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Research Article

Genetic diversity of brinjal (*Solanum melongena* L.) and its wild relatives

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Abstract

Genetic divergence analysis in brinjal genetic resources consisting of landraces, related cultivated species and wild relatives based on 22 morphological descriptors revealed distinct variation between cultivated and wild genotypes for the plant, flowering and fruiting characters. The multivariate D² analysis grouped the 30 accessions into eight clusters revealing a clear separation of wild relatives and cultivated types. The characters fruit yield per plant, leaf size and fruit number had high contribution towards the genetic divergence. SM- 27 (cluster V), SM- 25 (cluster III) and SM-23, SM-24, SM-20, SM-18, SM-10 and SM- 8 (cluster I) were the promising accessions identified based on superior performance for three yield attributes viz., fruit weight, number of fruits per plant and fruit yield per plant. The accessions SM- 25, SM- 27, SM- 28 (*Solanum incanum*) and SM-30 (*Solanum insanum*) of highly divergent clusters III, V and VIII respectively were identified as potential parents for future introgression breeding.

Keywords: Genetic divergence, cluster analysis, wild relatives, *Solanum melongena*

INTRODUCTION

Brinjal, eggplant or aubergine (*Solanum melongena* L.) belonging to Solanaceae family is a widely cultivated species in America, Europe and Asia. The other related species viz., scarlet eggplant (*S. aethiopicum* L.) and the gboma eggplant (*S. macrocarpon* L.), are cultivated mainly in Africa (Daunay *et al.*, 2001). It is an important source of phenols, vitamins and minerals with antioxidant, anti-microbial, hepatoprotective and cardio-protective properties (Pohl *et al.*, 2019). At present India is the second largest producer of brinjal after China at the global level with great increase in production (12660 MT) and area (728 ha) in the last years (NHB; 2018-2019). In spite of huge morphological variability, brinjal is having narrow genetic base which is the result of the major bottleneck of domestication syndrome and crop improvement (Meyer *et al.*, 2012). The wild relatives of brinjal are reported to have resistance and tolerance to biotic and abiotic stresses (Rotino *et al.*, 2014; Anushma *et al.*, 2018) which can

meet the challenges in the face of climate change, but still remain neglected as a potential source for development of new cultivars in brinjal as in case of tomato (Diez and Nuez, 2008).

One of the major hindrances in the utilization of wild species in the breeding program is the dearth of trait information. Even though lots of studies have been conducted in taxonomy and phylogeny of brinjal, the information regarding growth, reproductive and agronomic traits of importance in wild resources are lacking. The utilization of plant genetic resources for crop improvement primarily depends on the accurate assessment of the pattern and level of genetic diversity in these resources. Multivariate techniques are used for assessment of genetic divergence, classification of germplasm into different groups and selection of diverse parents to develop transgressive segregates or hybrids

for exploiting heterosis. Mahalanobis D^2 statistic is one such multivariate technique that helps in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components to the total divergence. Against this background, the present study was conducted to assess the genetic diversity in brinjal accessions collected from North Kerala including its wild relatives using morphological descriptors with the aim to identify the best genotypes for further crop improvement.

MATERIALS AND METHODS

The study was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Padannakkad, Kerala Agricultural University during 2019-2020. The experimental material consisted of 30 genotypes of brinjal comprising 25 local cultivars and five wild relatives collected from different localities of North Kerala as well as those indentified from Regional station NBPGR, Thrissur (Table 1). One-month-old seedlings of the 30 accessions were planted in Randomized Block Design (RBD) with three replications. Observations were recorded for 22 quantitative characters based on IPGRI (1990) descriptor. These included the vegetative characters like plant height (cm), plant breadth (cm), number of primary branches, leaf blade length (cm), leaf blade width (cm), petiole length (mm), flowering characters like days to first flowering, days to 50 per cent flowering, number of flowers per inflorescence, number of

long-styled flowers per inflorescence, number of medium-styled flowers per inflorescence, relative style length (mm) and fruit characters like fruit length (cm), fruit diameter (cm), relative fruit calyx length (%), fruit pedicel length (mm), fruit weight (g), number of days from anthesis to fruit set, number of days from fruit set to maturity, number of fruits per plant, number of seeds per fruit and fruit yield per plant (g).

The data obtained were subjected to statistical analysis and the diversity of 30 brinjal genotypes was assessed using the multivariate technique Mahalanobis (1936) D^2 statistic. The cluster analysis was performed using as dissimilarity measure and the inter and intra cluster distances were calculated and dendrogram constructed using Tocher's optimization method as mentioned by Rao (1952).

