

RESEARCH PAPER

Assessment of Trait Associations and Genetic Diversity in Finger Millet (*Eleusine coracana* L.) Germplasm

K. Jyothermayee Sree Satyavalli¹, N. Anuradha^{2*}, Lal Ahmed, M.¹ and T.S.S.K. Patro²

¹Department of Genetics and Plant Breeding, Agricultural College, Bapatla, India

²ANGRAU-Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

*Corresponding author: n.anuradha@angrau.ac.in (ORCID ID: 0000-0001-6244-9143)

Received: 06-04-2026

Revised: 03-05-2026

Accepted: 29-05-2026

ABSTRACT

Finger millet (*Eleusine coracana* L.) is a climate-resilient and nutritionally rich cereal crop with immense potential for ensuring food and nutritional security. The present study was conducted to evaluate the relationships among 13 quantitative traits using Pearson's correlation analysis and to assess the genetic diversity of 100 finger millet genotypes through principal component analysis (PCA). Correlation analysis revealed that grain yield per plant exhibited significant positive associations with ear length, finger length, number of fingers per ear, leaf length, finger width, and fodder yield per plant indicating their importance as selection criteria for yield improvement. PCA identified five principal components with eigenvalues greater than one, collectively accounting for 72.88% of the total phenotypic variation. The first principal component alone explained 24.18% of the variability and was mainly influenced by ear length, finger length, grain yield, fodder yield, and leaf length. The PCA biplot showed considerable overlap among genotypes from different geographical regions, suggesting that genetic diversity was independent of geographical origin. The identified variability and key yield-contributing traits provide valuable information for selecting diverse parental lines and developing high-yielding, climate-resilient finger millet cultivars through efficient breeding programmes.

HIGHLIGHTS

- ① Evaluation of 100 finger millet genotypes revealed substantial phenotypic variability for 13 quantitative traits.
- ② Finger length, ear length, number of fingers per ear, leaf length, and finger width were identified as key traits associated with grain yield.
- ③ The first five principal components explained 72.88% of the total phenotypic variation, indicating considerable genetic diversity.
- ④ PCA biplot revealed no distinct clustering based on geographical origin, emphasizing the importance of selecting parents based on genetic divergence rather than collection site.

Keywords: Finger millet, Genetic diversity, Pearson's correlation, Principal component analysis, Grain yield

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an allotetraploid ($2n = 4x = 36$) C4 cereal belonging to the family Poaceae and is recognized as one of the most climate-resilient and nutritionally superior small millets. It is believed to have originated in the highlands of East Africa, particularly Ethiopia, followed by domestication and subsequent

introduction into the Indian subcontinent, where it has become an important staple food crop. Today, finger millet is cultivated extensively across Asia

How to cite this article: Jyothermayee Sree Satyavalli, K., Anuradha, N., Lal Ahmed, M. and Patro, T.S.S.K. (2026). Assessment of Trait Associations and Genetic Diversity in Finger Millet (*Eleusine coracana* L.) Germplasm. *Int. J. Bioresource Sci.*, 13(01): 29-34.

Source of Support: None; **Conflict of Interest:** None



and Africa under diverse agro-ecological conditions because of its remarkable adaptability to drought, poor soil fertility, salinity, and erratic rainfall, making it an important crop for climate-smart agriculture (Wright and Devos, 2024; Gebreyohannes *et al.* 2024).

Finger millet has recently gained global attention owing to its exceptional nutritional profile and its potential contribution to food and nutritional security. Recognition of millets through the International Year of Millets (2023) has further stimulated research on their nutritional, genetic, and breeding potential, positioning finger millet as a promising crop for sustainable agriculture under changing climatic conditions (Kaur *et al.* 2024; Kayastha *et al.* 2024). Despite its immense potential, finger millet remains an underutilized and under-researched crop compared with major cereals. Global productivity remains relatively low due to several constraints, including limited genetic improvement, susceptibility to diseases such as blast, inadequate seed systems, and the narrow use of elite cultivars in breeding programmes (Wright and Devos, 2024).

Genetic diversity forms the cornerstone of crop improvement programmes by providing the raw material necessary for selection and breeding. Assessment of genetic diversity using agro-morphological traits continues to be an effective and economical approach for the preliminary characterization of germplasm. Estimates of genetic parameters such as variability, heritability, genetic advance, and genetic divergence provide valuable information for selecting diverse parental combinations capable of generating broad genetic recombination and transgressive segregants.

