | International rice research institute |
| G44 | SAMBA SUB-1 | Central Rice Research Institute (CRRI), Cuttack |
| G45 | HUR-36 | Banaras Hindu University. |

**Table 2.** Analysis of variance for 11 rice genotypes characters

| | Source of Variation | | |
|---|---|---|---|
| **Traits** | **Replication** | **Treatment** | **Error** |
| DF | 2 | 44 | 88 |
| DFF | 23.42 | 185.84* | 3.49 |
| DM | 1.27 | 155.32* | 4.28 |
| PH (cm) | 2.04 | 686.36* | 1.25 |
| NTT | 1.86 | 41.80* | 1 |
| NPT | 21.89 | 6.84* | 0.81 |
| PL | 0.12 | 17.36* | 0.12 |
| GPP | 3.81 | 368.77* | 1.1 |
| TSW | 0.3 | 52.00* | 2.19 |
| BY | 2.06 | 289.40* | 1.03 |
| HI | 9.47 | 246.97* | 8.6 |
| SYP | 5.44 | 82.44* | 4.05 |

**Note**: *, ** significant at 5 % and 1 % probability level, respectively, where, *=significant, **=highly significant. **Whereas** - **DFF**- *Days to 50 % flowering,* **DM** - *Days to Maturity*, **PH**- *Plant height*, **TT**- *tillers per plant*, **PT**- *productive tillers per plant*, **PL**- *panicle length*, **GPP**- *grains/panicle*, **BY**- *Biological yield per plant*, **HI**- *Harvest index*, **TSW**- *1000 seeds weight* and **SYP**- *Seed yield per plant,* **DF-** *degree of freedom*



| Genotypes | DFF | DM | PH | TT | PT | PL | GPP | TSW | BY | HI | SYP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DDR-119 | 114.33 | 144.33 | 136.72 | 21.33 | 10.13 | 22.34 | 131.37 | 17.43 | 76.03 | 40.44 | 30.75 |
| DDR-101 | 111 | 146.67 | 136.53 | 25.3 | 12.07 | 16.68 | 141.1 | 23.67 | 87.45 | 39.24 | 34.32 |
| Safari-2 | 97 | 127.67 | 145.27 | 16.77 | 11.6 | 22.9 | 151.4 | 24.47 | 85.54 | 41.55 | 35.54 |
| Bami Sundari | 86.67 | 133.67 | 134.79 | 21.27 | 12.57 | 21.28 | 138.93 | 35.93 | 84.4 | 41.77 | 35.27 |
| Shivanth | 92 | 131.33 | 124.75 | 23.2 | 11.07 | 22.73 | 121.17 | 25.67 | 67 | 39.98 | 26.78 |
| Sanchorma | 93.67 | 126.67 | 143.44 | 15.13 | 8.5 | 26.59 | 146.33 | 24.7 | 87.21 | 34.36 | 29.9 |
| Safari | 96 | 125 | 130.95 | 18.53 | 10.4 | 24.85 | 128.1 | 25.27 | 72.72 | 24.67 | 17.94 |
| Bhushu | 91.33 | 133 | 121.97 | 19.8 | 10.13 | 24.49 | 161.14 | 28.4 | 66.89 | 43.28 | 28.94 |
| IET-22020 | 91.67 | 122.67 | 118.37 | 17.5 | 8.7 | 26.62 | 159.58 | 21.17 | 63.7 | 48.71 | 31.04 |
| PR-110 | 102 | 133.67 | 129.07 | 25.83 | 12.53 | 24.64 | 135.47 | 23.83 | 71.48 | 41.25 | 29.49 |
| Kanchan | 108.33 | 138.67 | 103.1 | 15.5 | 9.03 | 24.43 | 140.83 | 23.17 | 64.68 | 44.59 | 28.83 |
| Asamiya Dhan | 115 | 145 | 117.85 | 20.07 | 9.33 | 26.79 | 151.38 | 25 | 69.56 | 32.85 | 22.86 |
| AAU DR-1 | 95.33 | 128.33 | 109.73 | 23.07 | 11.53 | 25.33 | 151.39 | 18.8 | 79.27 | 35.49 | 28.14 |
| DDR-100 | 89.67 | 129.67 | 124.36 | 19.77 | 9.33 | 22.85 | 140.09 | 26.67 | 67.1 | 36.45 | 24.45 |
| IET-20860 | 92.33 | 122.33 | 105.65 | 14.9 | 9.33 | 22.56 | 131.45 | 22.53 | 64.4 | 42.28 | 27.23 |
| DDR-130 | 96.33 | 128.67 | 117.87 | 26.27 | 10.97 | 23.5 | 122.14 | 23.57 | 71.11 | 51.1 | 36.35 |
| IET-22021 | 92.67 | 124.33 | 121.14 | 22.77 | 10.4 | 22.55 | 131.23 | 22.63 | 76.45 | 27.03 | 20.65 |
| Moha Dhan | 93.33 | 126.33 | 145.59 | 20.27 | 10.7 | 23.49 | 125.35 | 22.1 | 83.45 | 31.34 | 26.13 |
| 35/35 | 95.33 | 128.67 | 121.63 | 22.6 | 9.43 | 23.9 | 150.28 | 22.53 | 67.51 | 39.64 | 26.75 |
| Katak Dhan | 98 | 128 | 121.83 | 16.13 | 10.27 | 27.79 | 136.44 | 23 | 63.43 | 43.72 | 27.74 |
| Matko Dhan | 109.33 | 140 | 171.57 | 20.9 | 11.3 | 24.78 | 147.27 | 23.9 | 95.77 | 20.56 | 19.69 |
| Khajur | 117 | 146.33 | 114.51 | 21.83 | 11.53 | 26.15 | 126.94 | 25.2 | 68.63 | 52.2 | 35.82 |
| Mala Gauri | 95 | 125 | 109.73 | 23.9 | 7.63 | 24.47 | 129.73 | 25.97 | 66.25 | 41.99 | 27.82 |
| Panki guda | 90.33 | 129.67 | 104.64 | 12.77 | 10.3 | 23.71 | 151.21 | 26.32 | 59.23 | 41.08 | 24.34 |
| -2449-1037-1-463-1 | 92.33 | 122.33 | 101.89 | 23 | 11.83 | 26.32 | 123.6 | 26.56 | 61.45 | 38.61 | 23.69 |
| R-2307-43-3-1-38-1 | 96.33 | 126.33 | 113.78 | 11.63 | 10.4 | 24.33 | 125.31 | 36.35 | 68.66 | 52.21 | 35.85 |
| R-2370-112-2-90-1 | 94 | 125.33 | 106.57 | 22.53 | 10.2 | 22.56 | 131.95 | 19.05 | 57.32 | 44.04 | 25.2 |
| R-2370-115-1-93-1 | 98.33 | 128.33 | 146.04 | 20.73 | 9.63 | 22.45 | 131.93 | 25.2 | 80.42 | 27.02 | 21.72 |
| Ram Lakshman | 94.33 | 127.33 | 125.23 | 18.87 | 9.47 | 23.03 | 151.29 | 16.2 | 76.18 | 45.25 | 34.47 |
| Haldi Ghati | 101.67 | 133 | 135.16 | 15.57 | 10.67 | 22.39 | 140.19 | 13.37 | 76.88 | 38.59 | 29.66 |
| Tama Koni | 111 | 143 | 112.88 | 20.43 | 10.5 | 21.85 | 128.35 | 16.17 | 66.53 | 51.71 | 34.42 |
| Goyadi | 115 | 142.67 | 109.48 | 22.07 | 9.8 | 21.84 | 149.31 | 24.73 | 59.64 | 45.21 | 26.96 |
| Kani Dhan | 94 | 125.33 | 103.28 | 18.43 | 10.13 | 23.62 | 126.69 | 27.17 | 51.51 | 55.77 | 28.74 |
| Fara Dhan | 96 | 126.67 | 101.53 | 19.57 | 8.47 | 22.73 | 157.44 | 25.63 | 51.39 | 50.87 | 26.13 |
| Sonagathi | 95.33 | 132.33 | 107.86 | 18.37 | 9.97 | 24.48 | 134.52 | 26.9 | 60.47 | 67.05 | 40.53 |
| kalamati | 94.33 | 125 | 100.77 | 20.2 | 12.17 | 27.65 | 141 | 20.5 | 61.32 | 52.22 | 32 |
| IR 167 1662 | 94.67 | 126.33 | 98.94 | 23.1 | 10.17 | 19.35 | 131.37 | 26.23 | 59.52 | 54.82 | 32.65 |
| IR 82635-B-B-75-2 | 95 | 126.33 | 113.71 | 20.5 | 13.57 | 23.52 | 141.32 | 26.43 | 61.1 | 37.29 | 22.8 |
| CO-51 | 90.33 | 123 | 125.14 | 21.93 | 12.63 | 22.49 | 130.59 | 24.13 | 71.64 | 54.93 | 39.33 |
| SWARNA SUB-1 | 92 | 122.33 | 121.42 | 23.57 | 11.23 | 26.83 | 159.31 | 22.1 | 70.47 | 51.06 | 35.96 |
| SAMBA SUB-1 | 90.33 | 121.33 | 126.99 | 20.53 | 12.27 | 20.6 | 132.43 | 24.67 | 75.62 | 43.04 | 32.56 |
| HUR-36 | 90 | 121.67 | 108.89 | 24.63 | 13.6 | 21.64 | 141.11 | 25.9 | 61.28 | 43.86 | 26.89 |
| PR-131(CHECK) | 102 | 132.33 | 122.23 | 27.83 | 11.23 | 19.56 | 123.47 | 26.57 | 76.77 | 41.18 | 31.62 |
| Ruchi Dhan (CHECK) | 92.33 | 122.67 | 122.11 | 29.43 | 15.47 | 17.22 | 130.53 | 25.97 | 74.14 | 39.44 | 29.23 |
| Ashoka 200(CHECK) | 102.67 | 133.33 | 131.45 | 19.3 | 10.47 | 23.43 | 138.77 | 22 | 80.21 | 30.68 | 24.6 |
| Mean | 97.68 | 130.06 | 121.03 | 20.61 | 10.73 | 23.41 | 138.24 | 24.08 | 70.26 | 42.23 | 29.15 |
| Minimum | 86.67 | 121.33 | 98.94 | 11.63 | 7.63 | 16.68 | 121.17 | 13.37 | 51.39 | 20.56 | 17.94 |
| Maximum | 117 | 146.67 | 171.57 | 29.43 | 15.47 | 27.79 | 161.14 | 36.35 | 95.77 | 67.05 | 40.53 |
| C.V. | 1.91 | 1.59 | 0.93 | 4.86 | 8.41 | 1.54 | 0.76 | 6.15 | 1.45 | 6.95 | 6.91 |
| C.D. 5% | 3.03 | 3.36 | 1.82 | 1.63 | 1.46 | 0.58 | 1.71 | 2.4 | 1.65 | 4.76 | 3.27 |

