

Original Research Paper

Unveiling the genetic variability and principal component analysis for yield and yield attributing traits in brinjal

Singh T.H.^{1*}, Pandey S.², Chitra D. Pandey² and Shailesh K. Tiwari³

¹ICAR-Indian Institute of Horticultural Research, Bengaluru - 560 089, India

²ICAR-National Bureau of Plant Genetic Resources, New Delhi - 110 012, India

³ICAR-Indian Institute of Vegetable Research, Varanasi - 221 305, India

*Corresponding author Email: [ttejavathu41@gmail.com](mailto:ttejvathu41@gmail.com)

ABSTRACT

An experiment was conducted to assess 435 brinjal accessions for various growth and yield-related traits, in augmented randomized complete block design comprising five blocks. Traits such as plant spread, leaf length, leaf width, fruit length, fruit breadth, yield per plant, and average fruit weight exhibited high genotypic and phenotypic coefficients of variation. In contrast, plant height, number of fruits per plant, days to 50% flowering, and 100-seed weight displayed moderate levels of GCV and PCV. Except for the number of primary branches per plant, all traits showed high heritability and substantial genetic gain, indicating that additive gene effects predominantly govern these traits and that selection would be effective. Principal component analysis identified four major components with eigen values equal to or greater than one, accounting for 63.85% of the total variation. The promising accessions, such as IC-0285124, IC-0603134, IC-0261835, IC-0126664, IC-0126729, IC-012667, IC-0398177, IC-0127025, IC-0211841, IC-0510495, IC-0126840, IC-0126803, IC-01266841, IC-01266877, IC-0146670, IC-0261873, IC-0126836 and IC-0126769 identified for yield & yield attributing traits.

Keywords: Brinjal, genetic advance, genetic variability, heritability, principal component analysis

INTRODUCTION

Brinjal (*Solanum melongena* L.), belonging to the Solanaceae family, is a diploid species with a chromosome number of $2n=24$ and is considered native to India (Vavilov, 1931). It is among the most extensively cultivated vegetables in India as well as in several other countries. Globally, India ranks as the second-largest producer of brinjal, following China. India produces 12.78 million metric tonnes (MT) of brinjal annually on 676.70 thousand hectares of land, with a productivity of 18.90 MT/ha (Statistical data agriculture, 2023).

A thorough understanding of the extent of genetic variability among genotypes for different traits is fundamental to any crop improvement program. Variability is an inherent feature of all populations. The genotypic coefficient of variation (GCV) reflects the heritable portion of total variation by measuring the genetic contribution to overall variability. A higher GCV indicates a greater potential for a trait to be effectively used in selection strategies. However, GCV alone does not provide a complete picture of heritable

variability. To accurately estimate the potential genetic gain from selection, both heritability and genetic advance as a percentage of the mean must also be considered (Soumya et al., 2023). While phenotypic variability may fluctuate with environmental conditions, genetic variability remains stable and is therefore more valuable to breeders for selection and hybridization purposes. Since yield is a complex trait influenced by multiple contributing factors and environmental interactions, estimates of heritability and genetic progress are crucial for effective selection.

Principal component analysis (PCA) assists researchers in identifying significant relationships among various traits. The primary benefit of PCA over cluster analysis is that each genotype can only be assigned to one group, while cluster analysis is also a suitable technique for identifying familial links (Savankumar et al., 2018). The goal of the current study was to determine the possible genetic diversity among brinjal genotypes in order to choose parents for a hybridization program that would produce superior segregants in the next generation.



MATERIALS AND METHODS

The current study was conducted at the ICAR-Indian Institute of Horticultural Research, Bangalore, India, located at 13°8' 1.51" N and 77°29' 27.32" E at an altitude of 890 meter above mean sea level, during *kharif* season of 2023 to 2024. The meteorological data during June to November 2023 showing maximum and minimum temperature (29.45° and 20.32°C, respectively), mean relative humidity (87.15% and 63.01%) during 7 am and 1.30 pm, respectively, wind speed (4.13 km/h) and total rainfall (56.50 mm).

