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Genetic diversity analysis in *Solanuum surattense* – An endangered medicinal plant

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Abstract
Forty nine accessions of *Solanum surattense* were collected from different parts of India and used for study at the Department of Medicinal and Aromatic Crops, Tamil Nadu Agricultural University, Coimbatore during 2020-21. The field trial was laid out in Randomized Block Design (RBD) and replicated thrice. Diversity analysis was done by Mahalanobis D^2 method utilizing 34 traits of *Solanum surattense.* The accessions were grouped into six clusters indicating the presence of a huge amount of diversity among the accessions. The maximum intra cluster distance was registered in cluster VI (137.94) followed by cluster I (123.88). The lowest intra cluster distance was recorded in cluster II (20.62). Clusters I and VI had the highest inter cluster distance (128.25) followed by clusters V and VI (115.36). Cluster IV recorded the maximum mean value for nine traits. Maximum contribution towards divergence was observed for root dry weight (33.25%) followed by dry berry weight per plant (10.29%). From this study, a great insight to select promising traits / promising accessions for further breeding programmes can be visualized. The selection of diverged parents would be useful to get more variability in segregating generations.

Key words: Genetic diversity, *Solanum surattense,* Cluster analysis, Mahalanobis D^2, Intra and inter cluster distances.

INTRODUCTION

Kantakari (*Solanum surattense* Burm. F) is the plant belonging to the brinjal family, Solanaceae. It is a spreading annual plant with thorns in all parts except flowers. This plant can be seen in dry tracts, roadsides and wastelands. Due to over exploitation for its high medicinal value and indiscriminate and destructive collection from the habitat, the species is in threatened position and lead to an endangered status (Khan and Frost, 2001). *Solanum surattense* is also valued for its antispasmodic, antitumor, cardiotonic, hypotensive and anaphylactic activities. *Solanum surattense* produces glycolalkaloids, solanine, solamargine and solasodine. Solasodine is considered as a potential alternative to diosgenin for commercial steroid drug synthesis like progesterone and cortisone (Galanes *et al.,* 1984). There are huge numbers of literature describing the uses of *Solanum surattense.* But, information on breeding or evolving newer varieties of the species is scanty. Breeding is an important tool to develop a variety for a particular crop. For every crop improvement program, understanding the available diversity of the plant species is an important aspect to develop a variety and to indulge in crossins. Hence, an experiment was done to analyse the available diversity for *Solanum surattense.*

MATERIALS AND METHODS

Forty nine accessions of *Solanum surattense* were collected from different parts of Tamil Nadu, Rajasthan,

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Table 1. Passport data of collected germplasm of *Solanum surattense*

