Research Article

Elucidation of genetic diversity through Multivariate analysis in brinjal (*Solanum melongena* L.) landraces for varietal improvement

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How to Cite

Susmitha, J. *et al.* (2023). Elucidation of genetic diversity through Multivariate analysis in brinjal (*Solanum melongena* L.) landraces for varietal improvement. *Journal of Applied and Natural Science*, 15(3), 1012 - 1017. https://doi.org/10.31018/jans.v15i3.4694

Abstract

Genetic diversity plays a crucial role in harnessing the potential of crop genotypes for genetic improvement. It helps to identify, preserve, and utilize diverse landraces effectively. This research aimed to assess the level of genetic diversity and traits enhancing genetic variation among 46 brinjal genotypes (*Solanum melongena* L.) in preparation for a special breeding programme to utilize the potential landraces. Genetic divergence among 46 genotypes of brinjal for eleven characters was assessed using the D^2 method. The studied genotypes were categorized into eight clusters. Cluster I with 15 genotypes was the largest followed by Cluster IV (14 genotypes), Cluster V (7 genotypes), Cluster VII (4 genotypes), Cluster III (3 genotypes), Clusters II, VI, and VIII with one genotype each. The intra-cluster D^2 values ranged from 0.00 (Cluster II, VI and VII) to 103.53 (Cluster III). The inter-cluster distances varied from 117.00 to 791.17. Cluster II and Cluster VII had the greatest inter-cluster distance (791.17), followed by Cluster II and VIII (673.41), and Cluster VII and Cluster V had the smallest inter-cluster distance (117.00). Crossing genotypes in clusters with wide inter-cluster distances improves recombinant isolation in segregating generations. The three traits- number of flowers per inflorescence (23.8%), average fruit weight (17.68%) and days to first flowering (16.81%) altogether contribute to 57.8% of the total divergence. The combination of these traits could be useful to produce high-yielding climate resilient varieties from valuable landraces.

Keywords: Clusters, Genetic diversity, Intra and inter-cluster distance, MultivariateaAnalysis

INTRODUCTION

Brinjal, commonly known as eggplant or aubergine, is an economically and culturally significant crop grown in India (Kiranmai *et al.,* 2021). *Solanum melongena*, belonging to the "Nightshade" family of plants called "Solanaceae," and the genus Solanum has roughly 2000 different species (Ghosh, 2022). India is the world's second top brinjal producer, whereas China tops the list. Some of the important species of *Solanum* include *S. melongena*, *S. insanum*, *S. aethiopium*, *S. macrocarpon*, and others. *S. melongena* is the most widely grown of them, with over 5000 recorded incidences of variety. Brinjal is among the chief crops for resolving the global food shortage (Rajan *et al.,* 2022).

Eggplant has abundant potassium (229 mg/100gm), vitamin K (3.5 µg/100gm) and a significant number of antioxidants (Oladosu *et al.,* 2021). It is the best option for low-fat diet. In terms of plant type, fruit size, shape, stem colour, leaf size and colour, as well as yield, quality, pest and disease tolerance, and phenolic content, eggplant has varied native biodiversity.

Brinjal diversity includes a wide range of landraces, cultivars, varieties, and wild species. The categorization of available local germplasm is of utmost importance in understanding the taxonomic relationships in terms of both interspecific and intraspecific (Rakha *et al.,* 2021). It also highlights the valuable germplasms for special breeding programmes. The initial step in categorizing and classifying germplasm collections is

morphological characterization. Multivariate analysis is effective for characterising, assessing, and classifying plant genetic resources when several accessions must be evaluated for numerous agronomic and physiological characteristics. The study of genetic divergence among existing genetic pools allows for the selection of diverse parents for hybridization. In combination, such parents are predicted to generate excellent segregants. With the use of P.C. Mahalanobis' D^2 analysis given in 1936, genetic diversity can be calculated. For the first time, C. R. Rao in 1952 proposed using this method to evaluate the genetic variability in plants. Despite the presence of numerous landraces of brinjal in our country, many of them are not utilized completely. This is due to the lack of characterization of landraces. This research aimed to assess the level of genetic diversity and traits enhancing genetic variation among some landraces of brinjal in preparation for a special breeding programme to utilize the potential landraces.