**Fig. 1**. Heatmap illustrates the mean performance of different quality traits of rice. The rows correspond to genotypes, while the columns represent the mean trait values across observations. In the gradient color scale, pink shades indicate higher mean trait values, while blue shades denote lower mean values and green and yellow denote the intermediate mean trait values.

The GPP ranges from 121.17 to 161.14 with a mean value of 138.24. Biological yield ranged from 51.39 g to 95.77g with a grand mean of 70.26 g, HI ranged from 20.56 % to 67.05 % with an overall mean of 42.23 %. SYP ranged from 17.94 g to, with a general mean of 29.15 g, while TSW ranged from 13.37 g to 36.35, with a mean value of 24.08 g.

The average CV stood at 3.77, with figures fluctuating between 0.76 and 8.41. Notably, the CV for the elements affecting yield, such as TP, PT, TSW and SYP, exhibited considerable variability, indicating marked differences among the rice genotypes.

Previous researchers highlighted that the CV serves as a dependable indicator of the relationship between behaviors and the reliability of the study. They further noted that when CV values exceeded 20, the reliability of the experiment began to deteriorate (18, 19). The average CD value was recorded at 2.33, with a range between 0.58 and 4.76. There is a significant CV for yield-related traits like TT, PT, TSW and SYP plants, indicating a notable variability among the rice genotypes, with similar findings of (10).

## Determination of genetic variations

### Genotypic and phenotypic coefficient of variation

The genetic variation present in a population is measured using GCV values, which fall between 5.45 and 21.10. On the other hand, PCV values, reflecting both genetic and environmental factors, range from 5.53 to 21.48. The most significant figures for both PCV and GCV were found in HI, with SYP, TT and various TSW following closely behind. The result was in accordance with (20, 21) for TT which was like this study.

The minimum magnitude of GCV and PCV for DM, DFF, GPP and PL was observed (Fig. 2). The slight variation in the values of GCV and PCV for these traits indicates that genetic factors have a considerable impact on how these characteristics are manifested. These results concur with observations made by (21, 22) for the characteristics DFF, PL and are also supported by (23) for the characteristics DM, DFF and PL. When the PCV exceeds the GCV, it suggests that the differences we see are more likely shaped by environmental influences than by genetic variations. Occasionally, focusing on traits for selection can lead to misunderstandings.

### Heritability and genetic advance

Heritability refers to the portion of overall observable differences in traits that can be linked to genetic variations. It serves as an important measure for assessing how likely it is for traits to be passed down through generations. The eleven traits tested showed heritability estimates ranging from 88.10 % to 99.80 % (Fig. 2). Of these, PH, GPP, BY, DFF and PL showed exceptionally high heritability, with biological yield agreeing well with the results reported in reference (24). The characteristics of PH and GPP showed the highest expected genetic progress, suggesting that there will be significant improvements expected from selective breeding practices.

## Trait association

### Genotypic correlation

Days to 50 % flowering is closely and positively related to DM (r = 0.8913), meaning that there is a corresponding delay in maturity if flowering comes late. PH (r= 0.8787 is positively related to BY but negatively to HI (r = -0.6230), meaning tall plants are related to increased biomass but could detract from efficiency in harvesting. Total tillers (r = 0.5099) are positively related to PT (r = -0.3769) but negatively with PL (r = -0.4221), pointing towards a balance between tiller and panicle length, SYP (r = 0.7688) is highly related to HI, whereas BY (r = -0.6040) negatively affects HI, shown in (Table 3). The traits DFF, DM, TT, PT, HI and SYP are identified as key factors influencing rice SYP (25).