S. No.	Accession	Place of collection	Latitude^0 (N)	Longitude^0 (E)
1	*Ss* - 1	Govinthapuram,Thanjavur, TN	11.0083	79.4674
2	*Ss* - 2	Parivallikottai, Ottapidaram, TN	8.9212	77.8746
3	*Ss* - 3	Kollankinaru, Ottapidaram, TN	8.8899	77.8703
4	*Ss* - 4	Ottapidaram, Tuticorin, TN	8.9077	78.0210
5	*Ss* - 5	Onamakulam,Ottapidaram, TN	8.9647	77.8582
6	*Ss* - 6	Sillangulam, Ottapidaram. TN	8.9655	77.9432
7	*Ss* - 7	Kilakottai, Ottapidaram, TN	10.2800	77.9452
8	*Ss* - 8	Kalappanpatti, Devakottai, TN	10.4934	77.9369
9	*Ss* - 9	Maruthanvalvoo,Ottapidaram, TN	8.8680	77.8603
10	*Ss*- 10	Kothali, Belgum, Karnataka	16.4240	74.5068
11	*Ss* - 11	Seelaipilayarpudur, Trichy, TN	13.1356	80.1621
12	*Ss* - 12	Nagayanallur, Trichy, TN	11.0204	78.2348
13	*Ss* - 13	Karur, TN	10.9601	78.0766
14	*Ss* - 14	Kattuputhur, Trichy, TN	10.9961	78.2163
15	*Ss* - 15	Jabalpur, Madhya Pradesh	23.1815	79.9864
16	*Ss* - 16	Chennampatti, Trichy, TN	11.6772	77.6537
17	*Ss* - 17	Mayanur, Trichy, TN	10.9557	78.2369
18	*Ss* - 18	Unniyur, Trichy, TN	11.0022	78.1771
19	*Ss* - 19	Aalampalayampudur,Trichy, TN	13.1369	80.1637
20	*Ss* - 20	Chinnapallipalayam, Trichy, TN	10.9727	78.1917
21	*Ss* - 21	Sullipalayam, Trichy, TN	11.2631	77.9252
22	*Ss* - 22	Kalamboli, Maharashtra	19.0328	73.1012
23	*Ss* - 23	Manmad, Maharashtra	20.2607	74.4395
24	*Ss* - 24	Yeola, Maharashtra	20.0432	74.4840
25	*Ss* - 25	Andakudi, Sivagangai, TN	9.5844	78.6881
26	*Ss* - 26	Sithakur, Pudukottai, TN	10.0093	78.9916
27	*Ss* - 27	Keerani, Sivagangai, TN	9.9192	78.9029
28	*Ss* - 28	Devakottai, TN	9.9554	78.8162
29	*Ss* - 29	Okkur, Pudukottai, TN	9.9464	78.5235
30	*Ss* - 30	Pothuvakkur, Pudukottai, TN	10.8851	78.5908
31	*Ss* - 31	Thalamalaipatti, Trichy, TN	10.7749	78.6902
32	*Ss* - 32	Kadaladi, Ramnad, TN	9.1392	78.2974
33	*Ss* - 33	Madesampalayam,Namakkal, TN	11.1726	78.0029
34	*Ss* - 34	Mohanur, Namakkal, TN	11.0599	78.1422
35	*Ss* - 35	Puliyur, Karur, TN	10.6390	78.8326
36	*Ss* - 36	Sankari, Salem, TN	11.4745	77.8691
37	*Ss* - 37	Palmadai, Namakkal, TN	11.4208	77.8810
38	*Ss* - 38	Manaparai, Trichy, TN	10.6089	78.4233
39	*Ss* - 39	Tiruparankundram, Madurai, TN	9.8823	78.0720
40	*Ss* - 40	S.Pudhupalayam,Namakkal, TN	11.2734	78.0210
41	*Ss* - 41	Kagmala, Rajasthan	24.8387	72.2778
42	*Ss* - 42	Roadside, Rajasthan	28.5972	73.2557
43	*Ss* - 43	Bhatwas – 1, Rajasthan	24.7145	72.2509
44	*Ss* - 44	Bhatwas – 2, Rajasthan	27.6195	75.1245
45	*Ss* - 45	CSWRI, Avikanagar, Rajasthan	26.3092	75.4186
46	*Ss* - 46	CSWRI,Avikanagar, Rajasthan	26.2485	75.7541
47	*Ss* - 47	Bhatathali, Karnataka	16.4065	74.3876
48	*Ss* - 48	Ottanchathiram, TN	10.4897	77.7544
49	*Ss* - 49	Adikanpatti, Madurai, TN	11.2390	78.8702
50	*Ss* - 50	Ottampatti - 1, Trichy, TN	11.1954	78.1905
51	*Ss* - 51	Ottampatti - 2, Trichy, TN	11.1954	78.1905
52	*Ss* - 52	FC & RI, Mettupalayam, TN	11.3028	76.9383
53	*Ss* - 53	Pudukottai, TN	10.3833	78.8001
54	*Ss* - 54	Erode, TN	11.3410	77.7172
55	*Ss* - 55	Arkad, TN	11.9282	79.8135
56	*Ss* - 56	Kollidamriver,Ariyalur, TN	11.3306	79.7203
57	*Ss* - 57	Chinnamanur, Theni, TN	9.8427	77.3830
58	*Ss* - 58	Aniyapuram, Namakkal, TN	11.1259	78.1674

Gujarat, Maharashtra, Karnataka, Arunachal Pradesh, Madhya Pradesh and West Bengal was given in **Table 1**. The research was conducted at the Department of Medicinal and Aromatic Crops, Tamil Nadu Agricultural University, Coimbatore during 2020-21. The field trial was laid in Randomized Block Design (RBD) and replicated thrice. All the necessary intercultural operations were carried out.