The study consists of 435 brinjal accessions, received from the National Genebank, ICAR-National Bureau of Plant Genetic Resources, New Delhi, India (NBPGR) (Supplementary Table 1) and five standard checks, namely, IC-628873 (BR-14), Kashi Taru, Kashi Vijay, Arka Kusumakar, and Arka Keshav. The parameters were recorded as per the NBPGR descriptors such as plant height (cm), plant spread (cm), number of primary branches per plant, leaf length (cm), leaf width (cm), days to 50 per cent flowering, fruit length (cm), fruit breadth (cm), number of fruits per plant, yield per plant (kg), average fruit weight (g), and 100-seed weight (g). Five plants from each accession were tagged to document all observations.

An augmented randomized complete block design (ARCB) was employed. The checks were replicated in each block, and the treatments (germplasm/accessions) were not replicated. A total of 435 accessions were grown in 5 blocks, with 87 accessions in each block. Thirty-five-day-old plants were transplanted to the main field with 80 × 60 cm space between rows and plants. Good agriculture practices (GAPs) were followed to raise good crops.

Statistical analysis

The R package 'augmented RCBD' was employed to calculate adjusted averages for all considered traits across all genotypes (Aravind et al., 2018). The same R software was used to calculate frequency distributions, genetic variability parameters, and descriptive statistics. The following formulas were used to calculate phenotypic variance, genotypic variance, broad-sense heritability (h^2) (Lush, 1940), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and genetic advances (GA) (Johnson et al., 1955):

$$\text{Genotypic variance } (\sigma_g^2 = \bar{P} - \bar{e})$$

Where,

$\bar{P}$ = Phenotypic variance = Sum of squares of test treatments (genotypes)

$\bar{e}$ = Error Variance = Sum of squares of residuals (error)

Phenotypic Coefficient of Variation (PCV) =

$$\frac{\text{Phenotypic Variance}}{\sqrt{\text{mean}}} \times 100$$

Genotypic Coefficient of Variation (GCV) =

$$\frac{\text{Genotypic Variance}}{\sqrt{\text{mean}}} \times 100$$

$$\text{Broad sense heritability } (h^2) = \frac{\sigma_g^2}{\sigma_p^2}$$

$$\text{Genetic Advance (GA)} = k \times \sqrt{g} \times \frac{h^2}{100}$$

Where k is the selection intensity and g is the genotypic standard deviation. The R package 'FactoMineR' was used to perform PCA (Le et al., 2008).

RESULTS AND DISCUSSION

Genetic variability

A significant range of variance was observed among the twelve characters analyzed in the brinjal accessions. ANOVA results indicated that the variation for all characters was highly significant, highlighting inherent genetic differences. Each characteristic exhibited a wide range (Table 3), with the coefficient of variation ranging from 0.15 (fruit breadth) to 16.13 (number of primary branches per plant). The PCV and GCV were high for plant spread, leaf length, leaf width, fruit length, fruit breadth, yield per plant and average fruit weight. The traits such as plant height, days to 50 per cent flowering, number of fruits per plant and 100 seed weight has moderate PCV & GCV. Generally speaking, PCV was marginally greater than the corresponding GCV for every character in the study, suggesting that contextual factors frequently affect how these traits are expressed. However, the bulk of the traits have very little variation between PCV and GCV, indicating that genetic governance of these characters is more common and therefore phenotypic selection would be valid. Rathod et al. (2024), Sreevandana & Jana (2024), and Vankalas et al. (2024) also found similar results.

