



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.331>

PRINCIPAL COMPONENT ANALYSIS FOR YIELD, YIELD CONTRIBUTING AND NUTRITIONAL TRAITS IN INBRED LINES OF PEARL MILLET (*Pennisetum glaucum* L.)

P. Lakshmi Jyothika¹, N. Sabitha^{1*}, L. Madhavalatha² and G. Mohan Naidu³

¹Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati, ANGRAU, A.P, India.

²Department of Genetics and Plant Breeding, ARS, Kadiri, A.P, India.

³Department of Statistics and Computer Application, S.V. Agricultural College, Tirupati, ANGRAU, A.P, India.

*Corresponding author E-mail: nsabitha84@gmail.com

(Date of Receiving : 20-04-2026; Date of Revision : 17-06-2026; Date of Acceptance : 05-07-2026)

ABSTRACT

A study involving 97 inbred lines and three checks was conducted at ARS, Kadiri during *kharif*, 2024 in an alpha lattice design with two replications to study genetic divergence based on 14 quantitative and nutritional traits. Principal component analysis indicated five principal components were with Eigen value greater than 1.00 and accounted for a total variation of 66.4 percent. The analysis revealed that PC1 showed the highest variance of 21.95% with major contribution by traits such as grain yield per plant, panicle length and panicle girth. PC2 showed second highest variance of 15.13% with major contribution by days to 50% flowering and days to maturity. PC3 showed third highest variance of 11.68% and majorly contributed by zinc content and iron content. PC3 is followed by PC4 and PC5 with a variance of 9.07 percent and 8.51 percent, respectively. The biplot denoted that PC1 showed negative relation with iron content, zinc content and relative water content. While, PC2 showed negative relation with days to 50% flowering, days to maturity and SPAD chlorophyll meter readings and both the components showed positive relation with grain yield per plant, panicle length, panicle girth, number of productive tillers per plant, harvest index, thousand grain weight and plant height.

Keywords : Pearl millets, alpha lattice design, Principal component analysis, Eigen values, Biplot.

Introduction

Pearl millet (*Pennisetum glaucum* L.) is a C₄ crop known for its efficient photosynthesis and high biomass production (Varshney *et al.*, 2017). Its ability to withstand drought and thrive with minimal inorganic fertilizer input makes it an important crop for arid and semi-arid ecosystems. The hermaphroditic flowers of pearl millet exhibit protogyny, which facilitates a high degree of cross-pollination. In India, pearl millet ranks as the fourth most cultivated cereal after rice, wheat, and maize. During 2024–25, it was grown on 6.835 Mha, with a total production of 9.490 Mt and an average productivity of 1388 kg ha⁻¹ (Indiastat, 2025). In Andhra Pradesh, the crop covered 0.027 Mha, with a production of 0.059 Mt and productivity of 2199 kg ha⁻¹ in the same period (Indiastat, 2025). Nutritionally, pearl millet is superior to many staple cereals, being

rich in essential micronutrients such as iron and zinc and thus contributing to the alleviation of malnutrition and hidden hunger. On a dry weight basis, 100 g of grain contains approximately 17 MJ of energy, carbohydrates (60–70%), quality proteins (9.5–14.41 g), lipids (4.8–7.1 g), and minerals, including calcium (16–46 mg), iron (4–11.2 mg), and zinc (2.95–7.1 mg) (Hassan *et al.*, 2021). Additionally, pearl millet serves as a dual-purpose crop, offering both food and fodder, and is considered more palatable than sorghum. The success of a breeding programme relies on a clear understanding of the extent of variability, genetic differences in yield-attributing traits, and the associations among various traits. (Izge *et al.*, 2006). This investigation is designed to assess genotypic divergence among genotypes and traits which can serve as a basis for future crop improvement program.