Observations on days for germination, seedling length, shoot length, root length, number of leaves, seedling leaf length, seedling leaf width, seedling fresh weight, shoot fresh weight, root fresh weight, seedling dry weight, shoot dry weight, root dry weight, seedling fresh: dry ratio, plant spread [(North-South) and (East-West)], the number of branches, the number of flower clusters per plant, leaf length, leaf width, stem girth, petiole length, internodal length, the number of thorns at the upper surface of a leaf, the number of thorns at the lower surface of a leaf, days taken for first flowering and 50% flowering, the number of berries, berry diameter, fresh single berry weight, dry single berry weight, fresh berry weight per plant, fresh to dry ratio and dry berry weight per plant were recorded at an appropriate stage of the crop using appropriate methodology. Diversity analysis was done as described by Mahalanobis D^2 method (1936) for 34 traits of *Solanum surattense.*

RESULTS AND DISCUSSION

Genetic diversity analysis was done using the data generated for 49 accessions of *Solanum surattense* for 34 characters by calculating D^2 values for all possible n(n-1)/2 pairs of combinations. The accessions were grouped into six clusters indicating the presence of a huge amount of diversity among the accessions. The composition of clusters based on D^2 values of 49 accessions of *Solanum surattense* is presented in **Table 2**. Among six clusters, cluster VI had the highest number of genotypes (33) followed by cluster I (8). The remaining clusters *viz.,* cluster II, cluster III, cluster IV and cluster V had two accessions each in their clusters. The grouping was done based on the available diversity observed and not because of their geographical distributions. This is in accordance with the findings of Rathi *et al*. (2011), Ahmed *et al.* (2014), Madhavi *et al*. (2015) in brinjal and Mithlesh kumar *et al.* (2021) in ashwagandha.

The inter and intra cluster distances of six clusters are presented in **Table 3**. The maximum intra cluster distance was registered in cluster VI (137.94) followed by cluster I (123.88). The lowest intra cluster distance was recorded in cluster II (20.62). Clusters I and VI had the highest inter cluster distance (128.25) followed by clusters V and VI (115.36). The lowest inter cluster distance (23.61) was

Table 2. Composition of clusters based on D^2 values of 49 accessions of kantakari (*Solanum surattense*)

S. No.	Cluster name	Number of genotypes	Name of genotypes
1	Cluster I	8	Ss- 1, Ss- 2, Ss - 3, Ss - 4, Ss- 5, Ss- 6, Ss- 7 and Ss- 9
2	Cluster II	2	Ss – 27 and Ss - 32
3	Cluster III	2	Ss – 18 and Ss - 48
4	Cluster IV	2	Ss – 23 and Ss - 26
5	Cluster V	2	Ss – 42 and Ss - 44
6	Cluster VI	33	Ss - 10, Ss - 11, Ss - 12, Ss - 13, Ss - 14, Ss - 15, Ss - 17, Ss - 19, Ss - 20, Ss - 21 , Ss - 22, Ss - 24, Ss - 25, Ss - 31, Ss - 33, Ss - 34, Ss - 35, Ss - 36, Ss - 38, Ss - 39, Ss - 41, Ss - 43, Ss - 45, Ss - 49, Ss - 50, Ss - 51, Ss - 52, Ss - 53, Ss - 54, Ss - 55, Ss - 56, Ss -57 and Ss – 58

Table 3. Average intra (in bold) and inter cluster D^2 distances of kantakari (*Solanum surattense)*

Cluster	I	II	III	IV	V	VI
I	**123.88**	94.25	94.16	91.97	100.34	128.25
II		**20.62**	23.61	52.77	32.52	107.47
III			**20.97**	59.46	37.88	107.72
IV				**21.21**	65.00	102.82
V					**21.27**	115.36
VI						**137.94**

recorded between cluster II and III. The highest intra and inter cluster distance indicate the presence of a wide range of diversity within the cluster and between the clusters. This finding is in line with the results of Ravali *et al.* (2017), Singh *et al.* (2006) in *Solanum melongena* and Parthsinh *et al.* (2021) in chilli.

