Indian Journal of Traditional Knowledge
Vol 23(1), January 2024, pp 25-34
DOI: 10.56042/ijtk.v23i1.8140

Morpho-biochemical diversity in tree tomato (*Solanum betaceum* Cav.) genotypes grown under different altitudinal locations of north eastern Himalayas of India

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Received 14 December 2020; revised 14 December 2023; accepted 04 January 2024

Seventeen tree tomato (*Solanum betaceum* Cav.) genotypes were evaluated for their morpho-biochemical diversity in Randomized Block Design under three replications at Sikkim University, Gangtok in 2017-18. The genotypes were grouped into five clusters and cluster I possessed highest number of genotypes (6). Highest inter-cluster distance (372237) was recorded between clusters II & V. Intra-cluster was maximum in cluster III (28651.72) showing diversity within the cluster. The genotype STT-110 produced maximum value for average fruit weight (81 g) and other fruit yield contributing characters. Whereas, STT-40 produced maximum values for iron (1.86 mg/100 g), copper (0.47 mg/100 g) and manganese (1.38 mg/100 g). Genetic parameters (PCV, GCV) along with heritability and genetic advance were highest for anthocyanin (77.26%, 77.19%, 99% and 158.85%), flavonoid (56.91%, 56.90%, 100% and 117.22%), total phenol (52.76%, 52.72%, 99%, and 108.54%), manganese (50.87%, 49.26%, 93%, and 98.28%) and ascorbic acid (41.73%, 41.71%, 99% and 85.89%). Correlation coefficient analysis showed that polar and equatorial diameter of fruit was significantly correlated with average fruit weight. Genotypic correlation coefficients were higher than phenotypic correlation coefficients, which indicate the inherent association among the characters. This study highlights the potential utilization of STT-110 genotype for further selection in future breeding programme for enhancing yield.

Keywords: Tree tomato, Genetic diversity, Genetic variability, Genotypes, Multi-elemental profiling

IPC Code: Int Cl.^{24}: A01G 22/05, A61K 36/81

Tree tomato (*Solanum betaceum* Cav.) is a minor vegetable and commonly known as Tamarillo. It is a small, quick growing tree belonging to the family Solanaceae having chromosome number 2n=2x=24. Initially, botanical name of the plant was *Solanum betaceum* given by Spanish botanist Cavanilles and was later transferred to *Cyphomandra betacea* by Sendtner. Later on, it was reverted back to *Solanum betaceum*[1]. It is cultivated throughout the world; but in India, it is cultivated in north-eastern region especially in Sikkim and Darjeeling hills (West Bengal). Although it is a relatively under-exploited species, it is growing and shipping at a faster rate[2]. At present, demand for the tree tomato fruits remains strong due to increasing health awareness for its unique flavour and nutritional properties. The fruit is acidic in nature, recommended for its nutritional qualities such as provitamin A, vitamins C, B_6, E, iron and phenolics besides low carbohydrates contents[3-5]. It is also rich in pectin and contains a specific lectin in the cell walls of the fruit tissues and seed coat[6]. The presence of some anthocyanin pigments, flavonols and leucoanthocyanins is reported in the purple-red seed jelly, with delphinidin-3-rutinoside as the major anthocyanin.

Characterization of tree tomato is of great significance for the fruit yield and quality improvement. Its production is limited to the kitchen garden for availability and use; therefore, it cannot replace the conventional vegetables and only be used as supplement at its particular native place[7]. This study will provide information to the researchers for improvement of this crop and encourage farmers to produce tree tomato at commercial scale due to its potential in the market, especially when it is processed. Therefore, there is a need of screening tree tomato germplasm to select elite genotype(s) with improved quality and yield. An information on the nature and magnitude of variability presents in genetic stocks, heritability and genetic advance is of considerable importance for a breeder to start any effective crop improvement programme[8,9]. The

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correlation coefficient measures the mutual relationship between different traits and determines the associated characters on which selection to be made for yield enhancement[10]. The path coefficient analysis is a tool for partitioning of direct and indirect cause of association. Meager research work has been carried out in tree tomato to estimate the level of genetic diversity fall under north eastern Himalayan region for future genetic improvement. Hence, the study was undertaken to assess the extent of genetic diversity, variability and character association at both morphological and biochemical plateau in tree tomato genotypes grown in north eastern Himalayan region of India.