### Phenotypic correlation

The correlation analysis reveals key associations among yield-related traits in rice. DFF exhibits a strong positive correlation with DM (r = 0.8797), indicating that later flowering leads to delayed maturity. Plant height shows a significant positive correlation with BY (r = 0.8765), suggesting that taller plants contribute to increased biomass production. However, PH is negatively correlated with HI (r = -0.6122), implying that an increase in plant height may reduce harvest efficiency. Total tillers are positively correlated with PT (r = 0.4781), indicating that an increase in total tillers contributes to more productive tillers. However, PT has a negative correlation with PL (r = -0.3490), suggesting a potential trade-off between tillering ability and panicle length. Seed yield per plant is highly positively correlated with HI (r = 0.7765), indicating that higher HI leads to greater seed yield, whereas BY shows a strong negative correlation with HI (r = -0.5945), suggesting that increased biomass may lower harvest efficiency (Table 3).

## Path coefficient analysis

### Genotypic path

The path coefficient analysis reveals the direct & indirect impact of various agronomic traits on SYP. The results indicate that BY (0.8517) and HI (1.2002) exhibit very high direct effects, suggesting their critical roles in determining yield. Additionally, DFF (-0.0856), DM (0.0734) and PH (-0.1346) also contribute to yield variation, though with moderate effects. Among indirect effects, PH shows strong negative influences on HI (-0.7478) and BY (-0.1183), implying that an increase in PH may reduce overall harvest efficiency and biomass allocation. Total tillers and PT have minor indirect contributions, with PT positively influencing BY (0.1704) and negatively HI (-0.0199), while TT has minimal effects on yield-related traits (Table 4).

1000 seed weight exhibits a negative direct effect (-0.0312) but contributes positively to BY (0.0029) and negatively HI (-0.0033) indirectly. Grain per panicle shows negligible direct effects but exerts weak indirect influences on multiple traits. The negative indirect effects of BY on HI (-0.725) and HI on BY (-0.5144) suggest an inverse relationship between total biomass production and harvest efficiency. Overall, the findings emphasize the importance of optimizing HI and BY while managing traits such as PH and TSW to improve rice yield.

### Phenotypic path

The path coefficient analysis reveals significant direct & indirect impact of various agronomic traits on SYP. Biological yield (0.832) and HI (1.1932) exhibit strong positive direct effects on SYP, indicating that increasing these traits can significantly enhance seed yield. Additionally, PT (0.0336) and TSW (0.0265) show moderate direct effects on yield. Conversely, PH (0.1279) and DFF (-0.0728) have negative direct effects on SYP, suggesting that taller plants or longer flowering durations may reduce seed yield.

**Table 3.** Genotypic (G) and Phenotypic (P) correlation coefficient among rice (*Oryza sativa* L.) traits

| Traits | | DFF | DM | PH | TT | PT | PL | GPP | TSW | BY | HI | SYP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | G | 1 | 0.8913** | 0.16 | 0.062 | -0.1395 | -0.0052 | -0.014 | -0.289 | 0.1694 | -0.0918 | -0.0047 |
| | P | 1 | 0.8797** | 0.1582 | 0.0605 | -0.1263 | -0.0062 | -0.0142 | -0.2823 | 0.1675 | -0.094 | -0.0104 |
| DM | G | | 1 | 0.226 | 0.049 | -0.1172 | -0.0893 | 0.0634 | -0.124 | 0.2391 | -0.075 | 0.0787 |
| | P | | 1 | 0.2225 | 0.0437 | -0.104 | -0.0877 | 0.0623 | -0.1213 | 0.2354 | -0.0756 | 0.0722 |
| PH | G | | | 1 | 0.016 | 0.1189 | -0.0924 | 0.0588 | -0.085 | 0.8787** | -0.6230** | -0.124 |
| | P | | | 1 | 0.0165 | 0.1105 | -0.0915 | 0.0587 | -0.0823 | 0.8765** | -0.6122** | -0.1215 |
| TT | G | | | | 1 | 0.5099** | -0.4221** | -0.242 | -0.035 | 0.1043 | -0.0513 | 0.0382 |
| | P | | | | 1 | 0.4781** | -0.4158** | -0.2378 | -0.039 | 0.1046 | -0.0508 | 0.0383 |
| PT | G | | | | | 1 | -0.3769* | -0.228 | 0.1649 | 0.2001 | -0.0166 | 0.1708 |
| | P | | | | | 1 | -0.3490* | -0.2148 | 0.1424 | 0.1899 | -0.0136 | 0.1609 |
| PL | G | | | | | | 1 | 0.2664 | -0.07 | -0.1724 | 0.0185 | -0.1311 |
| | P | | | | | | 1 | 0.265 | -0.0726 | -0.1709 | 0.0157 | -0.1298 |
| GPP | G | | | | | | | 1 | -0.148 | 0.0196 | -0.048 | -0.052 |
| | P | | | | | | | 1 | -0.1439 | 0.0194 | -0.048 | -0.052 |
| TSW | G | | | | | | | | 1 | -0.0916 | 0.1069 | 0.0542 |
| | P | | | | | | | | 1 | -0.0902 | 0.099 | 0.0463 |
| BY | G | | | | | | | | | 1 | -0.6040** | 0.0217 |
| | P | | | | | | | | | 1 | -0.5945** | 0.0213 |
| HI | G | | | | | | | | | | 1 | 0.7688** |
| | P | | | | | | | | | | 1 | 0.7765** |
| SYP | G | | | | | | | | | | | 1 |
| | P | | | | | | | | | | | 1 |

**Table 4.** Path coefficient analysis showing direct and indirect influence of 11 characters on grain yield of rice at genotypic (G) and phenotypic (P) level.

| Traits | | DFF | DM | PH | TT | PT | PL | GPP | TSW | BY | HI |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | G | -0.0856 | -0.0763 | -0.0137 | -0.0053 | 0.0119 | 0.0004 | 0.0012 | 0.0247 | -0.0145 | 0.0079 |
| | P | -0.0728 | -0.0641 | -0.0115 | -0.0044 | 0.0092 | 0.0005 | 0.001 | 0.0206 | -0.0122 | 0.0069 |
| DM | G | 0.0655 | 0.0734 | 0.0166 | 0.0036 | -0.0086 | -0.0066 | 0.0047 | -0.0091 | 0.0176 | -0.0055 |
| | P | 0.0524 | 0.0595 | 0.0132 | 0.0026 | -0.0062 | -0.0052 | 0.0037 | -0.0072 | 0.014 | -0.0045 |
| PH | G | -0.0215 | -0.0304 | -0.1346 | -0.0022 | -0.016 | 0.0124 | -0.0079 | 0.0114 | -0.1183 | 0.0839 |
| | P | -0.0202 | -0.0285 | -0.1279 | -0.0021 | -0.0141 | 0.0117 | -0.0075 | 0.0105 | -0.1121 | 0.0783 |
| TT | G | -0.0006 | -0.0004 | -0.0001 | -0.0092 | -0.0047 | 0.0039 | 0.0022 | 0.0003 | -0.001 | 0.0005 |
| | P | -0.0002 | -0.0002 | -0.0001 | -0.004 | -0.0019 | 0.0017 | 0.0009 | 0.0002 | -0.0004 | 0.0002 |
| PT | G | -0.0057 | -0.0048 | 0.0048 | 0.0208 | 0.0407 | -0.0153 | -0.0093 | 0.0067 | 0.0081 | -0.0007 |
| | P | -0.0042 | -0.0035 | 0.0037 | 0.0161 | 0.0336 | -0.0117 | -0.0072 | 0.0048 | 0.0064 | -0.0005 |
| PL | G | 0.0000 | 0.0002 | 0.0002 | 0.0008 | 0.0007 | -0.0019 | -0.0005 | 0.0001 | 0.0003 | 0.0000 |
| | P | 0.0000 | 0.0003 | 0.0004 | 0.0016 | 0.0014 | -0.0039 | -0.001 | 0.0003 | 0.0007 | -0.0001 |
| GPP | G | 0.0001 | -0.0004 | -0.0004 | 0.0015 | 0.0014 | -0.0016 | -0.0061 | 0.0009 | -0.0001 | 0.0003 |
| | P | 0.0001 | -0.0003 | -0.0003 | 0.0011 | 0.001 | -0.0012 | -0.0047 | 0.0007 | -0.0001 | 0.0002 |
| TSW | G | 0.0090 | 0.0039 | 0.0026 | 0.0011 | -0.0051 | 0.0022 | 0.0046 | -0.0312 | 0.0029 | -0.0033 |
| | P | 0.0075 | 0.0032 | 0.0022 | 0.001 | -0.0038 | 0.0019 | 0.0038 | -0.0265 | 0.0024 | -0.0026 |
| BY | G | 0.1442 | 0.2036 | 0.7483 | 0.0888 | 0.1704 | -0.1469 | 0.0167 | -0.078 | 0.8517 | -0.5144 |
| | P | 0.1394 | 0.1958 | 0.7292 | 0.087 | 0.158 | -0.1422 | 0.0162 | -0.0751 | 0.832 | -0.4946 |
| HI | G | -0.1101 | -0.09 | -0.7478 | -0.0616 | -0.0199 | 0.0222 | -0.0576 | 0.1284 | -0.725 | 1.2002 |
| | P | -0.1122 | -0.0902 | -0.7304 | -0.0606 | -0.0162 | 0.0187 | -0.0572 | 0.1181 | -0.7093 | 1.1932 |

