

RESEACH ARTICLE

Principal component analysis for evaluating genetic diversity in turmeric (*Curcuma longa* L.) accessions

M. Bilashini Devi, VK Verma, Hammylliende Talang*, H. Rymbai, N. Uttam Singh, M. Bishonath Singh and S. Hazarika

Abstract

Turmeric (*Curcuma longa* L.) is one of the most important spice crops in India and is widely cultivated in the north-eastern region of the country, which represents a rich reservoir of genetic diversity. The current study was undertaken to assess the genetic diversity among turmeric accessions and to determine the contribution of rhizome yield and its associated traits to the overall genetic divergence using principal component analysis (PCA). A total of forty turmeric accessions were evaluated for yield and related morphological traits under field conditions. Principal component analysis revealed that two principal components had eigenvalues greater than one, indicating that these components accounted for a substantial proportion of the variability among the studied traits. The first 3 principal components (PC1, PC2 and PC3) explained 45.73, 6.77 and 6.05% of the total variation, respectively, collectively accounting for 58.66% of the overall variability. Traits viz., plant height, leaf length, leaf breadth, total number of leaves, yield per plant, number of mother rhizomes, weight of mother rhizomes, number of primary fingers and curcumin content showed positive contributions in PC1, PC2 and PC3, indicating their significant role in genetic divergence among the accessions. Among these traits, plant height exhibited the highest contribution towards total divergence (69.62%) in the ranked contribution analysis. The results indicate that these key traits are major contributors to variability and can be effectively utilised as selection criteria in genetic improvement programs aimed at improving yield and quality in turmeric.

Keywords: diversity, PCA, time rank, *Capsicum chinense* Jacq.

Introduction

Turmeric (*Curcuma longa* L.) is one of the most promising spice crops grown widely in India, particularly in the North Eastern Hill (NEH) region due to its favourable agro-climatic conditions, rich genetic diversity, and high curcumin content. The crop serves as a significant cash crop for farmers in this region and contributes substantially to the local economy. Turmeric occupies an area of about 38.6 thousand hectares with a production of 83.01 thousand tonnes in the North Eastern region (Anonymous, 2023–24), contributing approximately 8.30% of the total turmeric production in India. The agro-climatic conditions of the north-eastern hill region, characterized by warm and humid summers with abundant rainfall and relatively cool winters, provide an ideal environment for turmeric cultivation.

Apart from its culinary importance, turmeric holds a prominent place in pharmaceutical, nutraceutical, and cosmetic industries due to the presence of various bioactive compounds (Singh *et al.*, 2012). The most important phytochemical constituent of turmeric is curcumin, a polyphenolic compound also known as diferuloylmethane, which is primarily responsible for the characteristic yellow colour and medicinal value of turmeric. Curcumin exhibits various medicinal properties such as antioxidant,

ICAR Research Complex for NEH Region, Umiam-793103, Meghalaya, India

***Corresponding Author:** Hammylliende Talang, ICAR Research Complex for NEH Region, Umiam-793103, Meghalaya, India, E-Mail: hammylliende@gmail.com

How to cite this article: Devi, M. B., Verma, V. K., Talang, H., Rymbai, H., Singh, N. U., Singh, M. B., & Hazarika, S. 2025. Principal component analysis for evaluating genetic diversity in turmeric (*Curcuma longa* L.) accessions. *Indian J. Hill Farm.*, **38**(3):46-50.

Source of support: Nil

Conflict of interest: None.

Received: 21/04/2025 **Revised:** 26/05/2026 **Accepted:** 12/06/2026

antimicrobial, antimutagenic, anti-inflammatory and anticancer properties (Sharifi *et al.*, 2020). Because of these health-promoting properties, turmeric has gained increasing importance in global markets.

The north-eastern hill region of India is particularly popular for turmeric genotypes possessing a higher range of curcumin content and superior rhizome quality. However, despite the rich diversity of turmeric germplasm available in the region, only a limited number of well-characterized and stable varieties have been developed. Therefore,

exploration and evaluation of the existing genetic diversity are essential for identifying superior genotypes with higher yield potential and improved quality traits.

