



## RESEARCH ARTICLE

# Assessment of genetic diversity of bitter gourd (*Momordica charantia* L.) through morphological characterization and multi-variate analysis

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### Abstract

Bitter gourd (*Momordica charantia*) is a popular vegetable because of its rich nutritional profile and potent medicinal properties. In the present research, the genetic diversity of 38 bitter gourd genotypes was evaluated for 19 quantitative and 9 visual parameters. The trial was conducted during the spring-summer season of 2025 at the Vegetable Research Centre, GBPUA&T, Pantnagar and was laid out in RCBD with three replications. High GCV and PCV were observed for average yield per plant, number of primary branches per plant and stem diameter, whereas high heritability coupled with high genetic advance was recorded for average fruit weight and test weight, suggesting predominance of additive gene action and scope for direct selection. Average fruit yield per plant showed positive correlation with number of primary branches (0.925), stem diameter (0.921) and average fruit weight (0.710), while negative correlation with flowering and maturity traits such as days to first female flower (-0.291) and internodal length (-0.878). Path coefficient analysis revealed direct positive effects of key traits on average fruit yield per plant. Mahalanobis  $D^2$  statistics categorized the genotypes into six clusters, with clusters I and II being the largest. Intra-cluster distance was minimum in cluster IV, while maximum inter-cluster distance was noted between cluster I and cluster VI, suggesting the crosses between genotypes of these clusters may exploit maximum heterosis and develop superior recombinants, making them valuable for bitter gourd breeding. About 89.5% of the total genetic variance was explained by first six principal components and the PCA biplot clearly illustrated clustering, correlations and genetic divergence among the genotypes. Genotypes 2024/PBIG-38, 2024/PBIG-40 and 2024/PBIG-54 were found superior compared to standard check Pant Karela-1 for major yield-contributing parameters.

**Keywords:** Bitter gourd, genetic divergence, multi-variate analysis, principal component analysis

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**Citation:** Panchawatkar, V., Maurya, S.K., Kumar, V., Prasad, B., & Verma, A. (2026). Assessment of genetic diversity of bitter gourd (*Momordica charantia* L.) through morphological characterization and multi-variate analysis. *Vegetable Science*, 53(1), 38-45.

**Source of support:** Nil

**Conflict of interest:** None.

**Received:** 14/10/2025; **Revised:** 29/06/2026; **Accepted:** 29/06/2026

### Introduction

Bitter gourd (*Momordica charantia* L.;  $2n = 2x = 22$ ) is a major cucurbitaceous vegetable, also referred as bitter cucumber, bitter squash and maiden apple (Meghashree et al., 2024). The probable centre of domestication of Bitter gourd is Eastern Asia, Eastern India or Southern China (Behera et al., 2010). Bitter gourd is bitter in taste but not bitter for health. The presence of various bioactive compounds is responsible for its therapeutic benefits. It exhibits several important pharmacological properties such as anti-diabetic, anti-obesity, antifungal, antioxidant, digestion promoting, blood pressure lowering, cholesterol lowering and anticancer activities (Arun et al., 2021). Bitter gourd has gained a unique place among vegetables over the last 20 years because of its noteworthy hypoglycemic qualities and important nutritional benefits, earning it the title of "vegetable insulin" and "cornucopia of health" (Tan et al., 2016; Rathod et al., 2021).

Diversity is the essence of the biological world and crop improvement greatly benefits from genetic diversity.

The manifestation of various plant traits depends on a combination of both hereditary and environmental factors. Hence, studying genetic parameters is crucial for understanding the inheritance of desired traits and selecting desirable genotypes. Genetic diversity analysis allows plant breeders to produce superior cultivars with favorable traits consisting of both breeder-favoured and farmer-favoured traits and serves as a key foundation for successful hybridization programs aimed at improving yield and adaptability. Multivariate analysis serves as a powerful method for evaluating the extent of genetic divergence within biological populations at the genotypic level (Bhandari *et al.*, 2017). Therefore, the present research was conducted to evaluate genetic diversity among 38 bitter gourd genotypes, collected from diverse agro-climatic regions and the national germplasm collection to ensure broad genetic representation, using morphological traits and multivariate analysis, with the aim of identifying divergent elite genotypes as potential parents for future bitter gourd breeding programs.