RESULTS AND DISCUSSION

The results of ANOVA (Table 2) showed significant differences for all the quantitative characters indicating presence of high genetic variability. The mean performance of 30 genotypes for 22 quantitative characters revealed distinct variation between cultivated and wild genotypes for the plant, flowering and fruiting characters (Table 3).

The wild relatives had shown a wider variation for plant height ranging 28.89 cm (SM-30 *S. insanum*) to 86.46 cm (SM-22 *S. mammosum*) when compared with cultivated

Table 1. Details of 30 brinjal accessions studied

Accession number	Place of collection	Fruit colour at commercial ripening	Accession number	Place of collection	Fruit colour at commercial ripening
SM-1	Malappuram	Green	SM-16	Malappuram	Milky white
SM-2 (<i>S. macrocarpon</i>)	Kannur	Green	SM-17	Malappuram	Green
SM-3	Malappuram	Green	SM-18	Malappuram	Purple
SM-4	Malappuram	Purple	SM-19	Malappuram	Green
SM-5	Malappuram	Milky white	SM-20	Kozhikode	Purple
SM-6	Kozhikode	Purple	SM-21	Malappuram	Purple
SM-7	Kozhikode	Milky white	SM-22 (<i>S. mammosam</i>)	Kasaragod	Yellow
SM-8	Malappuram	Purple	SM-23	Kasaragod	Purple
SM-9	Kozhikode	Purple	SM-24	Kasaragod	Purple
SM-10	Kannur	Purple	SM-25	NBPGR	Green
SM-11	Kannur	Purple	SM-26	NBPGR	Purple
SM-12	Kannur	Green	SM-27	NBPGR	Green
SM-13	Malappuram	Green	SM-28 (<i>S. incanum</i>)	NBPGR	Green
SM-14	Wayanad	Purple	SM-29 (<i>S. gilo</i>)	NBPGR	Green
SM-15	Kozhikode	Purple	SM-30 (<i>S. insanum</i>)	NBPGR	Green

Table 2. Analysis of Variance for 30 brinjal genotypes

S.No	Characters	Mean Sum of Square		
		Replication	Genotype	Error
1	Plant height (cm)	8.481	341.875**	1.696
2	Plant breadth (cm)	24.096	347.792**	4.485
3	Number of primary branches	0.025	8.566**	0.057
4	Leaf blade length (cm)	0.036	29.937**	0.008
5	Leaf blade width (cm)	0.06	25.701**	0.009
6	Petiole length (mm)	0.089	8.896**	0.008
7	Days to first flowering	0.578	46.885**	0.371
8	Days to 50 per cent flowering	2.411	82.632**	0.285
9	Number of flowers per inflorescence	0.131	5.171**	0.054
10	Number of long styled flowers	0.036	2.249 **	0.081
11	Number of medium styled flowers	0.045	0.623**	0.034
12	Relative style length (mm)	0.016	0.597**	0.016
13	Fruit length (cm)	0.02	63.115**	0.011
14	Fruit diameter	0.005	9.377**	0.004
15	Relative fruit calyx length (%)	0.025	468.62**	1.51
16	Fruit pedicel length (cm)	0.026	4.078**	0.012
17	Fruit weight (g)	9.377	3714.184**	8.695
18	Number of days from anthesis to fruit set	1.211	85.58**	1.361
19	Number of days from fruit set to maturity	5.7	121.96**	1.781
20	Number of fruits/plant	0.184	45.348**	0.343
21	Fruit yield /plant (g)	1054.56	518657.89**	1405.82
22	Number of seeds/fruit	1196.98	323313.47**	1780.4

* Significant at 5 per cent level ** Significant at 1 per cent level

S. melongena (46.01-77.2 cm). The plant spread ranged from 58.37 cm (SM-14) to 96.75 (SM-30 ;*S. insanum*). The flowering duration parameters such as days to first flowering and 50% flowering are indicators of earliness as it allows for early harvest in brinjal. Days to first flowering ranged from 43 to 49 days and days to 50% flowering ranged from 43 to 53 days in *S. melongena*. The wild relatives required more days for first flowering ranging from 43 (*S. macrocarpon*) to 60 days (*S.gilo*) and days to 50% flowering 49 days (*S .macrocarpon*) to 71 days(*S. gilo*) which is in agreement with the observations of Lagat (2016) in case of *S.gilo*. Nyadanu *et al.* (2014) reported 87-100 days for days to 50% flowering in *S. macrocarpon* accessions of Ghana. *S. macrocarpon* is cultivated in Ghana for both leaves and fruits, therefore the divergent results in this case may be related to the distinct agroclimatic zones of research as well as cultivar variations.