In turmeric, rhizome yield is a complex quantitative trait determined by various morphological and contributing traits such as the number of mother rhizomes, the number of primary fingers, rhizome weight, plant height, leaf parameters, etc. Traits like plant height and leaf parameters influence photosynthetic efficiency and biomass production, while rhizome-related traits such as the number and weight of mother rhizomes and primary fingers directly contribute to yield. Quality traits such as curcumin content determine the commercial and medicinal value of the crop. Understanding the relationship and contribution of these traits to overall yield and quality is pivotal for efficient selection in improvement programmes.

Genetic divergence among germplasm is a prerequisite for achieving significant genetic improvement through hybridization and selection (Kumar *et al.*, 2019). Identification of genetically diverse accessions with desirable traits enables breeders to develop superior varieties with enhanced productivity and quality. Principal component analysis (PCA) is an effective multivariate statistical approach to assess genetic variability and identify the traits contributing most to the overall variation among genotypes. It reduces a large number of correlated variables into a smaller set of uncorrelated components, thereby simplifying the interpretation of complex datasets (Rao *et al.*, 1952). PCA helps in identifying key traits responsible for variability and assists in the selection of promising genotypes for crop improvement programmes (Kumar *et al.*, 2020).

Therefore, the present study was undertaken to evaluate the genetic divergence among turmeric accessions using principal component analysis and to identify the major yield and quality contributing traits for effective selection in turmeric breeding programmes.

Material and Methods

The present experimental trial was conducted at the Experimental Farm, ICAR Research Complex for NEH Region, Umiam, Meghalaya during 2023-24. The present field evaluation was laid out in a completely randomized block design with 3 replications. The treatments consist of 40 accessions of turmeric (Table 1). The Experimental farm is located at 950 m MSL altitude with latitude and longitude of 25°41'N and 91°54'E, respectively. The average annual rainfall of the area is 150 to 250 cm with a subtropical climate. The experimental bed of 3×1 m at 20 cm height is prepared after thorough ploughing. The accessions were planted at a spacing of (30 × 30) cm. Observations on rhizome yield and yield-contributing traits were recorded at the time of harvesting (220–230 days after planting), while other morphological parameters, viz., plant height, leaf length and

Table 1: List of 40 turmeric accessions used in the study with their sources

S.No.	Accessions	Source
1	IC-586749	ICAR(RC) for NEH Region, Umiam, Meghalaya
2	IC-586750	-do-
3	IC-586751	-do-
4	IC-586752	-do-
5	IC-586753	-do-
6	IC-586754	-do-
7	IC-586755	-do-
8	IC-586756	-do-
9	IC-586757	-do-
10	IC-586758	-do-
11	IC-586759	-do-
12	IC-586762	-do-
13	IC-586763	-do-
14	IC-586764	-do-
15	IC-586765	-do-
16	IC-586766	-do-
17	IC-586767	-do-
18	IC-586768	-do-
19	IC-586769	-do-
20	IC-586770	-do-
21	IC-586771	-do-
22	IC-586772	-do-
23	IC-586774	-do-
24	IC-586775	-do-
25	IC-586776	-do-
26	IC-586777	-do-
27	IC-586778	-do-
28	IC-586779	-do-
29	IC-586780	-do-
30	Lakadong Sel-1	Shangpung village, Laskein, West Jantia Hills District, Meghalaya
31	Dienglieng Sel	Mawkynrew, East Khasi District, Meghalaya
32	Umsohmatam Sel-1	Umsning Ri-Bhoi District, Meghalaya
33	Jonska Sel	Mawkynrew, East Khasi District, Meghalaya
34	Madan Kynsaw Sel	Laskein, West Jantia Hills
35	Mawpun Sel	Umsning Ri-Bhoi District, Meghalaya
36	Lakadong Sel-2	Shangpung village, Laskein, West Jantia Hills District, Meghalaya
37	Umsomatam Sel-3	Umsning Ri-Bhoi District, Meghalaya
38	Jokiang 1	Jokiang, Umsning, Ri-bhoi District, Meghalaya
39	Umsohmatam Sel-4	Umsning Ri-Bhoi District, Meghalaya
40	Jokiang 2	Jokiang village, Umsning, Ri-Bhoi District, Meghalaya

breadth, etc were recorded 150 to 160 days after planting. All the observations were recorded from five randomly taken plants in each accession and replication, followed by computing their means. The recorded data were analysed using Windostat version 9.2 software.