Materials and Methods

The experiment was carried out during *khari*f, 2024 at Agricultural Research Station, Ananthapuramu located at 14° 41'N latitude and 77° 40'E longitude from an altitude of 373 m above mean sea level, and situated in scarce rainfall zone of Andhra Pradesh. The experimental material comprising 97 pearl millet inbred lines developed at Agricultural Research Station, Ananthapuramu and three checks i.e., ABV04 (Composite variety), SBH 888 (Hybrid), Pittaganti (local variety) were evaluated in an Alpha lattice design with two replications. Each genotype was sown in single row of four meters' length with a spacing of 45 cm between rows and 15 cm between the plants within the rows. All the recommended cultural and agronomic measures were followed in raising a healthy crop. Observations on traits such as plant height (cm), number of productive tillers per plant, panicle length (cm), panicle girth (cm), SPAD chlorophyll meter reading (SCMR) at 60 DAS, Relative water content (%), thousand grain weight (g), harvest index (%) and grain yield per plant (g) were recorded on five randomly selected competitive plants in each genotype and each replication. Days to 50% flowering and days to maturity observations were recorded on whole plot basis. Iron content (ppm) and zinc content (ppm) in grain were estimated using AAS (Tandon, 1999) and protein content (%) in grain estimated by Kjeldahl method (AOAC 1990). PCA was assessed using the procedure outlined by Banfield (1978). Statistical analysis was done using R studio version 2024.12.1+563.

Results and Discussion

Principal Component Analysis a multivariate statistical procedure was used to transform and reduce data dimensions as it allows large datasets with multiple variables and summarize into a few representative components (Singh and Narayana, 1993). The study revealed that five principal components (PCs) were with Eigen value greater than 1.00 and accounted for a total variation of 66.4 percent. The eigen values, percentage of variance of each component were presented in Table 1 and loadings of each variable were present in Table 2. PC1 showed the highest amount of variance of 21.95% with major contribution by traits like grain yield per plant, panicle length and panicle girth, therefore PC1 identifies the characters related to grain yield. PC2 showed second highest amount of variance of 15.13% and cumulative variance of 37.08% with major contribution by days to 50% flowering and days to maturity, therefore PC2 mainly identifies the characters related to flowering and maturity. PC3 showed third highest amount

variance of 11.68% with cumulative variance of 48.76% and majorly contributed by zinc content and iron content, therefore PC2 mainly identifies the characters related to nutritional traits. PC3 is followed by PC4 and PC5 with a variance of 9.07 percent and 8.51 percent, respectively. Plant height and protein content contributed for variance in PC4, while SPAD chlorophyll meter reading (SCMR) and thousand grain weight in PC5. Similar results were reported by Shashibhushan *et al.*, 2022, Kaushik *et al.*, 2018, Singh *et al.*, 2018 and Ramya *et al.*, 2017. Percentage contribution of character on principal components was represented in Table 3. Scree plot showed the association of PCs with eigen values and variance% was presented in Figure 1.

Table 1: Eigen value, Percentage of variance and Cumulative percentage of variance of Principal components

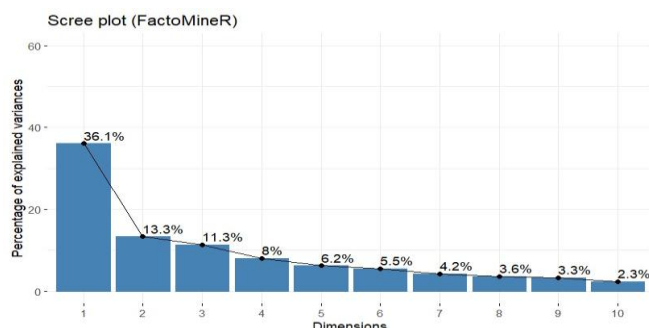
Principal component	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	3.073	21.949	21.949
PC2	2.119	15.135	37.083
PC3	1.635	11.676	48.76
PC4	1.271	9.077	57.837
PC5	1.192	8.514	66.35
PC6	0.939	6.705	73.055
PC7	0.88	6.289	79.344
PC8	0.738	5.27	84.614
PC9	0.665	4.748	89.361
PC10	0.483	3.449	92.81
PC11	0.437	3.125	95.935
PC12	0.352	2.511	98.446
PC13	0.176	1.26	99.707
PC14	0.041	0.293	100

Table 2: Loadings of each character with respect to different principal components