Comprehensive evaluation of germplasm collections or breeding lines not only supports the identification of superior donor parents but also contributes to the conservation and utilization of genetic resources in developing climate-resilient, nutrient-dense, and high-yielding cultivars. Therefore, understanding the extent of genetic diversity present in finger millet germplasm remains a prerequisite for designing efficient breeding programmes aimed at ensuring sustainable food and nutritional security under future climatic challenges (Wright and Devos, 2024; Gebreyohannes *et al.* 2024; Kasule *et al.* 2024).

MATERIALS AND METHODS

The present study was conducted at the Agricultural Research Station, Vizianagaram, utilizing a set of 100 finger millet genotypes, including the check varieties VR 929 and VL 376. Each genotype was planted in two rows of 3 m length following a randomized experimental layout. Recommended agronomic practices were uniformly adopted throughout the crop growth period to ensure the establishment of a healthy crop. Observations were recorded on 13 quantitative traits following standard guidelines. Pearson's phenotypic correlation analysis was carried out to determine the relationships among the studied traits. Furthermore, Principal Component Analysis (PCA) was performed using the agricolae package in PBTtools to evaluate the extent of genetic diversity among the genotypes and to identify the key traits contributing to the observed variability in the finger millet germplasm.

RESULTS AND DISCUSSION

Association analysis was carried out after confirming that significant differences were observed among genotypes for all the traits under study (ANOVA table not furnished). The phenotypic correlation coefficients among the thirteen quantitative traits are presented in Table 1. Grain yield per plant exhibited significant and positive correlations with finger length ($r = 0.383^{***}$), ear length ($r = 0.345^{***}$), number of fingers per ear ($r = 0.326^{***}$), leaf length ($r = 0.322^{**}$), and finger width ($r = 0.244^{*}$), indicating that these traits are the major contributors to grain yield and can serve as effective selection criteria in finger millet improvement programmes. Productive tillers and test weight showed positive but non-significant associations with grain yield, whereas days to 50% flowering, days to maturity, plant height, and leaf width exhibited weak or negative correlations, suggesting their limited direct influence on grain productivity. Similar associations between these yield-contributing traits and grain yield have been reported by Charitha and Lal (2023), Singh *et al.* (2024), and Gebreyohannes *et al.* (2024).

Among the component traits, ear length was highly and positively correlated with finger length ($r = 0.980^{***}$), while finger width showed significant positive associations with leaf length ($r = 0.466^{***}$), test weight ($r = 0.300^{**}$), and leaf width ($r = 0.219^{*}$), indicating coordinated development of vegetative

and reproductive traits. Grain yield per plant also exhibited a strong positive correlation with fodder yield per plant ($r = 0.712^{***}$), suggesting the possibility of simultaneous improvement of grain and fodder yield through selection. These findings are in agreement with recent reports by Wright and Devos (2024) and Kaur *et al.* (2024), who highlighted the importance of these traits in enhancing productivity.

Principal component analysis (PCA) revealed considerable genetic diversity among the 100 finger millet genotypes. The first five principal components had eigenvalues greater than one and together explained 72.88% of the total phenotypic variation (Table 2), indicating that these components adequately represented the variability present in the germplasm. PC1 accounted for the highest variation (24.18%), followed by PC2 (17.47%), PC3 (11.40%), PC4 (10.86%) and PC5 (8.97%). The high cumulative variance explained by the first few principal components suggests that these traits contributed substantially to the genetic divergence among the genotypes, which is consistent with earlier reports in finger millet (Singh *et al.* 2024; Gebreyohannes *et al.* 2024).

The first principal component was mainly influenced by ear length, finger length, grain yield per plant, fodder yield per plant and leaf length, indicating that these traits were the major contributors to genetic variability. PC2 was predominantly associated with days to 50% flowering, days to maturity and finger width, whereas PC3 was characterized by leaf width, grain yield and fodder yield. Test weight showed maximum contribution in PC4, while number of productive tillers and number of fingers per ear contributed substantially to PC5. These results indicate that yield and its associated component traits, together with phenological characters, played a significant role in differentiating the evaluated genotypes and may therefore be prioritized for selection in finger millet improvement programmes. Similar findings have been reported by Wright and Devos (2024) and Kaur *et al.* (2024), highlighting the usefulness of PCA in identifying key traits governing genetic diversity.

The scree plot (Fig. 1) further confirmed the findings by showing a distinct elbow after the fifth principal component, indicating that the first five principal components adequately explained the variability

among the finger millet genotypes. Together, these components accounted for 72.88% of the total phenotypic variation and were considered the most informative for diversity analysis and used for further interpretation (Jolliffe, 2002).