Materials and Methods

Experimental location

The experimental material comprised of 17 tree tomato genotypes from various geographical location of Sikkim, West Bengal, Nagaland and Meghalaya (Table 1). The experimental material was analyzed in Randomized Block Design with three replications. Morphological and biochemical study was carried out at Plant Ionome and Biochemical Analysis Laboratory, Department of Horticulture, Sikkim University during 2017-2018.

Data observation

Fruit yield contributing and biochemical parameters

The observations were recorded on fruit yield contributing and biochemical traits to estimate the extent of genetic diversity. Five fruits were randomly selected from each plant in each replication from every geographical location. Observations were recorded upon nineteen traits. Among biochemical traits, the estimation of ascorbic acid and titrable acidity was done as described by Rangana[11], reducing sugar and total sugar was examined with the method suggested by AOAC[12], total phenol estimation was as per the method by Thimmaiah[13], protein was estimated with the method of Lowry *et al.*[14], estimation of anthocyanin was as per the method by Swain *et al.*[15] and total flavonoid was measured through aluminum chloride colorimetric assay[16].

Multi-elemental profiling

Elements like iron, copper, zinc and manganese was analyzed by the PerkinElmer AAS (atomic absorption spectrophotometer) by following the procedure suggested by Ajai *et al.*[17]. Prior to AAS analysis, samples were acid digested to achieve clear and colorless solution. Open air acid digestion was performed with the use of di-acid solution (concentrated nitric acid and perchloric acid) in the ratio of 9:4. 1000 ppm stock solution of iron, copper, zinc and manganese was made in a volumetric flask to prepare standards of different concentrations *i.e.*, 5 ppm, 10 ppm, 15 ppm, 20 ppm and 25 ppm.

Statistical analysis

The data were subjected to D^2 statistics to determine the degree of genetic diversity as suggested by Mahalanobis[18]. Genotypic and phenotypic coefficients of variations were estimated by the procedure suggested by Burton and De Vane[19]. The broad sense heritability and genetic advance as percent of mean was calculated

Table 1 — Description of Tree Tomato genotypes

S. N.	Genotype	Source	GPS location
1	STT-10	Pangthang (East Sikkim)	27º22.58’N- 88º36.33’E
2	STT-20	Tangzi Bikmat (South Sikkim)	27º9.69’N- 88º27.16’E
3	STT-30	KVK farm (South Sikkim)	27º9.76’N- 88º28.24’E
4	STT-40	Mirik (West Bengal)	26º53.60’N- 88º11.43 ‘E
5	STT-50	Lava, Kalimpong (West Bengal)	27º5.29’ E- 88º39.62’E
6	STT-60	Sombaria (West Sikkim)	27º8.75’N- 88º8.54’E
7	STT-70	Phadamchen (East Sikkim)	27º14.30’N- 88º46.01’E
8	STT-80	Dzongu (North Sikkim)	27º31.733’N- 88º30.57’E
9	STT-90	Pakyong (East Sikkim)	27º14.65’N- 88º36.20’E
10	STT-100	Mangalbaria (West Sikkim)	26º53.02’N- 88.48.41’E
11	STT-110	Nagi Karek (South Sikkim)	27º10.06’N- 88º28. 18’E
12	STT-120	Namthang (South Sikkim)	27º10.00’N- 88º28.67’E
13	STT-130	Ranka (East Sikkim)	27º20.79’N- 88º34.91’E
14	STT-140	6th Mile (East Sikkim)	27º18.50’N- 88º35.27’E
15	STT-150	Kohima (Nagaland)	25º09.66’N- 94º6.44’E
16	STT-160	Ri Bhoi district (Meghalaya)	25º47.79’N- 91º59.55’E
17	STT-170	Assam Lingzey (East Sikkim)	27º17.04’N- 88º36.68’E

Table 2 — Clustering patterns of seventeen genotypes of tree tomato on the basis of genetic divergence

Cluster	Number of genotypes	Name of the genotypes
I	6	STT-20, STT-90, STT-150, STT-160, STT-30, STT-60
II	4	STT-40, STT-110, STT-10, STT-130
III	5	STT-50, STT-70, STT-80, STT-100, STT-170
IV	1	STT-120
V	1	STT-140