Results and Discussion

Principal component analysis (PCA) was performed on 40 turmeric accessions to understand the extent of genetic divergence and to identify the traits contributing most to variability among the genotypes. The eigenvalues, percentage of variance, cumulative variance, and factor loadings for the studied traits are given in Table 2. The analysis revealed 3 principal components accounting for 58.66% of the total variability observed among the traits. Among them, the 1st principal component (PC1) explained the major proportion of variation (45.73%), followed by PC2 (6.87%) and PC3 (6.05%). The eigenvalues recorded for PC1, PC2 and PC3 were 7.32, 1.10 and 0.97, respectively. Since the eigenvalues of the first two components were greater than one, they were considered significant contributors to the total variability among the turmeric accessions. These results indicate the existence of significant genetic diversity among the genotypes evaluated, which can be utilized in improvement programmes targeting yield and quality improvement. The high contribution of PC1 suggests that

the majority of the variability among the turmeric accessions is governed by morphological and yield-related traits. In PC1, plant height (0.35), leaf length (0.32), yield per plant (0.32), weight of mother rhizome (0.26), number of primary fingers (0.26) and total number of leaves (0.25) exhibited high positive factor loadings, indicating that these characters contributed significantly to the genetic divergence among the accessions. These traits are biologically important because plant height and leaf characteristics influence photosynthetic efficiency and vegetative growth, which ultimately affect rhizome development and yield. Similarly, rhizome-related characters such as the primary finger number and mother rhizome weight are directly associated with rhizome yield and are therefore key determinants of productivity in turmeric.

In the second principal component (PC2), leaf length (0.40) showed the highest positive contribution, suggesting that this trait plays an important role in differentiating the genotypes. Leaf length is associated with leaf area and photosynthetic capacity, which may indirectly influence biomass accumulation and rhizome yield. In the third principal component (PC3), dry matter content (0.99) showed a very high factor loading, indicating its importance as a quality-related trait. Dry matter content is an important quality parameter as it reflects the concentration of storage compounds in the rhizome, which is often associated with processing quality and curcumin concentration. The contribution of yield-contributing traits, viz., plant height, leaf parameters, rhizome number and rhizome weight, to the major principal component indicates that these traits are key determinants of yield variability among turmeric accessions. Similar observations were reported by Sigrist *et al.* (2011), Sanni *et al.* (2008) and Suresh *et al.* (2019), who also reported that morphological and rhizome-related traits contributed significantly to genetic divergence in turmeric germplasm. These findings highlight the biological relevance of these traits in determining productivity and variability within turmeric populations.

The principal component scores of the first three vectors (PCA I, PCA II and PCA III) for the forty accessions are presented in Table 3. Among the accessions, IC-586779 recorded the highest PCA I score (25.215), indicating its strong association with the traits contributing to the first principal component, while Lakadong Sel-2 recorded the lowest PCA I value (16.520). For PCA II, the highest score was observed in IC-586776 (1.581) and the lowest in Jokiang 2 (0.311). In PCA III, IC-586778 (11.199) recorded the highest value, whereas Lakadong Sel-2 (9.776) recorded the lowest value. These differences in PCA scores reflect the genetic diversity present among the accessions for the studied traits. The scatter plot based on the first 2 principal components (PC1 and PC2) provides a graphical representation of the genetic relationship among the

Table 2: The eigenvalue (root), percent variance and percent cumulative variance and factor loading between PCs and traits studied in Turmeric (*C. longa*)

	PC I	PC II	PC III
Eigene Value (Root)	7.32	1.10	0.97
% Var. Exp.	45.73	6.87	6.05
Cum. Var. Exp.	45.73	52.61	58.66
Characters	Factor Loading		
1. Plant Height (cm)	0.35	0.02	0.01
2. Leaf length (cm)	0.32	0.40	0.03
3. Leaf breadth (cm)	0.12	-0.89	-0.02
4. No. of tillers	-0.24	0.15	-0.02
5. Total no. of leaves	0.25	0.02	0.02
6. Stem diameter (cm)	-0.21	0.12	-0.02
7. Yield/plant (g)	0.32	0.002	0.02
8. No of Mother rhizomes	0.19	0.03	0.02
9. Weight of mother rhizome	0.26	-0.001	0.02
10. No. of primary fingers	0.26	0.01	0.02
11. Weight of primary fingers (g)	-0.31	-0.003	-0.02
12. No of secondary finger	-0.29	0.0003	-0.02
13. Weight of secondary finger (g)	-0.25	0.0004	-0.02
14. Yield t/ha	-0.13	-0.003	-0.05
15. Curcumin %	0.22	0.03	0.02
16. Dry Matter content (%)	-0.07	-0.03	0.99