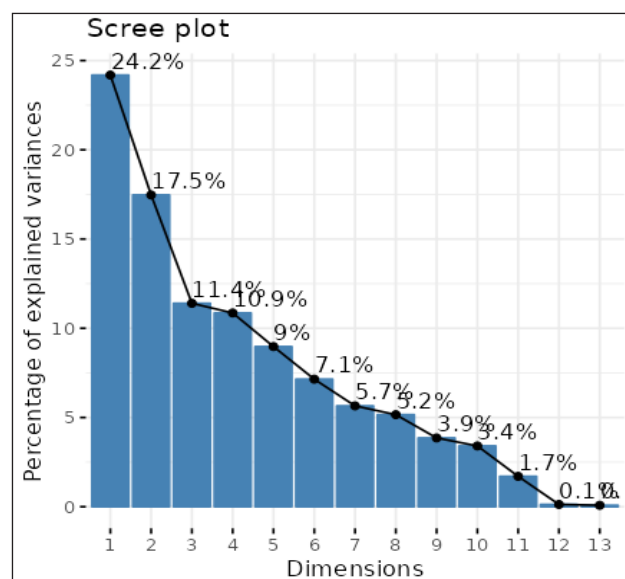


Fig. 1: Scree plot of principal components in finger millet

The PCA correlation circle (Fig. 2) indicated that the first two principal components explained 41.65% of the total phenotypic variation (PC1 = 24.18% and PC2 = 17.47%). Ear length (EL), finger length (FL), grain yield per plant (GY), fodder yield per plant (FYP), and finger width (FW) showed strong positive loadings on PC1, indicating that these traits were the major contributors to genetic divergence and were positively associated with each other. The close proximity of EL and FL vectors suggests a strong positive correlation between these traits, which agrees with the correlation analysis.

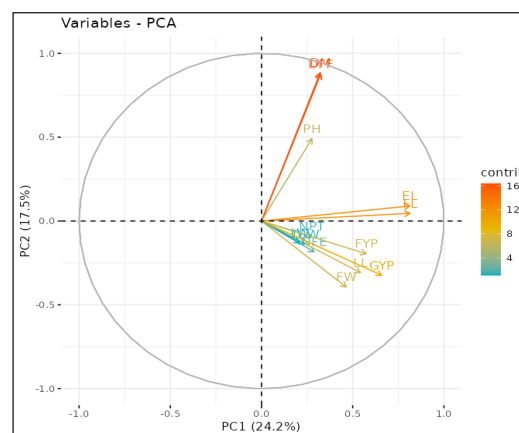


Fig. 2. Circle plot indicating the contribution of various traits towards divergence

Table 1: Associations among 13 traits in finger millet

Trait	Days to %0% flowering	Days to maturity	Plant height	Productive tillers	No. of fingers per ear	Ear length	Finger length	Finger width	Leaf length	Leaf width	Test weight	Grain yield per plant	Fodder yield per plant
Days to %0% flowering	1	0.988***	0.356***	0.029	0.046	0.199*	0.158	-0.116	-0.065	-0.024	0.014	-0.013	0.114
Days to maturity	0.988***	1	0.362***	-0.006	0.018	0.215*	0.172	-0.126	-0.073	-0.013	0.005	-0.017	0.108
Plant height	0.356***	0.362***	1	-0.027	-0.078	0.218*	0.196	0.083	0.08	0.076	0.101	-0.041	-0.072
Productive tillers	0.029	-0.006	-0.027	1	0.037	0.169	0.175	0.083	-0.05	-0.034	0.222*	0.163	0.235*
No. of fingers per ear	0.046	0.018	-0.078	0.037	1	0.054	0.082	0.101	0.161	0.181	-0.006	0.326***	0.195
Ear length	0.199*	0.215*	0.218*	0.169	0.054	1	0.980***	0.221*	0.372***	0.128	0.033	0.345***	0.215*
Finger length	0.158	0.172	0.196	0.175	0.082	0.980***	1	0.213*	0.378***	0.084	0.02	0.383***	0.239*
Finger width	-0.116	-0.126	0.083	0.083	0.101	0.221*	0.213*	1	0.466***	0.219*	0.300**	0.244*	0.200*
Leaf length	-0.065	-0.073	0.08	-0.05	0.161	0.372***	0.378***	0.466***	1	0.123	0.028	0.322**	0.142
Leaf width	-0.024	-0.013	0.076	-0.034	0.181	0.128	0.084	0.219*	0.123	1	0.307**	-0.031	0.003
Test weight	0.014	0.005	0.101	0.222*	-0.006	0.033	0.02	0.300**	0.028	0.307**	1	0.055	0.203*
Grain yield per plant	-0.013	-0.017	-0.041	0.163	0.326***	0.345***	0.383***	0.244*	0.322**	-0.031	0.055	1	0.712***
Fodder yield per plant	0.114	0.108	-0.072	0.235*	0.195	0.215*	0.239*	0.200*	0.142	0.003	0.203*	0.712***	1