The wild type SM-29 (*S. gilo*) had maximum (6.33) number of flowers per inflorescence followed by *S. melongena* accession SM-21 (5.33). The least number of flowers was recorded in SM-11 (1.00) and wild accessions SM-2 and SM-30 (2.00) among all the genotypes studied. This

is in confirmation with the findings of Page *et al.* (2019) and Ranil *et al.* (2017) in these respective species. The number of flowers per inflorescence has great implications in brinjal breeding as a lower value of this trait helps in maintaining uniformity in fruit size (Sekara and Bieniasz, 2008).

In the present study, only the long-styled and medium-styled flowers per inflorescence were counted as these are considered as functionally fertile flowers (Hazra *et al.*, 2003). The number of long-styled flowers was more than the medium-styled flowers per inflorescence in all *S. melongena* and wild relatives except SM-7 and SM-24. The accessions SM-25 and *S. mammosum* had shown only long-styled flowers with complete absence of medium-styled flowers per inflorescence. According to Karapanos *et al.* (2008), the percentage of long-styled and medium-styled flowers is a genotype dependent characteristic and the long-styled flowers are considered responsible for more effective fruit set in brinjal. They also reported that fruit set is more influenced by the relative style length *i.e.* relative position of stigma from the anther pore. In the present study, the relative style length was recorded only in long-styled flowers. All such accessions

Table 3. Mean performance of 22 characters in 30 brinjal genotypes

Accessions	Plant height [cm]	Plant breadth [cm]	Number of primary branches	Leaf blade length [cm]	Leaf blade width [cm]	Petiole length [mm]	Days to first flowering	Days to 50% flowering	Number of flowers/ inflorescence	Number of long-styled flowers/ inflorescence	Number of Medium styled flowers/ inflorescence
SM-1	64.51	67.45	6.73	16.64	9.23	42.5	44.33	50.67	5.00	3.70	1.13
SM-2 (W)	67.24	63.87	4.73	18.72	17.09	77.5	43.00	48.67	2.00	1.07	0.80
SM-3	65.52	63.95	5.67	16.06	13.23	69.3	43.33	48.33	2.80	1.47	0.93
SM-4	77.22	84.10	9.40	18.47	8.83	53.6	44.33	51.33	3.00	1.67	1.27
SM-5	71.67	85.15	7.73	19.71	12.38	67.0	45.33	50.67	1.67	1.07	0.80
SM-6	66.37	62.42	5.13	13.88	11.38	34.8	44.00	48.67	1.17	1.00	0.33
SM-7	67.84	66.79	8.13	21.58	13.31	65.8	44.00	49.67	2.00	0.87	1.33
SM-8	70.11	86.28	6.67	15.82	9.92	46.5	45.33	51.33	2.73	1.33	0.67
SM-9	46.01	70.43	7.93	15.73	11.72	55.0	44.67	49.67	2.13	0.93	0.93
SM-10	66.80	67.92	5.47	19.15	13.95	72.1	43.00	48.67	1.60	1.00	0.80
SM-11	60.42	60.27	4.73	19.74	12.76	53.0	42.67	48.00	1.00	0.87	0.89
SM-12	53.78	61.91	6.73	16.66	13.68	81.6	44.33	50.33	2.20	1.47	0.87
SM-13	53.78	62.55	6.87	14.14	9.66	44.3	44.33	50.67	2.60	2.07	0.87
SM-14	71.33	96.75	8.67	19.40	13.69	47.5	44.67	51.00	2.00	1.07	0.80
SM-15	68.02	87.05	7.67	15.31	10.97	61.5	44.67	51.00	4.00	2.47	1.60
SM-16	68.15	71.75	6.00	17.66	16.44	68.7	43.33	47.67	2.40	1.07	0.60
SM-17	63.86	68.71	5.80	18.66	14.68	56.2	43.67	48.33	3.60	1.87	1.47
SM-18	63.02	80.67	10.3	18.62	12.42	75.8	44.33	50.00	4.27	2.67	1.80
SM-19	56.97	58.66	7.60	18.42	13.37	67.6	44.67	50.00	4.53	3.00	1.67
SM-20	68.44	92.41	8.80	20.68	12.23	65.1	43.33	48.67	2.53	0.93	0.80
SM-21	71.60	68.30	6.07	20.14	16.78	47.9	44.33	49.33	5.33	2.83	1.53
SM-22 (W)	86.46	74.45	5.73	12.84	15.51	96.5	55.67	64.00	4.00	3.67	0.00
SM-23	59.81	85.57	9.13	16.72	11.51	66.1	43.33	43.33	2.80	1.13	1.27
SM-24	69.84	73.24	4.47	19.67	13.41	67.0	43.67	50.00	2.07	1.07	1.27
SM-25	47.00	67.55	6.73	13.54	8.34	33.4	49.33	53.67	2.77	1.67	0.00
SM-26	57.93	78.23	11.4	17.74	11.34	64.3	45.00	50.33	2.93	1.87	0.87
SM-27	67.25	85.49	7.67	19.73	14.24	57.4	44.33	50.33	3.73	1.93	1.40
SM-28 (W)	64.49	65.09	7.27	11.61	9.29	25.1	46.33	54.33	5.07	2.70	1.73
SM-29 (W)	74.33	65.97	8.67	17.77	16.50	69.5	60.33	71.33	6.33	3.00	1.07
SM-30 (W)	28.89	58.37	8.13	6.62	3.54	16.1	52.67	59.67	2.00	1.07	0.80
Mean	63.96	72.71	7.2	17.05	12.38	58.29	45.54	51.32	3.01	1.75	1.01
CV (%)	2.04	2.91	3.32	0.51	0.75	1.55	1.34	1.04	7.75	16.3	18.2
CD	2.13	3.46	0.39	0.14	0.15	0.15	0.99	0.87	0.38	0.47	0.3

