



RESEARCH ARTICLE

# Discerning of genetic variability and diversity of finger millet (*Eleusine coracana* L.) germplasm for yield and its components

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## Abstract

The present investigation was conducted to assess genetic variability, correlations among characters, direct and indirect effects and genetic divergence among 20 finger millet genotypes, with the aim of identifying promising lines for yield improvement. The genotypes were evaluated for 12 quantitative traits and their mean performance was recorded. The Analysis of Variance (ANOVA) revealed significant differences among genotypes for all studied traits, indicating sufficient genetic variability in the experimental material. High estimates of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were observed for traits like grain yield per plant (GYPP), number of fingers per ear (NFPE) and ear weight (EW), suggesting potential for genetic improvement. Moderate GCV and PCV were found for traits such as finger length (FL), number of productive tillers and plant height (PH). High heritability ( $H_{bs}$ ), coupled with high GA, was observed for GYPP, FL, NFPE, EW and the number of productive tillers per plant (NPTPP), indicating the predominance of additive gene action for these characters. Grain yield per plant showed a significant positive association with EW, NFPE and NPTPP at both phenotypic and genotypic levels. Path coefficient analysis revealed that EW exhibited the highest direct positive effect on GYPP, trailed by NPTPP, FL and NFPE. Mahalanobis  $D^2$  analysis divided the genotypes under study into three clusters, with clusters II and III exhibiting the maximum inter-cluster distance. Principal component analysis (PCA) identified the first five components %, which together explained 76.52 % of the total variation, with GYPP, EW, NFPE and FL as major contributors, further validating their importance in selection strategies.

**Keywords:** correlation coefficient; finger millet; genetic variability; path coefficient analysis; principal component analysis; quantitative traits; yield components

## Introduction

Finger millet (*Eleusine coracana* L.), popularly known as ragi or mandua, pertains to the Poaceae family and the genus *Eleusine* bearing a chromosome number of  $2n=36$ , subfamily Chloridoideae and is a highly self-pollinated allotetraploid (1), evolved from its wild tetraploid ancestor, *E. coracana* subsp. *Africana*. It is considered one of the major staple food crops, along with rice, wheat, sorghum and pearl millet and is predominantly cultivated in the southern regions of India. The crop's wide adaptability, rich nutritional value, dual-purpose utility and high multiplication rate make it an essential component of mixed crop-livestock farming systems commonly practiced in semi-arid tropical regions (2). As an ancient crop, finger millet is well-suited for cultivation in drylands, hilly terrains and tribal agricultural systems. Its remarkable resilience allows it to thrive under diverse ecological conditions, making it a highly suitable option for addressing climate change challenges and contingency planning in agriculture.

This cereal plays a vital role in the semi-arid regions of the world, accounting for about 12% of the total millet cultivation area, and is grown across more than 25 countries in Asia and Africa (3). According to an ASSOCHAM report, India cultivated finger millet across 1.01 million hectares during the 2021–22 crop year,

achieving a total production of 1.67 million tons (MT) and a yield of 1,747 kg per hectare. India leads the world in millet production, contributing approximately 15 % of the global output. As reported by the Ministry of Agriculture and Farmers Welfare, India stands as the largest producer of millets globally, with an annual production of 11.5 million tons (4). It is an important crop in developing countries, especially in Africa and Asia (5) and is cultivated across various regions of the world. In India, it is predominantly grown in the southern states such as Karnataka, Andhra Pradesh and Tamil Nadu, as well as in the northern hilly regions, particularly Uttarakhand.

Finger millet is represented by approximately 10 genera and 20 species distributed globally and is a drought-tolerant crop, cultivated during the Kharif season (6). Its flour offers a range of health benefits, like supporting weight loss, controlling blood cholesterol level, improving bone health, addressing anemia and managing other health conditions. It is an excellent source of calcium (Ca), phosphorus (P) and iron (Fe). With increasing consumer awareness of health benefits and a growing preference for processed products, it has gained prominence for its functional components, such as slowly digestible starch and resistant starch (7). To enhance production by improving the yield potential of different genotypes, plant breeders must recognize the extent of variability, genetic inheritance, the nature

and strength of relationships among various traits and their stability over different environments. Since grain yield is a complex trait with environmental effects, direct selection based solely on yield is often ineffective. Therefore, selecting genotypes based on yield-contributing traits is a more effective breeding strategy.