MATERIALS AND METHODS

The study was conducted in Sivapuri village, Cuddalore district, Tamil Nadu from Jan 2022 to June 2022. The experiment was conducted with three replications utilizing Randomized Block Design (RBD). A total of 46 genotypes (Table 1) were planted with 60 x 45 cm spacing in all three replications. Recommended practices were followed for growing the accessions. These genotypes were measured for eleven characters like days to first flowering, plant height, number of primary branches per plant, days to first harvest, fruit length, fruit thickness, average fruit weight, number of flowers per inflorescence, number of fruits per cluster, number of fruits per plant, fruit yield per plant. Mahalanobis D^2 statistics were used for assessing the genetic divergence between brinjal genotypes. Tocher's approach, originally described by Rao in 1952, was used to divide the accessions into various clusters based on the D^2 values. Using the Singh and Chaudhary (1985) formula, the inter- and intra-cluster distances and the percentage of each character contributing to diversity were calculated. The Statistical software of Tamil Nadu Agricultural University Statistical Pacakge (TNAUSTAT) was used for this study.

RESULTS AND DISCUSSION

Based on Mahalanobis's D^2 method suggested by Tocher (Rao, 1952), the 46 genotypes were categorized into nine different clusters depending on their D^2 values. Among them, cluster I was the largest with 15 genotypes followed by Cluster IV (14 genotypes), Cluster V (7 genotypes), Cluster VII (4 genotypes), Cluster III (3 genotypes), and Cluster II, VI, and VIII with one genotype each. The clustering pattern of 46 genotypes

Table 1. List of 46 Genotypes of Brinjal (*Solanum melongena* L.)

S. No	Name of the Genotype	Place of Collection (in Tamil Nadu)
1.	Sevanthampatti	Bhuvanagiri
2.	Karapadi	Bhuvanagiri
3.	Manaparai Gundu	Tirichirapalli
4.	Dindigul Pachai	Dindigul
5.	Mul Kathiri	PKR Greens
6.	Chevandhipati Kathiri	Erode
7.	Puliyambu	PKR Greens
8.	Kateri Green	Chennai
9.	Chitamur local	Chidambaram
10.	Pudhukottai local	Pudhukottai
11.	Vellai Kathiri	PKR Greens
12.	Thirunelveli Vellai Kathiri	Ambasamudhiram
13.	Green Round	Coimbatore
14.	Kannadi Kathiri	Erode
15.	Pachai Neelam	PKR Greens
16.	Ven Nira Ootha Kathiri	Karur
17.	Pudhukottai local-2	Pudhukottai
18.	Chidamabram local	Shivapuri
19.	Perambattu local	Chidambaram
20.	Half Stripped Brinjal	Karur
21.	Ottanchathiram Kathiri	Palani
22.	Ven Vari Kathiri	PKR Greens
23.	Pachai Kathiri	PDR Greens
24.	Erode Express	Erode
25.	Vari Kathiri	PDR Greens
26.	Vellore Mul Kathiri	Vellore
27.	Myna Kathiri	Salem
28.	Annamalai gold	Salem
29.	Pure White Brinjal	Chidambaram
30.	Ven Vari Urundai	Uzhavan Angaadi
31.	Velir Pachai Kathiri	Chidambaram
32.	Vellai Mul Kathiri	Uzhavan Angaadi
33.	Ootha Vari Vellai Kathiri	Karur
34.	Off White Brinjal	Pudhukottai
35.	Ootha Urundai Kathiri	Chidambaram
36.	Full Striped Brinjal	PKR Greens
37.	Purple Beauty	Salem
38.	Purple Long	PKR Greens
39.	Green Long	PKR Greens
40.	Pachai Vari Kathiri	Uzhavan Angaadi
41.	Violet Brinjal	Uzhavan Angaadi
42.	Pachai Ootha Kathiri	Karur
43.	Dhruva	Coimbatore
44.	Ven Vari Pachai	PDR Greens
45.	White Brinjal	Chennai
46.	Green Small Round	Karur

is presented in Table 3. The genetic diversity among the genotypes was differentiated into discrete clusters, indicating that the materials may be a viable source for choosing parents with a range of genetic backgrounds for a hybridization program. Ravali *et al.,* (2017) observed ten clusters among 35 genotypes, in which Cluster V (10 genotypes) was the largest cluster. In contrast, Gurve *et al.* (2019) observed only three clusters among 20 genotypes. The largest cluster was Cluster I comprising 18 genotypes of brinjal (*S. melongena* L.)