## Materials and Methods

### *Experimental material, site and layout*

In the present research, 38 diverse bitter gourd genotypes consisting two check varieties, i.e., Pant Karela-1 and Pusa Purvi, were analyzed to assess the genetic diversity among these genotypes by studying morphological traits. The research was carried out during the spring-summer season of 2025, at Vegetable Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. This region has a humid subtropical climate marked by considerable temperature fluctuations between summer and winter. During the experimental period, the temperature ranged from 10.7 to 38.2°C. Three replications were used in the experiment, which was arranged as randomized complete block design (RCBD). The genotypes used in the present research were randomly allotted to different plots. The sowing was carried out in the first week of March 2025 and a spacing of 150 × 75 cm was maintained.

### *Observation recorded*

Ten plants per genotype were planted in each of the three replications; border plants were excluded, and from the remaining plants, five plants were randomly picked to take observations. For morphological characterization, nineteen quantitative and nine visual traits were observed. Quantitative traits include days to first male flower (DFF), number of nodes to first male flower (NNFF), days to first female flower (DFMF), number of nodes to first female flower (NDFF), days to first fruit harvest (DTFFH), average fruit weight (g) (AFW), average fruit length (cm) (AFL), average fruit diameter (cm) (AFD), average fruit circumference (cm) (AFC), vine length at harvest (m) (VL), stem diameter

(mm) (SD), number of primary branches per plant (NPBPP), internodal length (cm) (IL), root length (cm) (RL), number of fruits per plant (NFPP), average fruit yield per plant (kg) (AYPP), fruit yield (q/ha) (Fyha), seed length (mm) (SL) and test weight (TW), while the visual traits includes leaf blade length, leaf blade width, number of lobes, depth of lobing, fruit color, fruit ridges, fruit shape, seed color and seed indentation of margin.

### *Statistical analysis*

Statistical analysis was conducted using the mean values of five randomly chosen plants. The data were verified for conformity to the assumptions of normality and homogeneity of variance, which were found to be satisfactorily fulfilled. Analysis of variance (ANOVA) was performed on the collected data according to Panse & Sukhatme (1961). Duncan's multiple range test (DMRT) was carried out for comparing means at a 5% level of significance. Genotypic and phenotypic coefficient of variations (GCV and PCV) were evaluated according to Burton & Devane (1953). The methods suggested by Johnson *et al.* (1995) and Allard (1960) were employed to calculate broad-sense heritability ( $h^2_b$ ) and genetic advance (GA). Correlation and path coefficient analysis were conducted using INDOSTAT software, with average fruit yield per plant as the dependent variable. Genetic divergence was analyzed through Mahalanobis  $D^2$  statistics and genotypes were grouped into clusters on the basis of  $D^2$  values. Intra- and inter-cluster distances were calculated to determine the extent of divergence using the formulae proposed by Singh & Chaudhary (1977). Cluster means and the relative contribution of each trait were calculated. Additionally, principal component analysis (PCA) was conducted to determine the major traits influencing variation and to visualize the diversity among the bitter gourd genotypes.

## Results and Discussion

### *Per se performance of bitter gourd genotypes using nineteen quantitative traits*

In the present research, significant variation was observed among the genotypes for all studied traits. For DFMF and NDFF, 2024/PBIG-38 was identified as the earliest, while 2024/PBIG-10 was the earliest for DTFFH. Among the fruit traits, 2024/PBIG-38 recorded for the highest value of AFW and maximum AFL was observed in 2024/PBIG-36. Among vegetative traits, 2024/PBIG-38 excelled in VL, NPBPP and RL, while the longest IL was observed in 2024/PBIG-10. In terms of yield, 2024/PBIG-10 showed the highest NFPP, while 2024/PBIG-38 emerged as the top performer for AYPP and Fyha. For the seed parameter, maximum TW was observed in 2024/PBIG-35. Detailed genotype-wise numerical values are presented in Table 1. Interestingly, 2024/PBIG-38 and 2024/PBIG-40 showed consistent superiority across multiple