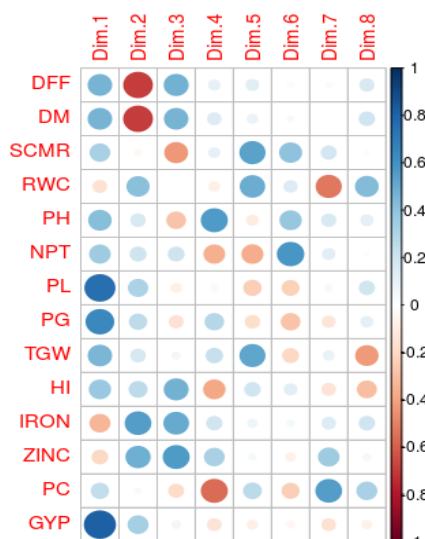
Character	PC1	PC2	PC3	PC4	PC5
DFP	0.264	-0.475	0.375	0.094	0.116
DM	0.264	-0.477	0.36	0.13	0.081
SCMR	0.185	-0.027	-0.341	0.089	0.487
RWC	-0.086	0.283	0.001	-0.08	0.458
PH	0.242	0.116	-0.226	0.505	-0.098
NPT	0.201	0.143	0.161	-0.318	-0.339
PL	0.432	0.214	-0.068	-0.033	-0.228
PG	0.366	0.173	-0.121	0.254	-0.156
TGW	0.261	0.118	0.04	0.198	0.481
HI	0.214	0.182	0.373	-0.339	0.18
IRON	-0.19	0.379	0.399	0.169	0.065
ZINC	-0.115	0.336	0.441	0.29	0.037
PC	0.142	0.023	-0.143	-0.504	0.24
GYP	0.465	0.228	0.046	-0.132	-0.079

Table 3: Percentage contribution of character on principal components

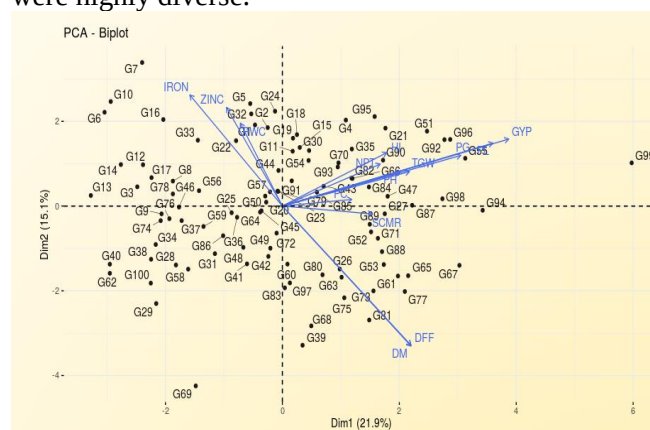
Character	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DFF	6.983	22.565	14.091	0.875	1.356	0.091	0.084	3.532
DM	6.975	22.782	12.958	1.688	0.654	0.123	0.006	5.241
SCMR	3.406	0.074	11.612	0.799	23.702	17.536	3.908	0.044
RWC	0.744	7.997	0	0.634	20.937	2.092	31.847	25.4
PH	5.837	1.339	5.129	25.518	0.967	15.389	2.969	1.907
NPT	4.034	2.049	2.587	10.137	11.471	36.436	1.81	0.04
PL	18.665	4.598	0.461	0.107	5.185	5.929	0.215	4.979
PG	13.417	2.977	1.476	6.443	2.448	8.916	2.019	1.723
TGW	6.814	1.381	0.16	3.94	23.105	4.619	0.924	23.962
HI	4.59	3.308	13.913	11.461	3.227	1.742	2.544	12.25
IRON	3.608	14.343	15.904	2.861	0.418	0.191	2.389	5.169
ZINC	1.315	11.319	19.449	8.393	0.136	0.593	13.914	0.274
PC	2.029	0.051	2.049	25.395	5.769	6.139	34.775	14.759
GYP	21.584	5.216	0.211	1.752	0.624	0.203	2.595	0.719

**Fig. 1 :** Screen plot with connecting curves

Correlation matrix of 14 yield and yield contributing traits were plotted against the five principal components was presented in Figure 2 and biplot between PC1 and PC2 for 14 characters of 100 genotypes was presented in Figure 3. The red dots from correlation matrix show the negative relationship between the respective characters with components and blue dot shows the positive relationship.

