



Estimates of Contribution, Clausturation and Principal Component Analysis in Different Genotype of Brinjal (*Solanum melongena* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2023/v35i224184

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/109833>

Original Research Article

Received: 24/09/2023

Accepted: 30/11/2023

Published: 06/12/2023

ABSTRACT

The present investigation was carried out in thirty-two genotypes of brinjal with a view to estimate the extent of variability, variance and genetic divergence. The experiment was conducted in Randomized Block Design with three replications at Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology Narendra Nagar, (Kumarganj), Ayodhya

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(U.P.), during Kharif, 2020-21. Each treatment consisted of twelve plants in two rows, having spacing of 60 cm x 50 cm with net plot size of 1.2 m x 3.0 m². Based on the Principal Component Analysis (PCA) with 15 parameters of cent percent diversity, it formed 6 Principal Components (PCs) with more than one Eigen value. These components indicate maximum variation among the variables with a diversity percentage of 75.46%. The first PC showed 19.59% variation, while the second, third, fourth, fifth and sixth (PCs) showed the variation of 19.18%, 11.48%, 9.37%, 8.29% and 7.54% respectively. Contribution of diverse traits in principal component analysis showed positive and maximum variable loaded component PCI for T.S.S (0.3321), PC II for number of primary branches per plant (0.0.6397), PC III for days to 50 % flowering (0.5158), PC IV for plant height (0.0.592), PC V for day to first fruit harvest (0.4073) and PC VI for day to first fruit harvest (0.5741).

Keywords: Percent contribution; clusters; principal component analysis; genotypes.

1. INTRODUCTION

An annual herbaceous plant, eggplant (*Solanum melongena* L.) is self-pollinating. Because it is inexpensive, eggplant is consumed. Iron, zinc, copper, calcium, magnesium, and potassium are all abundant in eggplant fruit. It has potential health benefits and is a fair source of fatty acids [1]. "In South Asia, which includes Bangladesh, India, Nepal, and Sri Lanka, eggplant is a significant produce and makes up over half of all agricultural soil. In terms of plant type, stem colour, leaf size, leaf tip, midrib colour, fruit size, fruit shape, fruit colour, fruit yield, fruit quality, cooking quality, and pest and disease tolerance, eggplant has a significant indigenous biodiversity" [2-4]. Improvement in eggplant can be achieved by exploiting available sources of variability.

Principal Component Analysis (PCA), a descriptive method, explains the distribution of character variance in individuals. It tends to reduce the dimension of multivariate data by removing inter-correlation between variables and makes it possible to depict a multi-dimensional connection on two or three principal axes. When employing cluster analysis, which is widely used to analyse genetic diversity, to group accessions with similar features into a single homogeneous category [5]. Clustering is also used to simplify data regarding the relationships between objects by grouping comparable units into groupings that make sense together [6,7].

2. MATERIALS AND METHODS

The study comprised 32 genotypes of brinjal including one check. The experiment was conducted in Randomized Complete Block Design with three replications at the Main Experiment Station, Department of Vegetable

Science, Narendra Deva University of Agriculture and Technology Narendra Nagar, (Kumarganj), Ayodhya (U.P.), during autumn-October to March 2020-21 with a wide range of diversity and variability, were selected based on fruit shape, colour, size and evaluated under field conditions. Each treatment consisted of 12 plants in two rows, having spacing of 60cm x 50cm with net plot size of 1.2x3.0 meter².

For variations among genotypes, the alternate hypothesis as tested [8]. In order to do the principal component analysis, SPSS (version 16.0, Chicago, IL) was used (Levesque, 2007). To define variation among accessions for agronomic and morphological parameters, PCA axes with eigen values 1.0 were chosen. Cluster analysis was performed on the mean values of 32 genotypes for 15 different variables using the PC programme numerical taxonomy and multivariate analysis system (NTSYS) [9].