W- Wild relatives

Table 3. (Cont.)

Accessions	Relative style length [mm]	Fruit length [cm]	Fruit diameter [cm]	Relative calyx length [%]	Fruit pedicel length [mm]	Fruit weight [g]	Number of days from anthesis to fruit set	Number of days from set to maturity	Number of fruits/plant	Fruit yield/plant [g]	Number of seeds/fruit
SM-1	1.37	12.48	3.98	11.80 (0.12)	34.5	71.67	14.00	31.00	14.00	765.33	715
SM-2 (W)	1.27	4.52	5.48	77.67 (0.89)	40.8	67.89	16.00	32.00	7.11	458.67	486.33
SM-3	1.13	5.47	4.46	11.27 (0.11)	43.6	37.67	12.67	28.33	9.11	565.33	1019.3
SM-4	2.77	11.27	3.41	21.67 (0.22)	43.8	100.0	17.00	30.67	8.67	770.67	681
SM-5	1.17	15.48	5.58	10.20 (0.10)	44.3	84.44	11.33	31.00	9.33	770.33	656
SM-6	1.17	8.19	6.47	20.87 (0.21)	19.7	95.00	16.00	39.00	9.00	902	907.67
SM-7	1.07	8.01	2.99	10.23 (0.10)	30.2	69.67	15.00	30.67	10.67	668.22	878
SM-8	1.00	10.00	4.42	10.17 (0.10)	38.1	88.33	17.33	31.33	11.67	1019.33	686
SM-9	1.00	4.99	4.02	10.27 (0.10)	19.4	62.00	15.33	30.67	9.33	592.33	939.33
SM-10	1.07	10.53	4.99	10.70 (0.11)	34.0	73.33	13.00	31.33	12.11	1285.67	642
SM-11	1.13	21.32	4.42	20.60 (0.21)	34.7	88.67	12.00	34.00	11.33	983	843.67
SM-12	0.93	5.12	3.02	22.03 (0.22)	31.2	29.04	12.00	32.67	11.45	292.67	492.67
SM-13	1.10	9.49	2.71	10.33 (0.10)	23.7	62.33	14.00	31.67	7.67	442.44	776.67
SM-14	1.20	9.14	8.01	20.53 (0.21)	44.4	79.00	11.00	33.00	12.00	905.33	993.67
SM-15	1.07	9.38	5.34	15.33 (0.15)	29.1	102.3	14.00	32.00	12.00	1144	614
SM-16	0.90	12.73	3.12	11.67 (0.12)	24.3	56.26	12.67	32.33	11.22	576.67	728
SM-17	1.03	11.98	3.45	10.63 (0.11)	41.6	72.22	13.33	32.33	13.67	867	785
SM-18	1.00	15.17	3.90	10.90 (0.11)	40.8	97.48	13.33	31.33	12.89	1185.56	477.67
SM-19	0.90	7.96	6.90	20.63 (0.21)	44.3	68.67	11.00	34.33	15.11	996.78	1067.3
SM-20	1.03	7.99	3.42	22.30 (0.22)	35.0	92.67	14.67	34.00	13.00	1275.67	629.67
SM-21	1.07	11.47	2.78	10.13 (0.10)	38.6	62.00	15.00	32.00	12.67	799.55	996.67
SM-22 (W)	0.96	4.40	3.13	12.67 (0.13)	19.5	20.22	31.00	31.67	26.67	519.45	174.67
SM-23	1.10	14.96	4.82	10.60 (0.11)	54.2	108.0	16.67	33.33	12.67	1434.11	1591.33
SM-24	1.00	18.03	5.46	11.63 (0.12)	44.9	99.67	11.00	30.67	11.67	1233.67	890.67
SM-25	0.87	5.53	4.40	10.63 (0.11)	27.4	96.33	18.00	45.00	11.22	1041	1222
SM-26	1.00	8.36	4.59	11.10 (0.11)	20.8	67.33	13.67	45.33	8.22	614.11	591.67
SM-27	1.60	11.45	10.5	20.13 (0.20)	59.4	192.7	12.67	46.00	11.67	2146.44	1050
SM-28 (W)	1.23	4.17	3.66	21.10 (0.21)	31.9	56.85	14.33	31.33	18.89	1072.89	1510.67
SM-29 (W)	0.93	2.75	2.68	11.67 (0.12)	17.2	11.43	35.67	53.67	18.22	199.22	261
SM-30 (W)	1.10	2.00	2.01	21.50 (0.22)	7.7	4.61	11.67	49.33	8.22	63.33	211
Mean	1.14	9.48	4.47	16.7 (0.17)	33.97	73.93	15.18	34.73	12.05	853.03	783.96
CV (%)	11.7	1.12	1.45	7.36	3.12	3.99	7.69	3.84	4.86	4.4	5.38
CD	0.21	0.17	0.11	2.01	0.17	4.82	1.91	2.18	0.96	61.28	68.96