Fig. 1 — Clustering pattern of seventeen tree tomato genotypes on the basis of genetic diversity

as per procedure suggested by Johnson *et al.*[20]. Genetic advance was computed by the formula of Lush[21]. Correlation coefficient among all characters at phenotypic (rp) and genotypic (rg) level were estimated by formulae given by Al-Jibouri *et al.*[22]. Path coefficient analysis at genotypic and phenotypic level was performed by taking iron as dependent variable as per the formulae given by Wright[23] and elaborated by Dewey and Lu[24]. Data analysis was carried out by using INDOSTAT software version 8.1 (Indostat services, Hyderabad, India).

Results

Genetic diversity (D^2 analysis)

Mahalanobis (1936) generalized distance estimated by D^2 statistics is an effective tool for the quantitative estimation of genetic diversity for a rational choice of potential material in breeding programme. On the basis of D^2 values, all the seventeen tree tomato genotypes were characterized into five divergent clusters (Table 2, Fig. 1). Cluster I contained maximum number of genotypes (6) followed by cluster III with 5 & II with 4 genotypes. However, cluster IV & V were found to be monotypic and contained only one genotype. Average intra and inter-cluster distances were also estimated (Table 3) and intra-cluster distance was maximum in cluster III (28651.72) indicated that genotypes included in this cluster were highly diverse. Minimum intra-cluster distance (0) was estimated in cluster IV & V, because only one genotype was included in these clusters. Whereas, maximum inter-cluster distance (372237.00) was calculated between cluster II & V exhibited maximum diversity followed by cluster III & V (233028.80). While, the lowest inter-cluster distance (38684.14) was observed between cluster I & III. Cluster II produced highest mean values for TSS (12.91°Brix), and multi-elements like Iron (1.43 mg/100 g), copper

Table 3 — Intra and inter-cluster distance of seventeen genotypes of tree tomato

Cluster	I	II	III	IV	V
I	23112.65	58955.32	38684.14	99557.34	229414.30
II		18467.28	39341.25	163271.70	372237.00
III			28651.72	84316.80	233028.80
IV				0.00	105176.90
V					0.00

Table 4 — Cluster wise mean values of nineteen characters in tree tomato

Cluster	Polar diameter (cm)	Equatorial diameter (cm)	Average fruit weight (g)	Peduncle length (cm)	Number of seeds /fruit	Test weight (g)	TSS (°Brix)	Acidity (%)	Ascorbic acid (mg/100 g)	Reducing sugar (%)	Total sugar (%)
I	4.82	2.00	44.30	4.53	162.72	5.28	11.53	2.06	35.26	8.22	13.29
II	4.71	1.96	44.93	4.59	156.91	5.46	12.91	2.01	21.06	11.80	17.47
III	4.95	2.15	50.13	4.74	194.93	5.39	12.18	1.43	18.49	11.86	17.36
IV	5.43	2.16	59.65	5.10	235.33	5.71	11.33	2.18	35.56	20.83	28.30
V	4.58	1.97	41.47	3.93	178.00	5.21	12.33	2.30	16.64	6.95	12.43
Percent contribution towards divergence	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.15	4.41	3.68

Cluster	Flavonoid (mg/100 g)	Total phenol (mg/100 g)	Protein (g/100 g)	Anthocyanin (mg/100 g)	Iron (mg/100 g)	Copper (mg/100 g)	Zinc (mg/100 g)	Manganese (mg/100 g)
I	39.48	417.53	1.02	1.64	0.88	0.25	4.00	0.68
II	19.95	326.94	0.91	0.64	1.43	0.36	4.68	1.08
III	39.98	353.05	0.91	0.79	1.04	0.28	4.24	0.76
IV	86.96	522.20	1.13	2.60	0.68	0.34	3.24	0.29
V	106.16	152.10	0.91	0.98	0.71	0.22	2.85	0.20
Percent contribution towards divergence	53.68	5.15	0.00	3.68	21.32	2.94	0.00	0.00

(0.36 mg/100 g), zinc (4.68 mg/100 g) and manganese (1.08 mg/100 g) (Table 4). Cluster IV showed highest mean values for yield contributing traits like polar diameter (5.43 cm), equatorial diameter (2.16 cm), average fruit weight (59.65 g), peduncle length (5.10 cm), number of seeds/fruit (235.33), test weight (5.71 g) and few biochemical parameters like ascorbic acid (35.56 mg/100 g), reducing sugar (20.83%), total sugar (28.30%), total phenol (522.20 mg/100 g), protein (1.13 g/100 g) and anthocyanin (2.60 mg/100 g). Cluster V recorded highest mean values for acidity (2.30%) and flavonoid (106.16 mg/100 g). The results also showed that flavonoid contributed maximum contribution (53.68 %) towards total divergence followed by iron (21.32%).