Cluster mean values for 34 characters of *Solanum surattense* for six groups are presented in **Table 4**. Cluster IV recorded maximum mean value for nine traits *viz.,* days taken for germination (15.00), shoot length (10.93 cm), the number of leaves (5.25), seedling leaf length (6.25 cm), root fresh weight (0.05 g), root dry weight (0.01 g), seedling fresh: dry (7.72), plant spread (North-South) (112.33 cm) and the number of flower cluster per plant (20.47). Cluster I had the maximum mean values for eight traits *viz.,* seedling fresh weight (0.59 g), shoot fresh weight (0.54 g), root dry weight (0.01 g), stem girth (9.08 mm), internodal length (9.14 cm), the number of berries (89.09), fresh berry weight per plant (209.21 g) and dry berry weight per plant (62.36 g).

Cluster V recorded the maximum mean value for seven traits *viz.,* seedling leaf width (3.90 cm), days for first flowering (54.83), days to 50% flowering (66.00), plant spread (East-West)(107.13 cm), the number of thorns at the upper surface of a leaf (14.03), the number of thorns at the lower surface of a leaf (14.07) and

Table 4. Cluster mean values for 34 characters of *Solanum surattense*

Cluster	Days taken for germination	Seedling length (cm)	Shoot length (cm)	Root length (cm)	Number of leaves	Leaf length (cm)	Leaf width (cm)	Seedling fresh weight (g)	Shoot fresh weight (g)	Root fresh weight (g)	Seedling dry weight (g)	Shoot dry weight (g)
I	13.73	18.87	9.91	6.50	3.73	5.08	2.87	0.59	0.54	0.04	0.09	0.08
II	12.50	21.37	9.65	7.25	4.75	5.13	3.37	0.44	0.40	0.05	0.10	0.09
III	13.50	13.51	8.98	6.38	4.25	4.90	3.63	0.51	0.47	0.04	0.11	0.11
IV	15.00	21.02	10.93	6.22	5.25	6.25	2.03	0.42	0.38	0.05	0.06	0.05
V	14.50	17.94	8.68	7.40	3.75	4.75	3.90	0.34	0.30	0.03	0.06	0.06
VI	14.67	17.90	10.15	7.07	3.80	4.67	2.74	0.58	0.53	0.05	0.09	0.08

Table 4. Contd….

Cluster	Root dry weight (g)	Seedling fresh: dry ratio	Days for first flowering	Days for 50 % flowering	Plant spread (N-S) (cm)	Plant spread (E-W) (cm)	Number of branches	Number of flower cluster per branch	Leaf width (cm)	Leaf length (cm)	Stem girth (mm)	Petiole length (cm)
I	0.01	7.18	35.82	52.21	105.39	103.34	5.23	15.19	5.97	8.87	9.08	5.45
II	0.00	4.67	48.33	51.67	103.27	103.97	5.90	18.03	6.49	8.67	7.88	4.89
III	0.00	4.75	47.67	52.83	98.00	98.43	6.77	16.77	8.20	10.09	7.39	6.08
IV	0.01	7.72	32.17	48.00	112.33	101.90	5.10	20.47	7.99	9.00	8.52	4.86
V	0.00	5.26	54.83	66.00	104.57	107.13	5.77	16.10	5.68	7.51	7.22	6.02
VI	0.01	7.25	39.59	55.36	99.91	107.13	5.62	15.26	7.41	9.96	8.77	4.74

Table 4. Contd….

Cluster	Internodal length (cm)	Number of thorns in upper side of the leaf	Number of thorns in lower side of the leaf	Number of berries	Berry diameter (mm)	Fresh single berry weight (g)	Dry single berry weight (g)	Fresh berry weight (g)	Fresh to dry ratio	Dry berry weight (g)
I	9.14	12.73	13.02	89.09	16.61	2.51	0.64	209.21	3.30	62.36
II	7.02	13.17	12.70	49.37	15.23	2.42	0.63	122.70	2.79	44.28
III	8.57	13.10	13.10	53.35	15.74	2.33	0.68	118.44	2.77	42.35
IV	7.40	13.43	13.63	63.40	17.22	2.04	0.62	130.06	2.86	44.74
V	8.31	14.03	14.07	47.63	16.93	2.57	0.77	117.64	2.79	42.10
VI	8.15	13.04	13.12	77.11	17.34	2.69	0.68	202.88	3.31	59.79