The average intra-cluster and inter-cluster values are mentioned in Table 4. The intra-cluster D^2 values ranged from 0.00 (cluster II, VI and VII) to 103.53 (cluster III). The intra-cluster values were lower than the inter-cluster values, indicating that the genotypes show homogeneity inside the cluster and heterogeneity between the clusters. The inter-cluster distances varied from 117.00 to 791.17. Cluster II and Cluster VII had the greatest inter-cluster distance (791.17), followed by Cluster II and VIII (673.41), and Cluster VII and Cluster V had the smallest inter-cluster distance (117.00). This

indicated that the genotypes in these clusters had a broad spectrum of genetic divergence. Islam *et al.* (2018) recommended crossing between the genotypes of clusters with wide inter-cluster distances would be beneficial to enhance the probability of isolating excellent recombinants in the segregating generations, but importance should also be given to the yield potentiality of the genotype. Kaur *et al.* (2021) cited pertinent reports on 110 local genotypes of brinjal (*S. melongena* L.), noting that the eighth and tenth clusters had the largest inter cluster distance (1584.40). Also, the inter-cluster values ranging from 35.96 to 1584.40 are different from the current study's findings.

Fig. 2 shows the percentage contribution of each attribute to genetic divergence and Fig. 1 shows the number of times each character ranked. The attribute number of flowers per inflorescence was shown to be the highest factor contributing towards genetic divergence, accounting for 23.28% of the total, followed by average fruit weight (17.68%) and days to first flowering (16.81%). These three traits contributed 57.8% of the total divergence. But, Balasubramaniyam *et al.,* (2020)

Table 2. Cluster means for 11 characters in brinjal (*Solanum melongena* L.)

S. No.	Characters	Cluster means of brinjal							
		I	II	III	IV	V	VI	VII	VIII
1	Days to first flowering	40.83	27.06	41.15	51.23	55.82	34.45	62.72	60.33
2	Plant height	90.85	109.33	67.56	85.21	81.68	75.75	74.17	86.55
3	Days to first harvest	44.34	39.48	44.67	50.88	55.02	46.69	61.50	60.55
4	Number of primary branches per plant	6.70	9.63	7.10	7.34	7.08	6.43	6.62	5.83
5	Number of flowers per inflorescence	4.53	4.00	5.12	2.91	4.13	1.02	3.81	3.50
6	Average fruit length	6.64	9.11	8.09	6.04	8.04	7.35	5.65	6.52
7	Average fruit weight	50.00	88.91	87.98	45.09	44.50	54.86	45.56	100.06
8	Fruit thickness	39.79	42.55	51.19	44.03	31.13	41.45	42.70	35.49
9	Number of fruits per cluster	2.84	3.26	2.23	1.72	2.40	1.27	2.14	1.41
10	Number of fruits per plant	34.63	58.45	24.33	28.28	29.28	27.07	28.24	20.37
11	Fruit yield per plant	1.71	5.22	2.18	1.25	1.23	1.43	1.20	2.05