A thorough understanding of genetic variability components, population diversity and the inter-relationships among various traits is fundamental to the success of any plant breeding program. Conventional breeding methods for genetic improvement largely rely on the accessibility of diverse germplasm with substantial genetic variance. Proper characterization and evaluation of germplasm are crucial prerequisites for its effective utilization, enabling the identification of valuable genetic resources and superior genotypes. Since yield is a quantitative trait affected by several component attributes, breeding for yield alone is not sufficient to produce improved genotypes. Hence, estimates of heritability ( $H_{bs}$ ), combined with genetic advance (GA), provide valuable insights for predicting selection outcomes and developing appropriate breeding strategies. Consequently, the correlation investigation shed light on the importance of a yield contributing character. It provides an assessment of the correlation and degree of association between traits, enabling yield improvement in a short time period. Therefore, understanding the correlation between yield and its contributing traits can aid in selecting an ideal plant type. To determine the actual contribution of individual traits to yield, it is important to break down the correlation into direct and indirect effects using path analysis. Combining correlation studies with path analysis helps identify effective selection criteria for yield improvement. For a systematic enhancement of yield and its components, analyzing trait correlations is highly beneficial. Understanding genetic divergence is crucial for breeders because it allows individuals with similar characteristics to be grouped together by classifying the subject samples into distinct groups based on a set of dissimilar factors. Consequently, employing clustering techniques such as  $D^2$  and Principal Component Analysis, the genetic diversity of finger millet genotypes for yield and related traits was evaluated and compared. Considering this, the current study was designed to assess the components of variability, trait associations and diversity among 20 finger millet genotypes.

## Materials and Methods

The experimental material exhibited 20 *Eleusine* germplasm accessions (Table 1) procured from the Indian Institute of Millets Research (IIMR), Hyderabad. The germplasm was evaluated in a Randomized Block Design (RBD) with three replications at the farm of Genetics & Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab. Randomized Block Design was chosen over other experimental designs as it allows better control over experimental error by accounting for block-to-block variation, thereby improving the precision and reliability of treatment comparisons. Additionally, it facilitates flexibility in handling missing plots and provides valid comparisons among genotypes using analysis of variance. All entries were sown on 27<sup>th</sup> February during the Rabi season of 2024. In each replication, every genotype was sown in two rows of 1 m length, with a spacing of 30 cm between rows and 10 cm between the plants within a row. Standard agronomic package of practices was employed to grow the genotypes % and the observations were recorded on five randomly selected plants in each plot for all the traits under investigation, except for days to 50 % flowering (D 50 % F) and days to 75 % maturity (D 75 % M) maturity, where data were recorded on a plot basis. Statistical analysis was carried out to compute the different parameters of variability, correlation (8) and path coefficient (9), Mahalanobis  $D^2$  analysis (10) and Principal Component Analysis (PCA), employing R core team software (11), before being clustered using Tocher's method.

## Results and Discussion

### Analysis of variance

In the present investigation, the summary statistics of the 12 traits were recorded in Table 2 with the help of descriptive statistics like Standard Error of Mean (Sem), Critical Difference (CD) and Coefficient of Variation (CV). The analysis of variance (ANOVA) revealed that the genotypes differ significantly for all the characters under study, viz., D 50 % F, D 75 % M, plant height (PH), number of productive tillers per plant (NPTTP) and number of spikelets per plant (SPP), number of ears per spikelet (NSPE), length of fingers (LOF), length of peduncle (LOP), 1000 seed weight (1000 SW), biological yield per plant (BYPP), harvest index (HI) and Grain yield per plant (GYPP). This highlights the presence of substantial genetic diversity in the initial breeding material, which is essential for the development of key component

**Table 1.** List of the genotypes used for the investigation

| SR.NO | GENOTYPE                                                    | STATUS    | SOURCE                                               |
|-------|-------------------------------------------------------------|-----------|------------------------------------------------------|
| 1     | GPU 28 (Krishna) - Indaf 5 x (Derived from Indaf 9×IE 1012) | Released  | Indian Institute of Millet Research (IIMR) Hyderabad |
| 2     | GPU 48                                                      | Released  | Indian Institute of Millet Research (IIMR) Hyderabad |
| 3     | GPU 67                                                      | Released  | Indian Institute of Millet Research (IIMR) Hyderabad |
| 4     | MR 6                                                        | Released  | Indian Institute of Millet Research (IIMR) Hyderabad |
| 5     | VL 376                                                      | Released  | Indian Institute of Millet Research (IIMR) Hyderabad |
| 6     | IC0473149                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 7     | IC0473306                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 8     | IC0473352                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 9     | IC0474764                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 10    | IC0474797                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 11    | IC0473193                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 12    | IC0477424                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 13    | IC0477980                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 14    | IC0478061                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 15    | IC0478078                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 16    | IC0478275                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 17    | IC0478291                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 18    | IC0478534                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 19    | IC0479799                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |
| 20    | IC0587935                                                   | Germplasm | Indian Institute of Millet Research (IIMR) Hyderabad |

**Table 2.** Analysis of variance for different agro-morphological characters in finger millet (*Eleusine coracana* L.) genotypes

