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# Genetic variability, character association and diversity studies in brinjal (*Solanum melongena* L.)

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**Abstract**

An experiment was conducted to assess the existing variability in brinjal germplasm based on Mahalanobis's $D^2$ statistic based on nine quantitative traits. The germplasm accessions were classified into six clusters, in which the highest inter-cluster distance was recorded between clusters III and IV. Cluster I exhibited a low mean estimate for days to 50% flowering; cluster VI showed high estimates of the mean for plant height, the number of primary branches per plant, average fruit weight, and 1000 seed weight. Cluster V recorded the highest number of fruits and fruit yields per plant. Principal component analysis revealed total variability of 53.09 per cent, contributed by PC 1 (30.83 %) and PC 2 (23.07 %). Traits *viz*., days to 50% flowering, plant height, an average number of branches per plant, fruit length, and 1000 seed weight contributed positive significant component loadings for the first two PCs. High heritability and high GAM were also recorded for a number of fruits per plant, fruit yield per plant, fruit length, fruit girth, fruit weight, and 1000 seed weight. Fruit yield and the number of fruits per plant were positively and significantly associated with each other. Hence, simultaneous selection of these traits is advised for the genetic improvement in the brinjal breeding program.

**Key words**: Brinjal, Correlation, Heritability, Genetic diversity, PCA

## INTRODUCTION

Brinjal (*Solanum melongena* L.) dominates the globe owing to its high vitamins, minerals and numerous nutraceutical properties (Daunay and Hazra, 2012). Approximately, 55.2 million tonnes of brinjal are being produced globally with productivity of 29.9 tonnes per hectare (Food and Agriculture Organization Statistics, 2019). However, the demand-supply gap is yet to be met owing to diversified consumer demand which is specific to the region. Several shapes, forms, and colors of brinjal are present throughout the Southeast Asia region. Being the center of origin, a vast diversity can be found in India for plant and fruit morphological traits, fruit quality, and cooking quality; hence possess ample scope for improvement of several horticultural traits suitable for diversified consumer requirements (Ullah *et al*., 2014).

The development of high-yielding cultivars of brinjal dictates the thorough knowledge and understanding of the available germplasm, existing genetic variation in the population, and the degree of association among the yield contributing traits. Studies on genetic variability and the associations among the yield contributing traits along with genetic divergence are helpful in designing a successful breeding programme in any crop. Various biometrical protocols have been developed through which the quantification of genetic divergence can be done, which can be used in isolating genetically dissimilar parents to carry out an efficient hybridization plan (Uddin *et al*., 2014). Hence, genetic diversity assessment is necessary to identify the genetic resources to be employed in the hybridization programme (Amin *et al*., 2014). The vast genetic diversity in the material provides better chances of obtaining diverse traits in the segregating generations and helps in the improvement of the crop. Choice of parents based on genetic divergence would be more fruitful for an efficient hybridization program (Kumar and Gurumurthi, 2000). Multivariate analysis can be successfully implemented to evaluate the extent of divergence existing in the germplasm. It can also be used to quantify the contribution of various traits to the total divergence at intra as well as inter-cluster levels (Quamruzzaman *et al*., 2009).

Hence, the current experiment was attempted to quantify the genetic diversity existing among the selected brinjal genotypes and to hand-pick suitable parents to use in future hybridization programs.

## MATERIALS AND METHODS

The trial was carried out at Central Horticultural Experiment Station (ICAR-IIHR), Odisha, India during 2019-2020. The experimental soil was red laterite with a pH of 4.4. The available nitrogen, phosphorus, and potassium content in the soil were 296, 3.92, and 157 kg/ha, respectively. Twenty-six germplasm accessions [CARI-1 (Central Island Agriculture Research Institute, Andaman and Nicobar Islands), IC0598430, Arka Neelachal Shyama (Central Horticultural Experiment Station, IIHR, Bhubaneswar, Odisha), Arka Harshitha, Arka Avinash, Arka Nidhi, Arka Anand, Arka Kusumkar, Arka Neelkanth, IIHR 7, IIHR-322 (Indian Institute of Horticultural Research, Bangalore, Karnataka), IIHR-B-NE-1, IIHR-B-NE-2, IIHR-B-NE-3 (North-Eastern Indian collection), Utkal Anushree, Utkal Keshari (OUAT, Bhubaneswar, Odisha), Pusa Uttam, Pusa Purple Long (IARI, New Delhi), Swarna Pratibha, Swarna Mohit, Swarna Shakti, Swarna Shyamali (ICAR Research Complex for Eastern Region, Bihar), Swetha, Haritha, Surya, Ponny (Kerala Agricultural University, Kerala) were studied for vigor and yield attributing traits. The treatments were planned out in a Randomized Complete Block Design with two replications consisting of 20 plants for each genotype. The genotypes were planted at a distance of 75 cm (R-R) x 60 cm (P-P). The required package of practices for a better stand of plants in the field was practised.