**Table 1:** Summary of morphological characters examined in 38 bitter gourd genotypes

| <i>Genotypes</i> | <i>DFF</i> | <i>DTFFH</i> | <i>AFW</i> | <i>VL</i> | <i>NFPP</i> | <i>AYPP</i> |
|------------------|------------|--------------|------------|-----------|-------------|-------------|
| 2024/PBIG-1      | 45.04      | 58.03        | 56.56      | 2.83      | 21.18       | 1.19        |
| 2024/PBIG-2      | 52.78      | 62.83        | 21.40      | 2.34      | 42.37       | 0.91        |
| 2024/PBIG-4      | 50.74      | 66.51        | 44.80      | 2.23      | 18.49       | 0.82        |
| 2024/PBIG-7      | 49.52      | 64.15        | 48.53      | 3.14      | 31.31       | 1.52        |
| 2024/PBIG-8      | 56.82      | 69.34        | 28.99      | 2.55      | 36.44       | 1.06        |
| 2024/PBIG-9      | 45.60      | 58.52        | 35.54      | 2.95      | 38.61       | 1.38        |
| 2024/PBIG-10     | 42.17      | 50.61        | 12.78      | 1.94      | 50.57       | 0.64        |
| 2024/PBIG-12     | 55.56      | 64.07        | 32.52      | 3.14      | 46.46       | 1.51        |
| 2024/PBIG-14     | 54.88      | 66.41        | 41.37      | 2.06      | 16.54       | 0.69        |
| 2024/PBIG-17     | 61.31      | 70.42        | 59.24      | 3.14      | 25.59       | 1.52        |
| 2024/PBIG-19     | 49.63      | 65.97        | 56.18      | 4.22      | 37.51       | 2.10        |
| 2024/PBIG-21     | 58.49      | 67.28        | 45.89      | 3.82      | 39.47       | 1.80        |
| 2024/PBIG-23     | 60.20      | 75.04        | 65.60      | 4.02      | 29.34       | 1.93        |
| 2024/PBIG-24     | 54.79      | 70.70        | 50.52      | 2.15      | 22.73       | 0.79        |
| 2024/PBIG-28     | 52.40      | 66.23        | 41.15      | 2.16      | 19.62       | 0.81        |
| 2024/PBIG-30     | 52.75      | 67.01        | 44.32      | 2.41      | 21.47       | 0.95        |
| 2024/PBIG-32     | 50.39      | 65.91        | 37.45      | 1.15      | 20.55       | 0.76        |
| 2024/PBIG-35     | 46.20      | 61.87        | 51.75      | 2.43      | 18.47       | 0.96        |
| 2024/PBIG-36     | 51.03      | 61.71        | 64.71      | 3.86      | 28.48       | 1.85        |
| 2024/PBIG-38     | 30.88      | 51.02        | 101.54     | 4.81      | 28.87       | 2.92        |
| 2024/PBIG-39     | 61.47      | 70.91        | 61.21      | 4.24      | 35.70       | 2.18        |
| 2024/PBIG-40     | 45.40      | 54.94        | 71.34      | 4.65      | 38.51       | 2.74        |
| 2024/PBIG-41     | 53.45      | 70.52        | 36.58      | 3.24      | 42.52       | 1.56        |
| 2024/PBIG-42     | 41.03      | 51.06        | 67.79      | 4.56      | 39.45       | 2.67        |
| 2024/PBIG-43     | 41.44      | 52.17        | 63.82      | 4.07      | 30.47       | 1.95        |
| 2024/PBIG-44     | 42.48      | 57.23        | 51.15      | 4.15      | 40.64       | 2.08        |
| 2024/PBIG-45     | 55.04      | 69.33        | 77.98      | 3.16      | 19.69       | 1.53        |
| 2024/PBIG-46     | 54.75      | 70.15        | 73.74      | 3.41      | 22.69       | 1.68        |
| 2024/PBIG-47     | 47.89      | 59.83        | 70.72      | 3.77      | 25.55       | 1.80        |
| 2024/PBIG-48     | 44.90      | 58.08        | 76.60      | 4.52      | 33.68       | 2.58        |
| 2024/PBIG-49     | 50.56      | 64.81        | 41.55      | 2.74      | 27.63       | 1.15        |
| 2024/PBIG-50     | 59.50      | 69.57        | 64.71      | 2.95      | 19.66       | 1.28        |
| 2024/PBIG-51     | 59.51      | 69.57        | 64.71      | 2.94      | 19.66       | 1.28        |
| 2024/PBIG-52     | 49.50      | 61.41        | 36.30      | 2.53      | 28.61       | 1.04        |
| 2024/PBIG-53     | 42.47      | 53.28        | 49.15      | 3.32      | 32.54       | 1.60        |
| 2024/PBIG-54     | 46.20      | 65.58        | 70.68      | 4.53      | 37.54       | 2.66        |
| Pant Karel-1 (C) | 53.53      | 60.94        | 51.32      | 4.06      | 37.65       | 1.94        |
| Pusa Purvi (C)   | 42.49      | 54.78        | 35.76      | 3.40      | 45.61       | 1.64        |
| S.E. (m) $\pm$   | 3.10       | 3.22         | 2.77       | 0.23      | 1.20        | 0.12        |
| C. D. at 5%      | 8.74       | 9.06         | 7.79       | 0.66      | 3.38        | 0.34        |
| C.V. (%)         | 10.68      | 8.83         | 9.07       | 12.39     | 6.74        | 13.30       |