| Source of variation | Replication | Treatment | Error   | S.E m | C.D at 5 % | C. V % |
|---------------------|-------------|-----------|---------|-------|------------|--------|
| Degree of freedom   | 2           | 19        | 39      | -     | -          | -      |
| D 50 % F            | 51.0500*    | 260.0518* | 15.3307 | 2.26  | 6.47       | 5.06   |
| D 75 % M            | 1.7167      | 303.1184* | 1.1026  | 0.60  | 1.73       | 1.14   |
| PH (cm)             | 1.4632      | 545.8072* | 3.436   | 1.07  | 3.06       | 1.82   |
| NPTTP               | 0.2172      | 1.9372*   | 0.2359  | 0.28  | 0.80       | 7.53   |
| NSPE                | 29.3932*    | 0.6300*   | 0.0293  | 0.09  | 0.28       | 3.41   |
| SPP                 | 0.2015      | 10.2054*  | 3.5192  | 1.08  | 3.100      | 12.74  |
| LOF (cm)            | 1.8305*     | 2.3570*   | 0.1177  | 0.19  | 0.56       | 4.06   |
| LOP (cm)            | 6.2530*     | 0.9543*   | 0.2259  | 0.27  | 0.75       | 7.49   |
| 1000 SW             | 9.4965*     | 1.9184*   | 0.1456  | 0.22  | 0.63       | 14.76  |
| BYPP (g)            | 0.3077      | 95.7692*  | 0.8871  | 0.54  | 1.55       | 1.98   |
| HI (%)              | 0.6604      | 21.5205*  | 1.2139  | 0.63  | 1.82       | 6.61   |
| GYPP (g)            | 0.1160      | 1.7915*   | 0.1965  | 0.25  | 0.73       | 5.70   |

\*5 % level of significance

traits and supports the effectiveness of future breeding programs. The results are in agreement with the previous analysis in the same crop (12, 13).

### Parameters of variability

In the present investigation, for parameters of variability (Table 3), the estimates of Phenotypic Coefficient of Variation (PCV) were slightly higher than those of Genotypic Coefficient of Variation (GCV) for all the characters under study, indicating that although environmental factors influenced trait expression, the magnitude of environmental variance was relatively low for most traits. The narrow differences between GCV and PCV values were observed for 1000 SW, BYPP and HI, representing the presence of substantial genetic variability and the potential for effective selection in improving these traits. Moderate GCV and PCV were recorded for D 50% F, D 75 % M, PH, number of fingers per plant, number of spikelets per spike and GYPP, suggesting that these traits are also amenable to selection but may require larger populations to achieve significant progress. Importantly, the proximity of GCV and PCV values for D 75 % M, PH, 1000 SW, BYPP, HI, as well as GYPP suggests that these characters are also amenable to improvement through selection, although genetic gain may be comparatively moderate.

The high estimates of  $H_{bs}$  coupled with high GA as percentage of mean were detected for the variables like PH, D 75 % M, 1000 SW, HI and BYPP. These results suggest that a significant proportion of the observed variation may be heritable; however, since ( $H_{bs}$ ) was estimated in a broad sense and derived from phenotypic evaluation without progeny testing, the nature of gene action cannot be definitively drawn. Significant ( $H_{bs}$ ) was also demonstrated for D 50 % F and HI, confirming their reliability for genetic transmission to the next generation; therefore, multi-location and multi-season evaluation would be required to estimate genetic parameters more efficiently and to validate selection efficiency. Traits such as peduncle length and the number of spikelets per plant, on the other hand, showed less genetic advancement and ( $H_{bs}$ ), indicating a stronger

environmental influence. Overall, the results demonstrate that 1000 SW, HI, PH, D 75 % M and BYPP are reliable and promising traits for genetic improvement due to their high variability, ( $H_{bs}$ ) and GA. These results are consistent with earlier research by which also noted strong ( $H_{bs}$ ) and genetic advancement in important yield variables (12, 13).

### Correlation coefficient

Since yield is a dependent trait governed by complex polygenic inheritance, understanding the extent of genetic associations among its components is crucial for identifying the most desirable genotypes. It deciphers that selecting one trait can significantly advance a positively correlated trait. The estimates of correlation coefficients for yield and its component traits at both the genotypic and phenotypic levels are shown in Fig. 1. The study focuses on correlation analysis among 12 yield and its components in 20 finger millet genotypes. Grain yield per plant showed significant positive correlation with traits like HI, NPTTP and length of fingers at both the levels, suggesting their significance for indirect selection in breeding. Additionally, moderate relationships were found between 1000-seed weight and PH, indicating that these characteristics significantly enhance production. These results support the importance of these traits in yield enhancement strategies and are consistent with previous studies which also revealed substantial trait relationships and variability in finger millet between yield and its components (12, 14–17).

### Path coefficient analysis

Path analysis determines how component traits influence grain yield, either directly or indirectly through their interactions with other traits, as the correlation coefficient alone cannot be able to provide the precise estimates of each component trait, as it only measures the nature and magnitude, not the cause, because of the non-independence of the associated characters. Therefore, path coefficient analysis serves as a discrimination to partition correlation into direct and indirect effects of a particular causal factor. Grain yield served as the dependent variable in this analysis,