Table 3. Clustering pattern of 46 genotypes of brinjal

| Clusters	Number of genotypes	Genotypes
I	15	Sevanthampatti, Vari Kathiri, Annamalai Gold, Purple Long, Ottanchathiram Kathiri, Violet Brinjal, Full Striped, Perampattu Local, Ven Vari Urundai, Ven Vari Mul, Pachai Ootha Kathiri, Pudukkottai Local, Dhruva, Dindigul Pachai, Manaparai Gundu
II	1	Karapadi
III	3	Chidambaram Local, Kannadi, Keeri
IV	14	Puliyambu, Kateri Green, Ven Vari Ootha, Pudukkottai Local-2, Velir Pachai, Ootha Vari Vellai, Ootha Urundai, Tirunelveli Vellai, Pachai Kathiri, Vellai Urundai, Mulkathiri, Erode Express, Pachai Vari Kathiri, Dindigul Vellai
V	7	Green Long, Half Striped, Myna Kathiri, Chevandhipatti Kathiri, Ven Vari Pachai, Green Round, Pachai Neelam
VI	1	White Brinjal
VII	4	Chitamur Local, Purple Beauty, Off White Brinjal, Green Small Round
VIII	1	Vellore Mulkathiri
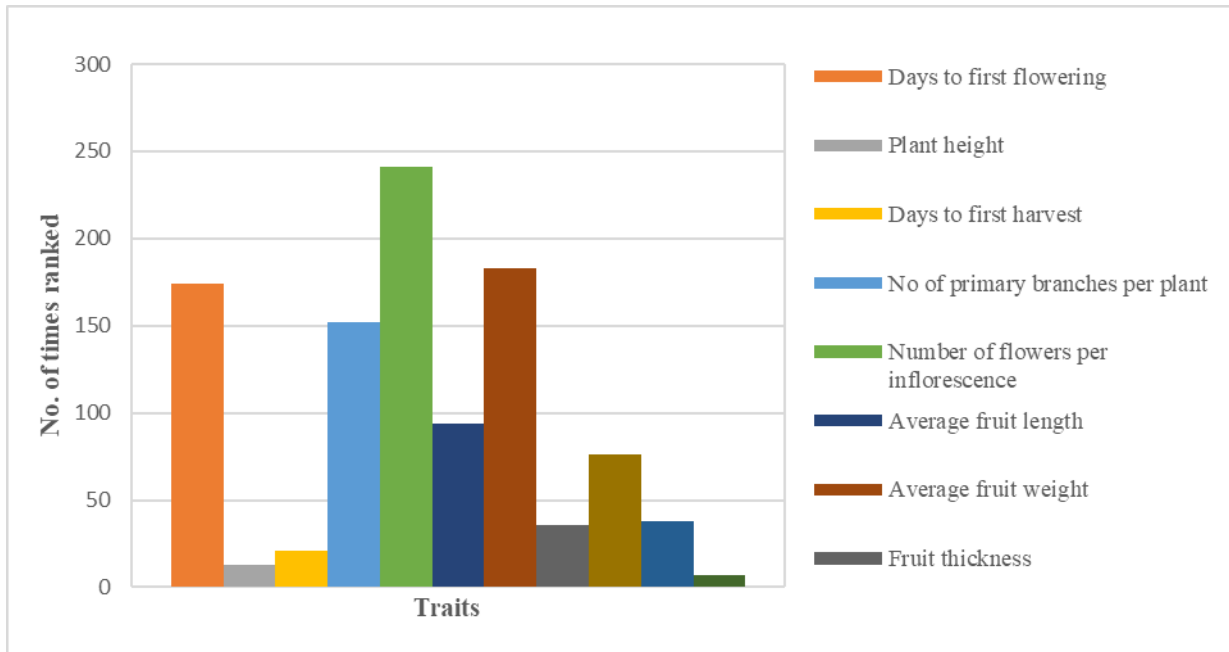
Fig. 1. *Relative contribution of traits of brinjal (Solanum melongena* L.*) to genetic diversity by rank*
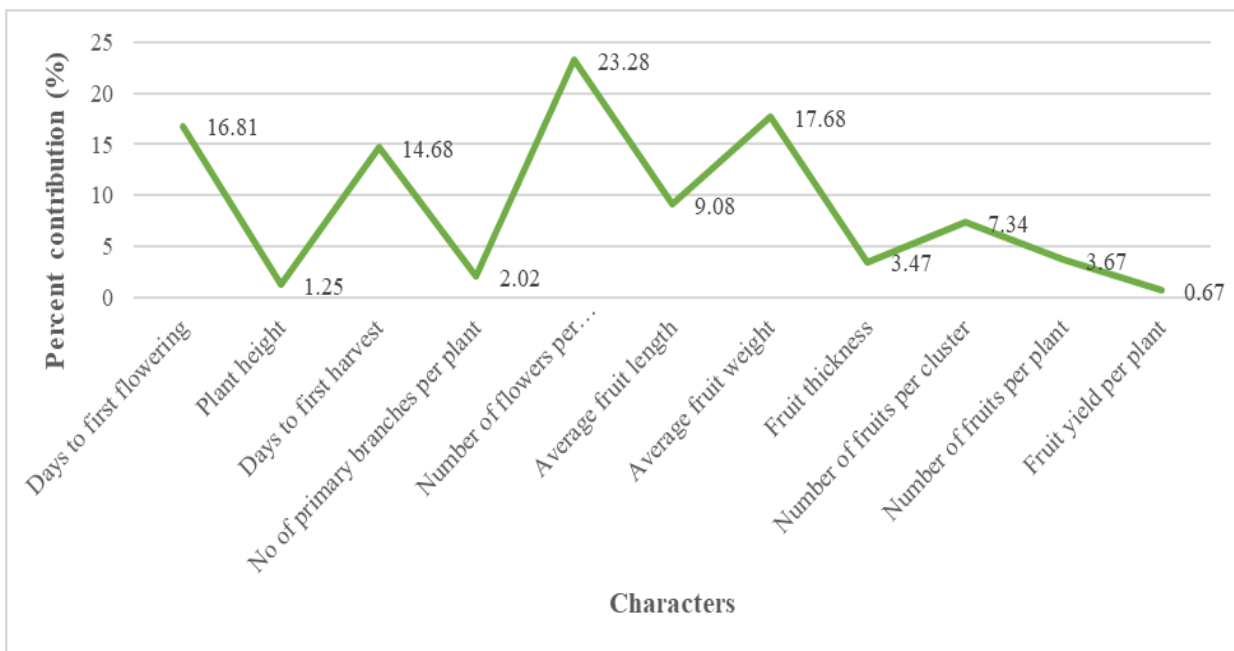