traits, representing their strong potential as parents in improvement programs. Despite their early bearing nature, 2024/PBIG-38 and 2024/PBIG-40 recorded comparatively higher AYPP and Fyha, suggesting a desirable balance between earliness and productivity. Furthermore, the stability of their performance across vegetative, fruit, and yield traits suggests their broader adaptability, which is a critical consideration for recommending genotypes as potential parents. The observed morphological superiority of these genotypes directly contributes to yield improvement by ensuring better canopy development, higher fruit set and increased harvest index. These findings are in agreement with Reddy *et al.* (2021), Mallikarjuna *et al.* (2023) and Mehta *et al.* (2024), who also identified morphologically superior genotypes as promising parents for bitter gourd improvement. According to Duncan's multiple range test (DMRT), a group of genotypes including 2024/PBIG-2, 2024/PBIG-4, 2024/PBIG-8, 2024/PBIG-24, 2024/PBIG-28, 2024/PBIG-30, 2024/PBIG-32, 2024/PBIG-35 and 2024/PBIG-52 were noted to be statistically *at par* with each other for average fruit yield per plant, but, all of these genotypes differed significantly from the highest-yielding genotype, 2024/PBIG-38. Remarkable variation was also noted in visual traits, including creamy-white fruit color in 2024/PBIG-23, glossy green color in 2024/PBIG-9, globose fruit shape in 2024/PBIG-10 and rhomboid fruit shape in 2024/PBIG-2, 2024/PBIG-12, 2024/PBIG-21, 2024/PBIG-41 and Pusa Purvi. Sharma *et al.* (2025) also noted similar findings on morphological characters such as fruit color, shape, ridges and presence of tubercles.

### Genetic variability parameters

For all the quantitative traits studied, considerable variability was recorded between the thirty-eight bitter gourd genotypes, as represented by the range of GCV and PCV,  $h^2_b$ , GA and genetic advance as percent of mean (GAM). The GCV values varied from 4.60% for seed length to 39.17% for average fruit yield per plant, while PCV values varied from 5.56% for seed length to 41.36% for average fruit yield per plant. For all 19 quantitative traits studied, PCV values were slightly greater than GCV values, representing the effect of environmental factors on the expression of traits. The maximum GCV and PCV were recorded for AYPP (39.17, 41.36%), representing significant genetic variability. High GCV was recorded for the traits like average fruit yield per plant (39.17%) and stem diameter (36.65%), representing the presence of considerable genetic variability, while high PCV values noted for the traits like AYPP (41.36%) and Fyha (37.88%), indicating the influence of both genetic and environmental factors. Similarly, Reddy *et al.* (2021) also found high values of GCV and PCV for traits like medium fruit weight, total fruit yield per vine, 100-seed weight, vine height and number of nodes per vine in bitter gourd. Heritability estimates (in broad sense) varied from 51.47 for

DTFFH to 95.31 for NPBPP, with high heritability recorded for NPBPP (95.31), followed by NFPP (95.16), suggesting that the expression of these traits is largely determined by genetic factors and can be effectively transferred to the next generation. Genetic advance (GA) varied from 0.91 for average fruit diameter to 65.75 for test weight, whereas GAM values varied from 7.84% for seed length to 76.40% for fruit yield per plant, representing greater expected improvement in these traits through selection. High values of GA were noted for the traits such as TW, Fyha and AFW. High  $h^2_b$  along with high GA was recorded for the traits like AFW (93.04, 34.77) and TW (87.09, 65.75), indicating that the traits are highly governed by additive gene action and may be effectively improved via selection. Similar results regarding heritability and GA were noted by Reddy *et al.* (2021), Nithinkumar *et al.* (2021), Sagar *et al.* (2024) and Sharma *et al.* (2025).