**Table 3.** Variation, heritability and genetic improvement potential in finger millet genotypes

| SL.NO | Characters | GCV % | PCV % | Environmental Coefficient of Variation (ECV) % | Heritability % | GA as % of Mean |
|-------|------------|-------|-------|------------------------------------------------|----------------|-----------------|
| 1     | D 50 % F   | 11.67 | 12.72 | 5.06                                           | 84.18          | 22.06           |
| 2     | D 75 % M   | 10.91 | 10.97 | 1.14                                           | 98.92          | 22.36           |
| 3     | PH         | 13.24 | 13.37 | 1.82                                           | 98.13          | 27.02           |
| 4     | NPTTP      | 11.68 | 13.90 | 7.53                                           | 70.62          | 20.23           |
| 5     | NSPE       | 8.92  | 9.55  | 3.41                                           | 87.23          | 17.17           |
| 6     | SPP        | 10.14 | 16.29 | 12.74                                          | 38.77          | 13.01           |
| 7     | LOF        | 10.24 | 11.02 | 4.06                                           | 86.38          | 19.61           |
| 8     | LOP        | 7.77  | 10.79 | 7.49                                           | 51.81          | 11.52           |
| 9     | 1000 SW    | 29.73 | 33.20 | 14.76                                          | 80.23          | 54.87           |
| 10    | BYPP       | 11.87 | 12.03 | 1.98                                           | 97.27          | 24.11           |
| 11    | HI %       | 15.63 | 16.97 | 6.62                                           | 84.79          | 29.65           |
| 12    | GYPP       | 9.37  | 10.97 | 5.70                                           | 73.01          | 16.507          |

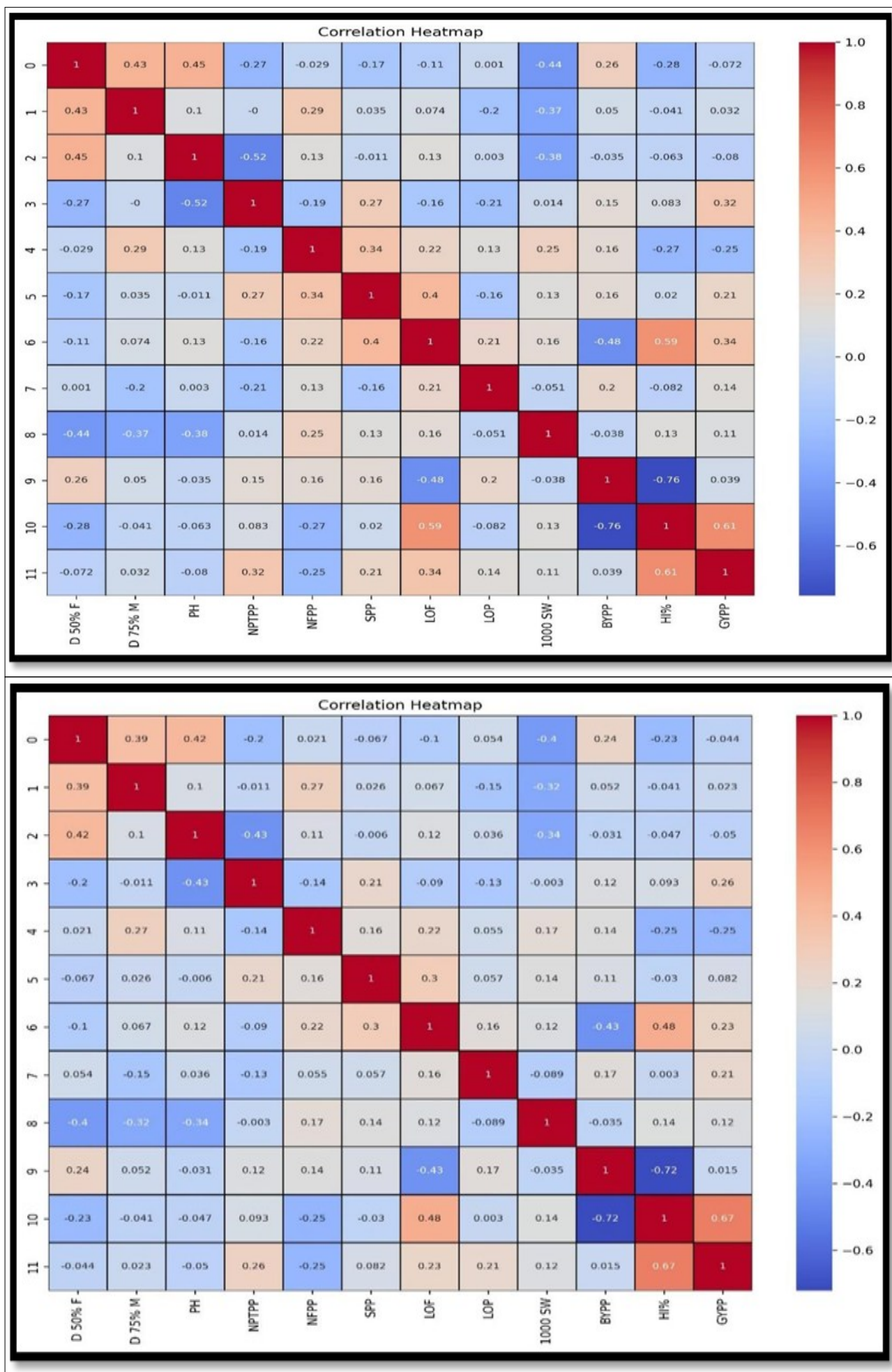


Fig. 1. Correlogram of genotypic (A) and phenotypic (B) correlations for yield and yield-contributing traits in finger millet.