Traits *viz*., days to 50 % flowering, plant height, the number of branches per plant, the number of fruits and yield per plant, fruit length, fruit girth, average fruit weight, and 1000 seed weight were recorded from freshly harvested marketable fruits and the average was taken. The genotypic coefficient of variation (GCV) along with the phenotypic coefficient of variation (PCV) was estimated as per Burton (1952). The heritability estimates were calculated according to Lush (1949) and Burton and Devane (1953) and expressed in percentage (Webber and Moorthy, 1952), while the genetic advance was determined as per Johnson *et al.* (1955). The genotypic correlation coefficient was calculated based on the formulae given by Snedecor (1961). The data were analyzed using Mahalanobis (1936) $D^2$ statistic and Tochers' method according to Rao (1952) for estimating group constellation. Average inter-cluster, as well as intra-cluster distances, were estimated according to Singh and Choudhary (1977). PCA analysis was also carried out through the statistical procedures suggested by Sneath and Sokal (1973). The statistical package R with the help of agricolae package (De Mendiburu, 2014) was used for the analysis.

## RESULTS AND DISCUSSION

The data on the mean performance of 26 genotypes for 9 quantitative traits are given in **Table 1**. The days to 50% flowering ranged from 36.50 (Arka Neelachal Shyama) to 57.00 (CARI-1) days. Plant height ranged from 31.75 cm (Arka Neelachal Shyama) to 58.50 cm (CARI-1). The maximum number of branches per plant was found for Swarna Pratibha (14.70) and the minimum was exhibited by CARI-1 (6.50). The genotypes *viz*., Swarna Mohit, Swarna Shakti, Swarna Shyamali, Arka Harshitha, Arka Avinash, Arka Nidhi, Arka Anand, and Utkal Keshari were found at par with Swarna Pratibha for a number of branches per plant. The maximum number of fruits per single plant was exhibited by Utkal Anushree (23.56), while the lowest number of fruits was exhibited by Pusa Uttam (0.98). The highest per plant fruit yield was obtained from CARI-1 (888.00 g), while the minimum quantity of fruits was obtained from Pusa Uttam (126.50 g). Utkal Anushree performed statistically on par with CARI-1 for per plant fruit yield. The highest fruit length was found in Arka Anand (23.25 cm), while the lowest fruit length was observed in IIHR-B-NE- 3 (4.85 cm). Arka Avinash and Swarna Pratibha were statistically on par with Arka Anand for fruit length. Fruit growth ranged from 4.40 cm (IIHR-B-NE-3) to 26.00 (Swarna Shyamali). Similarly, the maximum average fruit weight was exhibited by 238.00 g (CARI-1), while the minimum fruit weight was exhibited by IIHR-B-NE-3 (15.92). 1000 seed weight fluctuated from 2.52 (CARI-1) to 5.34 g (Swarna Shakti).

The phenotypic coefficient of variation component exceeded the genotypic coefficient of variation among the genotypes, referring that the existing variation was due to the combination of the inherent nature of the genotypes as well as the impact of environmental factors (**Table 2**). The PCV and GCV for the characters ranged