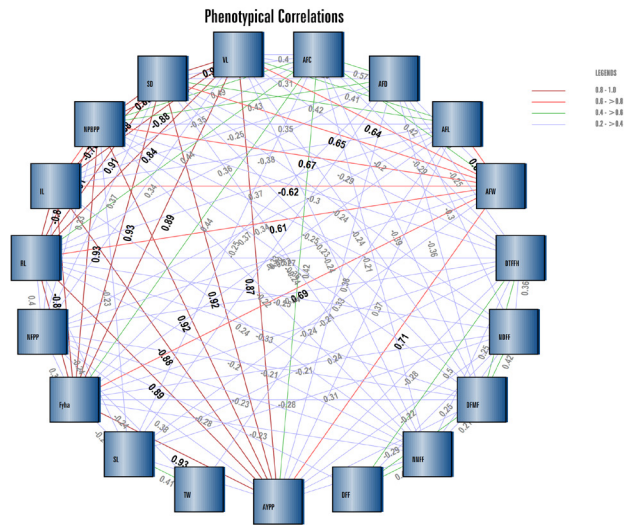
### Correlation and path coefficient analysis

The correlation analysis represented key relationships among the various traits examined in the study. The ultimate economic trait AYPP represented a highly significant and positive correlation with AFW (0.710), AFL (0.373), AFD (0.377), AFC (0.417), VL (0.870), NFPP (0.377) and Fyha (0.934), indicating that simultaneous improvement of these characters may be effective for enhancing overall productivity. Conversely, the trait, AYPP has a highly significant negative correlation with NNFF (-0.243), DFMF (-0.291), DTFFH (-0.278) and IL (-0.878) at the phenotypic level, representing that the earliness and compact plant architecture may be favorable for higher yield in bitter gourd. The correlation network diagram (Figure 1) represented interrelationships among 19 quantitative traits, demonstrating associations useful for indirect selection in bitter gourd breeding. However, these associations reflect statistical relationships and should not be directly interpreted as causal relationships. Path coefficient analysis helped partition trait correlations into direct and indirect effects, providing better understanding of the actual contribution of each trait towards yield. The phenotypic path coefficient analysis indicated that the highest positive direct effect on AYPP was contributed by AFW (0.4639), followed by NFPP (0.3462), NPBPP (0.3171) and Fyha (0.0986), while the maximum negative direct effect was contributed by NDFF (-0.0077), followed by TW (-0.0096), AFC (-0.0237) and RL (-0.0479). Similar results were noted by Aftab *et al.* (2024), Singh *et al.* (2024), Srinivasulu & Singh (2024), Srinivasulu (2025).

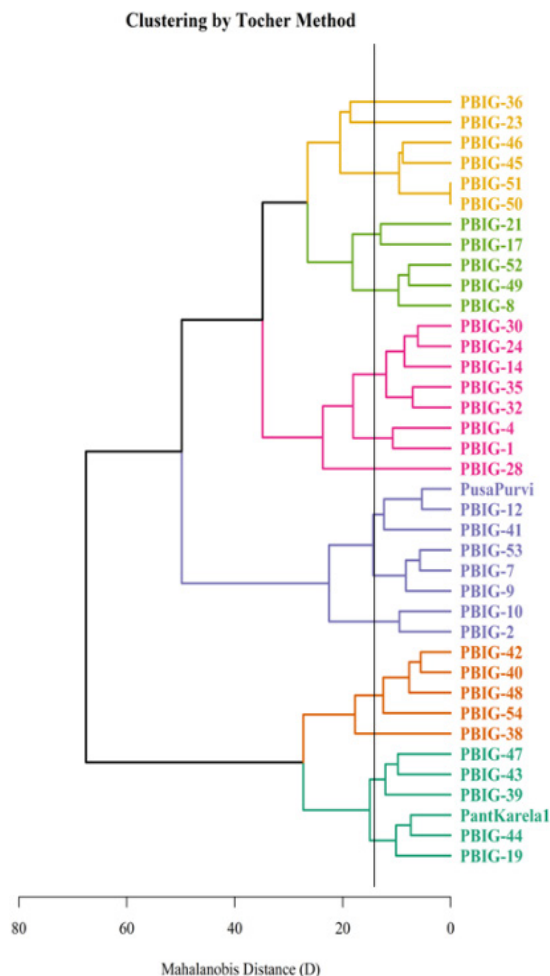
### Genetic divergence using Mahalanobis $D^2$ statistics