whereas the other 11 yield-associated traits were treated as independent variables. Genotypic and phenotypic correlation coefficients (Fig. 2) were calculated to assess the relationships between GYPP with each of the 11 independent variables. This analysis helped in understanding both the direct impact of these traits on grain yield and their indirect effects mediated by other yield components. The findings showed that BYPP (1.08715) and HI (1.39431) exhibited direct effects on GYPP greater than unity at the genotypic level, suggesting that they shouldn't be prioritized in breeding programs, as this might be due to multicollinearity between these independent traits. Traits such as NPTPP (0.02454) and 1000 SW (0.02281) also showed positive direct effects, suggesting their importance in trait selection. The number of fingers per plant (-0.1422), on the other hand, displayed the strongest adverse direct effect, indicating that the characteristic may reduce production. The results are in line with previous research which highlighted the significance of biomass output, 1000-seed weight and productive tillers as critical factors for finger millet yield enhancement (12, 13, 18, 19). The study found that NPTPP (0.02454) and 1000 SW (0.02281) showed positive direct effects on GY at the genotypic level, indicating their critical role in yield improvement, albeit to a lesser extent. In contrast, NFPP (-0.0684) had the effect, trailed by the largest negative direct effect, followed by D 50 % F and D 75 % M, suggesting these traits may hinder yield performance. These findings highlight the importance of prioritizing traits like HI and BYPP in breeding programs. The residual effects, phenotypic and genotypic, were observed to be 0.023 and 0.016, respectively, suggesting that the variability of the traits under investigation was fully captured. The results corroborate earlier findings which reported similar traits, such as the NPTPP and HI, influencing grain yield in finger millet (13, 19–22).

### Principal component analysis

To identify the Principal Component (PC) of variability, PCA was conducted & the result elucidated the five significant principal components with eigenvalue  $\geq 1$ , which aggregated 76.52 % of the total variability (Table 4). Principal Component1 exhibited 22.49 % of the variability %, especially through D 50 % F, BYPP and PH, while PC2 contained 17.02 % mainly via NPTP, BYPP and 1000 SW. PC3 attained 13.82 % of the total variability primarily through NFPP, NSPP, LF % and 1000 SW, whereas PC4 constituted 12.56 % of the variability through GYPP, D 75 % M, NSPP and BYPP. The PC5 had 10.63 % variability, where D 75 % M and NPTPP were the major contributing traits. Together, the first five components account for a significant part of the dataset's total variability. The PCA biplot (Fig. 3) displays the contribution of various traits to the first two principal

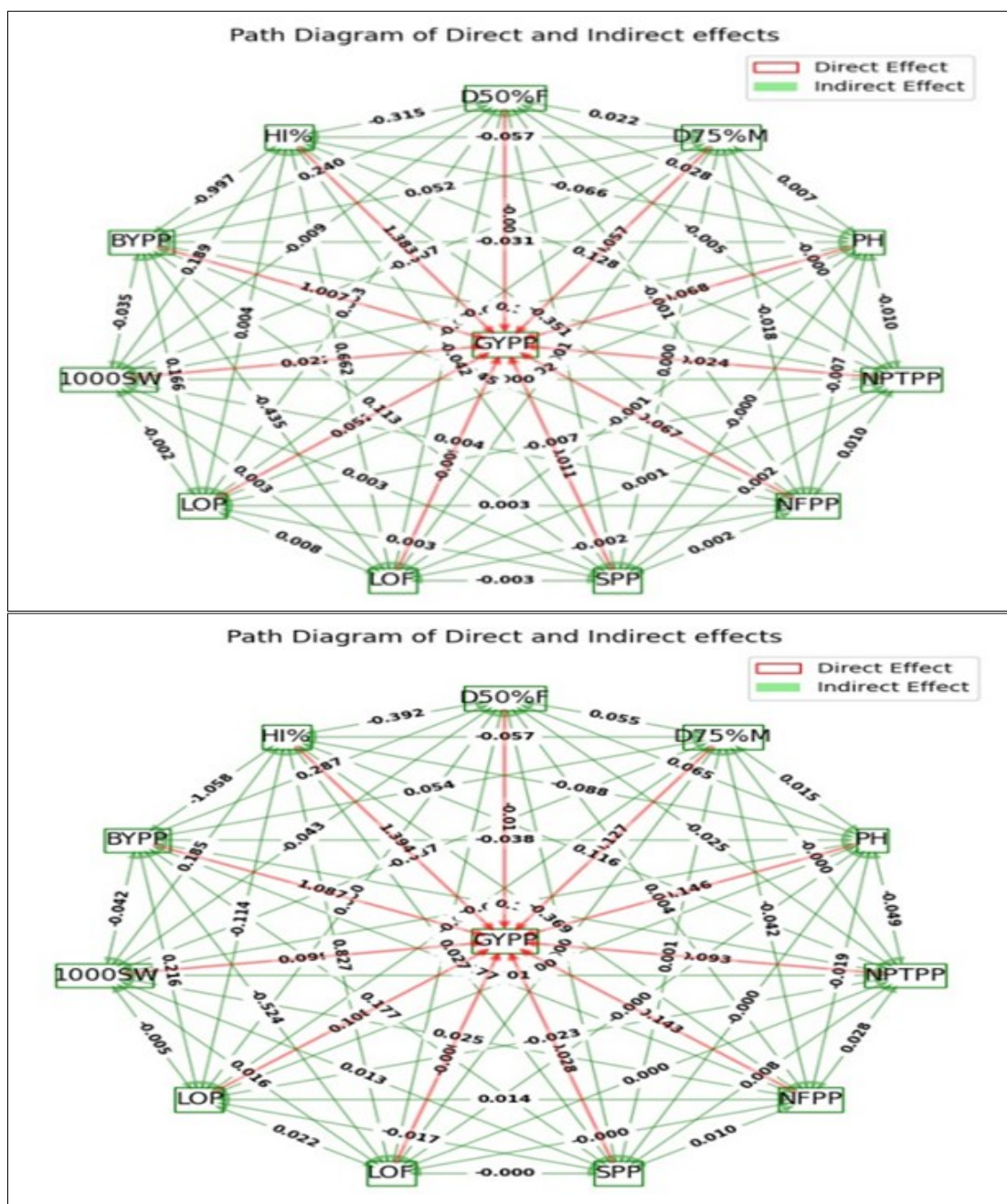
components, Dim1 (22.5 %) and Dim2 (17 %), which together account for 39.5 % of the total variance. Arrows represent individual traits, with their length and direction indicating the strength and nature of their contribution. An acute angle between the traits indicates positive correlation, an obtuse angle indicates negative correlation and a right angle indicates weak or no correlation among the traits. Traits like NPTPP and NFPP contributed strongly and positively to Dim1, as they had the longest vector lengths from the origin, indicating the maximum variability of these traits, while HI and LF showed negative associations, as they fall in the negative dimension of the biplot. The occurrence of BYPP as a singleton in Dim1 indicated that a large portion of variance is explained by the trait; therefore, selection solely for the trait may increase the biomass but not necessarily grain yield. Traits such as GYPP, 1000 SW and SPP contributed moderately to the variability in both the dimensions. Positively correlated traits point in the same direction, whereas opposite vectors indicate negative relationships, revealing key patterns in trait variability.