**Table 1. Mean performance of genotypes for yield and fruit traits in brinjal**

| Genotype | DT50%F | PH (cm) | NOB | NOFP | FYPP (g) | FL (cm) | FG (cm) | FW (g) | 1000SW (g) |
|---|---|---|---|---|---|---|---|---|---|
| CARI-1 | 57.00 | 58.50 | 6.50 | 3.73 | 888.00 | 13.90 | 24.15 | 238.00 | 2.52 |
| Arka Neelachal Shyama | 36.50 | 31.75 | 8.50 | 4.85 | 762.50 | 9.70 | 23.35 | 157.11 | 3.94 |
| IC0598430 | 47.00 | 38.30 | 9.10 | 5.22 | 462.50 | 8.45 | 14.75 | 88.57 | 3.88 |
| IIHR-B-NE-1 | 49.00 | 50.75 | 11.40 | 7.46 | 676.50 | 8.95 | 22.70 | 89.98 | 3.07 |
| Arka Harshitha | 47.50 | 47.75 | 12.60 | 3.00 | 203.75 | 17.90 | 5.00 | 67.90 | 2.53 |
| Arka Avinash | 49.00 | 48.00 | 12.30 | 4.24 | 312.25 | 22.40 | 5.40 | 73.70 | 2.56 |
| IIHR 7 | 49.00 | 46.25 | 12.10 | 4.45 | 287.00 | 18.90 | 5.95 | 64.46 | 2.68 |
| IIHR-322 | 48.00 | 52.25 | 14.40 | 4.26 | 260.75 | 18.65 | 6.50 | 61.16 | 4.59 |
| Arka Nidhi | 40.00 | 45.75 | 11.70 | 5.12 | 241.00 | 18.00 | 5.00 | 47.20 | 3.51 |
| Arka Anand | 41.00 | 46.50 | 11.70 | 10.34 | 597.00 | 23.25 | 4.80 | 57.64 | 4.24 |
| Arka Kusumkar | 43.00 | 45.50 | 10.80 | 6.51 | 468.25 | 17.85 | 5.05 | 72.03 | 3.25 |
| Arka Neelkantha | 48.50 | 47.00 | 11.90 | 6.02 | 381.50 | 17.90 | 4.90 | 64.52 | 4.84 |
| IIHR-B-NE-2 | 48.50 | 48.25 | 13.50 | 5.75 | 601.75 | 7.40 | 21.35 | 104.86 | 2.96 |
| Utkal Anushree | 49.00 | 37.75 | 11.30 | 23.56 | 866.25 | 5.60 | 5.05 | 37.01 | 4.01 |
| Utkal Keshari | 48.50 | 43.75 | 12.40 | 3.72 | 350.75 | 7.05 | 15.80 | 95.67 | 3.01 |
| Pusa Uttam | 45.00 | 45.00 | 9.20 | 0.98 | 126.50 | 8.50 | 20.75 | 131.16 | 2.85 |
| Swarna Pratibha | 50.00 | 53.25 | 14.70 | 4.63 | 652.50 | 22.95 | 12.90 | 140.86 | 3.77 |
| Swarna Mohit | 52.00 | 54.00 | 14.60 | 4.62 | 637.50 | 15.25 | 16.35 | 138.05 | 4.58 |
| Swarna Shakti | 52.00 | 50.50 | 13.65 | 3.84 | 601.25 | 12.95 | 18.65 | 156.69 | 5.34 |
| Swarna Shyamali | 51.00 | 52.00 | 14.10 | 3.57 | 600.00 | 8.35 | 26.00 | 168.03 | 4.86 |
| IIHR-B-NE-3 | 48.50 | 48.25 | 8.00 | 15.29 | 241.25 | 4.85 | 4.40 | 15.92 | 2.75 |
| Swetha | 47.00 | 39.75 | 7.20 | 4.67 | 200.38 | 12.75 | 8.00 | 43.53 | 2.54 |
| Haritha | 47.50 | 41.00 | 7.80 | 3.73 | 240.50 | 14.90 | 8.40 | 64.39 | 2.77 |
| Surya | 50.50 | 40.75 | 7.65 | 9.00 | 718.75 | 11.50 | 13.50 | 82.82 | 4.29 |
| Ponny | 52.50 | 43.75 | 7.50 | 6.17 | 617.50 | 13.40 | 6.45 | 110.60 | 2.87 |
| Pusa Purple Long | 45.50 | 54.70 | 10.60 | 2.95 | 211.00 | 20.90 | 6.10 | 71.29 | 3.57 |
| S. Em. | 0.68 | 1.09 | 1.09 | 0.80 | 30.89 | 0.30 | 0.30 | 8.97 | 0.03 |
| S. Ed. | 0.96 | 1.53 | 1.55 | 1.13 | 43.68 | 0.42 | 0.42 | 12.68 | 0.04 |
| CD $_{.05}$ | 1.97** | 3.16** | 3.19** | 2.34** | 89.96** | 0.87** | 0.86** | 26.12** | 0.09** |
| CV (%) | 2.00 | 3.29 | 14.04 | 18.69 | 9.30 | 3.05 | 3.53 | 13.50 | 1.23 |

