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## Genetic variability, character association, and diversity analysis of yield and yield-contributing traits in bottle gourd (*Lagenaria siceraria* L.)

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### Abstract

Bottle gourd (*Lagenaria siceraria* L.) is a vital vegetable crop requiring continuous genetic improvement to overcome stagnant yield barriers. A field experiment was conducted to assess the genetic variability, correlation, path coefficients, and genetic divergence among 15 bottle gourd genotypes. Analysis of variance revealed highly significant variations among genotypes for all 21 traits studied. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV), indicating environmental influence. High heritability (97.30%) coupled with high genetic advance as a percentage of the mean (56.78%) was observed for the node number of the first female flower, suggesting additive gene action and the potential for direct selection. Correlation studies revealed that yield per plant exhibited a highly significant positive association with the sex ratio (male to female) and days to germination. Path coefficient analysis demonstrated that fruit length (2.62) and days to first female flowering (2.31) exerted the highest positive direct effects on yield. Genetic divergence, assessed via Mahalanobis  $D^2$  and Principal Component Analysis (PCA), grouped the genotypes into five distinct clusters. The maximum inter-cluster distance (54.79) was observed between Cluster IV and Cluster V. Based on genetic distance and agronomic superiority, genotypes G8 (BD 4536) and G3 (BD 4527), alongside G13 and G10, were identified as highly divergent and promising parents for future hybridization programs aimed at maximizing heterosis.

**Key words:** *Lagenaria siceraria*, genetic variability, heritability, path analysis, genetic divergence, Mahalanobis  $D^2$

## Introduction

Bottle gourd (*Lagenaria siceraria* L.,  $2n = 22$ ) is a premier vegetable crop within the Cucurbitaceae family, widely cultivated across tropical and subtropical regions. Due to its monoecious flowering habit, it is predominantly cross-pollinated, with rates reaching up to 80% (Han et al., 2021; Islam et al., 2020). The crop is highly valued for its nutritional and medicinal properties, characterized by high water content (96.1g/100g) and a rich profile of essential minerals and vitamins (Bhardwaj et al., 2024). Despite its suitability for year-round cultivation in Bangladesh, the average productivity remains critically low at 8.37 ton.ha<sup>-1</sup> (Anjum, 2021), lagging significantly behind other tropical regions. This yield gap necessitates intensive genetic improvement. The success of any breeding program depends primarily on the magnitude of genetic variability within the germplasm and the degree to which yield-contributing traits are heritable. Because phenotypic expression is a result of the interaction between genotype and environment, it is crucial to partition total variability into heritable and non-heritable components. Parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2b$ ), and genetic advance provide the statistical foundation required for effective selection (Singh et al., 2025). Yield is a complex, polygenic trait determined by the interplay of various quantitative characters. While correlation studies identify the associations between yield and its components, they do not distinguish between cause and effect. Path coefficient analysis is therefore essential to partition these correlations into direct and indirect effects, allowing breeders to identify the specific traits that contribute most effectively to the final yield.

Furthermore, the development of superior hybrids or segregants requires the selection of genetically divergent parents. Hybridization between closely related genotypes often results in a narrow genetic base, whereas divergent parents are more likely to exhibit high heterosis. Multivariate analysis using Mahalanobis's D<sup>2</sup> statistics and Principal Component Analysis (PCA) are

robust tools for quantifying genetic diversity and clustering genotypes based on similarity (Defard et al., 2021; Das et al., 2026).

Given this context, the present investigation was aimed to evaluate the genetic variability, trait interrelationships, and genetic divergence among fifteen bottle gourd genotypes to identify superior parents for future breeding programs.

## Materials and methods

### *Experimental site and design*

The field experiment was conducted at the experimental farm of Dhaka, Bangladesh (23°74'N latitude, 90°35'E longitude) from April to September, 2025. The soil belongs to the Madhupur Tract (AEZ-28) with a clay-loam texture and a pH of 5.55. Fifteen genetically pure bottle gourd genotypes (collected from PGRC, BARI) were evaluated. Table 1 shows the origin status of gourd genotypes. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications.

### *Crop management*

Seeds were sown in polybags on April 25, 2024, and 18-day-old seedlings were transplanted to the main field maintaining a pit-to-pit spacing of 3 m. Standard agricultural practices, including the application of organic manure (cow dung at 10 ton.ha<sup>-1</sup>) and recommended doses of NPK, were strictly followed. Pesticides and pheromone traps (Mashed Sweet Gourd Trap) were utilized for pest management, particularly against the cucurbit fruit fly.

