**Journal of Environmental Biology**
p-ISSN: 0254-8704 • e-ISSN: 2394-0379 • CODEN: JEBIDP

JEB®

Original Research Paper
Volume 47 Issue 1 January 2026 pp. 126-134
*DOI: http://doi.org/10.22438/jeb/47/1/MRN-5315*

*J. Environ. Biol.*, 2026
© Triveni Enterprises, Lucknow (India)
Journal website : www.jeb.co.in ★ E-mail : editor@jeb.co.in

# Genetic divergence assessment through Principal Component and Single Linkage Cluster Analysis in pointed gourd (*Trichosanthes dioica* Roxb.) genotypes

**S.R. Singh[1]*, S. Rajan[1], G.L. Veena[2], D. Nayak[1], A.K. Trivedi[1], V. Soni[1] and V. Singh[3]**

[1]*ICAR-Central Institute for Subtropical Horticulture, Lucknow-226 101, India*
[2]*ICAR-Central Institute for Subtropical Horticulture, RSS Malda-732 103, India*
[3]*Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur-191 121, India*

**Received:** 27 March 2024 **Revised:** 14 July 2024 **Accepted:** 15 October 2025

***Corresponding Author Email:** srajparmar@gmail.com ***ORCiD:** https://orcid.org/009-00016038-4064

## Abstract

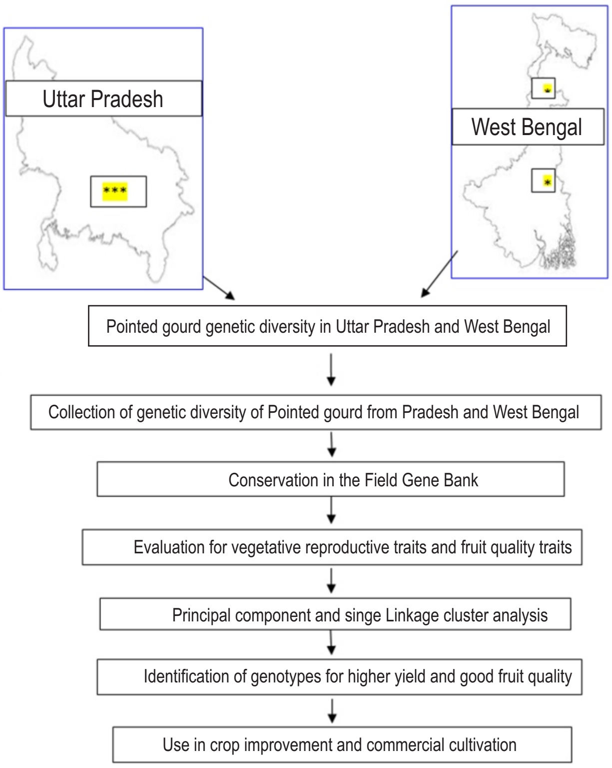
**Aim:** The study aims to assess the extent and nature of genetic divergence and relationships among the key yield attributing characters in pointed gourd (*Trichosanthes dioica* Roxb.) genotypes using advanced multivariate statistical approaches. The objective was strategic selection of genetically diverse and superior parental lines for their potential use in future breeding programs for yield improvement and quality enhancement.

**Methodology:** A comprehensive evaluation of morphological, yield-contributing, and fruit quality traits was carried out. PCA was employed to determine the relative contribution of each trait to overall variation, while Single Linkage Cluster Analysis was used to group genotypes based on trait similarity.

**Results:** Significant variability was observed among the genotypes, supported by high values of standard deviation, coefficient of variation, and broad trait ranges. All genotypes were distinctly separated at 100% dissimilarity, forming seven clusters at 85% and three clusters at 55% dissimilarity levels. Genotypes with high cluster means for specific desirable traits were identified as potential parents for the genetic improvement of pointed gourd through hybridization and selection.

**Interpretation:** The pointed gourd germplasm of Uttar Pradesh and West Bengal and hybrids exhibited considerable genetic diversity for desirable traits and suggested divergent parents can produce superior, high-yielding pointed gourd varieties.

**Key words:** Genetic divergence, Pointed gourd, Principal component analysis, Single linkage cluster analysis



Triveni Enterprises (Educational Services Set-up)

**How to cite:** Singh, S.R., S. Rajan, G.L. Veena, D. Nayak, A.K. Trivedi, V. Soni and V. Singh: Genetic divergence assessment through Principal Component and Single Linkage Cluster Analysis in pointed gourd (*Trichosanthes dioica* Roxb.) genotypes. *J. Environ. Biol.,* **47,** 126-134 (2026).

## Introduction

Pointed gourd (*Trichosanthes dioica* Roxb.) is an important dioecious perennial vegetable of the Cucurbitaceae family, well recognized for its nutritional and medicinal properties. The crop thrives in tropical and subtropical climates and plays a vital role in the vegetable basket of eastern and northern India. Presently, it occupies nearly 20,000 hectares of cultivated land, producing about 310,000 metric tons annually, with an average productivity of 14.89 t ha$^{-1}$ (NHB, 2021). The states of West Bengal, Bihar, Uttar Pradesh, Odisha, and Chhattisgarh dominate its cultivation, contributing 53.64%, 13.36%, 9.19%, 8.91%, and 5.13% of national production, respectively. Despite this significance, its productivity remains relatively low, posing a major limitation to wider adoption and commercialization. Nutritionally, pointed gourd fruits are enriched with proteins, vitamins, minerals, and bioactive compounds that impart therapeutic benefits (Yadav *et al.,* 2022). They are easily digestible and known for their diuretic, laxative, and cardio-protective properties, while also alleviating circulatory disorders (Mukherjee *et al.,* 2022).