*- statistically significant differences ($p \leq 0.05$); **- statistically significant differences ($p \leq 0.01$) [DT50%F- Days to 50 % flowering; PH- Plant height; NOB- Number of branches; NOFP- Number of fruits per plant; FYPP- Fruit yield per plant; FL- Fruit length; FG-Fruit girth; FW-Fruit weight,1000SW- 1000 seed weight ]

from medium to high. However, a very low difference between PCV and GCV pointed towards minimal involvement of the environmental factors. GCV and PCV estimates for earliness were found to be 8.70 and 9.93 per cent, respectively. Heritability was found to be high (94.97%) along with a lower genetic advance (17.48%). For plant height, GCV and PCV estimated were found to be low (12.74 % and 13.16 %, respectively). Heritability estimated was high (93. 73 %) with low GA (11.83%). For the number of branches, the estimates of GCV and PCV were found high at 45.91 and 51.26 per cent, respectively. The trait was mainly controlled by additive gene action which is indicated by high heritability (80%) and GA (84.66%). The estimates of GCV (73.38 %) and PCV (75.72 %) exhibited a high value with respect to the number of fruits per plant, along with high heritability (93.91 %) and GA (146.49 %). For yield per plant, GCV (47.80 %) and PCV (48.70) estimated were found to be high. Heritability estimated was high (96.35 %) besides high GA (96.61%). For fruit length, high GCV and PCV (40.17 % and 40.29 %, respectively) were estimated and heritability (99.42 %) and GA (82.52 %) were also

**Table 2. Estimate of mean, range, components of variance, heritability and genetic advance for various yield traits of brinjal**

| Characters | General mean | Range | GCV (%) | PCV (%) | $h^2$ (%) | GAM (%) |
|---|---|---|---|---|---|---|
| Days to 50 % flowering | 47.81 | 36.50-57.00 | 8.70 | 8.93 | 94.97 | 17.48 |
| Plant height (cm) | 46.58 | 31.75-58.50 | 12.74 | 13.16 | 93.73 | 25.40 |
| Number of branches | 11.01 | 6.50-14.70 | 20.58 | 24.91 | 68.23 | 35.01 |
| Number of fruits per plant | 6.06 | 0.97-23.56 | 73.38 | 75.72 | 93.91 | 146.49 |
| Fruit yield per plant (g) | 469.49 | 126.50-888.00 | 47.80 | 48.70 | 96.35 | 96.61 |
| Fruit length (cm) | 13.93 | 4.85-23.25 | 40.17 | 40.29 | 99.42 | 82.52 |
| Fruit girth (cm) | 11.97 | 4.40-26.00 | 62.43 | 62.53 | 99.68 | 128.41 |
| Average Fruit weight (g) | 93.97 | 15.91-238.00 | 51.87 | 53.60 | 93.66 | 103.41 |
| 1000 seed weight (g) | 3.53 | 2.52-5.34 | 24.20 | 24.24 | 99.74 | 49.81 |

found to be high. Similarly, in the case of fruit girth, GCV and PCV estimated were found to be high (62.43% and 62.53%, respectively). Heritability estimated was high (99.68%) with high GA (82.52 %). GCV and PCV estimate for fruit weight was found to be high (51.87 % and 53.60 %, respectively). Heritability was high (93.66%) coupled with high GA (103.41 %). The estimates of GCV and PCV for 1000 seed weight were found to be high with 24.20 and 24.24 per cent, respectively. The high heritability (99.74%) coupled with high GA (49.81 %) was recorded for this trait.

High phenotypic and genotypic coefficients of variation were found for most of the traits pointing towards the existence of high genetic variability for the evaluated traits and selection of these characters can be highly productive as the effectiveness of the selection relies upon the variability that exists in the germplasm. The results of the current study are supported by the result found by Baswana *et al.* (2002) and Vidhya and Kumar (2015). The moderate estimates of the PCV and GCV for days to 50 % flowering and plant height were also reported by Sujin *et al.* (2017) in brinjal. High heritability, high estimates of GCV, and genetic advance were also reported for per plant fruit yield and the number of fruits as well as individual fruit length, girth, weight, and 1000 seed weight by Sharma and Swaroop (2000) and Sujin *et al.* (2017) in brinjal.

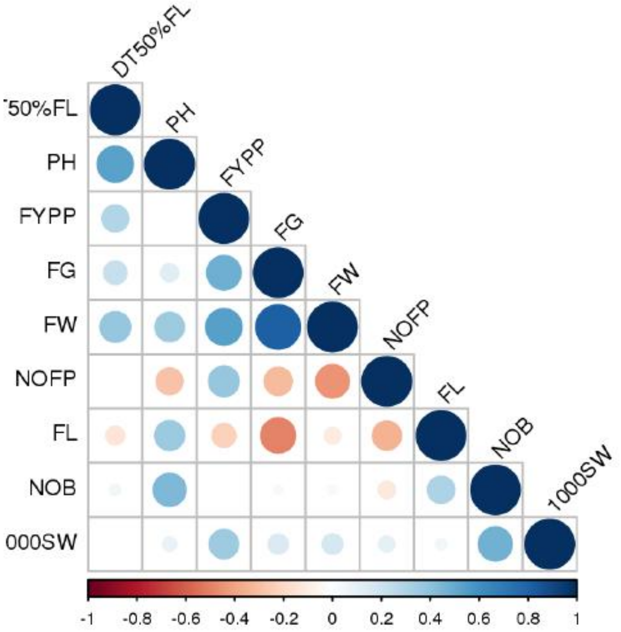

**Fig. 1. Correlation Matrix showing character correlation with each other**
**[A positive correlation is shown in blue and negative correlations in shown in red color. The color intensiveness and the size of the circle are relatively proportional to the correlation]**