Table 3: The principal component analysis (PCA) scores for 40 accessions of turmeric

	PCA I	PCA II	PCA III
Accessions	X Vector	Y Vector	Z Vector
IC-586749	22.077	1.421	10.301
IC-586750	23.843	1.443	10.649
IC-586751	21.108	1.091	10.778
IC-586752	21.313	1.036	10.312
IC-586753	20.824	1.109	9.983
IC-586754	20.485	1.063	10.453
IC-586755	22.834	0.803	10.053
IC-586756	21.183	1.391	10.280
IC-586757	24.486	1.395	10.845
IC-586758	21.601	1.383	10.525
IC-586759	21.441	1.414	10.425
IC-586762	22.892	1.328	10.915
IC-586763	22.720	1.475	10.361
IC-586764	20.898	1.040	10.225
IC-586765	21.081	0.647	10.541
IC-586766	20.627	1.415	10.905
IC-586767	24.083	1.160	10.765
IC-586768	23.219	1.351	10.193
IC-586769	20.207	1.556	10.043
IC-586770	23.959	1.329	10.553
IC-586771	20.254	0.896	11.066
IC-586772	22.564	1.188	10.134
IC-586774	24.687	0.988	10.343
IC-586775	22.146	1.125	10.402
IC-586776	20.543	1.581	10.342
IC-586777	22.150	1.066	10.617
IC-586778	20.961	1.017	11.199
IC-586779	25.215	1.433	10.414
IC-586780	21.311	1.134	9.888
Lakadong Sel-1	21.942	0.874	10.467
Dienglieng Sel	20.874	0.832	9.913
Umsohmatam Sel-1	19.123	0.560	10.711
Jonska Sel	20.033	0.791	9.949
Madan Kynsaw Sel	17.441	1.124	10.344
Mawpun Sel	18.327	0.536	10.834
Lakadong Sel-2	16.520	0.370	9.776
Umsomatam Sel-3	20.237	0.671	10.441
Jokiang 1	21.766	0.981	10.649
Umsohmatam Sel-4	19.866	0.256	10.099
Jokiang 2	18.624	0.311	10.712

accessions. Together, these two components explained 52.61% of the total variability, indicating that they effectively capture the major variation present in the dataset. The

dispersion of accessions in the scatter plot suggests the existence of substantial genetic diversity, which may be attributed to both genetic constitution and adaptation to different geographical environments. Similar observations were reported by Kumar *et al.* (2019), who emphasized that genetic diversity rather than geographical origin should be considered while selecting parental materials for crop improvement programmes. The positive contribution of plant height, leaf length, total number of leaves, yield per plant, number of mother rhizomes, weight of mother rhizome, number of primary fingers and curcumin content in PC1 and PC2 indicates that these traits play a pivotal role in determining productivity and quality in turmeric. Therefore, these characters may serve as reliable selection criteria for identifying superior genotypes with higher yield potential and improved quality.

The times-ranked contribution analysis (Table 4) further supported the importance of these traits in determining genetic divergence. Among the studied traits, plant height showed the highest contribution (62.62%), indicating its major role in differentiating the accessions. The strong contribution of plant height may be attributed to its influence on vegetative growth and assimilate production, which ultimately affects rhizome development and rhizome yield. Other traits, viz., stem diameter, number of tillers, yield per plant and rhizome-related traits also contributed moderately to the overall divergence. Overall, the results demonstrate that both morphological and rhizome-related traits contribute significantly to the genetic variability

Table 4: Times ranked contribution of traits under study

Sl. No.	Traits	Times Ranked 1st	(%) Contribution
1.	Plant height (cm)	543	62.62
2.	Leaf length (cm)	13	1.67
3.	Leaf breadth (cm)	0	0.00
4.	No. of tillers	16	2.05
5.	Total no. of leaves	18	2.31
6.	Stem diameter (cm)	25	3.21
7.	Yield/plant (g)	23	2.95
8.	No of mother rhizomes	11	1.41
9.	Weight of mother rhizome	9	1.15
10.	No. of primary fingers	15	1.92
11.	Weight of primary fingers (g)	20	2.56
12.	No of secondary finger	18	2.31
13.	Weight of secondary finger (g)	13	1.67
14.	Yield t/ha	17	2.18
15.	Curcumin %	16	2.95
16.	Dry Matter content (%)	23	2.05