The percentage of total variance explained by each of the first 10 principal components (PCs) from a PCA is displayed in the scree plot. The main components (PC1 through PC5) are represented by the dimensions along the X-axis and the percentage of variance explained by each component is shown on the Y-axis. A line graph connecting the tops of the bars illustrates the trend in variance contribution across components, while the height of each bar indicates the amount of variation recorded by the corresponding major component.

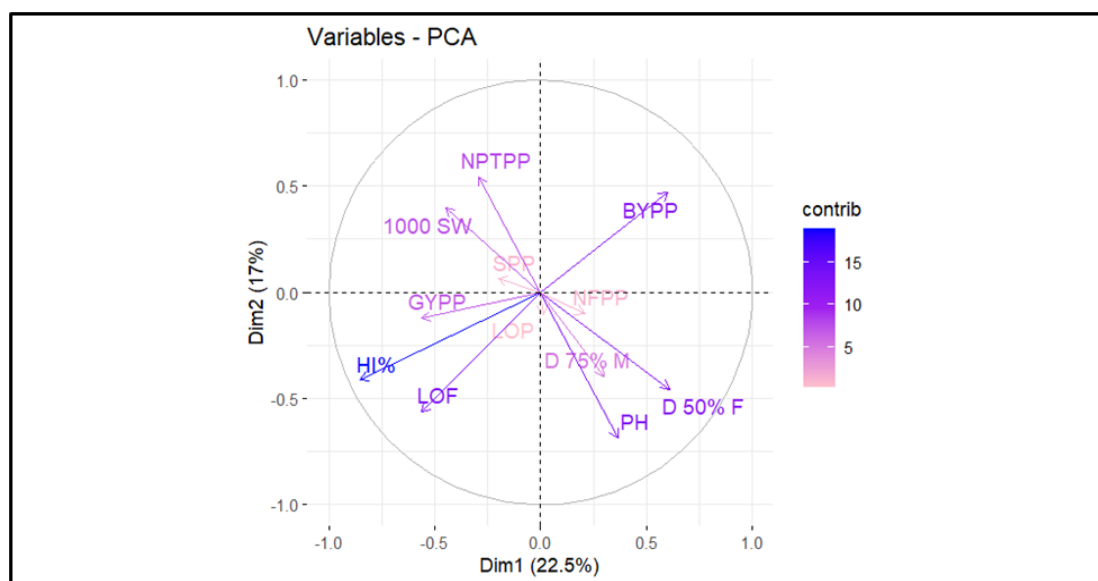
The plot has a semi-curved shape, with a visible elbow or bend between PC5 and PC6 (Fig. 4), after which the curve flattens. This pattern indicates that the top five to six components are the most relevant, accounting for most of the data's volatility. Components other than PC7 contribute minimally to the overall variance and may provide limited further insight. Thus, in terms of dimensionality reduction, preserving the first few components will likely preserve much of the fundamental data structure while simplifying the analysis. The scree plot demonstrated that the first six components accounted for most of the variation, indicating that they are suitable for genotype grouping and dimensionality reduction. Similar results of the Scree plot, where the first few principal components explain most of the variability, were evident in black gram (23, 24). These findings are consistent with earlier reports that highlighted PH and yield traits as the main contributors to the first PC in finger millet and identified D 50% F, PH and finger length (FL) as key traits influencing PCA variation in different genotypes (22, 25).