### *Data collection*

Data were recorded on five randomly selected plants per replication for 21 quantitative traits. Plant traits included leaf length/breadth and internodal distance. Inflorescence traits comprised days to first male/female flowering, node number for first male/female flower, and pedicel lengths. Fruit traits measured were number of fruits per plant, fruit length, fruit breadth, fruit weight, and total yield per plant. Seed traits included seed dimensions, 100-seed weight, and number of

**Table 1.** Name and origin of fifteen bottle gourd genotypes used in the present study

| S/N | Genotypes | BARI ACC Number | Origin     |
|-----|-----------|-----------------|------------|
| 01  | G1        | BD-4548         | PGRC, BARI |
| 02  | G2        | BD-4537         | PGRC, BARI |
| 03  | G3        | BD-4527         | PGRC, BARI |
| 04  | G4        | BD-4525         | PGRC, BARI |
| 05  | G5        | BD-4533         | PGRC, BARI |
| 06  | G6        | BD-4528         | PGRC, BARI |
| 07  | G7        | BD-4542         | PGRC, BARI |
| 08  | G8        | BD-4536         | PGRC, BARI |
| 09  | G9        | BD-4545         | PGRC, BARI |
| 10  | G10       | BD4526          | PGRC, BARI |
| 11  | G11       | BD-4530         | PGRC, BARI |
| 12  | G12       | BD-4546         | PGRC, BARI |
| 13  | G13       | BD-4535         | PGRC, BARI |
| 14  | G14       | BD-4547         | PGRC, BARI |
| 15  | G15       | BD-4549         | PGRC, BARI |

seeds per fruit.

*Statistical analysis*

The mean data were subjected to Analysis of Variance (ANOVA). Genotypic and phenotypic variances, PCV, GCV, broad-sense heritability (h<sup>2</sup><sub>b</sub>), and genetic advance (GA) were estimated following standard procedures (Nabi, 2025; Mohammad et al., 2025). Phenotypic and genotypic correlation coefficients and path coefficient analyses were computed as per Islam et al. 2025. Multivariate analysis, including Mahalanobis D<sup>2</sup> statistics, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), and Canonical Variate Analysis (CVA), was conducted using GENSTAT software to estimate genetic divergence and group the genotypes into clusters.

**Results and discussion**

*Morphological characterization and genetic variability*

The analysis of variance (ANOVA) indicated highly significant variations ( $p < 0.01$ ) among the 15 genotypes for all the studied traits, revealing a wide genetic base. Table 2 shows the estima-

tion of genetic parameters for morphological characters.

The phenotypic variance was consistently higher than the corresponding genotypic variance for all characters, indicating a degree of environmental influence. However, for traits like internode distance, the difference between phenotypic (5.79) and genotypic variance (5.37) was marginal, suggesting robust genetic control. The PCV and GCV were closely aligned for traits such as leaf length (12.15% and 11.71%) and fruit weight (14.89% and 12.79%). These findings align with Anjum, 2021, who reported similar PCV and GCV parameters in cucurbits.

High heritability (h<sup>2</sup><sub>b</sub>) coupled with high genetic advance as a percentage of the mean (GA%) is the most reliable index for effective selection (Baye et al., 2020; Alemu et al., 2024). In the present study, exceptionally high heritability was observed for the node number of the first female flower (97.30%), sex ratio (96.35%), 100-seed weight (95.79%), and number of fruits per plant (93.53%). The maximum GA% was observed for the node number of the female flower (56.78%) and the number of fruits per plant (52.19%). This indicates that these characters are governed by