**Fig. 2 :** Correlation plotted against different characters with respective principal components

The biplot analysis revealed that genotypes are diverse for the characters PC1 and PC2. PC1 components showed negative relationship with iron content, zinc content and relative water content. PC2 had negative relationship with traits like Days to 50% flowering and days to maturity and slightly negative SPAD chlorophyll meter reading (SCMR) and both components showed positive relation with grain yield per plant, panicle length, panicle girth, number of productive tillers per plant, harvest index, thousand grain weight and plant height. From biplot of PC1 and PC2 it is evident that genotypes such as API 1011, API 1012, API 1018, API 1026, API 1029, API 1049, API 1074, API 2001, API 2010, API2052 and SBS 888 were highly diverse.

**Fig. 3 :** Biplot against PC1 and PC2 for studied characters of 100 genotypes

Conclusions

Principal Component Analysis (PCA) is a valuable tool in both self and cross pollinated crops as it simplifies the assessment of genetic variability and trait significance. PCA identifies traits contributing to variability, clusters similar lines, and highlights the

lines which are promising. By reducing data complexity and focusing on traits driving variability, PCA improves the efficiency and accuracy of breeding strategies. The pearl millet lines that have been evaluated have a lot of variation that may be used in breeding programmes. The genotypes of Pearl millet belonging to PC1, PC2 and PC3 involving characters of major economic importance viz., number of effective tiller per plant, grain yield per plant, harvest index, panicle length, panicle harvest index, panicle weight, 1000 grain weight and zinc content might be employed in the crop enhancement programme to generate potential hybrids based on genetic distances.

Disclaimer (Artificial Intelligence)

Author(s) hereby declare that no generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Competing Interests

Authors have declared that no competing interests exist.

Acknowledgement

Necessary facilities provided by S. V. Agricultural college, Tirupati and Agricultural Research Station, Kadiri, ANGRAU are acknowledged.

References

- AOAC (1990) Official Methods of Analysis. Association of Official Analytical Chemists, Washington, D.C.
- Banfield, C.F. (1978). Multivariate analysis in genstat. *Journal of Statistical Computation and Simulation*, 6(3-4), .211-222.
- Hassan, Z.M., Sebola, N.A and Mabelebele, M. (2021). The nutritional use of millet grain for food and feed, a review. *Agriculture & Food Security*. 10,1–14.
- Indiastat. 2025. *Area and Production of Bajra in India*. <https://www.indiastat.com/>.
- Izge, A.U., Kadam, A. M. and Gungla, D.T. (2006). Studies on character association and path analysis of certain quantitative character among parental lines of pearl millet (*Pennisetum glaucum* L.) and their F1 hybrids in a diallel cross. *African. J.* 5, 194-198.
- Kaushik, J., Vart, D., Kumar, M. and Kumar, A. (2018). Genetic diversity analysis among maintainer lines of pearl millet [*Pennisetum glaucum* (L.) R. Br.] based on grain yield and yield component characters. *Chemical Science Review and Letters*. 7(28), 978-981.
- Ramya, A. R., Ahamed, M. L. and Srivastava, R. K. (2017). Genetic diversity analysis among inbred lines of pearl millet [*Pennisetum glaucum* (L.) R. Br.] based on grain yield and yield component characters. *International Journal of Current Microbiology and Applied Sciences*. 6(6), 2240-2250.
- Shashibhushan, D., Kumar, C.S. and Kondi, R.K.R. (2022). Principal Component Analysis for Yield and Yield Related Traits in Pearl Millet Cultivars. *Ecology Environment and Conservation*. 28, 104-107.
- Singh, O.V., Gowthami, R., Singh, K. and Shekhawat, N. (2018). Genetic divergence studies in pearl millet germplasm based on principal component analysis. *International Journal of Current Microbiology and Applied Sciences*. 7(06), .522-527.
- Singh, P. and Narayanan, S.S. (1993) *Biometrical Techniques in Plant Breeding*. New Delhi, India, Kalyani Publishers.
- Tandon, H.L.S. (1999). *Methods of Analysis of Soils, Plants, Waters and Fertilizers*. Fertilizer Development and Consultation Organisation, New Delhi, India. 86-96.
- Varshney, R.K., Shi, C., Thudi, M., Mariac, C., Wallace, J., Qi, P., Zhang, H., Zhao, Y., Wang, X., Rathore, A and Srivastava, R.K. (2017). Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. *Nature biotechnology*. 35 (10), 969-976.