Mean performance of tree tomato genotypes

Fruit yield contributing parameters

Mean performance of the genotypes for fruit yield contributing traits is presented in Table 5. Maximum value for polar diameter was in STT-110 (5.88 cm), while lowest in STT-40 (3.90 cm). Maximum value for equatorial diameter was recorded in genotype STT-110 & STT- 170 (2.42 cm), and lowest in STT-40 (1.65 cm). Whereas, average fruit weight was maximum in genotype STT-110 (81 g), while lowest in STT-40 (23.66 g). Among other traits, peduncle length was maximum in STT-70 (6.00 cm) and lowest in STT-40 (3.76 cm), number of seeds/fruit was maximum in STT-80 (240.66) and lowest in STT-10 (97.33). Test weight was highest in STT-70 (6.75 g), while lowest in STT-170 (3.85 g). All these genotypes were significantly superior over their respective population mean.

Biochemical and multi-elemental parameters

Significant variation was observed in biochemical and multi-elemental parameters among all the genotypes (Table 6). TSS was maximum in STT-130 (14.66°B) and lowest in STT-100 (11.10°B), acidity was highest in STT-10 (3.39%) and lowest was recorded in STT-80 (0.68%). Maximum ascorbic acid was observed in STT-60 (47.52 mg/100 g) and lowest in STT-50 (11.84 mg/100 g). Highest values for reducing sugar and total sugar were observed in STT-120 (20.83% & 28.30%); whereas, lowest value of reducing sugar was noted in STT-60 (6.57%), and

Table 5 — Mean performance of fruit yield contributing traits of tree tomato genotypes

S.N.	Genotype	Polar diameter (cm)	Equatorial diameter (cm)	Average fruit weight (g)	Peduncle length (cm)	Number of seeds/fruit	Test weight (g)
1	STT-10	4.65	1.99	41.42	5.50	97.33	5.54
2	STT-20	4.80	2.00	45.34	5.13	206.66	5.74
3	STT-30	4.79	2.00	45.12	4.36	105.33	5.60
4	STT-40	3.90	1.65	23.66	3.76	153.66	4.51
5	STT-50	4.81	2.11	50.01	4.06	107.66	5.77
6	STT-60	4.92	1.99	44.88	5.00	161.00	5.61
7	STT-70	5.50	2.35	63.14	6.00	210.66	6.75
8	STT-80	5.02	2.10	47.23	4.83	240.66	5.44
9	STT-90	4.60	1.87	35.29	3.80	185.66	4.99
10	STT-100	4.11	1.79	28.35	3.80	209.66	5.15
11	STT-110	5.88	2.42	81.00	4.80	218.00	6.55
12	STT-120	5.43	2.16	59.65	5.10	235.33	5.71
13	STT-130	4.41	1.79	33.66	4.30	158.66	5.24
14	STT-140	4.58	1.97	41.47	3.93	178.00	5.21
15	STT-150	4.76	2.03	43.31	4.53	125.33	4.20
16	STT-160	5.04	2.14	51.89	4.40	192.33	5.55
17	STT-170	5.31	2.42	61.94	5.00	206.00	3.85
	Mean	4.85	2.04	46.90	4.60	176.00	5.37
	SE (m)	0.10	0.04	3.18	0.27	1.66	0.07
	CD (P=0.05)	0.29	0.12	9.17	0.79	4.79	0.20
	CV	3.70	3.66	11.75	10.43	1.63	2.31
	Fratio	22.77	24.52	19.27	5.36	755.60	102.74
	Range Lowest	3.90	1.65	23.66	3.76	97.33	3.85
	Range Highest	5.88	2.42	81.00	6.00	240.66	6.75