**Table 2.** Estimation of genetic parameters for morphological characters related to yield

| Sl No. | Characters                    | Mean   | GCV (%) | PCV (%) | Heritability (%) | GA (5%) | GA (% of Mean) |
|--------|-------------------------------|--------|---------|---------|------------------|---------|----------------|
| 1      | Leaf length (cm)              | 22.21  | 11.71   | 12.15   | 92.99            | 5.17    | 23.27          |
| 2      | Leaf breath (cm)              | 20.05  | 11.29   | 11.89   | 90.05            | 4.42    | 22.06          |
| 3      | Internode length (cm)         | 13.70  | 16.91   | 17.57   | 92.71            | 4.60    | 33.55          |
| 4      | Days of 1st male flowering    | 59.13  | 2.45    | 4.19    | 34.07            | 1.74    | 2.94           |
| 5      | Days of 1st female flowering  | 65.40  | 4.19    | 5.28    | 62.91            | 4.48    | 6.85           |
| 6      | Node no. of 1st male flower   | 26.93  | 23.25   | 23.88   | 94.75            | 12.55   | 46.61          |
| 7      | Node no. of 1st female flower | 25.80  | 27.94   | 28.33   | 97.30            | 14.65   | 56.78          |
| 8      | Number of fruits/plant        | 9.80   | 26.20   | 27.09   | 93.53            | 5.11    | 52.19          |
| 9      | Fruit length (cm)             | 32.02  | 22.19   | 23.50   | 89.12            | 13.82   | 43.15          |
| 10     | Fruit diameter (cm)           | 30.16  | 15.74   | 17.69   | 79.11            | 8.70    | 28.84          |
| 11     | Fruit weight (kg)             | 1.81   | 12.79   | 14.89   | 73.73            | 0.41    | 22.62          |
| 12     | Length of petiole (cm)        | 8.78   | 23.90   | 26.87   | 79.07            | 3.84    | 43.77          |
| 13     | Peduncle length (cm)          | 11.53  | 22.38   | 23.25   | 92.59            | 5.12    | 44.36          |
| 14     | Sex ratio (M:F)               | 25.73  | 16.35   | 16.66   | 96.35            | 8.51    | 33.06          |
| 15     | Days to germination           | 7.18   | 11.79   | 16.87   | 48.80            | 1.22    | 16.96          |
| 16     | Seed length (cm)              | 1.51   | 7.93    | 11.35   | 48.86            | 0.17    | 11.42          |
| 17     | Seed breadth (cm)             | 0.63   | 17.73   | 19.12   | 86.05            | 0.21    | 33.89          |
| 18     | No. seed per fruit            | 456.51 | 15.51   | 15.95   | 94.61            | 141.89  | 31.08          |
| 19     | 100 seed weight (gm)          | 17.97  | 17.00   | 17.37   | 95.79            | 6.16    | 34.27          |
| 20     | Seed thickness (cm)           | 0.24   | 18.81   | 23.04   | 66.67            | 0.08    | 31.63          |
| 21     | Yield per plant (kg)          | 26.80  | 13.37   | 14.09   | 90.16            | 7.01    | 26.16          |

additive gene action, and directional selection based on phenotypic performance would be highly rewarding. Conversely, days to first male flowering exhibited low heritability (34.07%) and low GA% (2.94%), suggesting non-additive gene action and high environmental influence.

#### *Correlation coefficient analysis*

Selection for yield may not be effective unless the direct or indirect influences of other yield components are considered. In general, genotypic correlation coefficients were higher than phenotypic correlation coefficients, suggesting strong inherent associations masked slightly by

**Table 3.** Genotypic correlation coefficients (rg) among yield and yield-contributing characters in bottle gourd

| Characters                    | Sex ratio | Days to germination | Node no. of 1st female flower | Fruit diameter | 100-seed weight | Yield per plant (kg) |
|-------------------------------|-----------|---------------------|-------------------------------|----------------|-----------------|----------------------|
| Days of 1st male flowering    | 0.607*    | 0.036               | -0.165                        | 0.282          | 0.483           | 0.380                |
| Days of 1st female flowering  | 0.185     | 0.734**             | 0.303                         | 0.195          | 0.055           | 0.237                |
| Node no. of 1st female flower | 0.106     | -0.304              | —                             | 0.317          | 0.066           | -0.548*              |
| Number of fruits/plant        | -0.173    | -0.552*             | -0.568*                       | -0.155         | 0.082           | -0.190               |
| Fruit diameter (cm)           | 0.077     | 0.104               | 0.317                         | —              | 0.479           | -0.069               |
| Sex ratio                     | —         | -0.008              | 0.106                         | 0.077          | 0.140           | 0.567*               |
| Days to germination           | -0.008    | —                   | -0.304                        | 0.104          | 0.131           | 0.587*               |
| Yield/plant (kg)              | 0.567*    | 0.587*              | -0.548*                       | -0.069         | 0.103           | —                    |

environmental factors (Table 3).

Yield per plant showed a highly significant positive correlation with the sex ratio ( $rg = 0.567$ ,  $rp = 0.570$ ). This indicates that an increased proportion of female flowers directly elevates total fruit yield. Additionally, yield showed a highly significant positive correlation with days to germination ( $rg = 0.587$ ), suggesting early vigor plays a role in final biomass accumulation.