The inherent potential of a given crop is generally quantified in terms of yield per unit area. Direct selection to improve the yield is generally difficult as it is a polygenically controlled trait and largely influenced by its various component characters along with the environmental factors. The current study indicated that yield per plant correlated positively with average fruit weight, fruit girth, the number of fruits per plant, and 1000 seed weight at the genotypic level. The correlation values among the nine traits are illustrated in **Fig. 1**. Days to 50 % flowering was highly correlated with plant height (0.53**). Plant height exhibited a positive correlation with the number of branches (0.44*), fruit length (0.36*), and fruit weight (0.35*). The number of branches also correlated positively with 1000 seed weight (0.47*). The number of fruits per plant showed a positive correlation with fruit yield per plant (0.38*) and a negative correlation with average fruit length (-0.34*) as well as fruit weight (-0.45*). A significant positive correlation of fruit yield per plant was found with a fruit girth (0.48*), fruit weight (0.54**), and 1000 seed weight (0.35). Fruit length was negatively correlated with a fruit girth (-0.50**). Average fruit weight was observed to be correlated with a fruit girth (0.81***). The previous work of Kalda *et al*. (1996) and Sujin *et al.* (2017) in brinjal further confirmed the outcomes of the current experiment.

Divergence analysis revealed that fruit yield per plant (28 %) contributed the highest towards genetic divergence, while fruit length and average fruit weight contributed 15 per cent each (**Table 3**). The lowest contribution towards genetic divergence was recorded by the traits, the number of branches (2 %) followed by plant height (3 %). The twenty-six genotypes were grouped into six clusters and the highest number of genotypes were in cluster II (11 genotypes), while clusters IV, V, and VI were solitary clusters with a single genotype each (**Fig. 2**). The mean of intra- cluster $D^2$ values varied between 0.00 to 542.59, where the maximum intra-cluster distance (542.59) was noted in cluster III followed by cluster II (461.16) (**Fig. 3**). This result indicated that selection can be made from cluster III for the superior genotypes (Karim *et al*., 2016 and Sindhuja *et al*., 2019). Cluster III and cluster IV (3150.86) exhibited the maximum divergence indicating the selection of the divergent parents from these clusters will yield good segregation for the traits of interest (Chippy *et al*., 2021). The minimum divergence was found between cluster IV and cluster V (701.4).

The mean of cluster reveals the average performance of all the genotypes grouped in a single cluster. The highest mean value for earliest flowering (47.36) was recorded in cluster I (**Table 4**). The highest mean values recorded by cluster VI were plant height (52.00 cm); cluster VI for the number of branches per plant (14.1); Cluster V for the number of fruits and fruit yield per plant (23.56 and 866.25 g, respectively); cluster III for fruit length