Table 6 — Mean performance of biochemical and multi-elemental parameters of tree tomato genotypes

S.N.	Genotype	TSS (°Brix)	Acidity (%)	Ascorbic acid (mg/100 g)	Reducing sugar (%)	Total sugar (%)	Flavonoid (mg/100 g)	Total phenol (mg/100 g)	Protein (g/100 g)	Anthocyanin (mg/100 g)	Iron (mg/100 g)	Copper (mg/100 g)	Manganese (mg/100 g)	Zinc (mg/100 g)
1	STT-10	11.33	3.39	26.75	15.65	21.60	31.26	209.86	1.06	0.49	1.25	0.44	1.20	3.28
2	STT-20	11.33	1.52	42.90	7.80	13.60	46.60	383.36	0.77	2.32	0.84	0.31	1.08	5.92
3	STT-30	11.66	1.84	40.49	9.63	15.53	40.63	828.76	0.85	3.13	0.92	0.25	0.62	5.38
4	STT-40	12.00	1.28	14.61	11.07	16.30	18.10	364.86	0.91	0.22	1.86	0.47	1.38	5.22
5	STT-50	12.66	1.35	11.84	10.44	15.46	36.36	330.23	0.21	1.28	1.60	0.38	1.02	4.30
6	STT-60	11.33	1.77	47.52	6.57	11.36	37.13	213.23	1.04	1.27	1.39	0.27	1.13	3.38
7	STT-70	12.33	1.78	23.53	8.34	13.30	48.90	750.30	0.81	0.36	1.40	0.29	1.08	5.58
8	STT-80	12.06	0.68	16.69	11.34	16.20	39.56	207.73	1.02	1.72	0.75	0.25	0.57	4.90
9	STT-90	12.06	2.79	28.48	8.93	13.36	47.73	202.50	1.37	2.09	0.64	0.28	0.53	2.47
10	STT-100	11.10	1.92	11.89	11.35	18.23	25.00	218.83	1.49	0.35	0.72	0.22	0.75	2.88
11	STT-110	13.66	1.77	19.11	9.62	16.53	18.13	279.26	0.88	1.30	1.61	0.27	1.11	7.59
12	STT-120	11.33	2.18	35.56	20.83	28.30	86.96	522.20	1.13	2.60	0.68	0.34	0.29	3.24
13	STT-130	14.66	1.62	23.76	10.86	15.46	12.30	453.76	0.79	0.56	1.00	0.26	0.63	2.64
14	STT-140	12.33	2.30	16.64	6.95	12.43	106.16	152.10	0.91	0.98	0.71	0.22	0.20	2.85
15	STT-150	11.46	2.78	30.83	9.26	15.43	37.53	508.96	1.07	0.37	0.65	0.17	0.39	3.82
16	STT-160	11.33	1.66	21.36	7.14	10.46	27.26	368.40	1.04	0.67	0.86	0.22	0.32	3.00
17	STT-170	12.76	1.42	28.48	17.85	23.60	50.10	258.16	1.05	0.27	0.75	0.24	0.37	3.57
Mean		12.08	1.88	25.91	10.80	16.30	41.75	367.79	0.96	1.17	1.04	0.29	0.75	4.12
SE (m)		0.38	0.03	0.17	0.06	0.10	0.13	4.11	0.03	0.02	0.00	0.03	0.05	0.55
CD (P=0.05)		1.10	0.10	0.50	0.18	0.30	0.40	11.84	0.10	0.06	0.01	0.10	0.15	1.58
CV		5.48	3.23	1.18	1.04	1.11	0.57	1.93	6.49	3.43	0.84	20.63	12.68	23.18
Fratio		6.16	340.96	3732.41	3589.93	1879.73	29120.01	2223.45	56.78	1515.41	6128.30	5.23	46.22	6.68
Range Lowest		11.10	0.68	11.84	6.57	10.46	12.30	152.10	0.21	0.22	0.64	0.17	0.20	2.47
Range Highest		14.66	3.39	47.52	20.83	28.30	106.16	828.76	1.49	3.13	1.86	0.47	1.38	7.59

total sugar was minimum in STT-160 (10.46%). Highest flavonoid was recorded in STT-140 (106.16 mg/100 g) and lowest in STT-130 (12.30 mg/100 g). Total phenol was maximum in STT-30 (828.76 mg/100 g), and minimum in STT-140 (152.10 mg/100 g). Protein was highest in STT-100 (1.49 g/100 g) and lowest in STT-50 (0.21 g/100 g). Highest anthocyanin was observed in STT-30 (3.13 mg/100 g) and lowest in STT-40 (0.22