Conversely, the node number of the 1st female flower exhibited a significant negative correlation with yield per plant ( $-0.548$  at the genotypic level). This is a critical finding for breeders: genotypes that produce female flowers at lower (earlier) nodes yield significantly higher. Fruit breadth and fruit weight were also highly significantly correlated ( $rg = 0.663$ ), corroborating findings by (Rahman et al., 2021; Hasan, 2021).

*Path coefficient analysis*

While correlation establishes mutual associations, path analysis partitions these into direct and indirect effects, providing an exact picture of relative trait importance. A strong positive genotypic correlation was observed between yield per plant and sex ratio (Table 4).

Path analysis revealed that fruit length exerted the highest positive direct effect (2.62) on yield per plant, followed by days to first female flowering (2.31), seed breadth (1.33), and 100-seed weight (1.06). Therefore, direct selection based

on fruit length and seed mass will be highly effective for yield improvement. Similar positive direct effects of fruit parameters were reported by Negi et al. 2025 in snake gourd. In contrast, the node number of the first female flower exerted a massive negative direct effect ( $-4.15$ ) on yield, further validating the correlation findings that early-node flowering is a prerequisite for high yield. The number of fruits per plant also showed a negative direct effect ( $-3.28$ ); however, it contributed to yield indirectly through its robust positive indirect effects via fruit length (0.558) and days to germination (1.004). The residual effect was low (0.0820 phenotypic; 0.2427 genotypic), indicating that the morphological characters selected for this study sufficiently accounted for the majority of the variation in yield.

*Genetic diversity and cluster analysis*

To select diverse parents for future hybridization, multivariate analysis was performed. Principal Component Analysis (PCA) yielded eigenvalues where the first five principal component axes accounted for 84.77% of the total variation, with PC1 alone contributing 43.25%. Figure 1 shows the relationship between the first two principal components, which account for the majority of the total genetic variation.

Using non-hierarchical clustering, the 15 genotypes were grouped into five distinct clusters. Cluster I was the largest (6 genotypes), followed

**Table 4.** Combined path coefficient analysis showing direct and indirect effects of components on fruit yield per plant

| Characters                    | Direct effect (Genotypic) | Direct effect (Phenotypic) | Total correlation with yield (rg) |
|-------------------------------|---------------------------|----------------------------|-----------------------------------|
| Days of 1st male flowering    | -0.481                    | -1.70                      | 0.380                             |
| Days of 1st female flowering  | -0.575                    | 2.31                       | 0.237                             |
| Node no. of 1st male flower   | 1.579                     | -0.87                      | 0.079                             |
| Node no. of 1st female flower | -2.66                     | -4.15                      | -0.548*                           |
| Number of fruits/plant        | -3.93                     | -3.28                      | -0.190                            |
| Fruit length (cm)             | -0.987                    | 2.62                       | -0.262                            |
| Fruit diameter (cm)           | -4.85                     | 0.674                      | -0.069                            |
| Fruit weight (kg)             | 5.25                      | -0.579                     | -0.013                            |
| Sex ratio (M:F)               | -0.601                    | 0.527                      | 0.567*                            |
| Days to germination           | -3.41                     | -1.94                      | 0.587*                            |
| Seed length (cm)              | 1.01                      | -0.154                     | 0.187                             |
| Seed breadth (cm)             | -0.124                    | 1.33                       | -0.271                            |
| Seeds/fruit                   | -0.496                    | 0.299                      | 0.284                             |
| 100-seed weight (gm)          | 4.77                      | 1.06                       | 0.103                             |
| Residual Effect               | 0.2427                    | 0.0820                     | —                                 |