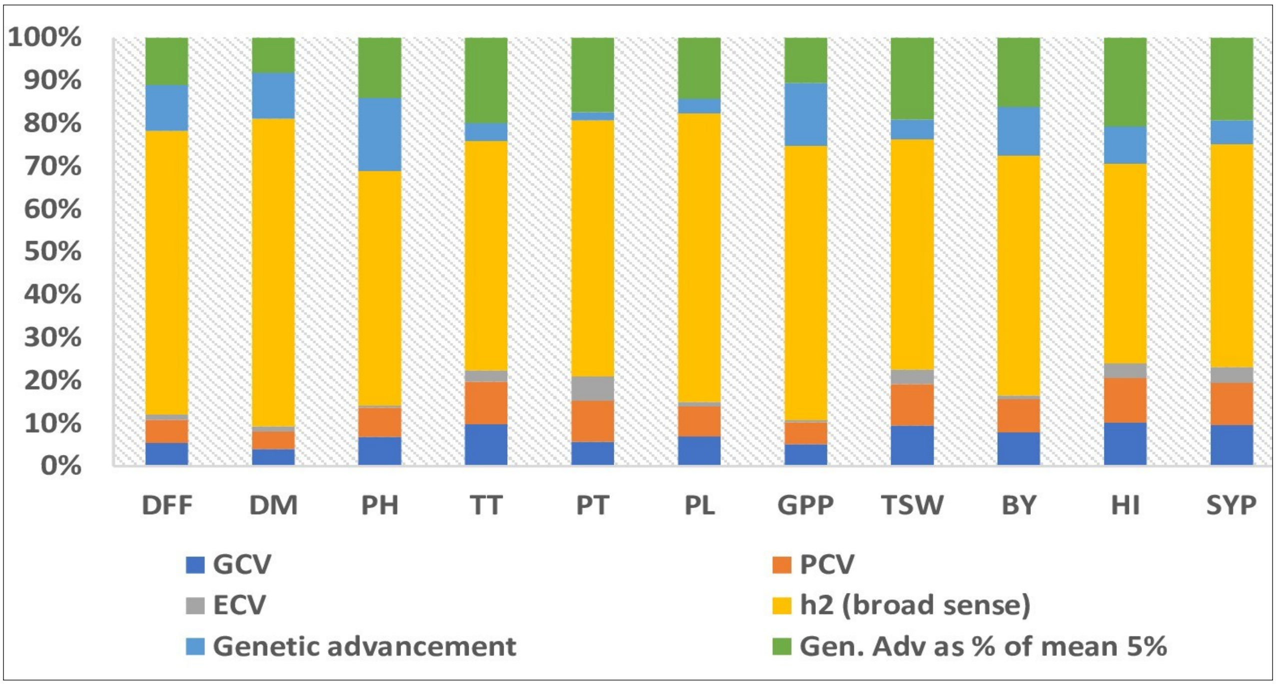


**Fig. 2.** Graphic illustration of genetic advance and heritability as % of mean in rice genotypes. (**PCV**= *Phenotypic Coefficient of Variation*, **GCV**= *Genotypic Coefficient of Variation*, **ECV**= *Environmental Coefficient of Variation*, **GA**= *Genetic advancement %*, **h2**= *Heritability %*).

Traits such as TT (0.004), PL (-0.0039) and GPP (-0.0047) exhibit low negative direct effects, indicating a minimal impact on yield. The result was in accordance with (26) for the trait TT and PL.

Indirect effects also play a crucial role in determining yield. Days to 50 % flowering, DM and PH have both positive and negative indirect effects through various traits such as PT, TSW, BY and HI. Biological Yield has maximum positive indirect impact on DFF, DM and PH but exerts a very high negative indirect impact on HI. On the other hand, HI has negative indirect impact on BY, DFF, DM and PH, reinforcing the complex relationship between these traits. Overall, BY and HI emerge as the most critical determinants of seed yield, while traits like DFF and PH negatively influence productivity. TSW contributes both directly and indirectly to yield, whereas traits like PL and GPP have minimal influence. This analysis underscores the importance of selecting genotypes with high BY and HI to improve seed yield (Table 4). The similar result was observed by (27) for the trait HI and BY for positive direct effect and DFF and TT for negative direct effect on seed yield and (28) for DFF and PH with negative influence.

## Cluster analysis

### Cluster analysis by Torcher's method

The results shown in Fig. 3 from the touch analysis revealed that Cluster I displayed the highest level of genetic diversity, followed by Cluster II and Cluster V. The degree of genetic variation found within Clusters I, II and V was measured at 27, 11 and 3, respectively. The results were consistent with the conclusions drawn in reference (29). Clusters III, IV, VI and VII each contained a single genotype (Fig. 3). This pattern of clustering revealed unique genotypic trends, providing important information for choosing the best genotypes, which will aid in developing a strong breeding strategy moving forward.

### Intra-Inter cluster distances among eight different clusters

Cluster V displayed the highest level of internal variation, followed closely by Clusters I and II regarding the differences within the groups. Clusters (III, IV, VI, VII) each containing a single genotype, have exhibited the highest mean, indicating their potential as parents in hybridization programs aimed at yield improvement, so no variation within the cluster. Cluster combinations V and VI, III and VII, VI and VII, as well as II and VII, exhibited significant inter-cluster distances. The largest distance between clusters was noted between clusters IV and VII. On the other hand, the smallest distance was recorded between clusters IV and VI, with the distances between clusters III and VI, as well as IV and III, coming next (Table 5).