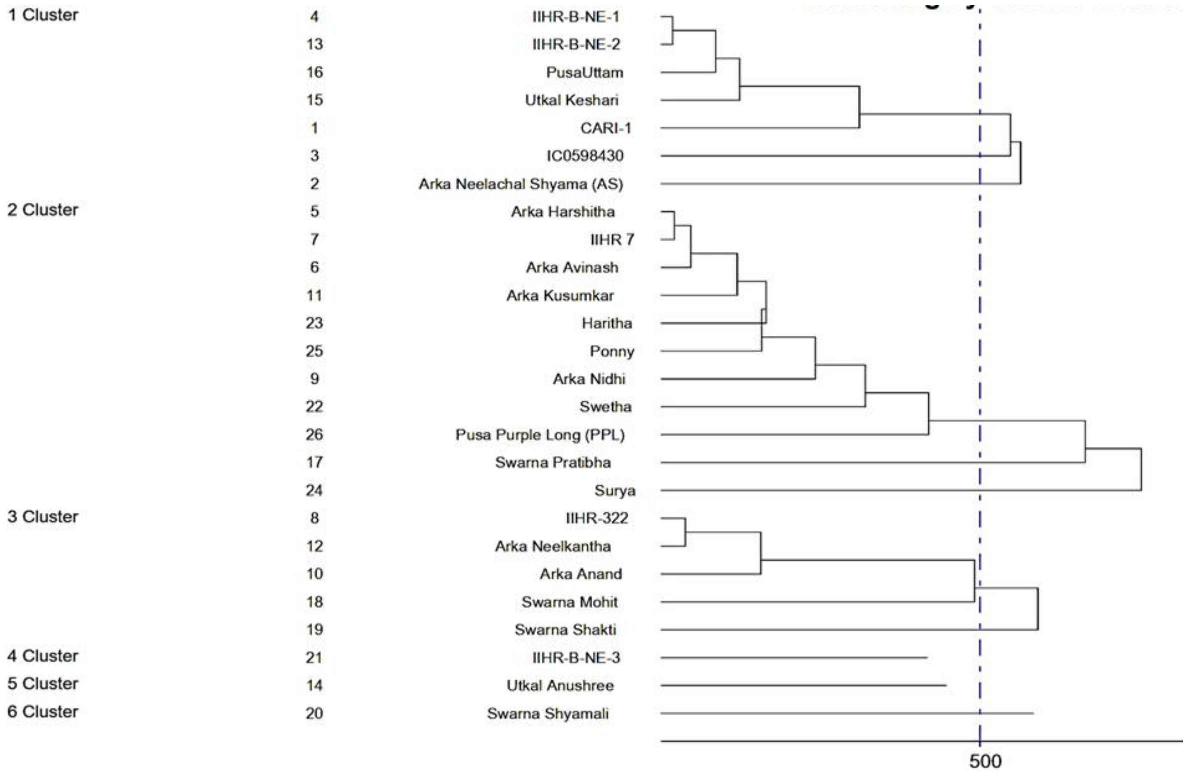

**Fig. 2. Dendrogram showing the clustering pattern of twenty-six genotypes of brinjal**

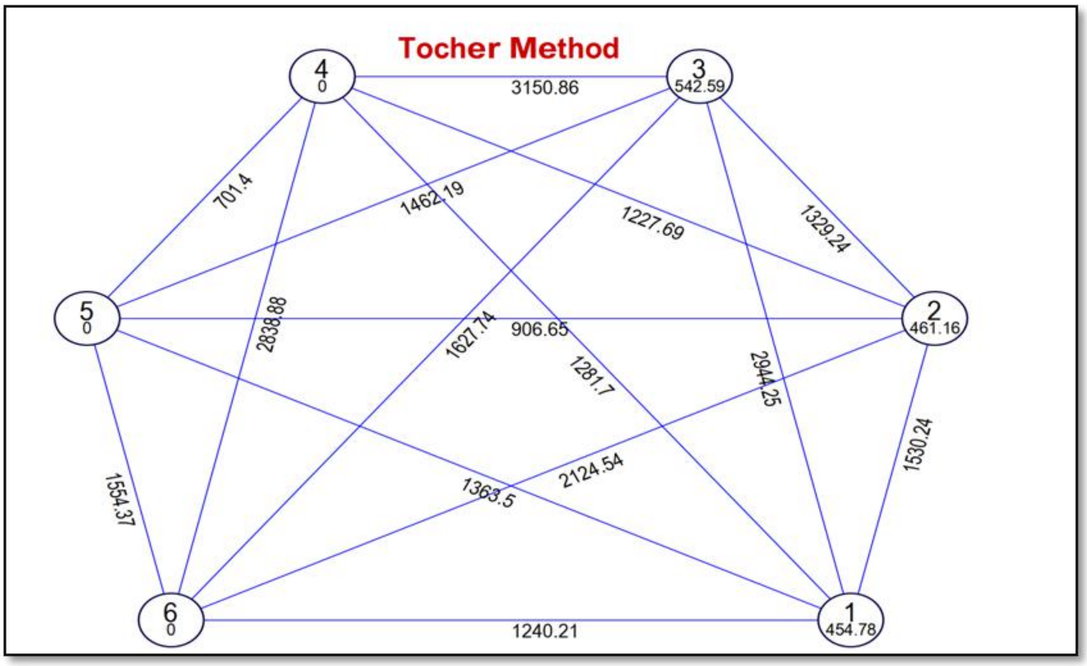

**Fig. 3. Intra- and inter-cluster distance among six groups of brinjal genotypes.**

**Table 3. Relative contribution of different characters to genetic divergence in brinjal**

| S. No. | Source | Contribution % | Times ranked 1st |
|---|---|---|---|
| 1 | Plant height | 3 | 10 |
| 2 | Number of branches | 2 | 7 |
| 3 | Days to 50 % flowering | 4 | 13 |
| 4 | Number of fruits per plant | 8 | 26 |
| 5 | Fruit yield per plant | 28 | 91 |
| 6 | Fruit length | 15 | 49 |
| 7 | Fruit girth | 13 | 42 |
| 8 | Average fruit weight | 15 | 91 |
| 9 | 1000 seed weight | 12 | 49 |