W- Wild relatives; Transformed values are given in parentheses

had short relative style length ranging from 0.87 mm (SM-25) to 1.6 mm (SM-27) except SM-4 which had relative style length of 2.7 mm.

Fruit characters such as size, weight and number showed considerable variation. The accession SM-11 had longest fruits in terms of length and SM-27 had the largest fruits in terms of diameter. The wild relatives had small sized fruits in general with a size range varying from short and small (2.0 cm; 2.01cm) in *S. insanum* to intermediate and large (4.52cm; 5.48cm) in *S. macrocarpon* which is in agreement with the observations of Page *et al.* (2019) and Ranil *et al.* (2017). The cultivated genotypes showed wide range of variability from 29.04 g (SM -12) to 192.7 g (SM-27) for fruit weight. Similar findings were reported by Kumar *et al.* (2013) in the *S. melongena* collection of Tamil Nadu. In wild relatives, the fruit weight was comparatively less due to its small fruit size. According to Banik *et al.* (2018), fruit weight in brinjal is highly dependent on the flowering habit, fruits produced from solitary flower being heavier than fruits produced from flower in clusters.

The duration from flowering to fruit set was in general two weeks for both *S. melongena* and wild relatives with exception of *S. gilo* which recorded maximum duration (35.67 days). The wild relatives and the cultivated accessions showed difference in the maturity duration. The maturity duration in *S. melongena* ranged from with maximum duration in SM27(46 days) and minimum SM-3 (28.33 days) The duration of fruit development from anthesis to maturity is a trait showing high variability between species and is strongly related to biomass composition at various stages of fruit development (Roch, 2020). The wild relatives showed wide range of variability for number of fruits per plant with maximum number of fruits recorded in *S. mammosam* (26.67) and minimum in *S. macrocarpon* (7.11). The *S. gilo* and *S. incanum* recorded higher number of fruits (18) than *S. melongena*. In the present study, *S. melongena* cultivars did not show much variability with a range from 7 (SM-7) to 15 (SM-19).

Fruit yield per plant in brinjal is a complex quantitative character dependent on various other fruit component

characters, flowering characters and their mutual interrelationships. The *S. melongena* genotypes showed wide range of variation for this character with maximum of 2146.44 g in SM-27 which also recorded maximum fruit weight and minimum in SM-12 (292.67 g) which also recorded least fruit weight. Seven accessions viz., SM-8, SM-10, SM-20, SM-18, SM-23, SM-24 and SM-25 had shown fruit yield more than 1000 g. These findings are in confirmation with those reported by Gavade and Ghadage (2015). However, Ahmed *et al.* (2014) reported a very high fruit yield of 5320 g per plant in a study. The wild relatives recorded fruit yield ranging from 63.33 g in SM 30 (*S. insanum*) to 1072.89 g in SM 28 (*S. incanum*). The wild relatives had small sized and lighter fruits which resulted in low fruit yield.