dry single berry weight (0.77 g). Cluster VI had the maximum mean values for six traits *viz.,* root fresh weight (0.05 g), root dry weight (0.01 g), plant spread (East-West)(107.13 cm), berry diameter (17.34 mm), fresh single berry weight (2.69 g) and fresh to dry ratio (3.31). Cluster III recorded the maximum mean value for six traits *viz.,* seedling dry weight (0.11 g), shoot dry weight (0.11 g), the number of branches (6.77), leaf length (8.20 cm), leaf width (10.09 cm) and petiole length (6.08 cm). Cluster II had the maximum mean values for three traits *viz.,* seedling length (21.37 cm) and root length (7.25 cm). Similar findings have also been reported by Senapathi *et al.* (2009) and Dutta *et al*. (2009) in brinjal. Crossing the accessions from the most divergent clusters will be useful to get better hybrids with desirable segregants. This result is in agreement with the divergence studies done by Vidhya and Kumar (2014) in brinjal.

Table 5. Relative contribution of 34 traits towards genetic divergence in 49 *Solanum surattense* accessions

S. No.	Character	Number of first rank	Per cent contribution
1.	Days taken for germination	2	0.17
2.	Seedling length	0	0.00
3.	Shoot length	2	0.17
4.	Root length	11	0.94
5.	Number.of leaves	8	0.68
6.	Leaf length	36	3.06
7.	Leaf width	40	3.40
8.	Seedling fresh weight	0	0.00
9.	Shoot fresh weight	58	4.93
10.	Root fresh weight	2	0.17
11.	Seedling dry weight	42	3.57
12.	Shoot dry weight	0	0.00
13.	Root dry weight	391	33.25
14.	Seedling fresh:dry ratio	95	8.08
15.	Days for first flowering	0	0.00
16.	Days for 50 % flowering	0	0.00
17.	Plant spread (N-S)	7	0.60
18.	Plant spread (E-W)	0	0.00
19.	Branch number	0	0.00
20.	Flower cluster per branch	13	1.11
21.	Leaf length	5	0.43
22.	Leaf width	87	7.40
23.	Stem girth	27	2.30
24.	Petiole length	55	4.68
25.	Internodal length	96	8.16
26.	Number of thorns in upper side of the leaf	2	0.17
27.	Number of thorns in lower side of the leaf	0	0.00
28.	Number of berries	3	0.26
29.	Berry diameter	0	0.00
30.	Fresh single berry weight per plant	3	0.26
31.	Dry single berry weight	15	1.28
32.	Fresh berry weight	41	3.49
33.	Fresh to dry ratio	14	1.19
34.	Dry berry weight per plant	121	10.29

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The relative contribution of characters towards divergence is presented in **Table 5**. Maximum contribution towards divergence was observed for root dry weight (33.25%) followed by dry berry weight per plant (10.29%). The contribution towards divergence ranged from 0.1 to 1.0 per cent for days taken for germination, shoot length, root fresh weight, the number of thorns at the upper surface of a leaf, the number of leaves, plant spread (North-South), leaf length, the number of berries, fresh single berry weight and root length. Seedling leaf length, seedling leaf width, shoot fresh weight, seedling dry weight, seedling fresh: dry, the number of flower cluster per plant, leaf width, stem girth, petiole length, internodal length, dry single berry weight, fresh berry weight per plant and fresh to dry ratio registered 1 to 10 per cent of contribution towards divergence. Contribution towards the divergence is important to know the variability that exists in the traits of interest which are reflected by the increased per cent of the contribution. This will offer more scope to practice selection for that trait. The trait (dry berry weight per plant) with a high contribution towards divergence, high mean yield and high intra cluster distance may help in realizing diversity in segregating generations on planned crosses as reported by Patel *et al*. (2014).

From this study, it is concluded that significant diversity among the accessions of *Solanum suarttense* was observed for seed germination, seedling characters, morphological and yield traits of plants. Wide divergence was recorded for dry berry weight per plant among the 34 characters studied. Selection of genotypes based on the above trait for the crossing programme would be useful since it is an economic part of the plant. Cluster analysis resulted in grouping 49 accessions into six clusters. From this analysis, promising traits can be improved through breeding promising accessions from selected clusters.

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