**Table 4. Mean performance of 9 characters in different clusters of brinjal**

| | DT50%F | PH (cm) | NOB | NOFP | FYPP (g) | FL (cm) | FG (cm) | FW (g) | 1000SW (g) |
|---|---|---|---|---|---|---|---|---|---|
| Cluster 1 | 47.36 | 45.19 | 10.26 | 4.53 | 552.64 | 9.14 | 20.41 | 129.34 | 3.18 |
| Cluster 2 | 47.41 | 46.04 | 10.45 | 4.95 | 377.53 | 17.4 | 7.43 | 76.25 | 3.12 |
| Cluster 3 | 48.30 | 50.05 | 13.25 | 5.82 | 495.60 | 17.6 | 10.24 | 95.61 | 4.72 |
| Cluster 4 | 48.50 | 48.25 | 8.00 | 15.30 | 241.25 | 4.85 | 4.40 | 15.92 | 2.75 |
| Cluster 5 | 49.00 | 37.75 | 11.30 | 23.56 | 866.25 | 5.60 | 5.05 | 37.01 | 4.01 |
| Cluster 6 | 51.00 | 52.00 | 14.10 | 3.57 | 600.00 | 8.35 | 26.00 | 168.03 | 4.86 |

DT50%F- Days to 50 % flowering; PH- Plant height; NOB- Number of branches; NOFP- Number of fruits per plant; FYPP- Fruit yield per plant; FL- Fruit length; FG-Fruit girth; FW-Fruit weight,1000SW- 1000 seed weight

(17.6 cm); cluster I for fruit girth (20.41 cm); cluster VI for average fruit weight (168.03 g), and cluster IV for 1000 seed weight (2.73 g). Hence, crossing programme among these genotypes would result in getting transgressive segregants (Chippy *et al*., 2021).

The principal component analysis (PCA) was conducted to dispense the aggregate variance into the PCs to select the superior germplasm based on the average amount of different traits. The principal factor PC is a powerful practical method that provides easiness for obtaining suitable parental genotypes to generate useful breeding programs (Nazir *et al*., 2013). With the help of the correlation matrix, the principal components were estimated and genotype scores of the components with latent roots more than the unity were observed (**Table 5**). Four out of nine component factors (PCs) were found with an Eigenvalue of more than 1. These principal factors (PCs) contributed 83.61 per cent towards the total variability existing among brinjal genotypes (**Table 5**). The first principal component (PC 1) contributed the maximum towards the total variability (30.83%). Days to 50% flowering, plant height, the number of branches, and fruit yield per plant, fruit girth, fruit weight, and 1000 seed weight were positively loaded, while average fruit length and the number of fruits were negatively loaded (**Table 5**). Sunseri *et al*. (2010) studied principal component analysis (PCA) of 70 brinjal accessions and found that the first three principal components accounted for 74 per cent of the total variance. The second principal component (PC 2) contributed 23.07 per cent towards total variability. The traits including days to 50% flowering, plant height, the average number of branches per plant, fruit length, and 1000 seed weight were positively loaded, while average fruit weight and girth, the number of fruits and fruit yield per plant were negatively loaded. The third principle component (PC 3) contributed to the total variability of 16.85 per cent. Plant height, the number of branches, the number of fruits, fruit yield per plant, fruit length, and 1000 seed weight were positively loaded, while days to 50 % flowering, average fruit girth, and weight were negatively loaded. The fourth principal component (PC 4) contributed to the total variability of 12. 87 per cent. Days to 50% flowering, plant height, the number of fruits, and fruit yield per plant were positively loaded, while all the fruit traits along with 1000 seed weight were negatively loaded. The PC bi-plot (**Fig. 4**) demonstrated the genotypes distribution and variables and the gap within traits concerning PC 1 and PC 2 depicted the contribution of these traits in creating variation among the genotypes.