In traditional medicine as well as modern nutraceutical development, pointed gourd has secured a unique niche. Consumer preference, however, is strongly governed by fruit attributes such as shape, size, color, flesh texture, and seed softness. Green, fleshy fruits with tender seeds and high yield are most desirable traits of pointed gourd. The absence of high yielding varieties combining these traits is a critical reason behind the existing yield gap (Singh *et al.,* 2024). India is regarded as the primary center of origin of pointed gourd, and extensive genetic variability is present in its native germplasm. Variations in fruit shape, size, color, yield components, and bearing habit offer valuable opportunities for genetic improvement (Sharma *et al.,* 2023). Breeding efforts aimed at reorienting the genetic structure toward consumer-preferred traits—such as creamy-green fruits with reduced seed hardness, higher productivity, and stress resilience—are therefore essential to enhance the crop's acceptance and profitability. The breeding work in India so for done by previous workers rely upon natural diversity but first time efforts have been made at ICAR –CISH to create genetic variability through hybridization.

Genetic diversity is the foundation of any crop improvement program, as it enables selection and recombination of favorable alleles (Swarup *et al.,* 2021; Begna *et al.,* 2024). For generating novel allelic combinations, parental lines with wide genetic backgrounds are indispensable. Detailed knowledge of variability is not only vital for identifying promising traits but also for advancing the genetic base of the crop. Genetic divergence studies help address multiple breeding goals including yield enhancement, uniformity, quality traits, and resistance to biotic and abiotic stresses. Local landraces, adapted to specific edaphic and climatic conditions, are particularly important since they harbor useful variability and safeguard against genetic erosion (Nissar *et al.,* 2011). Classifying and characterizing this variability also aid in the maintenance breeding, conservation, and identification of elite parental lines for hybridization (Begna and Teressa, 2024). Multivariate statistical tools are indispensable in such analysis. Among them, Principal Component Analysis (PCA) is widely used to quantify variability in morphological and quantitative traits. It reduces complex trait data into principal components, thereby highlighting the most important contributors to overall divergence (Sheela *et al.,* 2020; Vaidya *et al.,* 2024). However, while PCA effectively summarizes total variation, it may not fully explain the relative contribution of each character when numerous traits are evaluated simultaneously (Nwangburuka *et al.,* 2011).

To strengthen PCA results, Single Linkage Cluster Analysis (SLCA) is frequently used. SLCA is an agglomerative method that classifies genotypes into groups based on trait similarities and differences, thereby revealing genetic relationships within populations (Vijaya *et al.,* 2019). The combined application of PCA and SLCA offers a robust framework for genetic diversity analysis: PCA identifies the major axes of variation, while SLCA organizes genotypes into meaningful clusters. Recognizing the critical importance of genetic variability for pointed gourd improvement, the present study was undertaken to identify key traits contributing to variation among genotypes and to classify potential parents into distinct groups through integrated use of PCA and SLCA. Such comprehensive characterization is expected to facilitate better utilization of genetic resources, accelerate breeding progress, and ultimately contribute to the development of high-yielding, consumer-preferred varieties of pointed gourd adapted to diverse agro-ecological conditions.

## Materials and Methods

The research was carried out during the year 2019-20 and 2020-21 at the Experimental farm Block-I of ICAR- Central Institute of Subtropical Horticulture at Rehmankhera, Lucknow situated at 26º 45' to 27º 10' N latitude, 80º 30' to 80º 5' E longitude, 123 m above the mean sea level. A total of thirty diverse genotypes of pointed gourd (*Trichosanthes dioica* Roxb.) were utilized for the study. These genotypes were collected from different agro-ecological regions of India to capture maximum variability, along with certain heterotic selections derived from breeding lines maintained at ICAR–CISH, Lucknow (Table 1). The material was selected on the basis of variability in fruit shape, size, color, yield potential, and quality attributes, thereby ensuring a broad genetic base for evaluation.

Ten plants of each genotype were transplanted in the month of October at 2 x 1m inter and intra row spacing with female and male ratio 9:1. The experiment was conducted in a complete randomized block design with three replications. The soil of the experimental field, was sandy loam in nature having 6.8 pH and 0.36 dsm$^{-1}$ electric conductivity. To obtain good phenotypic expression of characters, uniform agronomic cultural practices were adopted. For recording observations, five competitive plants were randomly selected from each replication, and data were

**Table 1:** Genotypes with their geographical information used in study

| Genotypes | Collection site | Latitude | Longitude | Altitude (M) |
|---|---|---|---|---|
| CISH-P-1 | Vinodpur, Malda, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-2 | Vinodpur, Malda, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-3 | Manikpur, Malda, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-4 | Nandapur, Malda, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-5 | Manikpur, Malda, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-6 | Jat Basant, Malada, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-7 | Jat Basnt, Malada, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-8 | Brahman gram, Malada, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-9 | Brahman gram, Malada, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-10 | Chunar, Mirzapur, UP | 25° 0 N | 82° 54' E | 84.00 |
| CISH-P-11 | Koilabad, Malada, West Bengal | 24.40 0 N | 87.450E | 17.00 |
| CISH-P-12 | Milkhipur, Faizabad, U.P. | 26.74 0 N | 81.010E | 94 .00 |
| CISH-P-13 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-14 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-15 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-16 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-17 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-18 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-19 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-20 | Mursidabad, West Bengal | 24.180 N | 88.270E | 10.00 |
| CISH-P-21 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-22 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-23 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-24 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-25 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-26 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-27 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-28 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-29 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |
| CISH-P-30 | ICAR-CISH, Lucknow | 27º 10'N | 80º 5' E | 123.00 |

recorded on eighteen quantitative and qualitative traits encompassing vegetative, reproductive, and fruit quality attributes. Phenological traits such as vine length, number of nodes, and days to first female flower were recorded along with yield-contributing traits like fruit length, fruit diameter, fruit weight, number of fruits per plant, and total fruit yield. Quality-related parameters included ascorbic acid, total carotenoids, total phenols, and total soluble solids (TSS).