Fig. 2. *Percentage contribution of traits to genetic diversity*

Table 4. Intra and Inter-cluster D^2 Values of 46 genotypes of brinjal (*Solanum melongena* L.)

Cluster	I	II	III	IV	V	VI	VII	VIII
I	87.55	278.99	145.89	183.97	186.71	341.23	285.88	294.05
II		0.00	287.36	516.38	582.92	521.59	791.17	673.41
III			103.53	277.47	274.69	429.63	377.53	261.63
IV				98.95	146.74	196.64	171.16	187.24
V					102.73	391.50	117.00	162.46
VI						0.00	461.66	366.18
VII							100.22	148.74
VIII								0.00

reported that the number of fruits per plant (27.42%) contributed the most to divergence, which is in contrast with the present findings. Rani *et al.* (2018) stated that early flowering leads to early fruit maturity, and fruit weight directly imparts an effect on fruit yield. So, the presence of diverse range of genotypes for days to first flowering in the present study could be highly useful for producing early yielding varieties. Zhao *et al.* (2023) agreed that early maturing varieties enhance the adaptability of a crop to changing climate. The combination of these traits could be useful to produce high yielding, climate resilient varieties of brinjal (*S. melongena* L).

Establishing the values of cluster means given in Table 2, it could be figured that for the yield improvement program, the accessions of cluster II characterized by the highest mean value for plant height (109.33), number of fruits per cluster (3.26), number of fruits per plant (58.45) and fruit yield per plant (5.22), number of primary branches per plant (9.63), average fruit length (9.11), and the cluster III having highest mean values for the number of flowers per inflorescence (5.12) and fruit thickness (51.19) could be utilized and using the genotypes in these clusters for hybridization program is predicted to escalate the probability of obtaining superior segregants. The least mean value for days to first flowering was observed in cluster II, indicating that this cluster's genotypes were early flowering and can be considered as a parent, if the objective of drought breeding. Banerjee *et al.* (2018) reported in their study comprising 38 genotypes of brinjal (*S. melongena* L.) that Cluster II and Cluster IV could be utilized for breeding an early variety.

Conclusion

The present study showed substantial genetic divergence across the 46 brinjal (*S. melongena* L.) genotypes. The factors contributing the most to genetic diversity were average fruit weight, days to first flowering, and number of flowers per inflorescence. Selection of diverse parents for fruit weight could yield recombinants with increased productivity per plant. Similarly, identifying brinjal varieties that exhibit early flowering allows for quicker harvest and reduced crop duration. Increasing the number of flowers per inflorescence can enhance pollination and improve fruit set, further boosting the yield. Overall, the traits in the studied genotypes could be exploited for producing high-yielding early maturing varieties of brinjal that adapt to changing climatic conditions. The choice of parents for hybridization between clusters II and III can result in high levels of hybrid vigor and good recombination. Using molecular markers could further aid in identifying superior genotypes and accelerating the breeding process.

Conflict of interest

The authors declare that they have no conflict of interest.

REFERENCES

1. Kiranmai, C., Pullaiah, T. & Rajam, M. V. (2021). Genetically Modified Brinjal (*Solanum melongena* L.) and Beyond. *Genetically Modified Crops: Current Status, Prospects and Challenges Volume* 2, 31-52.