Table 2: Eigenvalues and Eigenvectors

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
Eigen values and Variance %													
Eigen Value	3.14	2.27	1.48	1.41	1.17	0.93	0.73	0.67	0.5	0.44	0.22	0.02	0.01
Variance %	24.18	17.47	11.4	10.86	8.97	7.15	5.65	5.16	3.85	3.41	1.7	0.13	0.08
Cumulative Variance %	24.18	41.65	53.05	63.91	72.88	80.02	85.67	90.83	94.69	98.09	99.79	99.92	100
Eigenvectors													
Days to 50% flowering	-0.18	-0.58	-0.11	-0.16	0.13	0.05	0.06	-0.26	-0.02	0	0.07	-0.04	0.7
Days to maturity	-0.18	-0.59	-0.09	-0.14	0.13	0.05	0.01	-0.25	-0.03	0.01	0.08	0	-0.71
Plant height (cm)	-0.16	-0.33	0.32	-0.05	-0.02	0.26	0.17	0.8	-0.11	-0.02	-0.08	0	0
Productive tillers (No.)	-0.16	0.06	-0.22	-0.22	-0.6	-0.23	0.58	-0.04	-0.33	-0.12	0.04	0	-0.03
Fingers per ear (No.)	-0.16	0.12	-0.21	-0.16	0.56	-0.44	0.44	0.19	0.35	0.08	-0.15	0.02	-0.02
Ear length (cm)	-0.46	-0.06	0.15	0.33	-0.2	-0.25	-0.12	-0.04	0.14	0.1	-0.06	0.71	0.03
Finger length (cm)	-0.46	-0.03	0.12	0.36	-0.19	-0.24	-0.11	-0.01	0.18	0.09	-0.06	-0.7	-0.01
Finger width (cm)	-0.26	0.26	0.3	-0.19	0.07	0.4	0.25	-0.25	-0.06	0.66	0.03	-0.01	-0.01
Leaf length (cm)	-0.31	0.2	0.25	0.18	0.28	0.3	0.25	-0.25	-0.11	-0.67	-0.1	0	-0.01
Leaf width (cm)	-0.12	0.09	0.41	-0.38	0.21	-0.49	-0.31	-0.01	-0.53	-0.04	0.07	-0.04	0.01
Test weight (g)	-0.13	0.09	0.21	-0.61	-0.28	0.07	-0.18	-0.02	0.61	-0.26	0.08	0	0
Grain yield per plant (g)	-0.37	0.21	-0.41	0	0.13	0.15	-0.18	0.23	-0.09	-0.04	0.72	0.01	0.01
Fodder yield per plant (g)	-0.32	0.13	-0.47	-0.23	-0.01	0.21	-0.34	0.07	-0.19	0.02	-0.64	0.01	0

Days to 50% flowering (DFF), days to maturity (DM), and plant height (PH) were strongly associated with PC2 and formed a separate group from the yield-related traits, indicating that phenological characters contributed independently to the observed variability. Most vectors were positioned close to the circumference of the correlation circle, indicating that these traits were well represented by the first two principal components. The acute angles observed among EL, FL, GYP, and FYP indicate positive correlations, whereas the wider angles between phenological and yield traits suggest relatively weak associations. These findings demonstrate that yield-contributing traits and phenological traits were the major determinants of genetic diversity among the evaluated finger millet genotypes, corroborating previous reports by Singh *et al.* (2024) and Wright and Devos (2024).