The ascorbic acid content was estimated by the titration method using 2, 6-dichlorophenol indophenols dye solution (DCPIP) (Ranganna, 1986) whereas total carotenoids were determined by the method of Yang *et al.* (1998). Total phenol content (TPC) was estimated as per protocol of Singleton *et al.* (1999). TSS was determined with an Autago Digital Hand Refractometer model 3810. Data collected on quantitative characters for two consecutive years was analyzed by SAS Microsoft Windows 9.2 (SAS Institute, 2011). Multivariate techniques of SLCA and PCA were used to assess the genetic variation and percentage similarity within the genotype. PCA produced Eigen – vectors and principal component score were used to assess the relative discriminatory power of its axis and their associated characters. Cluster procedure was used to identify the distinct groups in 30 genotypes on the basis of genetic relationship using character variation. SLCA was used to analyse the position of genotypes into a dendogram at an interval of 5% level of dissimilarity, starting from 100% level of dissimilarity multivariate.

## Results and Discussion

A significant genetic diversity among the evaluated genotypes was revealed through the analysis of variance and descriptive statistics such as coefficient of variation, standard deviation, and range, clearly highlighting the extent of morphological and biochemical variability present within the collected material (Table 2). This diversity is of considerable importance for crop improvement programs, as it provides a broad base of genetic variability upon which effective selection and hybridization strategies can be built. The vine length, one of the most fundamental growth traits that reflect overall plant vigor and photosynthetic potential, ranged substantially from 382.67 cm in genotype CISH-P-28 to 1527.33 cm in genotype CISH-P-10. The remarkable difference of more than 1100 cm in vine length between the shortest and longest genotypes is indicative of diverse genetic makeup and possible adaptations to different

**Table 2:** Variation in quantitative traits of pointed gourd genotypes in term of range, mean, standard deviation and covariance

| Variables | Range | | Genotypes | | Mean | SD | CV (%) |
|---|---|---|---|---|---|---|---|
| | Min | Max | Min | Max | | | |
| Vine length (cm) | 382.67 | 1527.33 | CISH-P-28 | CISH-P-10 | 790.78 | 223.27 | 28.23 |
| Number of internodes per vine | 35.00 | 105.33 | CISH-P-9 | CISH-P-10 | 77.93 | 14.42 | 18.51 |
| Inter nodal length (cm) | 6.75 | 15.17 | CISH-P-16 | CISH-P-28 | 10.18 | 2.04 | 20.05 |
| No. of primary branches | 6.33 | 21.67 | CISH-P-16 | CISH-P-30 | 13.19 | 5.23 | 39.62 |
| Female flower length (cm) | 5.17 | 7.33 | CISH-P-7 | CISH-P-12 | 6.07 | 0.54 | 8.85 |
| Fruit length (cm) | 5.97 | 12.28 | CISH-P-19 | CISH-P-29 | 9.30 | 1.56 | 16.79 |
| Fruit width (cm) | 2.39 | 4.40 | CISH-P-5 | CISH-P-23 | 3.55 | 0.43 | 12.21 |
| Fruit circumference (cm) | 9.17 | 15.40 | CISH-P-20 | CISH-P-24 | 12.16 | 1.30 | 10.69 |
| Average fruit weight (g) | 22.38 | 81.46 | CISH-P-12 | CISH-P-20 | 45.40 | 14.35 | 31.61 |
| T.S.S. (%) | 1.71 | 5.67 | CISH-P-3 | CISH-P-27 | 3.37 | 1.21 | 35.71 |
| Dry mater content (%) | 5.81 | 14.00 | CISH-P- 19 | CISH-P-20 | 25.56 | 61.83 | 36.23 |
| Seed per fruit | 14.00 | 33.33 | CISH-P-25 | CISH-P-28 | 21.01 | 4.46 | 21.22 |
| Vit C (mg 100g$^{-1}$) | 25.00 | 81.78 | CISH-P-10 | CISH-P-4 | 53.24 | 15.88 | 29.83 |
| Total carotenoids (mg 100g$^{-1}$) | 1.85 | 6.54 | CISH-P-10 | CISH-P-29 | 3.99 | 1.08 | 26.94 |
| Total phenols (mg 100g$^{-1}$) | 4.16 | 41.88 | CISH-P-7 | CISH-P-25 | 13.41 | 8.91 | 66.47 |
| Seed weight per fruit (g) | 0.39 | 8.33 | CISH-P-2 | CISH-P-26 | 2.56 | 2.11 | 82.66 |
| No. of fruit per plant | 23.00 | 108.13 | CISH-P-24 | CISH-P-12 | 50.44 | 21.45 | 42.53 |
| Fruit yield per plant (g) | 504.00 | 4923.07 | CISH-P-24 | CISH-P-26 | 1787.36 | 1323.96 | 74.07 |

**Table 3:** Principal component latent vector for Eigen values and proportion of variance accounted for different components with respect of different traits