The clustering based on Tocher's method (Fig.1) grouped the 30 brinjal genotypes into eight clusters. The clustering pattern of 30 genotypes (Table 4) revealed a clear separation of wild relatives and cultivated types. All *S. melongena* genotypes were grouped into cluster I (22 Nos.), cluster II (SM-11), cluster III (SM-25) and cluster V (SM-27) with those collected from North Kerala grouped into one single cluster (cluster I) suggesting the parallelism between geographical diversity and genetic diversity. This may be due to the fact that maximum accessions (11 Nos.) were collected from Malappuram district and its neighboring district Kozhikode (4) and the remaining from Kannur, Kasaragod and Wayanad. All the wild accessions (Fig.2) were grouped in five different clusters (III, IV, VI, VII and VIII). The accession SM-28 (*S. incanum*) was grouped into cluster III along with cultivated accession SM-25 obtained from NBPGR. Similar observations were made by Mutege *et al.* (2015) in the diversity analysis consisting of natural populations of wild/weedy eggplant and cultivated populations in Southern India where the wild brinjal populations appeared to cluster according to their geographic origin. The closest wild relatives of brinjal are *S. insanum* and *S. incanum* with *S. insanum* being the wild progenitor of brinjal having Asian origin. *Solanum incanum* is considered to be of African origin occurring widely in dry regions (Knapp *et al.*, 2013). Gboma eggplant *S. macrocarpon* and scarlet eggplant *S. gilo* belong to the brinjal domesticated and cultivated

Table 4. Clustering pattern of quantitative characters of 30 brinjal genotypes

Clusters	Accessions
Cluster I	SM-1, SM-3, SM-4, SM-5, SM-6, SM-7, SM-8, SM-9, SM-10, SM-12, SM-13, SM-14, SM-15, SM-16, SM-17, SM-18, SM-19, SM-20, SM-21, SM-23, SM-24, SM-26
Cluster 2	SM-11
Cluster 3	SM-25, SM-28
Cluster 4	SM-2
Cluster 5	SM-27
Cluster 6	SM-29
Cluster 7	SM-22
Cluster 8	SM-30