**Table 4.** Principal component analysis of quantitative traits in finger millet accessions

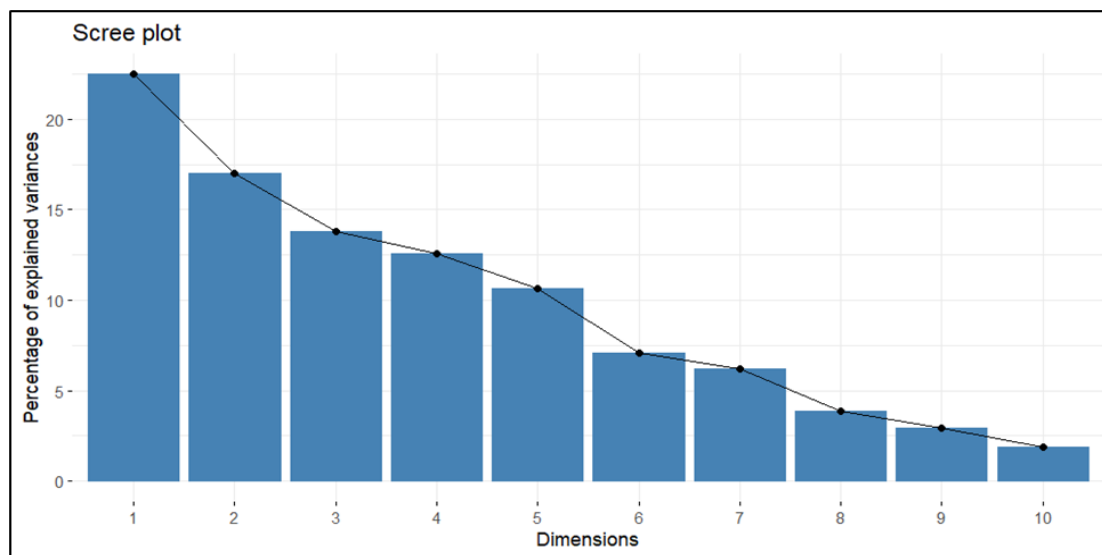
| <b>Eigen Vectors</b>    |             |             |             |             |             |
|-------------------------|-------------|-------------|-------------|-------------|-------------|
| <b>Characteristics</b>  | <b>PC 1</b> | <b>PC 2</b> | <b>PC 3</b> | <b>PC 4</b> | <b>PC 5</b> |
| D 50 % F                | 0.37        | -0.32       | -0.11       | 0.25        | -0.07       |
| D 75 % M                | 0.18        | -0.28       | 0.07        | 0.43        | 0.37        |
| PH                      | 0.22        | -0.48       | 0.03        | -0.08       | -0.1        |
| NPTPP                   | -0.18       | 0.38        | -0.1        | 0.5         | 0.13        |
| NSPE                    | 0.13        | -0.07       | 0.64        | -0.06       | 0.17        |
| SPP                     | -0.12       | 0.04        | 0.49        | 0.34        | 0.08        |
| LOF                     | -0.34       | -0.39       | 0.34        | 0.03        | -0.04       |
| LOP                     | 0.01        | -0.07       | 0.17        | -0.05       | -0.75       |
| 1000 SW                 | -0.27       | 0.28        | 0.33        | -0.27       | 0.02        |
| BYPP                    | 0.37        | 0.33        | 0.18        | 0.3         | -0.33       |
| HI %                    | -0.52       | -0.29       | -0.18       | 0.06        | 0.02        |
| GYPP                    | -0.34       | -0.09       | -0.08       | 0.46        | -0.36       |
| Eigen Values            | 2.7         | 2.04        | 1.66        | 1.51        | 1.28        |
| Variance (%)            | 22.49       | 17.02       | 13.82       | 12.56       | 10.63       |
| Cumulative variance (%) | 22.49       | 39.51       | 53.33       | 65.89       | 76.52       |



**Fig. 2.** Genotypic and phenotypic path diagram for grain yield and its components in 20 finger millet accessions. Residual 0.016 (genotypic) & 0.023 (phenotypic)