| Variables | PC-I | PC-II | PC-III | PC-IV | PC-V | PC-VI |
|---|---|---|---|---|---|---|
| Vine length (cm) | -0.354 | -0.165 | 0.744 | 0.193 | 0.432 | 0.052 |
| Number of internodes per vine | -0.407 | -0.099 | 0.035 | 0.507 | 0.685 | 0.069 |
| Inter nodal length (cm) | -0.152 | -0.083 | 0.919 | -0.197 | -0.049 | 0.041 |
| No. of primary branches | -0.140 | -0.767 | -0.060 | 0.283 | -0.046 | 0.082 |
| Female flower length (cm) | 0.177 | 0.399 | -0.119 | -0.464 | 0.471 | 0.260 |
| Fruit length (cm) | -0.176 | 0.785 | 0.196 | 0.213 | -0.002 | 0.127 |
| Fruit width (cm) | 0.409 | 0.511 | 0.299 | 0.265 | -0.433 | -0.164 |
| Fruit circumference (cm) | 0.196 | 0.835 | -0.082 | 0.302 | 0.189 | -0.001 |
| Average fruit weight (g) | 0.273 | 0.860 | 0.031 | 0.231 | 0.064 | -0.233 |
| T.S.S. (%) | 0.854 | -0.310 | 0.031 | -0.048 | 0.147 | -0.168 |
| Dry mater content (%) | 0.560 | -0.038 | 0.258 | 0.170 | 0.307 | 0.392 |
| Seed per fruit | 0.242 | 0.097 | -0.172 | 0.103 | -0.355 | 0.675 |
| Vit C (mg 100g$^{-1}$) | 0.291 | -0.092 | -0.746 | 0.232 | 0.337 | 0.013 |
| Total carotenoids (mg 100g$^{-1}$) | 0.709 | 0.047 | 0.165 | -0.542 | 0.066 | 0.196 |
| Total phenols (mg 100g$^{-1}$) | 0.685 | -0.300 | 0.143 | 0.214 | 0.075 | -0.389 |
| Seed weight per fruit (g) | 0.905 | -0.131 | 0.175 | -0.027 | 0.112 | 0.076 |
| No. of fruit per plant | -0.059 | -0.180 | 0.095 | 0.600 | -0.327 | 0.289 |
| Fruit yield per plant (g) | 0.833 | -0.226 | 0.084 | 0.390 | -0.085 | 0.004 |
| Eigen value | 4.351 | 3.414 | 2.299 | 1.837 | 1.602 | 1.097 |
| Proportion of variance (%) | 24.173 | 18.968 | 12.773 | 10.204 | 8.899 | 6.092 |
| Cumulative variance (%) | 24.173 | 43.141 | 55.914 | 66.118 | 75.017 | 81.109 |

agro-climatic conditions. Genotype CISH-P-10, with the longest vine, may contribute to higher vegetative biomass, supporting a greater photosynthetic surface, which can subsequently enhance reproductive output. In contrast, shorter vines like CISH-P-28 might represent compact growth habits that are desirable for high-density planting systems and may be better suited for resource-limited environments. Such variability in vine architecture has been reported earlier in cucurbit crops, where genotypes with vigorous vines tend to produce more fruits per plant, while compact types are preferred for commercial cultivation owing to their manageability (Islam *et al.,* 2024; Singh *et al.,* 2024).

The number of internodes per vine, another trait closely associated with plant size and reproductive efficiency, exhibited a wide variation ranging from 35.00 in CISH-P-9 to 105.33 in CISH-P-10. The variation in internodes number highlights the

**Table 4:** Grouping of 30 pointed gourd genotypes in three cluster based on agglomerative hierarchical clustering analysis

| Component | Cluster-I | Cluster-II | Cluster-III |
|---|---|---|---|
| Number of genotypes | 9 | 14 | 7 |
| Percent share of total genotypes | 30 | 46 | 24 |
| Position of genotypes in cluster | CISH-P-1 | CISH-P-2 | CISH-P-12 |
| | CISH-P-3 | CISH-P-5 | CISH-P-23 |
| | CISH-P-4 | CISH-P-6 | CISH-P-25 |
| | CISH-P-7 | CISH-P-10 | CISH-P-26 |
| | CISH-P-8 | CISH-P-11 | CISH-P-27 |
| | CISH-P-9 | CISH-P-13 | CISH-P-28 |
| | CISH-P-22 | CISH-P-14 | CISH-P-30 |
| | CISH-P-24 | CISH-P-15 | |
| | CISH-P-29 | CISH-P-16 | |
| | | CISH-P-17 | |
| | | CISH-P-18 | |
| | | CISH-P-19 | |
| | | CISH-P-20 | |
| | | CISH-P-21 | |

**Table 5:** Cluster means for 18 characters in 30 pointed gourd genotype based on agglomerative hierarchical cluster analysis

| Variables | Cluster -I | Cluster -II | Cluster-III |
|---|---|---|---|
| Vine length(cm) | 681.83 | 884.00 | 815.67 |
| Number of internodes per vine | 89.00 | 78.00 | 72.00 |
| Inter nodal length (cm) | 7.67 | 11.33 | 11.33 |
| No. of primary branches | 18.33 | 6.33 | 15.00 |
| Female flower length (cm) | 5.33 | 6.32 | 6.17 |
| Fruit length (cm) | 9.43 | 11.29 | 9.90 |
| Fruit width (cm) | 3.52 | 4.19 | 4.40 |
| Fruit circumference(cm) | 12.43 | 15.40 | 13.90 |
| Average Fruit weight (g) | 36.30 | 81.46 | 59.67 |
| T.S.S. (%) | 2.58 | 3.19 | 4.10 |
| Dry mater content (%) | 9.76 | 13.79 | 8.47 |
| Seed per fruit | 23.00 | 20.00 | 20.67 |
| Vit C (mg 100g$^{-1}$) | 78.33 | 47.10 | 63.89 |
| Total carotenoids (mg 100g$^{-1}$) | 2.05 | 3.94 | 4.72 |
| Total phenols (mg 100g$^{-1}$) | 4.17 | 5.87 | 29.17 |
| Seed weight per fruit (g) | 0.41 | 1.10 | 2.97 |
| No. of fruit per plant | 68.00 | 43.00 | 59.67 |
| Fruit yield per plant (g) | 1564.00 | 860.00 | 4020.73 |

differences in nodal density, which directly impacts the number of potential fruiting sites. A higher internodes number often increases the probability of flower initiation and fruit bearing, thus enhancing yield potential. However, excessively dense nodes may sometimes result in competition for assimilates and may negatively affect fruit size and quality. Alongside the number of nodes, the internodal length, which varied from 6.75 cm in CISH-P-16 to 15.17 cm in CISH-P-28, plays a critical role in determining plant architecture and bearing intensity. Short internodes, as seen in CISH-P-16, lead to compact vines with clustered leaves and nodes, possibly increasing photosynthetic efficiency per unit area, but reducing air circulation and increasing disease incidence. Conversely, longer internodes, like in CISH-P-28, contribute to a more spreading growth habit, which can enhance light interception and reduce intra-plant competition but may delay flowering and fruiting due to increased vegetative growth. Previous studies in cucurbits have confirmed that intermodal length has a strong correlation with flowering behavior and fruit