#### Clustering of genotypes

Based on Mahalanobis  $D^2$  statistics, 38 bitter gourd genotypes were classified into six clusters, indicating substantial diversity among genotypes (Figure 2). Cluster I



**Figure 1:** Network diagram indicating phenotypic correlation relationships among nineteen quantitative traits in bitter melon genotypes



**Figure 2:** Dendrogram showing clustering of bitter melon genotypes based on Mahalanobis D2 statistics

and cluster II were the largest clusters, each consisting of eight genotypes, while cluster VI contained five genotypes. All major clusters were further subdivided into sub-clusters, reflecting significant genetic differentiation within the population. Detailed cluster composition is presented in Figure 2. From a breeding perspective, genotypes grouped into distantly placed clusters are expected to possess greater genetic divergence, making them more suitable as parents for heterotic cross combinations. Crosses between genotypes from cluster I and cluster VI or cluster III and V are therefore recommended as potentially promising combinations for developing high-yielding hybrids and superior segregating populations. The presence of sub-clusters within major clusters further suggests exploitable variability even among genetically similar groups, which can be strategically utilized in recurrent selection programs. Similar clustering patterns were reported by Dey *et al.* (2006) in bitter melon.

#### **Determination of intra-cluster and inter-cluster distances**

Table 2 summarizes the intra- and inter-cluster distances among the six clusters of bitter melon genotypes, offering a measure of genetic divergence both within and between clusters based on Mahalanobis  $D^2$  statistics. The intra-cluster distances varied from 104.27 in cluster IV to 163.38 in cluster I. The low intra-cluster distance indicated that the genotypes in cluster IV were highly homogeneous, while the high intra-cluster value in cluster I indicated relatively greater variability within cluster I. The lowest inter-cluster distance, *i.e.*, 245.08, was recorded between cluster IV and cluster VI, indicating close genetic resemblance between these two clusters. The highest inter-cluster distance, *i.e.*, 953.14, was observed between cluster I and cluster VI, suggesting significant genetic divergence. Collectively, the findings revealed that cluster I and cluster VI were the most divergent clusters, consisting of potential genotypes for hybridization to maximize heterosis. On the other hand, clusters with the lowest inter-cluster distance, cluster IV and cluster VI, are likely to have relatively similar genetic backgrounds.

#### **Cluster mean analysis for quantitative traits**

The mean performance of six clusters for nineteen quantitative traits is shown in Table 3. Significant variability was recorded among clusters for all traits. Cluster VI was recorded as superior for yield-contributing parameters like AFW, NFPP, AYPP and Fyha. Highest values for fruit quality parameters such as AFL, AFD and AFC were found in cluster V. Cluster IV showed earliness by expressing the lowest mean values for the traits like DFF, DFMF and DTFFH. Cluster VI was characterized by higher RL and more branches per plant, whereas late flowering was observed in cluster III. The cluster mean analysis suggested that cluster VI was promising for yield trials, cluster IV for earliness and cluster V for quality

**Table 2:** Average intra- and inter-cluster distance

|             | <i>Cluster I</i> | <i>Cluster II</i> | <i>Cluster III</i> | <i>Cluster IV</i> | <i>Cluster V</i> | <i>Cluster VI</i> |
|-------------|------------------|-------------------|--------------------|-------------------|------------------|-------------------|
| Cluster I   | 163.38           | 455.51            | 295.34             | 581.63            | 335.42           | 953.14            |
| Cluster II  |                  | 136.10            | 259.45             | 297.39            | 492.66           | 634.06            |
| Cluster III |                  |                   | 131.08             | 352.03            | 272.50           | 621.12            |
| Cluster IV  |                  |                   |                    | 104.27            | 342.25           | 245.08            |
| Cluster V   |                  |                   |                    |                   | 156.35           | 499.19            |
| Cluster VI  |                  |                   |                    |                   |                  | 112.05            |