### Estimation of mean values of clusters

Cluster VII achieved the highest average for DFF at 109.33 days. It was closely followed by clusters V, II, I, III, VI and IV. Notably, cluster IV also recorded the longest DM at 140.00 days. Additionally, plant height varied, with cluster VII measuring 171.57 cm and cluster III at a shorter 98.94 cm. This indicates that these clusters could be significant for improving plant height in rice breeding initiatives. When assessing PH as a factor for enhancing yield, it is important to consider the usual distances between internodes and the width of the stem. Unfortunately, these characteristics were not analyzed in this study. Of the various traits related to yield, the TT demonstrated a range of variation, with values spanning from 18.43 in cluster VI to 23.10 in cluster III. Productive tillers are essential characteristics, with objectives for crop enhancement differing between cluster IV (11.83) and cluster II (10.02). The potential PL varied from cluster IV (26.32) to cluster III (19.35), the maximum GPP was in cluster VII (147.27) and then in cluster IV (123.60). Biological yield varied from 95.77 for cluster VII to 51.51 for cluster VI. Harvest index varied between 55.77 for cluster VI and 20.56 for cluster VII. Thousand seed weight varied from 22.91 for cluster II to 27.17 for cluster VIII. Seed yield per plant was 33.26, as indicated in Fig. 4.

### Percent contribution of traits

The ranking statistics show the comparative contribution of various traits to entire performance in rice which shows PH is ranked 1st with the highest percentage (36.06 %), indicating its strong influence. GPP comes next with 32.73 %, pointing to its role in determining yield. Other characteristics such as TT, TSW and HI contribute less and DM and PT show no contribution (Table 6).

## Principal component analysis (PCA)

PCA revealed eleven distinct morphological characteristics, leading to the formation of eleven principal components (PC1 through PC11), with each one reflecting various aspect. Kaiser's Rule was used in PCA to decide the number of principal components (PCs) that should be retained based on eigenvalues. PCs with eigenvalues larger than 1 are retained based on Kaiser's Rule as they capture useful variability. Retaining these components can help plant breeders improve genetic progress (Table 7).

The scree plot demonstrates that the initial four principal components (Dim1, Dim 4) explain 72.3 % of the overall variance, with Dim1 contributing 25.3 %, Dim 2 at 19.2 %, Dim 3 at 16.9 % and Dim 4 at 10.9 %. This suggests that these components effectively capture the underlying structure of the data. The

**Table 6.** Percent contribution of different traits towards divergence in rice genotypes

| Sr no. | Traits | Times Ranked 1st | Contribution % |
|---|---|---|---|
| 1 | DFF | 45 | 4.55 |
| 2 | DM | 0 | 0.00 |
| 3 | PH | 357 | 36.06 |
| 4 | TT | 17 | 1.72 |
| 5 | PT | 0 | 0.00 |
| 6 | PL | 123 | 12.42 |
| 7 | GPP | 324 | 32.73 |
| 8 | TSW | 12 | 1.21 |
| 9 | BY | 100 | 10.10 |
| 10 | HI | 9 | 0.91 |
| 11 | SYP | 3 | 0.30 |

**Table 5.** Estimates of average inter and intra- cluster distances for 7 clusters in Rice

| Cluster | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | 24.81 | 32.85 | 30.51 | 32.22 | 36.42 | 33.21 | 56.18 |
| II | 32.85 | 22.64 | 33.50 | 35.78 | 42.12 | 36.49 | 65.23 |
| III | 30.51 | 33.50 | 0.00 | 22.10 | 52.29 | 17.20 | 75.55 |
| IV | 32.22 | 35.78 | 22.10 | 0.00 | 56.50 | 15.86 | 77.57 |
| V | 36.42 | 42.12 | 52.29 | 56.50 | 25.42 | 57.60 | 36.18 |
| VI | 33.21 | 36.49 | 17.20 | 15.86 | 57.60 | 0.00 | 77.20 |
| VII | 56.18 | 65.23 | 75.55 | 77.57 | 36.18 | 77.20 | 0.00 |