**Table 6:** Average Inter and intra cluster distance

| | Cluster-I | Cluster-II | Cluster-III |
|---|---|---|---|
| Cluster-I | 0.00 | 896.83 | 2317.56 |
| Cluster -II | | 0.00 | 3193.73 |
| Cluster-III | | | 0.00 |

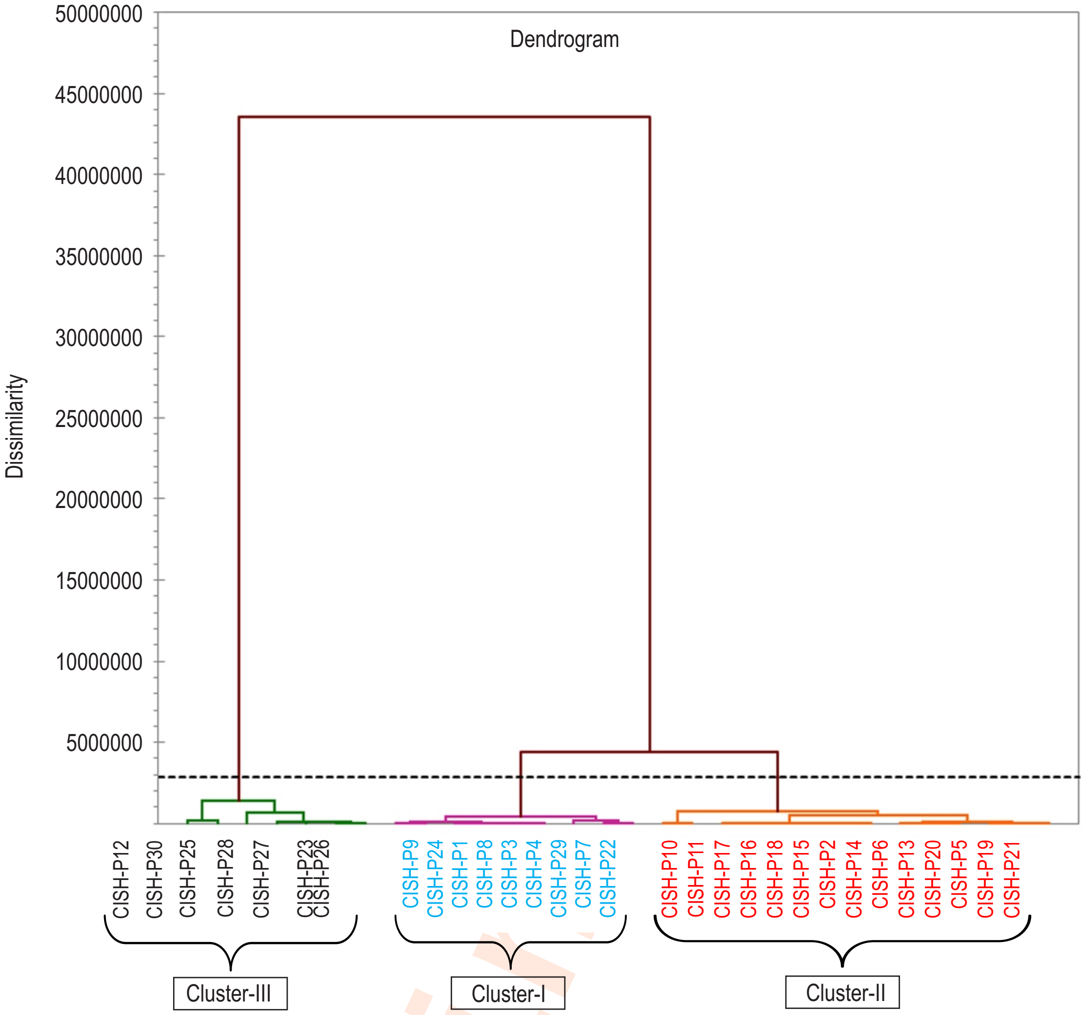


**Fig. 1:** Dendogram depicting genetic relationships among 30 genotypes based on horticultural traits produced by complete linkage analysis (Scale-Euclidean distance at .05).

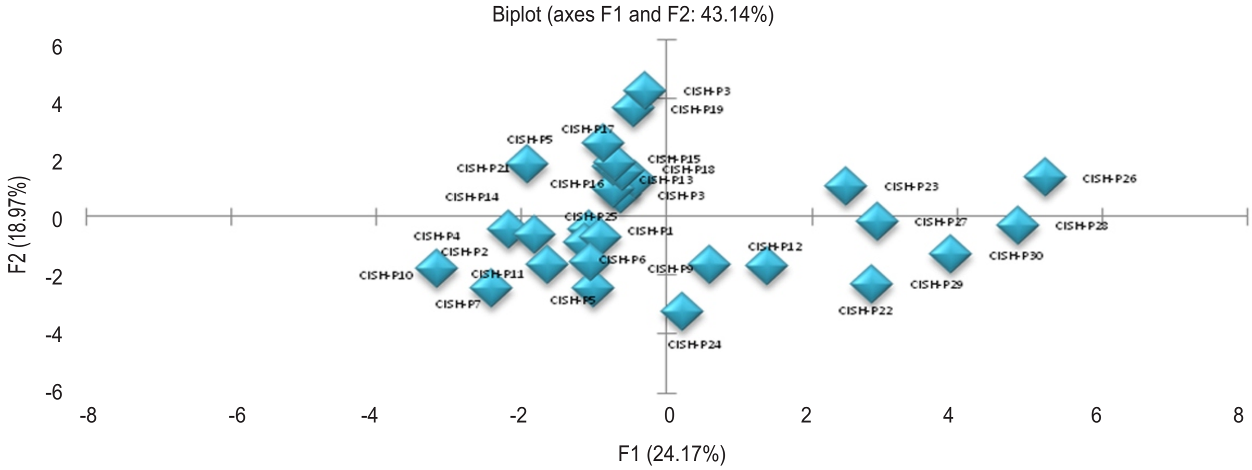


**Fig. 2:** Bi-plot for 1st and 2nd PC for genotypes of pointed gourd in relation to horticultural traits. N.

load (Malek *et al.,* 2007), and similar patterns were evident in the present study. Primary branching, which significantly contributes to canopy structure and reproductive potential, varied from 6.33 branches in CISH-P-5 to 21.67 branches in CISH-P-30. Plants with higher branching, such as CISH-P-30, are generally more prolific bearers due to increased number of fruiting axes, thereby contributing positively to yield. However, branching must be balanced with resource allocation, as excessive vegetative proliferation may reduce assimilate partitioning to developing fruits. Female flower length, another critical reproductive trait, varied between 5.17 cm (CISH-P-7) and 7.33 cm (CISH-P-12). Longer female flowers, as in CISH-P-12, may indicate greater ovary size and potential for larger fruit development.