**Fig. 3.** Scatter plot of 12 characters of finger millet.



**Fig. 4.** Scree plot showing variation for different PC values.

### Genetic divergence

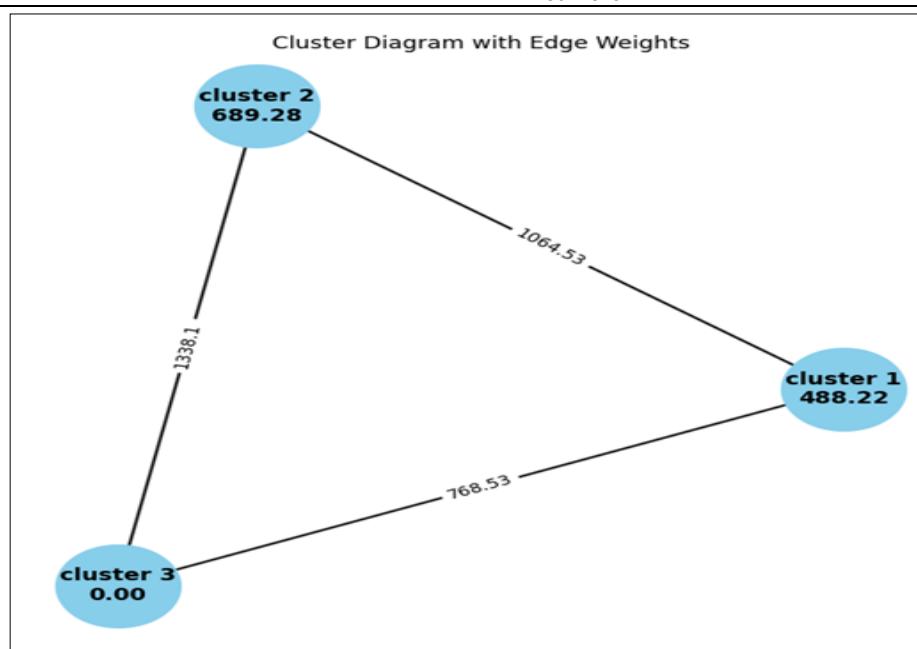
The Mahalanobis  $D^2$  statistics grouped the finger millet genotypes into three clusters (Table 5) by Tocher's method based on the performance of various yield and yield-related traits. Among them, Cluster I had the highest number of genotypes, indicating a high level of genetic similarity among the included genotypes (17). This cluster comprised: GPU 48, GPU 67, MR 6, VL376, IC0473149, IC0473306, IC0473352, IC0474764, IC0474797, IC0473193, IC0477980, IC0478061, IC0478078, IC0478275, IC0478534, IC0479799 and IC0587935.

Cluster II included 2 genotypes (GPU 28 and IC0477424), showing moderate diversity from other clusters. Cluster III was a singleton cluster, containing only IC0478291, suggesting its distinctness and high divergence from the other genotypes.

Cluster distance was further classified into intra & inter cluster distances. Fig. 5 represents intra- and inter-cluster distances. The maximum intra-cluster distance was recorded in cluster II (689.28), followed by cluster I (488.22). Cluster III showed an intra-cluster distance of 0.0. The maximum inter-cluster distance was observed between cluster II and cluster III (1338.10), followed by cluster I and cluster II (1064.53) and cluster I and cluster III (768.53). The highest inter-cluster distance was observed between Clusters II & III, suggesting that crossing genotypes from these clusters could yield superior segregants due to their genetic diversity. This strategy aligns with earlier studies that emphasized the potential of distant clusters to generate heterotic hybrids in finger millet breeding programs and with subsequent research that reported significant divergence among 148 genotypes based on traits such as ear length, days to flowering and grain yield (26–28).

**Table 5.** Clustering pattern among finger millet genotypes for various yield and yield-related traits

| Cluster Groups | No. of Genotypes | List of Genotypes                                                                                                                                                          |
|----------------|------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Cluster 1      | 17               | GPU 48, GPU 67, MR 6, VL376, IC0473149, IC0473306, IC0473352, IC0474764, IC0474797, IC0473193, IC0477980, IC0478061, IC0478078, IC0478275, IC0478534, IC0479799, IC0587935 |
| Cluster 2      | 2                | GPU 28, IC0477424                                                                                                                                                          |
| Cluster 3      | 1                | IC0478291                                                                                                                                                                  |



**Fig. 5.** Cluster diagram representing the inter- and intra-cluster distance of finger millet genotypes.

## Conclusion

In the present investigation, finger millet genotypes were effectively classified into distinct groups based on the evaluation of 11 agromorphological traits, indicating substantial genetic diversity. This diversity can be strategically exploited in hybridization programme (s) by selecting the genetically divergent genotypes as parents for the development of new, improved varieties. High estimates of both genotypic and phenotypic variance were recorded for 1000 SW, BYPP and HI, confirming the existence of significant genetic variability and highlighting the potential for impact full selection in improving these traits. Correlation and path coefficient analysis revealed that HI, NPTTP and BYPP exhibited significant positive correlations and direct effect on GYPP, underscoring their importance as key yield-determining traits. Furthermore %, PCA indicated that the first five components constituted 76.52 % of the total variation, with major contributions from HI, BYPP, NPTTP and PH, emphasizing their relevance in genotype differentiation and selection. The Mahalanobis D<sup>2</sup> statistics grouped the finger millet genotypes into three clusters by Tocher's method, reflecting wide genetic divergence among the genotypes studied. Overall, the identified traits and divergent genotypes provide valuable opportunities for targeted selection and hybridization. Therefore, these characteristics should be prioritized in *Eleusine* breeding for yield improvement.

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## Authors' contributions

AS, ASR participated in the design of the study and performed the statistical analysis, funding acquisition, writing original draft, reviews and editing. All authors read and approved the final manuscript.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interest to declare.

**Ethical issues:** None

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