Table 2 : Genetic variability parameters of the brinjal germplasm

Trait	Mean	Range	CV (%)	GCV	PCV	ECV	hBS(h ²) (%)	GA	GAM (%)
PH	97.71	47-153	2.37	17.84	17.84	2.40	100.00	35.97	36.81
PS	65.20	34-102	4.89	22.29	22.29	4.92	100.00	30.00	45.99
NPB	4.00	2-8	16.13	18.49	24.61	16.24	56.45	1.17	28.67
LL	15.81	5.25-32.30	5.01	24.35	24.86	5.03	95.91	7.78	49.19
LW	10.06	3.17-23.17	5.08	27.91	28.37	5.11	96.76	5.70	56.64
DF	35.00	29-54	5.16	17.54	18.28	5.13	92.11	12.22	34.73
FL	9.14	1.52-26.00	0.21	36.85	36.85	0.22	100.00	6.95	76.03
FB	5.13	1.50-14.30	0.15	28.76	28.76	0.18	100.00	3.04	59.33
FP	22.00	16-37	6.85	12.46	14.23	6.87	76.69	4.96	22.52
YPP	1.84	0.14-4.11	8.84	41.55	42.48	8.83	95.68	1.54	83.85
FW	86.96	5.80-221.80	1.50	47.34	47.37	1.50	99.90	84.89	97.62
100SW	0.50	0.30-0.50	0.32	11.93	11.93	0.35	100.00	0.11	24.61

PH: plant height (cm), PS: plant spread (cm), NPB: number of primary branches per plant, LL: leaf length (cm), LW: leaf width (cm), DF: days to fifty per cent flowering, FL: fruit length (cm), FB: fruit breadth (cm), FP: number of fruits per plant, YPP: yield per plant (kg), FW: average fruit weight (g), 100 SW: 100 seed weight (g)

Heritability and genetic advance

Because broad sense heritability is based on total genetic variance, which includes both fixable (additive) and non-fixable (dominance and epistatic) variances, both broad sense heritability and GAM are required throughout the selection process for the improvement of any character. Genetic advancement will be minimal when heritability is primarily caused by non-additive genetic effects, but a significant genetic advance may be anticipated when heritability is primarily caused by additive gene effects (Nagar et al., 2024). High heritability and high GAM have been found for all the characters in the current study, except for the number of primary branches per plant. This suggests that additive genetic effects (fixable) are prevalent in their expression and that they will respond well to phenotypic-based selection in crop improvement programs. Therefore, to improve these traits, straight phenotype-based selection is advised. Kousalya et al. (2024), Rathod et al. (2024), and Tabasum et al. (2024) all were obtained high heritability and high GAM values in their studies. By using the right breeding techniques, existing variability can be exploited to further increase the brinjal cultivars' yield level. Characteristics that contribute significantly to production have been found, and selection for these attributes will assist boost crop yield. Diverse genotypes can also be used for hybridization programs.

Yield frequency distribution

The average yield per plant among the germplasm varied from 0.15 kg to 4.14 kg. The promising accessions, such as IC-0285124 (4.14 kg), IC-0603134 (4.14 kg), IC-0261835 (3.96 kg), IC-0126664 (3.90 kg), IC-0126729 (3.86 kg), IC-0126677 (3.85 kg), IC-0398177 (3.83 kg), IC-0127025 (3.66 kg), IC-0211841 (3.64 kg), IC-0510495 (3.57 kg), IC-0126840 (3.57 kg), IC-0126803 (3.38 kg), IC-01266841 (3.36 kg), IC-01266877 (3.32 kg), IC-0146670 (3.30 kg), IC-0261873 (3.24 kg), IC-0126836 (3.17 kg) and IC-0126769 (3.04 kg) had superior fruit yield, as also reported by Rathod et al. (2024) and Tabasum et al. (2024).

Principal component analysis

Principal component analysis (PCA) measures the relevance of the largest contributor to total variation at each axis of differentiation (Sharma, 1998). The Eigen value of a primary component is the amount of variation explained by that component. The sum of all Eigen values is the total variance of the twelve attributes. In the current investigation, four principal components (PC-1 to PC-4) were identified from the original data set with eigen values greater than one. These four major components account for 63.85% of the overall variation (Table 3). Fig. 1 depicts a 2D dispersed diagram of 435 brinjal accessions based on

Table 3 : Eigen values, proportion of the total variance represented by the twelve principal components, cumulative per cent variance and component loading of different characters in brinjal