3. RESULTS AND DISCUSSION

The study of genetic divergence among the thirty two genotypes of brinjal was carried out using Mahalanobis D² statistics. The thirty two genotypes were grouped into eight different non overlapping clusters (Table 1). Cluster II had highest number of genotypes (11) followed by cluster I (7), cluster III (6), cluster IV (3), cluster V (2) and cluster VI, VII, VIII, each have one genotypes group constellation of brinjal genotypes through genetic divergence has been also reported by Mangi et al. [10]; Nand et al. [11].

The estimates of inter and intra cluster distances represented by D² values are given in Table 2. The intra cluster D² values ranged from 0.00 cluster (VI to VIII) to 298.71 cluster (V) lowest VI

to VIII and maximum cluster V, respectively. The maximum inter-cluster distance was observed between clusters II and VI (2142.25) which suggested that members of these two clusters were genetically very diverse to VIII (1871.17), cluster III and VI (1786.93), cluster V and VIII (1618.91), cluster V and VII (1461.20), cluster VI and VII (1361.91), cluster IV and VI (1123.87), cluster I and II (1068.41) were very high. "The minimum inter-cluster D² values was recorded between cluster VII and VIII (401.03). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of these clusters while lower inter cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other Das and Das [12] studied the genetic divergence in brinjal and grouped 26 genotypes into 11 clusters and also reported maximum and minimum inter and intra cluster distances". [13]

A perusal of Table 3 total fruit yield per plant showed the highest contribution (41.10%) followed by total phenol content (20.93%), ascorbic acid (10.89%), non-reducing sugar (10.19%), reducing sugars (4.94%), average fruit weight (4.50%), total sugars (2.21%), number of primary branch per plant (1.36%), days to 50% flowering (1.24%), plant height (0.96%), T.S.S (0.67%), days to first fruit harvest (0.45%), fruit circumference (0.28%), number of fruits per plant (0.15%) and fruit polar length (0.14%) for total divergence among the available genotypes of egg plant. Such contribution towards the genetic divergence has been also reported by Das and Das [8]. This suggest that maximum variability

were present for the traits like total fruit yield per plant, phenol, ascorbic acid, non- reducing sugar. Similar results were also reported by Ravali et al. [14].

Result of (PCA) for quantitative characters contributing to divergence in brinjal (Table 4). The result of principle component analysis showed that PCI to PCVI have more than one eigen values (%) highest in PCI (2.94) followed by PCII (2.88), PCIII (1.72), PCIV (1.41), PCV (1.24) and PCVI (1.13).

The result of principal component analysis showed that highest proportion (%) found in PCI (19.59%) followed by PCII (19.18%), PCIII (11.48%), PCIV (9.37%), PCV (8.29%) and PCVI (7.54 %).

The result of principal component analysis showed that highest cumulative proportion (%) found in PCVI (75.46%), PCV (67.92%), PCIV (59.62%), PCIII (50.25%), PCII (38.77%), PCI (19.59%).

The study of contribution of diverse traits in principal component analysis among the thirty two genotypes of brinjal was carried out using Harman statistics. The thirty two genotypes were grouped into six different groups (Table 5) positive maximum variable loaded component PC I for T.S.S (0.3321), PC II for number of primary branches per plant (0.0.6397), PC III for days to 50% flowering (0.5158), PC IV for plant height (0.0.592), PC V for day to first fruit harvest (0.4073), and PC VI for day to first fruit harvest (0.5741).

Table 1. Clustering pattern of thirty two genotypes of brinjal on the basis of Mahalanobis D² statistics

Cluster Number	Number of Genotypes	Genotypes
I	7	2019/BRRVAR-13, NDB-161, NDB-166, 2019/BRRVAR-5, 2020/BRRVAR-9, 2019/BRRVAR-2, NDB-163
II	11	2020/BRRVAR-7, 2019/BRRVAR-3, 2019/BRRVAR-11, 2020/BRRVAR-1, NDB-127, 2019/BRRVAR-14, 2019/BRRVAR-7, NDB-133, 2020/BRRVAR-3, 2020/BRRVAR-2, 2020/BRRVAR-4
III	6	2019/BRRVAR-9, NDB-165, Pant Rituraj, NDB-127, 2019/BRRVAR-1, 2020/BRRVAR-8, NDB-167
IV	3	2020/BRRVAR-6, 2019/BRRVAR-8, 2019/BRRVAR-12
V	2	2019/BRRVAR-6, NDB-164
VI	1	2019/BRRVAR-15
VII	1	NDB-162
VIII	1	2020/BRRVAR-5