Hence, it can be concluded that the clusters exhibiting the maximum inter-cluster distances (clusters *viz*., III & IV and I & III, respectively) and possessing high means for desired traits could be successfully utilized in hybridization programs. The yield and yield attributing traits registered

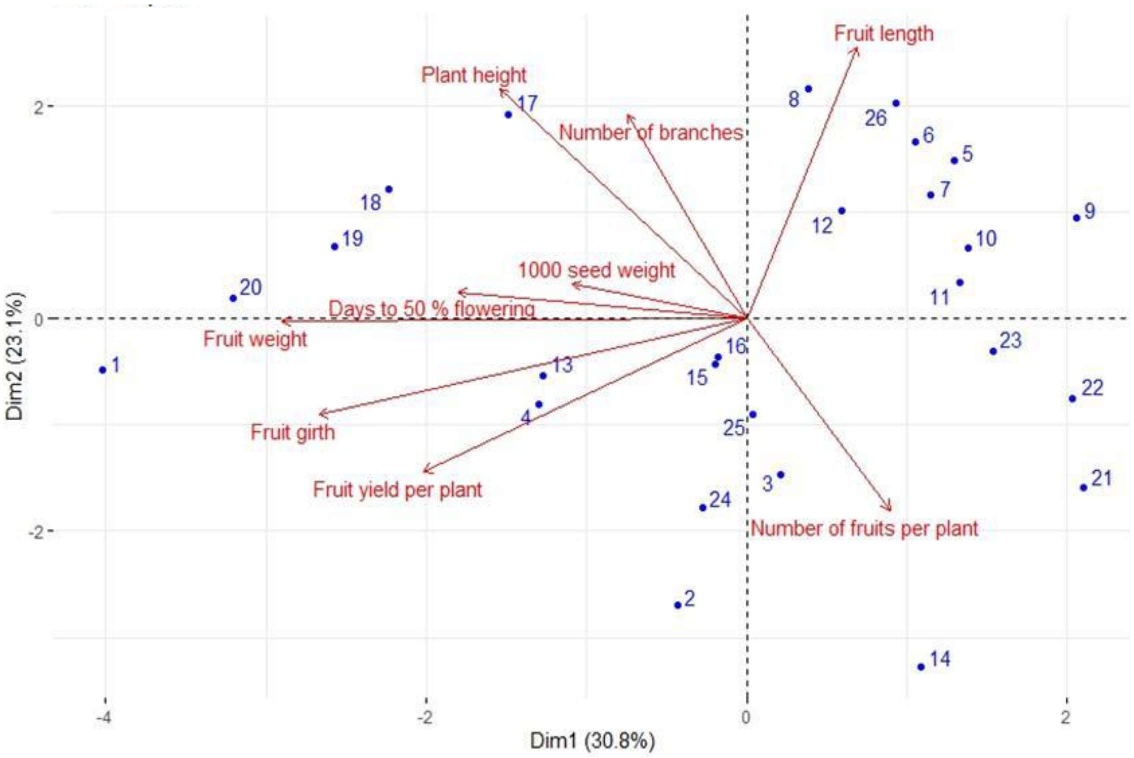

**Fig. 4. Biplot of 26 genotypes of brinjal using PCA analysis**

**Table 5. Eigen values, percent contribution towards variation and component loading in respect of 9 characters in brinjal**

| Component axis | Principal component characters | Eigen value | Percentage of total Variation accounted for | Cumulative (%) | Component loading | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | 1 Vector | 2 Vector | 3 Vector | 4 Vector |
| 1 | Days to 50 % flowering | 2.77 | 30.83 | 30.83 | 0.565 | 0.078 | -0.038 | 0.734 |
| 2 | Plant height | 2.08 | 23.07 | 53.90 | 0.484 | 0.676 | 0.008 | 0.413 |
| 3 | Number of branches | 1.52 | 16.85 | 70.74 | 0.233 | 0.600 | 0.539 | -0.169 |
| 4 | Number of fruits per plant | 1.16 | 12.87 | 83.61 | -0.282 | -0.565 | 0.623 | 0.400 |
| 5 | Fruit yield per plant | 0.70 | 7.82 | 91.43 | 0.632 | -0.451 | 0.405 | 0.082 |
| 6 | Fruit length | 0.41 | 4.59 | 96.03 | -0.216 | 0.799 | 0.081 | -0.027 |
| 7 | Fruit girth | 0.26 | 2.86 | 98.89 | 0.836 | -0.284 | -0.238 | -0.303 |
| 8 | Fruit weight | 0.07 | 0.78 | 99.67 | 0.909 | -0.009 | -0.247 | -0.154 |
| 9 | 1000 seed weight | 0.03 | 0.33 | 100.00 | 0.341 | 0.100 | 0.740 | -0.372 |

high heritability and GAM showed that the selection efficiency is high and it is due to the preponderance of additive gene action. Since fruit yield per plant exhibited a positive correlation with the number of fruits per plant, selection of this trait would be more valuable to bring the desired advancement in the brinjal breeding program.

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