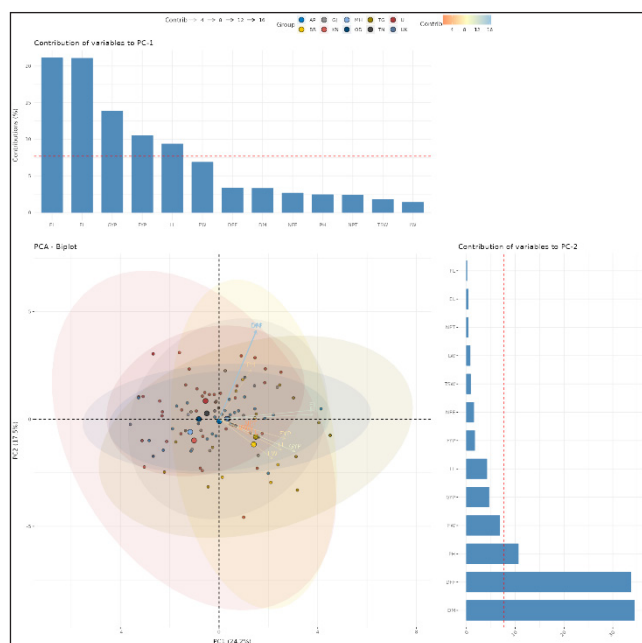


Fig. 3: Biplot showing genetic diversity among finger millet genotypes

The PCA biplot (Fig. 3) illustrated the distribution of finger millet genotypes from different geographical regions based on the first two principal components. The genotypes exhibited considerable overlap irrespective of their state of origin, indicating the absence of distinct geographical clustering. The wide dispersion of genotypes within and across groups suggests substantial genetic variability within each region, which may be attributed to germplasm exchange, selection history, and breeding activities. Similar observations have been reported in finger

millet, where clustering was found to depend more on genetic constitution than geographical origin (Singh *et al.* 2024; Wright and Devos, 2024).

The biplot further revealed that finger length (FL), ear length (EL), grain yield per plant (GYP), fodder yield per plant (FYP), and finger width (FW) were positively associated with PC1, whereas days to 50% flowering (DFF), days to maturity (DM), and plant height (PH) contributed predominantly to PC2. Genotypes positioned in the direction of these vectors are expected to possess higher values for the corresponding traits, while those located near the origin exhibited average performance. The lack of clear separation among state-wise groups indicates that geographic origin alone is not a reliable indicator of genetic diversity, highlighting the importance of selecting parents based on phenotypic and genetic divergence rather than place of collection.

CONCLUSION

The present study revealed substantial genetic variability among the 100 finger millet genotypes, indicating the availability of ample genetic resources for crop improvement. Correlation analysis identified finger length, ear length, number of fingers per ear, leaf length, and finger width as the major yield-contributing traits, suggesting that these characters can be effectively utilized as indirect selection criteria for improving grain yield. Principal component analysis further demonstrated that the first five principal components explained 72.88% of the total phenotypic variation, with yield-related and phenological traits contributing most to the observed diversity. The PCA biplot showed considerable overlap among genotypes from different geographical regions, indicating that genetic diversity was independent of geographical origin. Therefore, selection of parental lines should be based on genetic divergence and superior agronomic performance rather than place of collection. Overall, the identified diverse genotypes and key yield-associated traits provide valuable resources for developing high-yielding and climate-resilient finger millet cultivars through effective breeding programmes.

ACKNOWLEDGEMENTS

Facilities provided by Agricultural Research Station,

Vizianagaram are highly acknowledged. The work was carried out by utilizing the grants received from Acharya N.G. Ranga Agricultural University, Guntur

REFERENCES

- Charitha, A.V. and Lal, G.M. 2023. Genetic diversity analysis for yield and yield attributing traits in finger millet (*Eleusine coracana* L.). *International Journal of Plant & Soil Science*, **35**(20): 677–687.
- Gebreyohannes, A., Shimelis, H., Mashilo, J., Odeny, D.A., Tadesse, T. and Ojiewo, C.O. 2024. Finger millet (*Eleusine coracana*) improvement: Challenges and prospects—A review. *Plant Breeding*, **143**(2): 350–374.
- Jolliffe, I.T. 2002. *Principal Component Analysis*. 2nd Edition. Springer, New York.
- Kasule, F., Diack, O., Mbaye, M., Nuwamanya, E., Odeny, D.A. and colleagues. 2024. Genomic resources, opportunities and prospects for accelerated improvement of millets. *Theoretical and Applied Genetics*, **137**: 273.
- Kaur, S., Kumari, A., Seem, K., Sharma, R., Kumar, S. and colleagues. 2024. Finger millet (*Eleusine coracana* L.): From staple to superfood—A comprehensive review on nutritional, bioactive, industrial and climate resilience potential. *Planta*, **260**: 75.
- Singh, A., Sehrawat, A.R., Anish, Manjeet, Pankaj and Sehrawat, K. 2024. Genetic diversity assessment in Indian finger millet (*Eleusine coracana* L.) germplasm via qualitative traits. *Electronic Journal of Plant Breeding*, **15**(2): 633–642.
- Wright, H. and Devos, K.M. 2024. Finger millet: A hero in the making to combat food insecurity. *Theoretical and Applied Genetics*, **137**: 139.