Table 2. Average of intra and inter-clusters D² values for six clusters in brinjal

Clusters	I	II	III	IV	V	VI	VII	VIII
I	222.54	1068.41	906.71	596.72	812.14	658.58	532.74	699.62
II		232.06	599.67	608.12	1949.89	2142.25	665.15	412.70
III			268.58	539.05	987.94	1786.93	1024.30	603.68
IV				199.13	937.94	1123.87	547.60	658.00
V					298.71	719.21	1461.20	1618.91
VI						0.00	1361.91	1871.17
VII							0.00	401.03
VIII								0.00

Table 3. Per cent contribution of fifteen characters towards total genetic divergence in brinjal

S. No.	Traits	Percent contribution (%)
1	Day to 50% flowering	1.24
2	Day to first fruit harvest	0.45
3	Number of primary branches per plant	1.36
4	Plant height	0.96
5	Fruit Polar length	0.14
6	Fruit circumference	0.28
7	Average fruit weight	4.50
8	Number of fruits per plant	0.15
9	T.S.S	0.67
10	Total sugars	2.21
11	Reducing sugars	4.94
12	Non-reducing sugar	10.19
13	Total phenol content	20.93
14	Ascorbic acid	10.89
15	Total fruit yield per plant	41.10

Table 4. Principal Component Analysis (PCA) for quantitative characters contributing to divergence in brinjal

Principal component	Eigenvalues (%)	Proportion (%)	Cumulative Proportion (%)
PC1	2.94	19.59	19.59
PC2	2.88	19.18	38.77
PC3	1.72	11.48	50.25
PC4	1.41	9.37	59.62
PC5	1.24	8.29	67.92
PC6	1.13	7.54	75.46