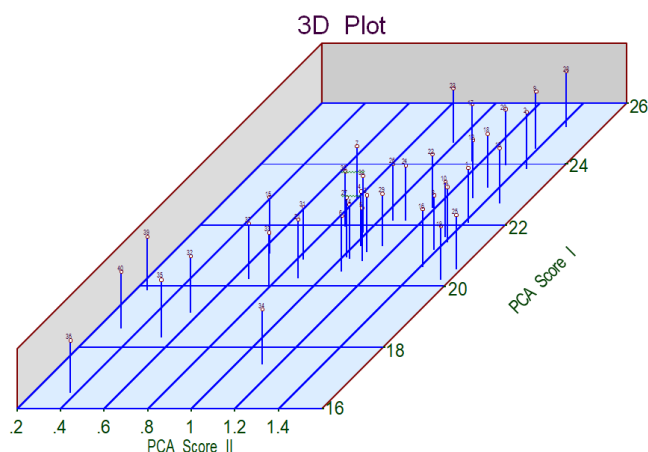


Figure 1: 3-Dimensional principal components scatter plot

present in turmeric germplasm. Identification of such key traits is important for trait prioritization in breeding programmes, as selection based on these characters can effectively enhance yield and quality in turmeric cultivars.

Conclusion

The present study revealed substantial genetic variability among the forty turmeric (*C. longa* L.) accessions evaluated through principal component analysis. The first two principal components contributed for a major proportion of the total variability, indicating the existence of significant diversity among the genotypes. Traits viz., plant height, leaf length, total number of leaves, yield per plant, number of mother rhizomes, weight of mother rhizome, number of primary fingers and curcumin content showed positive and significant contributions to the principal components, suggesting their important role in determining yield and quality in turmeric. Among the studied traits, plant height exhibited the highest contribution towards total genetic divergence, highlighting its importance as a key selection

parameter. The distribution of accessions in the PCA scatter plot further confirmed the presence of considerable genetic diversity, which can be effectively utilized in breeding programmes.

Therefore, selection based on the identified key traits and genetically diverse accessions could be utility for developing high-yielding and quality turmeric varieties. The findings of the study provide valuable information for trait prioritization and germplasm utilization in turmeric crop improvement programmes.

References

- Anonymous (2023-24). Department of Agriculture and Farmer's Welfare (first advance estimate). Ministry of Agriculture and Farmers' Welfare, Government of India.
- Kumar A and Singh S (2019). Genetic evaluation of *Melia composita* progenies for growth performance and productivity. *Indian Journal of Tropical Biodiversity* 27(1): 36-41.
- Rao CR (1952). *Advanced statistical methods in biometrical research*. Willey and Sons, New York.
- Sanni KA, Fawole I, Guei RG, Ojo DK, Somado EA, Sanchez I *et al.*, (2008). Geographical patterns of phenotypic diversity in *Oryza sativa* landraces of Cote d'Ivoire. *Euphytica* 160:389-400.
- Sigrist MS, Pinheiro JB, Azevdo filho JA and Zucchi MI (2011). Genetic divergence among Brazilian turmeric (*Curcuma longa* L.) using morpho-agronomical descriptors. *Crop Breed. Appl. Biotech.* 11(1):70-76.
- Suresh R, Ramar A, Balakrishnan S, Rajeswari S and Kumaravivel N (2019). Genetic divergence in turmeric (*Curcuma longa* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry* 8(6): 256-260
- Singh S, Panda MK and Nayak S (2012). Evaluation of genetic diversity in turmeric (*Curcuma longa* L.) using RAPD and ISSR markers. *Industrial Crops and Products* 37(1): 284-291
- Sharifi-Rad J, Rayess YE, Rizk AA, Sadaka C, Zgheib R *et al.*, (2020). Turmeric and its Major Compound Curcumin on Health: Bioactive Effects and Safety Profiles for Food, Pharmaceutical, Biotechnological and Medicinal Applications. *Front. Pharmacol.* 11:01021