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen value	3.44	1.69	1.44	1.10	1.00	0.80	0.73	0.62	0.55	0.46	0.18	0.01
% variance expressed	28.64	14.11	11.97	9.13	8.29	6.65	6.07	5.20	4.56	3.85	1.47	0.06
Cumulative variance expressed	28.64	42.75	54.72	63.85	72.14	78.79	84.87	90.06	94.62	98.47	99.94	100.00
PH	0.112	-0.503	-0.204	0.086	-0.272	-0.021	0.247	0.730	-0.125	-0.005	-0.003	0.001
PS	0.050	-0.116	-0.700	0.249	0.073	-0.061	0.566	-0.454	-0.021	0.156	-0.016	0.001
NPB	-0.083	0.004	-0.147	0.761	-0.261	0.341	-0.447	-0.039	0.075	0.023	-0.013	0.004
LL	0.356	-0.463	-0.030	-0.089	0.107	-0.010	-0.276	-0.225	0.049	-0.055	0.710	0.014
LW	0.352	-0.444	-0.033	-0.100	0.173	-0.078	-0.329	-0.171	0.087	0.114	-0.686	-0.008
DF	-0.065	0.070	-0.486	-0.494	-0.139	0.584	-0.103	0.029	0.293	-0.223	-0.042	-0.019
FL	0.129	-0.241	0.502	0.041	-0.375	0.362	0.380	-0.320	-0.044	-0.367	-0.113	0.037
FB	0.344	0.248	-0.174	0.170	-0.026	-0.408	-0.016	0.068	0.241	-0.725	-0.059	0.008
FP	-0.352	-0.240	0.157	0.051	-0.043	-0.199	0.119	0.010	0.841	0.116	0.035	0.108
YPP	0.460	0.250	0.095	0.005	-0.022	0.046	0.104	0.056	0.266	0.342	0.047	-0.680
FW	0.468	0.281	0.028	-0.029	-0.198	0.063	0.056	0.065	0.128	0.331	0.022	0.722
100 SW	0.177	0.040	0.143	0.238	0.748	0.431	0.219	0.250	0.158	-0.082	0.006	0.014

PH: plant height (cm), PS: plant spread (cm), NPB: number of primary branches per plant, LL: leaf length (cm), LW: leaf width (cm), DF: days to fifty per cent flowering, FL: fruit length (cm), FB: fruit breadth (cm), FP: number of fruits per plant, YPP: yield per plant (kg), FW: average fruit weight (g), 100 SW: 100 seed weight (g)