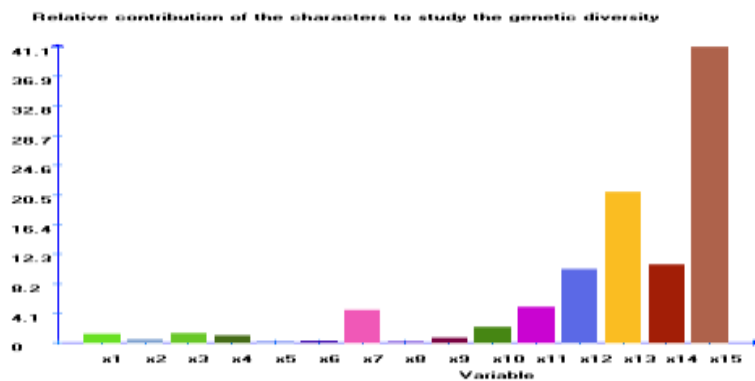


Fig. 1. Relative contribution of the charecters to study the genetic diversity

Table 5. Principal components of eggplant germplasm - non-rotated loadings

Traits	PC1	P2	PC3	PC4	PC5	PC6
Day to 50% flowering	-0.7898	-0.3419	0.5158	-0.3828	-0.0082	0.2327
Day to first fruit harvest	0.01	0.1748	-0.0374	0.0195	0.4073	0.5741
Number of primary branches per plant	0.0407	0.6397	-0.6555	0.4999	-0.3384	-0.0393
Plant height	-0.1511	-0.0949	0.0549	0.592	-0.1792	0.3596
Fruit Polar length	0.1324	-0.206	0.0469	-0.2356	-0.6538	0.2787
Fruit circumference	-0.1625	0.2301	0.0796	0.1475	-0.0898	0.0395
Average fruit weight	-0.1026	0.3507	0.1061	-0.0658	0.3289	-0.3557
Number of fruit per plant	0.1076	-0.2808	-0.172	0.0192	0.1538	-0.254
T.S.S	0.3321	-0.2409	0.228	0.2613	-0.1299	-0.3724
Total Sugars	0.2972	-0.0023	0.1617	0.1547	0.2821	0.2249
Reducing Sugars	-0.0478	-0.2392	-0.4069	-0.1098	0.0998	-0.0551
Non-reducing Sugar	-0.2795	-0.115	0.0486	0.2439	-0.0199	-0.1211
Total phenol content	-0.0797	-0.0137	0.0143	0.032	0.0941	0.0273
Ascorbic acid	-0.0087	0.0921	0.064	-0.0771	-0.0663	-0.0856
Total fruit yield per plant	-0.007	0.0009	-0.0043	-0.0085	-0.0048	-0.008

4. CONCLUSION

On the basis of present investigation, it might be concluded that there exists sample variation within the brinjal genotypes. This suggests that maximum variability was present for the traits like total fruit yield per plant, phenol, ascorbic acid, non-reducing sugar.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Shafeeq A. Heterosis and combining ability studies in brinjal (*Solanum melongena* L.). M.Sc Thesis, Department of Horticulture, University of Agricultural Sciences, Dharwad, India; 2005.
- Ullah S, Ijaz U, Iqbal Shah T, Najeebullah M, Niaz S. Association and genetic assessment in brinjal. *European J. Biotech. Biosci.* 2014;2(5):41-45.
- Quamruzzaman AKM, Rashid MA, Ahmad S, Moniruzzaman M. Genetic divergence analysis in eggplant (*Solanum melongena* L.). *Bangladesh J. Agric. Res.* 2009; 34:705-712.
- Senapati N, Mishra HN, Bhoi MK, Dash SK, Prasad G. Genetic variability and divergence studies in brinjal (*Solanum melongena* L.). *Veg. Sci.* 2009;36(2):150-154.
- Ulaganathan V, Nirmalakumari A. Finger millet germplasm characterization and evaluation using principal component analysis. *SABRAO J Breed. Genet.* 2015; 47:79-88.
- Kumar SR, Arumugam T, Ulaganathan V. Genetic diversity in eggplant germplasm by principal component analysis. *SABRAO J. Breed. Genet.* 2016;48:162-171.
- Mahendran R, Veerabhadhiran P, Robin S, Raveendran M. Principal component analysis of rice germplasm accessions under high temperature stress. *Int. J. Agric. Sci. Res.* 2015;5:355-360.
- Panse VC, Sukhatme PV. *Statistical methods for agricultural workers*, Indian Council of Agricultural Research, New Delhi; 1967.
- Rohlf FJ. *NTSYS-pc. Numerical taxonomy and multivariate analysis system*, version 2.02. Exeter Software, Setauket, NY; 1998.
- Mangi V, Patil HB, Karadi SM, Sanganamoni M, Shivam MK, Satish D. Character association and path analysis studies in brinjal (*Solanum melongena* L.) genotypes. *J. Appl. Nat. Sci.* 2017;9:29-33.
- Nand N, Adarsh A, Kumar A, Akhtar S, Kumar R, Ray PK. Morphological characterization of different genotype of brinjal (*Solanum Melongena* L.). *Int. J. Curr. Microbiol. Appl. Sci.* 2018;7:2218-2226.

12. Das, Das. Assessment of genetic diversity for brinjal in Terai Zone of West Bengal, India. Int. J. Curr. Microbiol. Appl. Sci. 2017;6:2401-2406.
13. Hari Shanker Verma, GC Yadav, Shravan Kumar, Prashant Verma. Estimation of genetic diversity among the genotypes of brinjal (*Solanum melongena* L.). The Pharma Innovation Journal 2021;10(8): 847-849.
14. Ravali B, Reddy KR, Saidaiah P, Shivraj N. Variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). Int. J. Curr. Microbiol. Appl. Sci. 2017; 6:42-47.

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