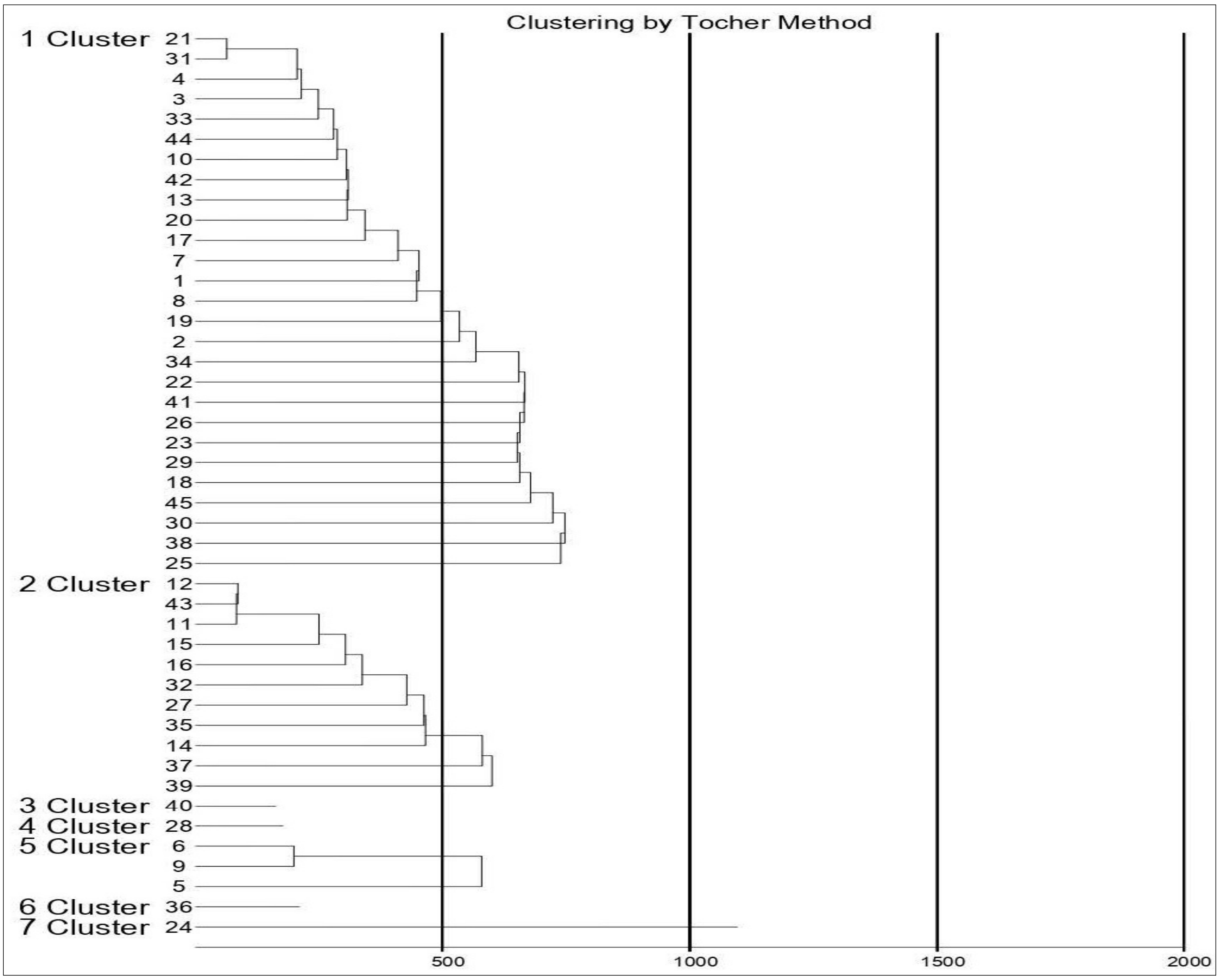
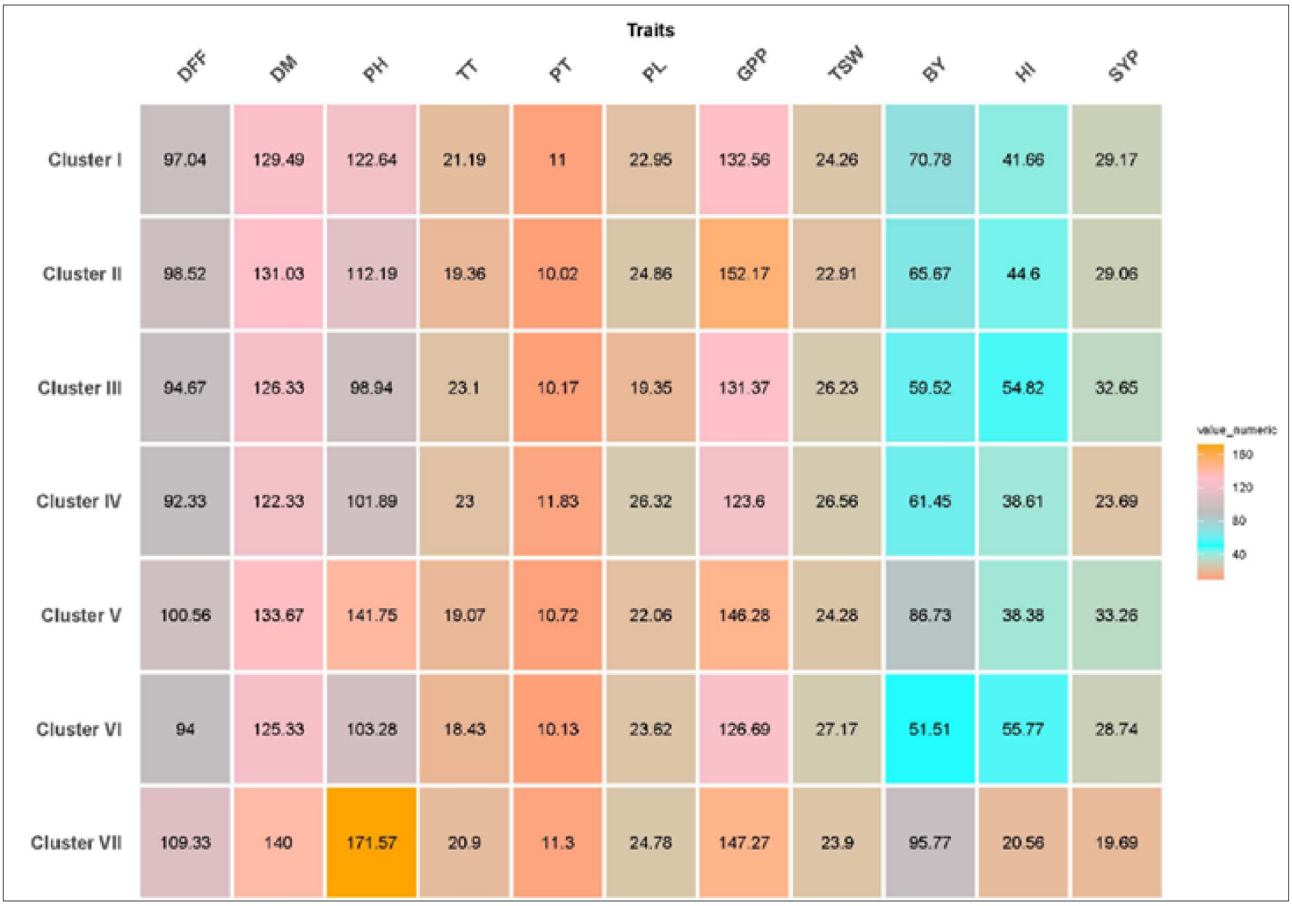


**Fig. 3.** Graphical representation of the mean values for eight clusters, as determined by Tocher's procedure, across 45 rice genotypes.



Traits

| | DFF | DM | PH | TT | PT | PL | GPP | TSW | BY | HI | SYP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 97.04 | 129.49 | 122.64 | 21.19 | 11 | 22.95 | 132.56 | 24.26 | 70.78 | 41.66 | 29.17 |
| Cluster II | 98.52 | 131.03 | 112.19 | 19.36 | 10.02 | 24.86 | 152.17 | 22.91 | 65.67 | 44.6 | 29.06 |
| Cluster III | 94.67 | 126.33 | 98.94 | 23.1 | 10.17 | 19.35 | 131.37 | 26.23 | 59.52 | 54.82 | 32.65 |
| Cluster IV | 92.33 | 122.33 | 101.89 | 23 | 11.83 | 26.32 | 123.6 | 26.56 | 61.45 | 38.61 | 23.69 |
| Cluster V | 100.56 | 133.67 | 141.75 | 19.07 | 10.72 | 22.06 | 146.28 | 24.28 | 86.73 | 38.38 | 33.26 |
| Cluster VI | 94 | 125.33 | 103.28 | 18.43 | 10.13 | 23.62 | 126.69 | 27.17 | 51.51 | 55.77 | 28.74 |
| Cluster VII | 109.33 | 140 | 171.57 | 20.9 | 11.3 | 24.78 | 147.27 | 23.9 | 95.77 | 20.56 | 19.69 |

**Fig. 4.** Graphical representation of mean value of seven clusters by torcher’s method for 45 genotypes of rice.

**Table 7**. Eigenvalues and eigenvectors for the first four PCs in 11 traits of rice

| PCs | PC1 | PC2 | PC3 | PC4 |
|---|---|---|---|---|
| Eigenvalue | 2.7804 | 2.115 | 1.86 | 1.199 |
| Variance % | 25.276 | 19.23 | 16.91 | 10.9 |
| Cumulative % | 25.276 | 44.51 | 61.42 | 72.32 |
| DFF | -0.287 | -0.15 | 0.564 | -0.221 |
| DM | -0.298 | -0.112 | 0.563 | -0.086 |
| PH | -0.507 | 0.033 | -0.134 | 0.364 |
| TT | -0.103 | 0.473 | 0.083 | -0.316 |
| PT | -0.066 | 0.526 | -0.056 | 0.042 |
| PL | 0.1062 | -0.474 | -0.095 | 0.112 |
| GPP | -0.023 | -0.354 | -0.032 | 0.31 |
| TSW | 0.1413 | 0.184 | -0.179 | 0.122 |
| BY | -0.503 | 0.117 | -0.083 | 0.402 |
| HI | 0.4763 | 0.1 | 0.369 | 0.245 |
| SYP | 0.2144 | 0.234 | 0.39 | 0.604 |

heatmap depicts the impact of 11 agricultural traits, indicating that Dim1 is significantly shaped by factors such as PH (0.71), BY (0.63) and HI (0.45), underscoring the variability related to growth. Dim 2 is associated with developmental traits, including days until maturity (0.65) and days to reach DFF (0.42). Dim 3 is linked to the weight of a TSW (0.68), while Dim 4 is influenced by PL and SYP (0.43). The NGPP (0.37) adds to Dim 5. Consequently, dim.1 to Dim 4 provides essential insights for breeding strategies Dim 2 focuses on early maturation, Dim1 emphasizes plant strength and Dim 3 and Dim 4 concentrate on improving seed weight and yield attributes (Fig. 5), demonstrates how much variance is accounted for by each PCs. The first PC1 shows an eigenvalue of 2.7804, reflecting a significant amount of variability that this component captures. The first four principal components PC1(25.276), PC2(19.23), PC3(16.91), PC4(1.199) explain 72.32 % of the total variance, making them the most important for distinguishing genotypes. As a result, these key components are sufficient to validate how the best-performing treatments influence the variations seen in various parameters.