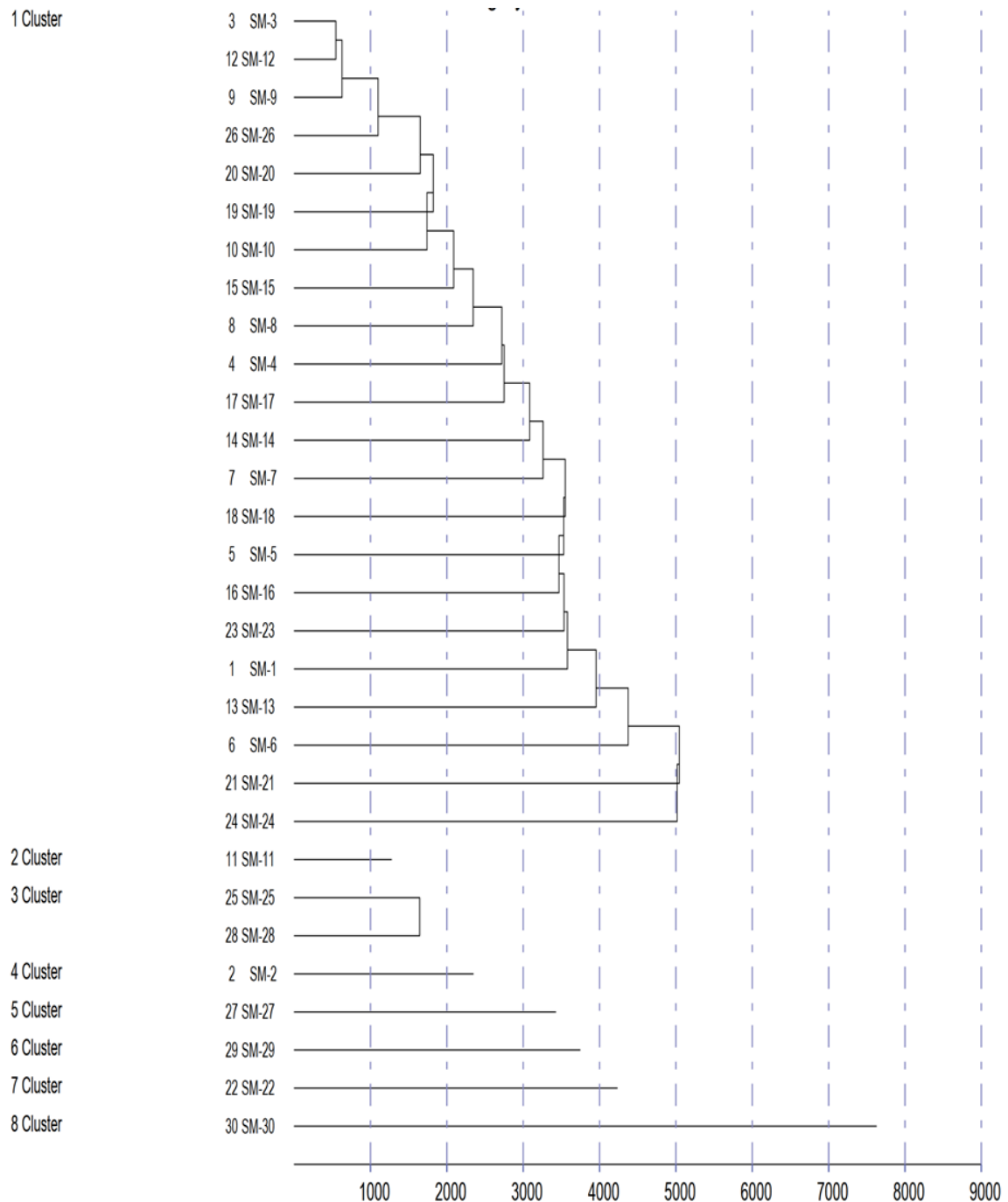


Fig.1. Dendrogram showing the relationship among 30 brinjal genotypes developed by Tocher method based on 22 quantitative characters

in Africa conventionally grouped as ‘Occidental’ and differ from *S. melongena* grouped as ‘Oriental’ grown in East and Southeast Asia (Cericola *et al.*, 2013). Hence, in the present study, two accessions SM-2 and SM-29 belonging to these respective species were grouped into separate clusters Cluster IV and Cluster VI respectively. *S. mammosum* belonging to cluster VII, is considered to be an invasive weedy species introduced into India

as an ornamental plant for its fancy udder-shaped fruits (Singh *et al.*, 2017).

The intra-cluster distance was observed to be maximum for cluster I (3784.88) (Table 5) pointing out greater heterogeneity of genotypes within the cluster. Similar results were also reported by Sindhuja *et al.* (2019) in brinjal. According to Murty and Arunachalam (1966) the



SM-2
(*S. macrocarpon*)

SM-22
(*S. mammosum*)

SM-28
(*S. incanum*)

SM-29
(*S. gilo*)

SM-30
(*S. insanum*)

Fig. 2. Five wild relatives of brinjal included in the study

effectiveness of hybridization followed by selection is substantially determined by the choice of parents with high genetic diversity for the desired traits. As a result, such an intra cluster heterogeneity among the component genotypes discovered in this study might be used as a guideline for selecting parents for the recombination

breeding programme. The highest inter-cluster distance (44564.7) was recorded between solitary clusters VIII having *S. insanum* (SM-30) and V having SM-27 followed by cluster II (SM-11) and VIII indicating maximum divergence between these clusters. The contribution of each character towards genetic divergence was obtained

Table 5. Intra and inter-cluster distance in 30 brinjal genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	3784.88	7792.36	8400.57	5740.69	9127.76	6658.72	7388.82	27419.6
Cluster 2		0	19333.07	14200.8	14143.1	15017.1	15475.5	41962
Cluster 3			1643.19	11709.7	17094.1	11594.6	7080.64	8671.7
Cluster 4				0	10500.3	4651.88	7265.34	33117.8
Cluster 5					0	15246.8	16289.4	44564.7
Cluster 6						0	5723.43	29839.5
Cluster 7							0	20382.2
Cluster 8								0

Diagonal values indicate intra-cluster distances

Table 6. Percentage contribution of characters towards genetic divergence in 30 brinjal genotypes

Source	Contribution (%)
Fruit yield / plant	39.77
Leaf Blade width	20.92
Number of fruits /plant	16.09
Leaf Blade length	10.8
Fruit length	3.22
Petiole length	2.76
Fruit diameter	2.76
Relative fruit calyx length	1.38
Number of seeds/fruit	1.15
Fruit pedicel length	0.69
Days from anthesis to fruit set	0.46