Table 7 — Genetic parameters of different traits of tree tomato genotypes

S.N.	Characters	General mean	Range	Co-efficient of variation (%)			Heritability % (broad sense)	Genetic advance at 5%	Genetic advance as % of mean
				GCV	PCV	ECV			
1	Polar diameter (cm)	4.85	3.90-5.88	9.97	10.63	3.70	87	0.93	19.26
2	Equatorial diameter (cm)	2.04	165-2.42	10.25	10.89	3.66	88	0.40	19.90
3	Average fruit weight (g)	46.90	23.66-81.00	29.01	31.30	11.75	85	25.98	55.40
4	Peduncle length (cm)	4.60	3.76-6.00	12.58	16.34	10.43	59	0.91	19.95
5	Number of seeds/fruit	176.00	97.33-240.66	25.96	26.01	1.63	99	93.94	53.37
6	Test weight (g)	5.37	3.85-6.75	13.50	13.70	2.31	97	1.47	27.42
7	TSS (°Brix)	12.08	11.10-14.66	7.19	9.05	5.48	63	1.42	11.79
8	Acidity (%)	1.88	0.68-3.39	34.46	34.61	3.23	99	1.33	70.67
9	Ascorbic acid (mg/100 g)	25.91	11.84-47.52	41.71	41.73	1.18	99	22.25	85.89
10	Reducing sugar (%)	10.80	6.57-20.83	36.17	36.19	1.04	99	8.04	74.49
11	Total sugar (%)	16.30	10.46-28.30	27.84	27.87	1.11	99	9.34	57.32
12	Flavonoid (mg/100 g)	41.75	12.30-106.16	56.90	56.91	0.57	100	48.94	117.22
13	Total phenol (mg/100 g)	367.79	152.10-828.76	52.72	52.76	1.93	99	399.21	108.54
14	Protein (g/100 g)	0.96	0.21-1.49	28.00	28.74	6.49	94	0.54	56.19
15	Anthocyanin (mg/100 g)	1.17	0.22-3.13	77.19	77.26	3.43	99	1.87	158.85
16	Iron (mg/100 g)	1.04	0.64-1.86	38.05	38.06	0.84	100	0.81	78.38
17	Copper (mg/100 g)	0.29	0.17-0.47	24.50	32.03	20.63	58	0.11	38.61
18	Zinc (mg/100 g)	4.12	2.47-7.59	31.92	39.45	23.18	65	2.19	53.21
19	Manganese (mg/100 g)	0.75	0.20-1.38	49.26	50.87	12.68	93	0.73	98.28

mg/100 g). Among the multi-elemental profile, STT-40 produced highest value for iron (1.86- mg/100 g), copper (0.47 mg/100 g) and manganese (1.38 mg/100 g). Whereas, lowest value for iron was observed in STT-90 (0.64 mg/100 g), copper was lowest in STT-150 (0.17 mg/100 g) and manganese was minimum in STT-140 (0.20 mg/100 g). Zinc was highest in STT-110 (7.59 mg/100 g) and lowest in STT-90 (2.47 mg).

Genetic parameters

High range of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was noted in anthocyanin (77.26% & 77.19%) followed by flavonoid (56.91% & 56.90%), total phenol (52.76% & 52.72%), manganese (50.87% & 49.26%) and ascorbic acid (41.73% & 41.71%). Whereas, moderate range of PCV and GCV were recorded in traits like peduncle length (16.34% & 12.58%), test weight (13.70% & 13.50%), equatorial diameter (10.89% & 10.25%) and polar diameter (10.63% & 9.97%) (Table 7). Almost all the characters under study showed a high value of heritability in broad sense with maximum in flavonoid and iron (100%). The data revealed that genetic advance as percentage of mean was ranged as 11.79-158.85% for different characters (Table 7). The highest genetic advance as percentage of mean was noted for anthocyanin (158.85%) followed by flavonoid (117.22%), total phenol (108.54%), manganese (98.28%), ascorbic acid (85.89%) and iron (78.38%).