### Biplot analysis

Biplot analysis showed correlations among the various parameters and treatments in relation to PC1, PC2, PC3 and PC4, which accounted for 72.32 % of the data variance. The PCs were graphed as four points in a two-dimensional Cartesian plane to determine the prominent features in the observations (Fig. 6).

In coordinate 1 of the biplot, the genotypes G38, G39, G16, G42, G37, G25, G27, G35 were Clustered, where these traits SYP, TSW, HI are projecting, confirming the strong association between them. In coordinate 2, the genotypes G44, G2, G43, G4, G10, G5, G17, G18, G22, G3 were clustered where traits PT, TT, BY and PH are projecting, confirming the strong association of them (Fig. 6).

The PC1 and PC2 were negative in G28, G13, G1, G45, G7, G30, G32, G29, G19, G21, G6, G12 at coordinate3. These are associated with traits like DM, DFF and GPP. The vectors of all traits are almost at different distance from the origin especially G12 and G21 are far away from the origin. In coordinate 4, G26, G33, G40, G36, G14, G23, G32, G15, G8, G20, G11, G24 and G9 were clustered which were associated with a single trait PI. In PCA, PC1 (25.3 %) is dominated by TSW, SYP and DFF, which shows their strong influence on genotype distinction. PC2 (19.2 %) is led by PH, BY and HI, which indicate plant growth-related differences. Other characters such as PL, GPP, TT and PT contribute moderately, representing finer-scale differences.

## Discussion

The variance analysis showed considerable differences in the traits examined, indicating that there is a promising opportunity for enhancing genetics through careful selection and crossbreeding of essential yield traits and their related features within the tested genotypes (30). All the characters had significant results with sufficient variation between major traits, allowing the variability needed to start a breeding program. Previous studies reported similar findings with significant variation observed in some of the rice traits (31).

Genotype 4, G22 and G41 had the minimum and maximum value of DM and DFF which means some genotypes mature previously than others. Early maturing rice varieties have a short life cycle and this renders them economically valuable for crop improvement. They grow intensively in the vegetative growth stage, which allows them to compete with weeds, release land early for the subsequent crops, avoid pests' attacks and use less water. This renders them extremely valuable in rice-based cropping systems (32). Genotype 4 and G22 had the least and greatest PH values, respectively and are henceforth identified as the greatest varying characteristics among all. This variance can be exploited for generating rice with low shelf life. In a similar fashion, previous studies (1) demonstrated that the vast differences in PH and reported it can be used in rice breeding.

In this experiment, the rice lines with accelerated maturity were developed and it was observed that all the high-yielding genotypes had a moderate plant height during all the seasons. This reflects that a medium plant height is preferred while breeding rice (32). Coefficient of variation suggested that the GCV estimates of all the characters under investigation were slightly lower than PCV estimates suggesting mild effect of environment on the performance of genotype. The findings are similarly supported by former studies in rice (33). The minimal variation between the PCV and GCV of most of the characteristics in this work, such as DFF, DM, PH, PL, GPP, HI and TSW, indicated some extent of environmental effect on the phenotypic expression of these characteristics.

The research shows that people who possess favorable characteristics while having a low impact on their surroundings can be chosen for breeding initiatives designed to enhance future production. Among the yield-attributing traits, HI, TT, BY and SYP exhibited the highest PCV and GCV (1, 34). Understanding both heritability and genetic advance offers more value than considering heritability alone for these traits (35, 36). The heritability values of the traits were found to be around the moderate to low range, with certain traits such as DFF, PL, BY, PH and GPP with highest heritability values (37). The high genetic advance observed for such characteristics as PH, GPP, BY, HI and DFF indicates that these characteristics are controlled by additive genes and can be improved through selection. The results agree with those documented by (35).

The major economic character, grain yield was highly positively correlated with some of the characters both for genotypic and phenotypic correlation. Thus, selecting these traits will indirectly improve grain yield. The relationships between yield and other traits, such as DM, PT and BY, were also shown by (38). Understanding the association of phenotypic traits with yield and their influence on yield is necessary for