This observation aligns with previous findings where floral morphology was significantly associated with fruit size and seed set in cucurbits (Islam *et al.,* 2024; Anil *et al.,* 2017 ). Fruit traits, which directly influence consumer acceptance and marketability, displayed pronounced variability. Fruit length varied from 5.97 cm in CISH-P-19 to 12.28 cm in CISH-P-29, while fruit diameter ranged between 2.39 cm (CISH-P-5) and 4.40 cm (CISH-P-23). Fruit circumference further highlighted the morphological diversity, with values ranging from 9.17 cm in CISH-P-20 to 15.40 cm in CISH-P-24. These differences in fruit dimensions reflect the underlying genetic variation and are crucial determinants of fruit shape, which has a direct bearing on consumer preference. Longer fruits, such as those of CISH-P-29, are often preferred in certain markets, whereas smaller, rounder fruits may be more acceptable in others, highlighting the role of genotype-specific breeding in meeting diverse consumer demands. Average fruit weight, an integral component of total yield, ranged widely from 22.38 g in CISH-P-12 to 81.86 g in CISH-P-20. Such a fourfold difference among genotypes emphasizes the scope for selection and improvement of fruit size, which remains one of the most economically significant traits in pointed gourd cultivation (Jena *et al.,* 2017).

Fruit quality attributes, including total soluble solids (TSS), dry matter content, seed number, and biochemical composition, further reinforced the extent of genetic variability. TSS, an indicator of sweetness and flavor, ranged from 1.71% in CISH-P-3 to 5.97% in CISH-P-27. Genotypes with higher TSS are particularly desirable for fresh consumption, as sweetness strongly influences consumer acceptance. Dry matter content, another important quality determinant influencing both texture and storability, ranged from 5.81% in CISH-P-19 to 14.00% in CISH-P-20. A higher dry matter content, as recorded in CISH-P-20, suggests improved postharvest shelf life and consumer-preferred firm texture, making such genotypes attractive for commercial exploitation. Seed number per fruit, a critical trait influencing consumer acceptability, varied between 14.00 seeds in CISH-P-25 and 33.33 seeds in CISH-P-28. Fewer seeds per fruit, as observed in CISH-P-25, are highly desirable since consumers prefer seedless or less-seeded fruits for better palatability. Conversely, higher seed content often reduces edible portion and market value, although it may be advantageous for breeding purposes where seed propagation is required.

Nutritional traits showed equally significant variability. Vitamin C content varied from 25.00 mg/100 g in CISH-P-10 to 81.78 mg 100 g$^{-1}$ in CISH-P-4, indicating more than a threefold variation among genotypes. Vitamin C, an essential antioxidant, enhances the nutritional and therapeutic value of pointed gourd, and genotypes with higher concentrations, like CISH-P-4, can contribute to biofortification programs. Total carotenoids ranged between 1.85 mg/100 g (CISH-P-10) and 6.54 mg 100 g$^{-1}$ (CISH-P-29), which is notable since carotenoids are precursors of vitamin A and play a key role in enhancing dietary quality. Such variation provides opportunities for improving the health-promoting potential of pointed gourd through selective breeding. Total phenol content (TPC), which contributes to antioxidant activity, also exhibited a wide range, corroborating earlier reports that cucurbits harbor substantial variation in secondary metabolites (Sinha *et al.,* 2025). The observed biochemical variability underscores the potential of pointed gourd not only as a yield-oriented crop but also as a functional food with significant nutraceutical potential.

Seed weight per fruit, ranging from 0.39 g in CISH-P-2 to 8.33 g in CISH-P-26, further contributed to the diversity observed. Lower seed weight is generally desirable for fresh consumption, while higher seed weight may reflect increased allocation of assimilates to reproductive sinks. Number of fruits per plant, a direct yield determinant, varied enormously from 23.00 in CISH-P-24 to 108.13 in CISH-P-12. Such a nearly fivefold variation demonstrates the presence of prolific genotypes that can substantially enhance productivity under commercial cultivation. Ultimately, fruit yield per plant, the most integrative trait encompassing all yield components, varied from 504 g in CISH-P-24 to 4923.07 g in CISH-P-26, highlighting the tremendous scope for yield improvement through careful selection and hybridization. The magnitude of variability among traits was confirmed by the coefficient of variation (CV). The highest CV was observed for number of seeds per fruit (82.66%), followed by fruit yield per plant (74.07%), total phenols (66.48%), and number of fruits per plant (42.53%). These high CV values highlight the potential of these traits as effective selection indices for genetic improvement. Traits with higher variability are often under polygenic control, and thus provide greater scope for recombination and selection, as noted in previous studies clone on cucurbits (Singh *et al.,* 2024; Malek *et al.,* 2007). Multivariate analysis through Single Linkage Cluster Analysis (SLCA) and principal component analysis (PCA) provided further insights into the structuring of genetic variability. Based on SLCA, all genotypes were grouped into three major clusters, with Cluster III containing the largest number of genotypes (14), followed by Cluster I (9) and Cluster II (7). The clustering pattern revealed that genotypes collected from same geographic origin were dispersed across different clusters, suggesting that genetic diversity was not strictly associated with geographic distribution. This observation corroborates with the findings of Debata *et al.* (2017), who reported similar results in cucurbit germplasm, emphasizing that natural and artificial selection pressures play a more significant role in shaping genetic variability than geographic origin alone (Arya *et al.,* 2017)