Character association analysis

The genotypic and phenotypic correlation coefficient was estimated for fruit yield contributing traits as well as biochemical and multi-elemental parameters in tree tomato (Table 8). At genotypic level; among multi-elemental parameters, iron was positively and significantly correlated with copper (rg=0.73), manganese (rg=0.84) and zinc (rg=0.55). Among fruit yield contributing traits, polar diameter showed significant positive correlation with average fruit weight (rg=0.98). Likewise, equatorial diameter showed significant positive correlation with average fruit weight (rg=0.96). At phenotypic level, iron expressed a significant positive correlation with manganese (rp= 0.81), copper (rp= 0.56), and zinc (rp= 0.44). Fruit yield contributing traits like polar diameter showed significant and positive correlation with average fruit weight (rp= 0.96). Likewise, equatorial diameter showed significant and positive correlation with average fruit weight (rp= 0.93). Partitioning of the correlation coefficient was done by path coefficient analysis through direct and indirect effect of all characters on iron (dependent variable) at both genotypic and phenotypic level (Data not shown). Path coefficient analysis showed that average fruit weight produced high positive direct effect on iron via indirect effect of test weight, reducing sugar and total phenol at both genotypic and phenotypic level, respectively.

Table 8 — Genotypic(rg) and phenotypic (rp)correlation coefficient for different traits of tree tomato

Traits		PD	ED	AFW	PL	NSF	TW	TSS	AD	AA	RS	TS	FN	TP	PT	AC	Cu	Zn	Mn	Fe
PD	rg	-	0.95**	0.98**	0.70**	0.43*	0.50*	0.18	-0.09	0.23	0.18	0.20	0.20	0.21	-0.17	0.23	-0.26	0.47*	-0.12	0.02
	rp	-	0.9**	0.96**	0.59*	0.40	0.47*	0.16	-0.10	0.21	0.17	0.18	0.19	0.20	-0.15	0.22	-0.16	0.37	-0.11	0.01
ED	rg		-	0.96**	0.68**	0.35	0.35	0.20	-0.14	0.08	0.20	0.21	0.20	0.16	-0.23	0.03	-0.30	0.42*	-0.14	0.01
	rp		-	0.93**	0.54*	0.33	0.31	0.13	-0.13	0.07	0.19	0.20	0.18	0.15	-0.20	0.03	-0.17	0.38	-0.14	0.01
AFW	rg			-	0.62**	0.38	0.49*	0.28	-0.13	0.11	0.18	0.21	0.16	0.18	-0.25	0.15	-0.21	0.56*	-0.05	0.12
	rp			-	0.54*	0.35	0.46*	0.17	-0.12	0.10	0.16	0.19	0.14	0.17	-0.23	0.14	-0.12	0.42*	-0.06	0.11
PL	rg				-	0.21	0.48*	-0.10	0.08	0.47*	0.27	0.27	0.10	0.32	-0.11	0.01	0.08	0.36	0.25	0.10
	rp				-	0.18	0.38	-0.07	0.04	0.36	0.21	0.21	0.08	0.25	-0.10	0.00	0.12	0.26	0.19	0.07
NSF	rg					-	0.18	0.05	-0.40	-0.09	0.14	0.15	0.24	-0.17	0.36	0.08	-0.33	0.15	-0.24	-0.30
	rp					-	0.18	0.03	-0.40	-0.09	0.14	0.15	0.24	-0.17	0.35	0.08	-0.26	0.12	-0.24	-0.30
TW	rg						-	0.09	-0.08	0.02	-0.25	-0.21	-0.00	0.27	-0.33	0.31	0.17	0.52*	0.38	0.37
	rp						-	0.07	-0.08	0.02	-0.25	-0.21	-0.00	0.27	-0.32	0.31	0.10	0.39	0.36	0.36
TSS	rg							-	-0.30	-0.35	-0.01	-0.04	-0.26	0.00	-0.45	-0.21	-0.02	0.23	0.04	0.29
	rp							-	-0.24	-0.27	-0.00	-0.03	-0.20	0.00	-0.35	-0.17	-0.06	0.06	-0.00	0.23
AD	rg								-	0.21	0.11	0.14	0.21	-0.05	0.39	-0.05	0.04	-0.42*	-0.11	-0.23
	rp								-	0.21	0.10	0.14	0.21	-0.05	0.38	-0.05	0.03	-0.34	-0.11	-0.23
AA	rg									-	0.00	0.02	0.16	0.31	0.10	0.51*	-0.13	0.02	-0.00	-0.22
	rp									-	0.00	0.02	0.16	0.31	0.09	0.51*	-0.09	0.01	-0.01	-0.22
RS	rg										-	0.98**	0.17	0.00	0.18	0.03	0.34	-0.19	-0.18	-0.15
	rp										-	0.98**	0.17	0.00	0.18	0.03	0.26	-0.15	-0.17	-0.15
TS	rg											-	0.20	0.02	0.20	0.07	0.31	-0.09	-0.14	-0.15
	rp											-	0.20	0.02	0.20	0.07	0.24	-0.08	-0.14	-0.15
FN	rg												-	-0.02	0.05	0.33	-0.18	-0.26	-0.54*	-0.45
	rp												-	-0.02	0.05	0.33	-0.14	-0.21	-0.52*	-0.45
TP	rg													-	-0.27	0.27	-0.06	0.35	-0.00	0.05
	rp													-	-0.26	0.27	-0.04	0.29	-0.00	0.05
PT	rg														-	-0.07	-0.36	-0.44*	-0.32	-0.54
	rp														-	-0.06	-0.24	-0.38	-0.30	-0.52
AC	rg															-	-0.02	0.23	-0.16	-0.26
	rp															-	-0.01	0.18	-0.15	-0.26
Cu	rg																-	0.21	0.75**	0.73
	rp																-	0.14	0.58*	0.56
Zn	rg																	-	0.56*	0.55
	rp																	-	0.46*	0.44
Mn	rg																		-	0.84
	rp																		-	0.81