2. Ghosh, S. K. (2022). Eggplant (*Solanum melongena* L.) and Climate Resilient Agricultural Practices. *New Delhi Publishers, New Delhi*. Page 1-24. DOI: 10.30954/NDP-climatev2.4

3. Mahalanobis P. C. (1936). On generalized distance in statistics. *Proceedings of National Institute of Science.* 2, 49- 55. http://hdl.handle.net/10263/6765

4. Rao, C. R. (1952). Advanced statistical methods in biometrical research. *John Wiley and Sons, inc., New York*, 357-363.

5. Ravali, B., Ravinder Reddy, K., Saidaiah, P. & Shivraj, N. (2017). Genetic Diversity in Brinjal (*Solanum melongena* L.). *Int. J Curr. Microbiol. App. Sci.*, 6(6), 48-54. https://doi.org/10.20546/ijcmas.2017.606.005

6. Islam, M. T., Chhanda, R. A., Pervin, N., Hossain, M. A. & Chowdhury, R. U. (2018). Characterization and genetic diversity of brinjal germplasm. *Bangladesh Journal of Agricultural Research*, 43(3), 499-512. http://dx.doi.org/10.3329/bjar.v43i3.38396

7. Gurve, V. R., Waskar, D. P., Khandare, V. S. & Mehtre, S. P. (2019). Genetic diversity studies in brinjal (*Solanum melongena* L.). *Int. J. Chemical Studies*, 7(6), 730-733. http://dx.doi.org/10.13140/RG.2.2.31073.12649

8. Banerjee, S., Yashpal Singh Bisht & Alka Verma (2018). Genetic Diversity of Brinjal (*Solanum melongena* L.) in the foot hills of Himalaya. *Int. J. Curr. Micro. Appl. Sci.,* 7(4), 3240- 3248. http://dx.doi.org/10.20546/ijcmas.2018.704.367

9. Oladosu, Y., Rafii, M. Y., Arolu, F., Chukwu, S. C., Salisu, M. A., Olaniyan, B. A., Fagbohun, I. K. & Muftaudeen, T. K. (2021). Genetic Diversity and Utilization of Cultivated Eggplant Germplasm in Varietal Improvement. *Plants*, 10, 1714. https://doi.org/10.3390/ plants10081714

10. Kaur, Sukhninder & Sidhu, Mohinder & Dhatt, Ajmer. (2021). Genetic diversity analysis through cluster constellation in Brinjal (*Solanum melongena* L.). *Genetika*, 53, 629-640. DOI: http://dx.doi.org/10.2298/GENSR2102629K

11. Rajan, N., Debnath, S., Dutta, A. K., Pandey, B., Singh, A. Kr., Singh, R. Kr., Singh, A. K. & Dugbakie, B. N. (2022). Elucidation of nature of gene action and estimation of combining ability effects for fruit yield improvement and yield attributing traits in brinjal landraces. *Journal of Food Quality*, 1-12. https://doi.org/10.1155/2022/8471202

12. Rakha, M., Prohens, J., Taher, D., Wu, T. H., & Solberg, S. Ø. (2021). Eggplant (*Solanum melongena, S. aethiopicum* and *S. macrocarpon*) breeding. *Advances in Plant Breeding Strategies: Vegetable Crops: Volume 9: Fruits and Young Shoots*, 163-203. https://doi.org/10.1007/978-3-030-66961-4_5

13. Zhao, H., Xianzhong Huang, Zhaoen Yang, Fuguang Li & Xiaoyang Ge (2023). Synergistic optimization of crops by

combining early maturation with other agronomic traits. *Trends in Plant Science*, 1360 - 1385. https://doi.org/10.1016/j.tplants.2023.04.011.

14. Rani, M., Kumar, S. & Kumar, M. (2018). Estimation of heterosis for yield and its contributing traits in brinjal. *Journal of Environmental Biology*, 39(5), 710-718.

https://doi.org/10.22438/jeb/39/5/mrn-609

15. Balasubramaniyam, K., Haripriya, K., Kumar, T. B. & Elangaimannan, R. (2020). Genetic Diversity in Brinjal (*Solanum Melongena* L.). *Plant Archives*, 20(2), 3754-3758. https://doi.org/10.51470/plantarchives.2021.v21.s1.285