**Table 3:** Cluster mean analysis of bitter gourd genotypes for nineteen quantitative traits

| <i>Sl. No.</i> | <i>Trait</i>                           | <i>Cluster I</i> | <i>Cluster II</i> | <i>Cluster III</i> | <i>Cluster IV</i> | <i>Cluster V</i> | <i>Cluster VI</i> |
|----------------|----------------------------------------|------------------|-------------------|--------------------|-------------------|------------------|-------------------|
| 1              | Days to first male flower              | 40.1             | 36.93             | 40.54              | 35.74             | 42.78            | 38.52             |
| 2              | Number of nodes to first male flower   | 8.71             | 7.08              | 8.93               | 5.71              | 8.57             | 7.3               |
| 3              | Days to first female flower            | 50.9             | 48                | 55.34              | 49.41             | 56.67            | 41.68             |
| 4              | Number of nodes to first female flower | 15.93            | 15.46             | 22.69              | 14.07             | 19.71            | 14.32             |
| 5              | Days to first fruit harvest            | 65.33            | 59.85             | 66.65              | 61.18             | 69.23            | 56.14             |
| 6              | Average fruit weight                   | 45.99            | 34.03             | 42.39              | 59.07             | 68.57            | 77.59             |
| 7              | Average fruit length                   | 13.67            | 10.11             | 12.31              | 14.75             | 17.5             | 15.89             |
| 8              | Average fruit diameter                 | 3.53             | 3.45              | 3.24               | 3.69              | 3.27             | 4.23              |
| 9              | Average fruit circumference            | 11.17            | 11.3              | 11.03              | 12.08             | 10.86            | 14.33             |
| 10             | Vine length                            | 2.18             | 2.93              | 2.96               | 4.08              | 3.39             | 4.61              |
| 11             | Stem diameter                          | 3.03             | 4.31              | 4.39               | 7.07              | 5.45             | 8.17              |
| 12             | Number of primary branches per plant   | 4.37             | 5.53              | 5.5                | 7.52              | 6.23             | 11.36             |
| 13             | Internodal length                      | 6.22             | 4.84              | 4.83               | 3.33              | 4.14             | 3.08              |
| 14             | Root length                            | 17.29            | 21.5              | 20.82              | 27.07             | 22.6             | 33.93             |
| 15             | Number of fruits per plant             | 19.88            | 41.25             | 31.55              | 34.58             | 23.25            | 35.61             |
| 16             | Average fruit yield per plant          | 0.87             | 1.34              | 1.32               | 2.01              | 1.59             | 2.71              |
| 17             | Fruit yield (q/ha)                     | 83.84            | 122.12            | 120.21             | 177.09            | 143.36           | 234.8             |
| 18             | Seed length                            | 13.64            | 13.44             | 13.11              | 13.51             | 13.35            | 12.92             |
| 19             | Test weight                            | 187.41           | 164.43            | 134.15             | 174.51            | 182.12           | 157.92            |

attributes, indicating that genotypes from these clusters may result in desirable combinations of yield, earliness and fruit quality.

#### **Trait-wise contribution to total genetic divergence**

The share of different traits toward genetic divergence was evaluated using Mahalanobis  $D^2$  statistics. The findings indicated that the contribution of individual traits varied significantly. Among the 19 parameters studied, NFPP showed maximum contribution, accounting for 26.17% of total genetic divergence, followed by NPBPP (18.49%), NDFF (16.07%) and NNFF (7.40%). These traits played a major role in governing genetic divergence. Few traits, such as VL and DTFFH, did not contribute to genetic diversity, indicating that these traits are relatively uniform and didn't contribute

to categorization in the present research. Similar results were also reported by Prasanth et al. (2020), Nithinkumar et al. (2021), Mallikarjuna et al. (2023), Bhardwaj et al. (2024), Singh & Biyyala (2024).