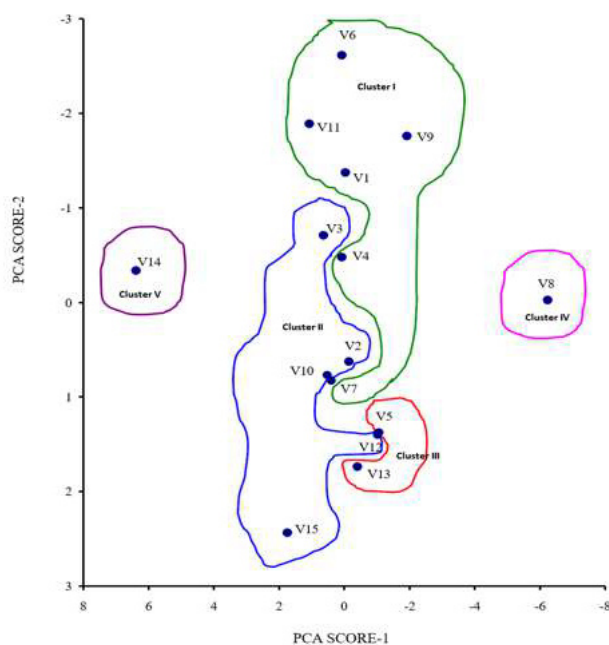


**Fig. 1.** Scatter diagram of 15 bottle gourd genotypes of based on their principal component scores

**Table 5.** Cluster means and inter-cluster distances ( $D^2$ ) for 15 bottle gourd genotypes

| Characters                       | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
|----------------------------------|-----------|------------|-------------|------------|-----------|
| Days of 1st female flowering     | 65.11     | 66.93      | 61.50       | 62.33      | 70.33     |
| Node no. of 1st female flower    | 25.83     | 27.80      | 20.50       | 37.00      | 15.00     |
| Number of fruit per plant        | 10.00     | 8.40       | 11.50       | 15.00      | 7.00      |
| Fruit length (cm)                | 29.67     | 34.33      | 34.17       | 42.33      | 20.00     |
| Fruit diameter (cm)              | 29.22     | 29.53      | 35.67       | 39.00      | 19.00     |
| Fruit weight (kg)                | 1.68      | 1.89       | 2.08        | 2.12       | 1.27      |
| Sex ratio (M:F)                  | 23.67     | 27.00      | 27.50       | 34.00      | 20.00     |
| 100-seed weight (gm)             | 18.76     | 17.21      | 18.35       | 22.80      | 11.40     |
| Yield per plant (kg)             | 25.83     | 27.80      | 28.50       | 31.00      | 20.00     |
| Inter-cluster distance ( $D^2$ ) |           |            |             |            |           |
| Cluster I                        | 26.43     | 26.29      | 28.05       | 31.70      | 36.15     |
| Cluster II                       |           | 22.80      | 26.62       | 33.55      | 31.73     |
| Cluster III                      |           |            | 27.50       | 35.98      | 29.74     |
| Cluster IV                       |           |            |             | 0.00       | 54.79     |
| Cluster V                        |           |            |             |            | 0.00      |

by Cluster II (5 genotypes). Cluster IV and Cluster V were monotypic, consisting only of G8 and G14, respectively. The maximum inter-cluster distance was observed between Cluster IV and V (54.79), suggesting that hybridization between parents from these groups would maximize heterotic expression (Table 5).

The inter-cluster distances were larger than the intra-cluster distances, suggesting a wide genetic diversity among the evaluated germplasm. The maximum inter-cluster distance (54.79) was observed between Cluster IV and Cluster V, followed by Cluster I and Cluster V (36.15). Crossing genotypes from highly divergent clusters is known to produce a wide spectrum of segregating populations and maximum heterosis (Alemu et al., 2024; Alemu et al., 2025). Cluster means indicated that Cluster IV (comprising only genotype G8) was agronomically superior, recording the highest mean values for yield per plant (31.00 kg), number of fruits per plant (15.00), 100-seed weight (22.80 g), and the earliest germination (5.67 days). Conversely, Cluster V (genotype G14) recorded the lowest yield (20.00 kg) and longest days to flowering, confirming it as a late-

maturing, low-yielding genotype. The clustering pattern confirmed that genotypes originating from the same geographic region (Baye et al., 2020; Das et al., 2026; Mohammad et al., 2025; Islam et al., 2025; Rahman et al., 2021) distributed into different clusters. This supports the assertion by Ahmad et al. 2022 that geographic diversity is not necessarily synonymous with genetic diversity, and selection forces or genetic drift play a larger role in driving divergence.

## Conclusion

The present investigation revealed substantial genetic variability among the 15 bottle gourd genotypes. Traits such as the node number of the first female flower, sex ratio, and number of fruits per plant exhibited high heritability and high genetic advance, suggesting their governance by additive genes and suitability for direct selection. Path analysis highlighted fruit length and early female flowering as the primary direct contributors to yield. Based on the magnitude of genetic distance, contribution of characters toward divergence, and agronomic performance, genotype G8 (BD

4536) from Cluster IV and G3 (BD 4527) from Cluster II emerged as highly promising. Therefore, to achieve maximum heterosis and recover desirable transgressive segregants, hybridization between G8 and G3, as well as G13 and G10, is strongly recommended for future bottle gourd breeding programs.

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