Cluster mean analysis provided valuable insights into the traits characterizing each group. Cluster I was distinguished by higher numbers of fruits per plant, vitamin C content, number of primary branches, and internode number per vine, indicating its superiority in traits contributing to prolificacy and nutritional quality. Cluster II was superior in vine length, fruit size (length, diameter and circumference), fruit weight, and dry matter content, making it particularly suitable for selection aimed at improving fruit size and postharvest qualities. Cluster III excelled in seed weight per fruit, fruit yield per plant, intermodal length, TSS and total carotenoids, making it a valuable source for improving both yield and nutritional attributes. Genotypes from these clusters can be utilized as parents in breeding programs to develop superior recombinants by targeting specific desirable traits. Hybridization between divergent clusters, particularly Cluster II and Cluster III, which exhibited the highest inter-cluster distance (3193.73), is expected to generate transgressive segregants with improved yield and quality traits. Such crossing strategies align with the observations of Kujur *et al.* (2017) and Roy *et al.* (2013), who emphasized that crosses between genetically distant parents tend to maximize heterosis and broaden the genetic base of the segregating population.

Dendrogram constructed using Euclidean distances provided a clear visualization of genetic relationships among 30 genotypes. At 100% dissimilarity, all genotypes were distinct, while at 85% dissimilarity, they formed seven clusters, which further condensed into three clusters at 55% dissimilarity. The wide range of dissimilarity (55–100%) strongly indicates the presence of substantial genetic variability in the studied material. Among the genotypes, CISH-P-12, CISH-P-21, CISH-P-30, CISH-P-29, CISH-P-28 and CISH-P-5 emerged as the most divergent and, therefore, highly promising candidates for use in future hybridization programs aimed at isolating superior recombinants with higher fruit yield and better quality. The implications of such genetic variability are profound. In pointed gourd, yield-attributing traits like fruit weight, number of fruits per plant, and fruit yield per plant often exhibit high heritability (Verma *et al.,* 2017; Pramila *et al.,* 2023), making them amenable to early-generation selection. Moreover, nutritional traits such as vitamin C and carotenoids, although influenced by environmental conditions, displayed sufficiently high variation in the present study to justify their consideration in breeding strategies aimed at biofortification. Selecting and crossing genotypes with complementary traits—for instance, those with high fruit yield and those with superior nutritional profiles—can lead to the development of cultivars that are both high yielding and nutritionally enhanced, contributing to food and nutritional security.

The present investigation unequivocally demonstrated the existence of substantial genetic diversity among 30 pointed gourd genotypes for a wide range of morphological, yield, and quality traits. The variability observed provides a valuable foundation for designing effective breeding programs. Divergent genotypes identified from different clusters can be strategically exploited in hybridization programs to develop elite cultivars with improved yield potential, nutritional quality, and consumer-preferred fruit attributes. Such genetic enhancement of pointed gourd, a nutritionally rich and regionally important vegetable, holds promise for enhancing its role in sustainable horticultural production systems and addressing nutritional security in tropical and subtropical regions.

## Acknowledgment

Authors are thankful to the Director, ICAR - Central Institute for Subtropical Horticulture, Rehmankhera, Lucknow for his keen interest and providing necessary facility for the study.

**Authors' contribution: S.R. Singh:** Collection of Germplasm and experimentation of trial; **S. Rajan:** Designing of experiment and collection of germplasm; **G.L. Veena:** Quality analysis of the fruit; **D. Nayak:** Collection of Germplasm from West Bengal; **A.K. Trivedi:** Recording of Phenological Data; **V. Soni:** Data recording; **V. Singh:** Statistical analysis and Graph prepration.

**Funding:** CISH Funded Project.

**Research content:** The research content of manuscript is original and has not been published elsewhere.

**Ethical approval:** Not applicable.

**Conflict of interest:** The authors declare that is there is no conflict of interest.

**Data availability:** Data is provided in the paper. Additional data will be made available on reasonable request.

**Consent to publish:** All authors agree to publish the paper in *Journal of Environmental Biology.*

## References

Anil, K.J., T. Susheela, P. Kiran and R.V. Sujatha: Studies on genetic variability, hritbility and genetic advance in pointed gourd (*Trichosanthes dioica* Roxb). *Int. J. Curr. Microbiol. Appl. Sci.,* **6**, 1857-1863 (2017).

Arya, J.S., N. Singh, P. Arya and A. Kant: Morphological variation and relationship among the onion germplasm for quantitative and qualitative traits at Trans-Himalayas Laddakh India. *Australian J. Crop Sci.,* **11**, 229-37 (2017).

Begna, T., G. Alemayehu and D. Tadesse: Genetic variability and heritability studies in crop improvement. *J. Plant Bree. Gene.,* **12**, 45–58 (2024).

Begna, T. and T. Teressa: Genetic variability and its benefits in crop improvement: A review. *Middle East J. Agricul. Res.,* **13**, 128-136 (2024)

Debata, J., S.K. Maurya, H. Yadav and B. Lalit: Study on genetic diversity of pointed gourd using morphological traits. *Int. J. Curr. Microbiol. Appl. Sci.,* **6**, 1511-1519 (2017).

Islam, S., S. Datta, B. Das, S. Basfore, R. Chatterjee and R.K. Sarkar: Variation of fruit morphology and genetic divergence of indigenous pointed gourd. *Bangladesh J. Bot.,* **53**, 193-201 (2024).

Jena A.K., T. Suseela, T.S.K.K. Kiran, and R.V. Sujatha: Studies on genetic variability, heritability and genetic advance in pointed gourd (*Trichosanthes dioica* Roxb). *Int. J. Curr. Microbiol. Appl. Sci.,* **6**, 1857-1863 (2017)

Kujur, P.K., V. Bahadur and P. Pankaj: Study on genetic variability, heritability and genetic advance in Dolichos bean (*Lablab pursuers* L.) genotypes. *Trends in Biosci.,* **10**, 2418-2421 (2017).