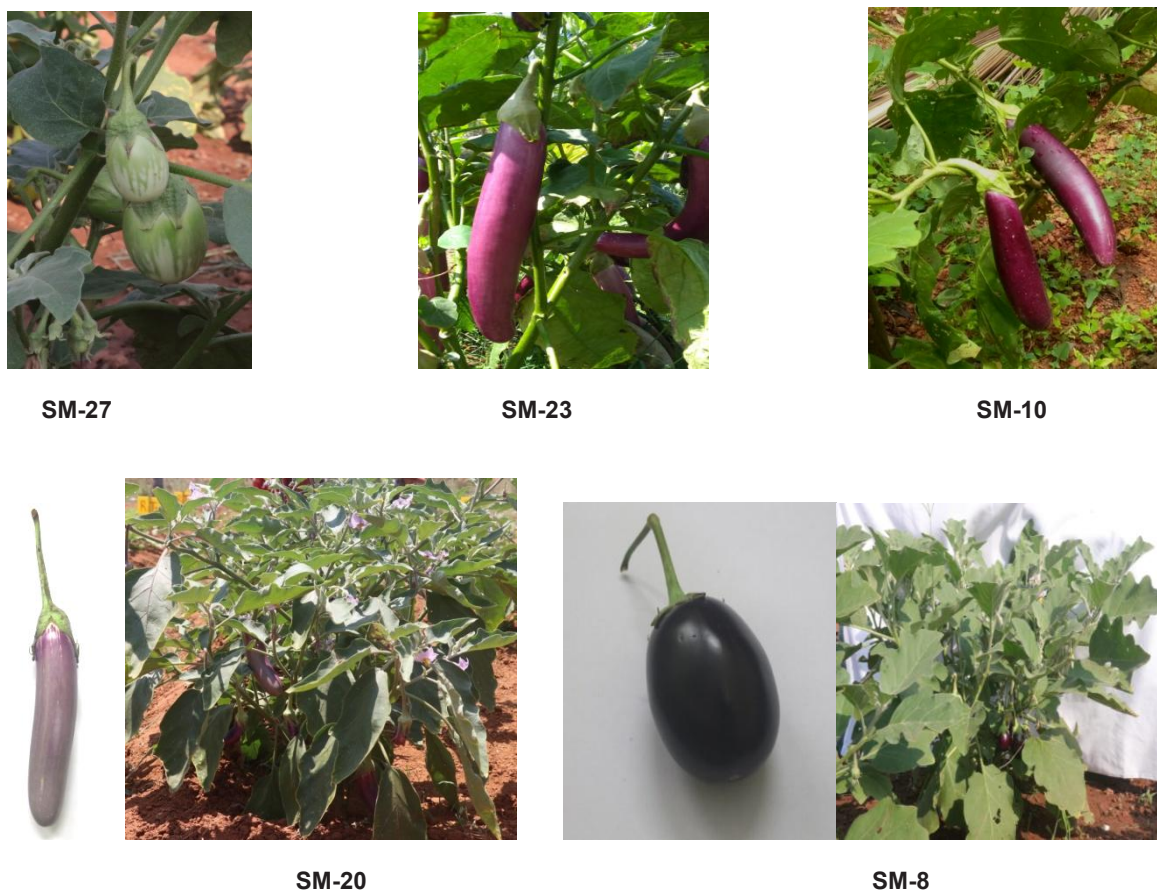


Fig. 3. Superior brinjal genotypes identified in the study

through Wilks test (**Table 6**). Among the characters fruit yield per plant exhibited the maximum contribution (39.77%) towards diversity followed by leaf blade width (20.92%) and number of fruits per plant (16.09%) which is comparable to the findings of Anbarasi and HariPriya (2021).

The crosses between genotypes showing superior performance in terms of yield and yield related traits and belonging to clusters having high inter-cluster distance are considered to yield better segregates. The *S. melongena* genotypes like SM 20, SM 10, SM 23, SM 24, SM 8 and SM 18 belonging to cluster I with maximum intra-cluster distance and the clusters showing high inter cluster distance SM 25(cluster III) and SM 27 (Cluster V) are identified as promising based on their superior performance for fruit weight, number of fruits per plant and fruit yield per plant and earliness in case of SM-10 and SM-23 (**Fig.3**). These genotypes can be used for intraspecific hybridization based on compatible colour combinations. In general the purple fruited genotypes are preferred to cross with purple fruited genotypes, and it is true with respect to green fruited and white fruited accessions also. The accessions SM-25, SM-27 and *S. insanum* of highly divergent clusters III, V and VIII

respectively are identified as potential parents for inter specific hybridization for developing introgression line (ILs) an important step towards broadening of eggplant genetic base. The wild species *S. insanum* is classified under primary gene pool (GP1) based on its crossability with cultivated *S. melongena* species as reported by Plazas *et al.* (2016) who could obtain large amount of seeds per fruit when using *S. melongena* as a female parent in hybridization with *S. insanum*. Crosses involving *S. insanum* gives partially fertile hybrid progeny as it belongs to secondary gene pool and *S. mammosum* may lead to high incompatibility as it belongs to tertiary gene pool (Nishio, 1984) and may require special techniques for recovery of hybrid progeny.

The present investigation concludes that the green fruited SM-27 with high fruit yield can be considered as one of the promising parent for future crop improvement programs. Similarly, the genotypes SM-20, SM-10, SM-23, SM-24, SM-8, SM-25 and SM-18 were identified as superior genotypes with respect to yield characters. The accessions from highly divergent clusters like cluster III (SM-28), cluster V (SM-27), and cluster VIII (SM-30) can be exploited for developing ILs which will thus allow an expeditious use of genes from the wild species in present

and future breeding programs in particular for traits related to climate change adaptation.

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