#### **Principal component analysis**

Principal component analysis (PCA), using the correlation matrix of nineteen traits, was employed to assess diversity among the bitter genotypes. The highest eigenvalue *i.e.*, 8.631, was exhibited by PC1, representing it accounted for maximum variability among the genotypes. The scree plot was constructed to examine the number of principal components contributing significantly to total diversity. PC1 contributed 45.4% of the total diversity, followed by PC (15.8%), PC3 (9.7%) and PC4 (9.3%). Most of the genetic

diversity was captured by first six principal components, which collectively contributed 89.5%. Hence, the first six principal components were utilized for further multivariate analysis. The PCA biplot was constructed to visualize the correlation between traits and genotypes simultaneously. PC1 and PC2 accounted for 45.5 and 15.8% of the total diversity, respectively. Six clusters were formed, which are represented in different color codes in the PCA biplot. Long vectors pointing towards the positive direction of PC1 were noted for the traits such as DFF, DFMF and DTFFH, indicating a clear effect on genotype separation along that axis. Similarly, traits such as AFW and SL contributed significantly to the diversity captured by PC2. Strong positive correlation among the traits like DFF, DFMF and DTFFH was clearly represented by the acute angle between the vectors of these traits, while a wide angle between these traits and NFPP suggested a strong negative correlation. The distribution of traits on the PCA biplot indicated which traits contributed majorly to the differentiation, offering an idea for selecting key traits in crop improvement programs. Similar results were noted by Prasanth *et al.* (2020), Mallikarjuna *et al.* (2023), Bhardwaj *et al.* (2024) and Mehta *et al.* (2024).

## Conclusion

Analysis of bitter gourd genotypes revealed the wide range of genetic diversity among the evaluated germplasms. Among all the parameters examined, NFPP and NBPBP indicated maximum contribution to genetic divergence, pinpointing their importance as a key selection criterion in bitter gourd breeding programs. For traits like AYPP and Fyha, genotypes 2024/PBIG-38 (2.92, 251.64), 2024/PBIG-40 (2.74, 237.05), and 2024/PBIG-54 (2.66, 230.03) were found superior to the standard check Pant karela-1 (1.94, 171.48), representing their strong practical breeding utility. Therefore, these three genotypes may serve as parents to develop high-yielding cultivars in future bitter gourd breeding. Since the present study is based on a single location, multi-location evaluation across diverse agro-climatic conditions is recommended to assess yield stability, so these genotypes may be used as commercial cultivars after following the standard varietal release procedure.

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## सारांश

करेला (मोमोर्डिका चारेण्टिया) अपनी समृद्ध पौष्टिक संरचना एवं प्रबल औषधीय गुणों के कारण एक लोकप्रिय सब्जी के रूप में प्रसिद्ध है। वर्तमान शोध में 19 मातात्मक एवं 9 दृश्यात्मक लक्षणों के लिए करेले के 38 जीनप्ररूपों की आनुवंशिक विविधता का मूल्यांकन किया गया। प्रस्तुत अध्ययन वर्ष 2025 के ग्रीष्म ऋतु के दौरान, सब्जी अनुसंधान केन्द्र, जी०बी०पी०यू०ए०टी० पंतनगर में किया गया। यह प्रयोग यादृच्छिक खंड अभिकल्पना में तीन आवृत्तियों के साथ किया गया। जीनप्ररूपीय एवं दृश्यात्मक विचरण गुणांक, आनुवंशिकता एवं आनुवंशिक लाभ के उच्च मूल्यों ने महत्वपूर्ण आनुवंशिक परिवर्तनशीलता और प्रत्यक्ष चयन की गुंजाइश का प्रतिनिधित्व किया। प्रति पौधा औसत फल उपज ने पौधे की वृद्धि एवं फल लक्षणों के साथ सकारात्मक सहसंबंध दर्शाए, तथा पुष्पन एवं परिपक्वता लक्षणों के साथ नकारात्मक सहसंबंध दर्शाए। पथ गुणांक विश्लेषण ने प्रति पौधे औसत फल उपज पर प्रमुख लक्षणों के प्रत्यक्ष सकारात्मक प्रभावों को दर्शाया। कुल आनुवंशिक विविधता का 89.5 प्रतिशत पहले छह प्रमुख घटकों द्वारा समझाया गया था, एवं सिद्धांत घटक विश्लेषण द्विआयामी चित्र ने जीनप्ररूपों के अंतर्गत समूह वर्गीकरण, सहसंबंध एवं आनुवंशिक विचलन को स्पष्ट रूप से दर्शाया। प्रमुख उपज योगदान मापदंडों के लिए मानक जांच पंत करेला-1 की तुलना में जीनप्ररूप 2024/पीबीआईजी-38, 2024/पीबीआईजी-40 एवं 2024/पीबीआईजी-54 बेहतर पाए गए।