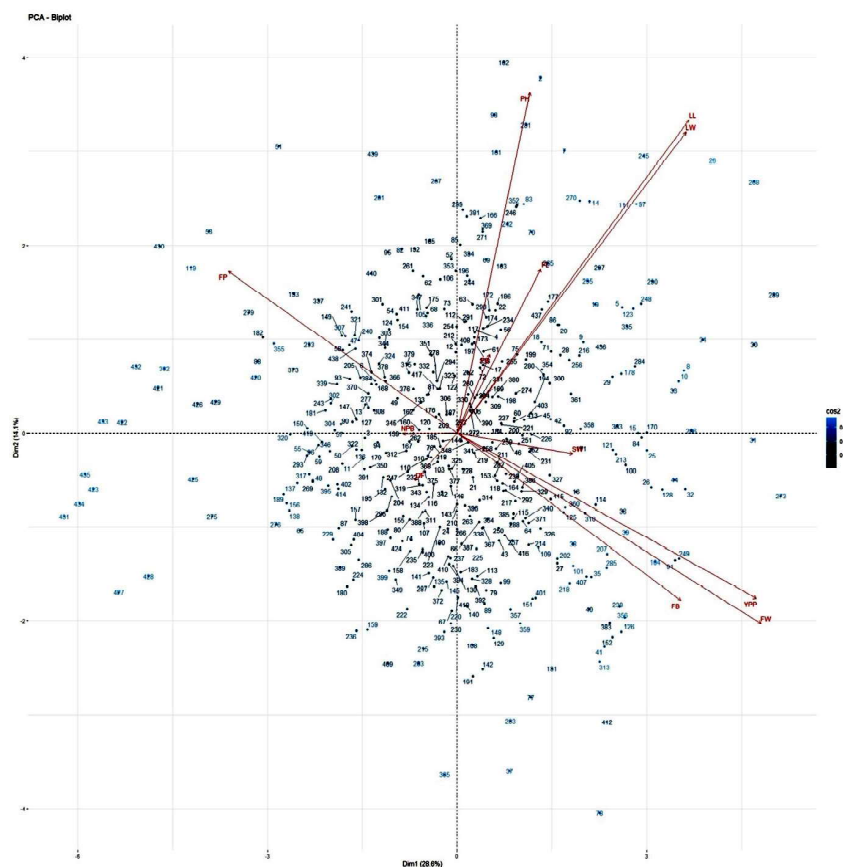


Fig. 1 : Two-dimensional graphical representations of component patterns along with different variables based on PC1 and PC2

their first two principal component scores. The first major component alone accounts for approximately 28.64% of the gross variability among accessions, owing primarily to average fruit weight, yield per plant, leaf length, leaf width, fruit breadth, 100 seed weight, fruit length, and plant height. The second primary component accounted for 14.11% of overall variability, primarily due to average fruit weight, yield per plant, and fruit breadth. The third principal component, which accounts for around 11.97% of total variation, is mostly related to fruit length, number of fruits per plant, and 100 seed weight. The fourth principal component, which accounted for 9.13% of total variability, was determined by the number of primary branches per plant, plant spread, 100 seed weight, and fruit breadth. These findings suggest that characters such as plant height, plant spread, number of primary branches per plant, leaf length, leaf width, fruit length, fruit breadth, number of fruits per plant, yield per plant, average fruit weight, and 100 seed weight could be used to distinguish brinjal germplasm. Fruit features contributed significantly to variance among Brinjal germplasm in similar research conducted by Ramesh Kumar et al. (2016), Alekhya & Namboodiri (2024), and Prashant et al. (2024).

CONCLUSION

According to the findings, the majority of the variables linked to earliness, growth, yield, and their components displayed significant genetic variability and heritability estimations, indicating the presence of additive genetic factors (fixable) affecting their expression. As a result, direct selection based on these characteristic combinations facilitates the use of desirable genotypes with high yield per plant in development endeavors. The promising accessions, such as IC-0285124, IC-0603134, IC-0261835, IC-0126664, IC-0126729, IC-0126677, IC-0398177, IC-0127025, IC-0211841, IC-0510495, IC-0126840, IC-0126803, IC-01266841, IC-01266877, IC-0146670, IC-0261873, IC-0126836 and IC-0126769 identified for yield and yield attributing traits. These diverse germplasm accessions serve as reservoirs of important genes/alleles that helps to get higher yield and can be utilized as foundational material in future breeding programs to develop new, improved varieties and advanced breeding lines in brinjal.

ACKNOWLEDGMENT

With sincere appreciation, the authors thank the Director of the ICAR-National Bureau of Plant Genetic Resources, New Delhi, for funding the ICAR-IIHR's acquisition of the germplasm for this work through the CRP-Agro Biodiversity initiative. The Director and Head of the Division of Vegetable Crops at the Indian Institute of Horticultural Research (ICAR) in Bengaluru are also acknowledged by the authors for providing the facilities required to conduct this study.

REFERENCES

- Alekhya, C., & Namboodiri, R. V. (2024). Exploring genetic diversity in brinjal (*Solanum melongena* L.)-Insights from D² analysis and principal component analysis. *Journal of Tropical Agriculture*, 62, 65-71.
- Aravind, J., Sankar, M. S., Dharma prakash, P. W., & Kaur, V. (2018). *Augmented RCBD: Analysis of augmented randomized complete block designs* (R package version 0.1.0). github.io
- Indiastat. (2023). *Statistical data agriculture*. <https://www.indiastat.com>
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47, 314-318. doi: 10.2134/agronj1955.00021962004700070009x
- Kousalya, R., Praneetha, S., Irene Vethamoni, P., Ravichandran, V., Iyanar, K., & Varanavasiappan, S. (2024). Unveiling the genetic variability, character association and principal component analysis for yield and yield contributing traits in brinjal (*Solanum melongena*) genotypes. *Indian Journal of Agricultural Sciences*, 94(10), 1039–1044. 10.56093/ijas.v94i10.152248
- Le, S., Josse, J., & Husson, F. (2008). FactoMineR: An R package for multivariate analysis. *Journal of Statistical Software*, 25, 1-17. doi: 10.18637/jss.v025.i01
- Lush, J. L. (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics.