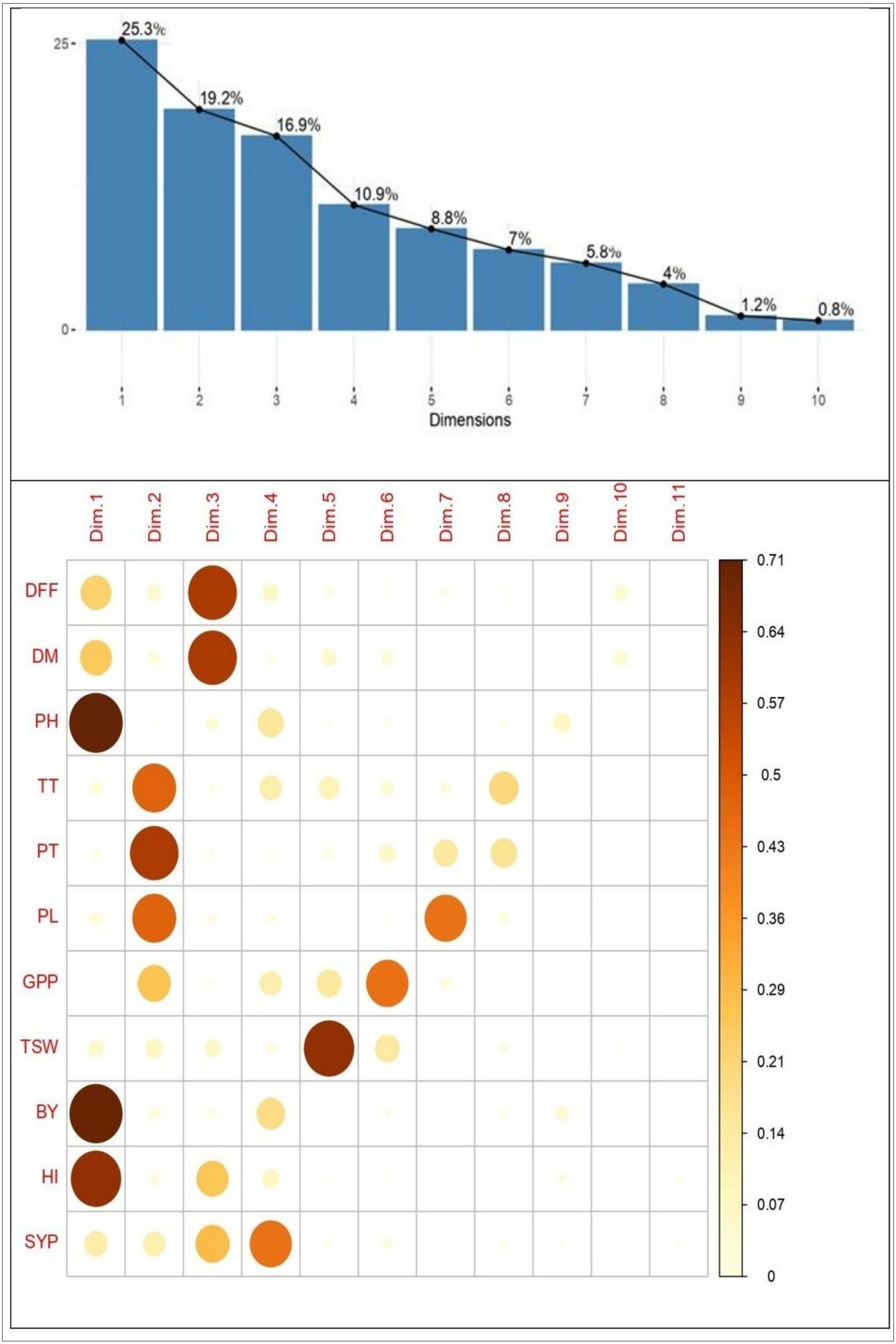


**Fig. 5.** Scree plot showing the variation between their Eigen value and the number of principal components.

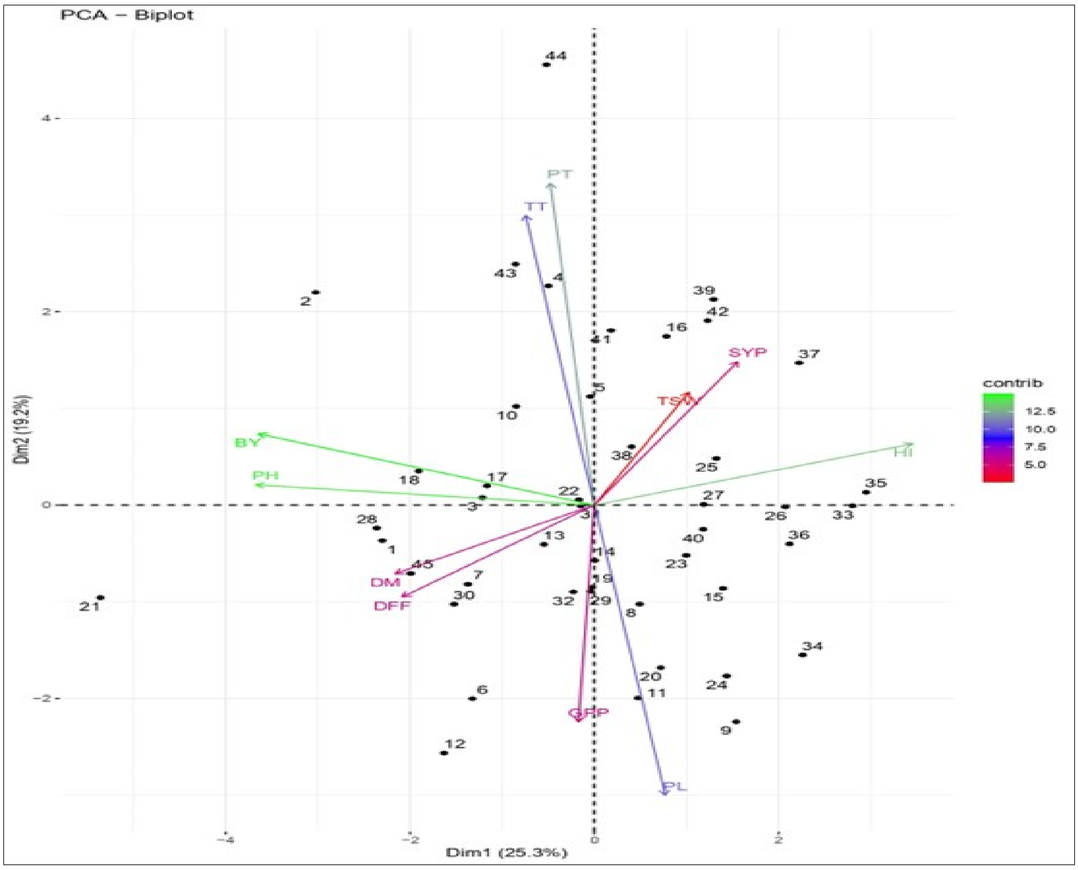


**Fig. 6**. Biplot for rice and 11 traits along the first 2 principal components.

effective selection in breeding programs. Path coefficient analysis shows direct and indirect effects of characters on yield, indicating the inter-relationship among yield components and helping in specific varietal improvement (39). The present study revealed that BY, HI, TSW and PL had maximum and positive direct impact on grain yield. It was suggested that assortment of these parameters is liable to carry on overall improvement on plant yield directly (14, 39, 38, 8).

Clusters of rice germplasm (Clusters IV and VII, Clusters III and VII and Clusters VI and VII) showed high inter-cluster distances, indicating significant genetic divergence among the genotypes. This divergence is essential for hybridization programs focused on developing high-yielding, short-duration and early maturing rice varieties (10). Cluster V showed the maximum intra-cluster distance representing high variation within the cluster and it was learned that genotypes with a high degree of heterogeneity in a cluster would produce better breeding materials to achieve maximum genetic progress (40). Clusters (IV and VI) remained improved suitable for creating early maturity isolates while other clusters (III) were better ideal for developing semi dwarf lines due to their high cluster mean values and cluster (V and III) have genotypes that can be used to develop transgressive breeding lines for maximum yield. The results of this research were concurrent with that of the previous research (2).

Principal Component Analysis simplifies multivariate data by condensing the number of original characteristics into fewer new components that account for the largest possible percentage of the total variation in the dataset, hence retaining much of the information in the first few components. The study revealed that just a small number of eigenvectors were sufficient to accurately represent the primary morphological differences among the genotypes. The PC1, which had an eigenvalue of 2.78 along with PC2, PC3 and PC4, explained 72.32 % of the total variation and was mainly reflecting characteristics related to early maturity and semi-dwarf PH. (12, 41) reported the highest variation explained by PC1 in their study on rice lines. Other major components, having eigenvalues of 2.115, 1.86 and 1.199, explained 19.23 %, 16.91 % and 10.9 % variation, respectively, these components are useful for constructing efficient selection criteria and selecting better lines in breeding populations (28).

## Conclusion

This study concludes that the evaluated rice genotypes exhibited significant genetic variability. Genotypes G35, G39, G16, G40 and G26 demonstrated the highest potential for superior seed yield per plant (SYP) and showed consistently strong performance across other yield-contributing traits, making them ideal candidates for breeding programs aimed at enhancing productivity. For reduced plant height (PH), genotypes G37, G36, G34, G25 and G11 were most promising and may serve as valuable male parents in hybridization. The highest PCV and GCV values were recorded for harvest index (HI) and SYP, indicating substantial genetic influence with minimal environmental impact. Cluster analysis showed minimum intra-cluster distance in Cluster II (high homogeneity) and maximum in Cluster IV, with the greatest inter-cluster divergence between Clusters IV and VII. Traits like PH and grains per panicle (GPP) contributed most to genetic divergence. Principal Component Analysis (PCA) revealed that PC1 was primarily influenced by TSW, SYP and DFF, while PC2 to PC4 also contributed significantly to yield enhancement. These findings support the development of high-yielding and early maturing varieties to help meet future food demands.

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## Authors' contributions

NC, SP and AP played key roles in conceptualizing the research and drafting the manuscript. SP edited the manuscript and maintained communication. SG and SP performed the data analysis and statistical analysis using R-Studio. Additionally, SP was involved in achieving the research goals. All authors read and approved the final version of the manuscript.

## Compliance with ethical standards

**Conflict of interest:** The authors have no conflicts of interest to report.

**Ethical issues:** None

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