Malek, M.A., M.A. Bari Miah, M.O. Islam, A.M.M. Mosiul Hoque and R. Gomes: Genetic varbility, heritability and genetic advance in pointed gourd (*Trichosanthes dioica* Roxb). *Bangladesh J. Pl. Breed. Genet.,* **20**, 47-52 (2007)

Mukherjee, P.K., S. Singha, A. Kar, J. Chand, S. Banerjee, B. Dasgupta, P.K. Haldar and N. Sharma: Therapeutic importance of Cucurbitaceae: A medicinally important family. *J. Ethnopharmacol.,* **282**, Article 114599 (2022).

National Horticulture Board. Area and Production Statistics of Horticultural Crops: Pointed gourd (*Trichosanthes dioica*). Ministry of Agriculture & Farmers Welfare, Government of India. (2021) https://agriexchange.apeda.gov.in/India%20Production/India_Productions.aspx

Nissar, M., A. Gafoor and M. Khan: Phenotypic variation in agronomic and morphological traits of *Pisum savium* L germ plasm obtained from different part of world. *Rus. J. Genet.,* **47**,19-25 (2011).

Nwangburuka, C.C., O.B. Kehinde, D.K. Ojo, O.A. Dentan and A.R. Popoola: Morphological classification of genetic diversity in cultivated Okra *Abelmoschus esculentus* L Moench using principal component analysis (PCA) and single linkage cluster analysis (SLCA). *Afric. J. Biot.,* **10**, 11165-11172 (2011).

Pramila, Dinesh, S.P. Singh, L.P. Nana, U. Kumar and S.N. Dhaker: Variability and divergence study in Pointed gourd (*Trichosanthes dioica* Roxb.). *Pharma. Innova. J.,* **12**, 4219-4224 (2023).

Ranganna, S.: Handbook of Analysis and Quality Control for Fruit and Vegetable Products. Tata Mc Graw Hill Publishing Co. Ltd., New Delhi, pp. 190-210 (1986).

Roy, S., M.A. Islam, A. Sarkar, M.A. MaliK, M.Y. Rafi and M.R. Ismail: Determination of genetic diversity in lentil germplasm based on quality traits. *Aust. J. Crop Sci.,* **7**, 14-21 (2013).

SAS Institute: SAS Institute Inc., SAS 9.1.3 Help and Documentation, Cary, NC: SAS Institute Inc., 2002-2004. (2011).

Sharma, S., R. Sinha, A.K. Singh and Y. Meena: An umbrella review on ethnomedicinal, pharmacological and phytochemical profile of pointed gourd (*Trichosanthes dioica* Roxb): A bioactive healthy vegetable of Indian subcontinent. *Food Chemi. Advan.,* **3**, 100433 (2023).

Sheela, K.S., S. Robin and S. Manonmani: Principal component analysis for grain quality charactersion rice germplasm. *Electro. J. Plant Bree.,* **11**,127-131(2020).

Singh, S.R., S. Rajan, D. Kumar, K.K. Srivastava and V.K. Soni: Assessment of genetic variability and correlation in pointed gourd (*Trichosanthes diuoica* Roxb) genotypes for yield and attributing Traits. *Indian J. Plant Genet. Resour.,* **37**, 447-453 (2024).

Singleton, V.L., R. Orthofer and R.M. Lamuela-Raventós: Analysis of total phenols and other oxidation substrates and antioxidants by means of Folin-Ciocalteu reagent. *Method Enzymol.,* **299**, 152–158 (1999).

Sinha, A.K., P. Bhavana, A. Singh, J. Ranjan, H. Choudhary, G. Mishra, K. Thamilarsi, P. Chaukhande, R. Shinde, P. Kumar, J. Rajak and S. Ekbal: Unravelling genetic diversity in pointed gourd (*Trichosanthes dioica*) genotypes from India's Eastern plateau and hill region: Insights from morphological and molecular markers. *J. Gene. Enginee. Biotechnol.,* **23**, 100542 (2025).

Swarup , S., E.J. Cargill, K. Crosby, L. Flagel, J. Kniskern and K.C. Glenn: Genetic diversity is indispensable for plant breeding to improve crops. *Crop Sci.,* **61**, 839–852 (2021).

Vaidya, N., G. Nayak, M. Parida, C. Parameswaran, R.S. Sharma, R. Verma, J.L. Katara, S. Samantaray, S. Sharma, S., Nema, V.S. Gaur, A. Kumar and R.S. Ramakrishnan: Principal component analysis of grain yield and its attributing traits in recombinant inbred lines of rice (*Oryza sativa* L.) developed for submergence tolerance. *Int. J. Plant Soil Sci.,* **36**, 143–148 (2024).

Verma, P., S.K. Maurya, A. Panchbhaiya and D. Shivani: Studies on variability, heritability and genetic advance for yield and yield contributing characters in pointed gourd (*Trichosanthes dioica* Roxb). *J. Pharmacog. Phytochem.,* **6**, 1296 (2017)

Vijaya, S. Sharma and N. Batra: Comparative Study of Single Linkage, Complete Linkage, and Ward Method of Agglomerative Clustering, International Conference on Machine Learning, Big Data, Cloud and Parallel Computing (COMITCon), Faridabad, India, **2019**, 568-573 (2019)

Yadav, N., A.K. Singh, T.B. Emran, R.G. Chaudhary, R. Sharma, S. Sharma and K. Barman: Salicylic acid treatment reduces lipid per oxidation and chlorophyll degradation and preserves quality attributes of pointed gourd fruit. *J. Food Qual.,* **2022**, 2090562, 1–7 (2022).

Yang, C.M., K.W. Chang, M.H. Yin, H.M. Huang: Methods for the determination of the chlorophylls and their derivatives. *Taiwania,* **43**, 116-122 (1998).