- Proceedings of American Society of Animal Production*, 33(1), 293–301. doi: 10.2527/jas1940.19401293x
- Nagar, K. L., Rana, D. K., Barela, A., & Rahangdale, S. (2024). Study of genetic diversity and genetic advance in brinjal for morpho-economic traits (*Solanum melongena* L.). *International Journal of Environment and Climate Change*, 14(3), 437–444. doi: 10.9734/ijecc/2024/v14i34054
- Prashant, Yadav, G. C., Singh, D. B., Tiwari, A., & Singh, N. K. (2024). Estimation of genetic diversity using D² and PCA in brinjal (*Solanum melongena* L.). *Journal of Advances in Biology and Biotechnology*, 27(6), 542–549. doi: 10.9734/jabb/2024/v27i111638
- Ramesh Kumar, S., Arumugam, T., & Ulaganathan, V. (2016). Genetic diversity in eggplant germplasm by principal component analysis. *SABRAO Journal of Breeding and Genetics*, 48(1), 162–171.
- Rathod, D., Tandel, T., Sarkar, M., Ahlawat, T. R., Patel, A. I., Vashi, J. M., Bambharolia, R. P., Varshney, N., Emmi, S., & Chaudhari, B. N. (2024). Genetic variability analysis in brinjal (*Solanum melongena* L.). *International Journal of Advanced Biochemistry*, 8, 04–06. doi: 10.33545/26174693.2024.v8.i1Sa.275
- Savankumar, N., Patel, R. C., Popat, P. A., Patel, & Vekariya, R. D. (2018). Genetic diversity analysis in brinjal (*Solanum melongena* L.) genotypes: A principal component analysis approach. *International Journal of Current Microbiology and Applied Sciences*, 7, 3296–3301. doi: 10.20546/ijcmas.2018.701.392
- Sharma, J. R. (1998). *Statistical and biometrical techniques in plant breeding*. New Age International (P) Limited Publishers.
- Soumya, B. K., Deo, C., Singh, S., Bhutia, N. D., Tayeng, T., Hazarika, B. N., Debbarma, A., Sakhamo, K., & Dutta, R. (2023). Genetic variability studies in brinjal (*Solanum melongena* L.) for quantitative and qualitative characters. *International Journal of Environment and Climate Change*, 13(10), 4463–4473. doi: 10.9734/ijecc/2023/v13i103124
- Sreevandana, K., & Jana, J. C. (2024). Studies on genetic variability, heritability and genetic advance for yield and its attributed traits in brinjal (*Solanum melongena* L.). *International Journal of Environment and Climate Change*, 14(3), 275–282. doi: 10.9734/ijecc/2024/v14i44115
- Tabasum, S., Nazir, G., Hussain, K., Ali, G., Nazir, N., Mushtaq, F., Hussain, Z., & Arizoo. (2024). Analysis of genetic variability and heritability in brinjal (*Solanum melongena* L.) genotypes. *Journal of Advances in Biology and Biotechnology*, 27(3), 198–205. doi: 10.9734/jabb/2024/v27i4754
- Vankalas, C. N., Khapte, P. S., Agale, M. G., Shitole, P. A., & Shinde, G. S. (2024). Genetic variability studies in brinjal (*Solanum melongena* L.). *International Journal of Advanced Biochemistry*, 8(1), 1241–1245. doi: 10.33545/26174693.2024.v8.i10p.2728
- Vavilov, N. I. (1931). The role of central Asia in the origin of cultivated plants. *Bulletin of Applied Botany, Genetics and Plant Breeding*, 26, 43–44.

(Received : 15.5.2025; Revised : 29.5.2026; Accepted : 04.6.2026)