** significant at 1% level; *significant at 5% level

PD= Polar diameter (cm) PL= Peduncle length (cm) TSS= Total soluble solid (°Brix) RS= Reducing sugar (%) TP= Total phenol (mg/100 g) Fe= Iron (mg/100 g)
ED= Equatorial diameter (cm) NSF= Number of seeds/fruit AD= Acidity (%) TS= Total sugar (%) PT= Protein (g/100 g) Cu= Copper (mg/100 g)
AFW= Average fruit weight (kg) TW= Test weight (g) AA= Ascorbic acid (mg/100 g) FN= Flavonoid (mg/100 g) AC= Anthocyanin (mg/100 g) Zn= Zinc (mg/100 g)
Mn= Manganese (mg/100 g)

Discussion

Our study revealed a wide range of genetic diversity among tree tomato genotypes for most of the traits related to fruit yield contributing, multi-elemental and biochemical parameters. The clustering pattern of the genotypes revealed no parallelisms between genetic diversity and their geographical distribution[25]. Selection of genotypes for hybridization will be effective up on genetic diversity rather than geographical diversity. In our investigation, inter-cluster distance was more than intra-cluster distances revealing considerable amount of genetic diversity which might be due to both natural and artificial selection forces among the genotypes. The clustering of genotypes helps in the selection of improved genotypes for crop improvement programs, as genotypes from different groups with a high genetic divergence must be chosen to guarantee the selection gain[26,27]. Clustering of genotypes also restricts the number of crosses, and increases genetic advance in successive breeding cycles[28,29]. Considering the genotypes in present investigation differed in morpho-biochemical and multi-elemental traits and belong to different groups, heterosis can be expected in future breeding programs[30,31]. High genetic diversity has been found in the tree tomato genotypes in present investigation may be exploited for further breeding programs to develop the tree tomato as a commercial crop in Sikkim[32,33]. Genetic variability among the fruit yield contributing traits might be due to the genetic variation and morphological differentiation, and would be a selection criterion for increasing the yield[34,35]. Using fruit size characterization data like diameter and weight, considerable variations has been proved to guaranty selection of suitable breeding lines in tree tomato improvement program aimed for higher productivity. The wide variation in the biochemical traits like TSS, acidity and total sugar might be due to the genotypic potential and environmental influence as transpiration at maturity stage leads to the water loss and may decrease the water content and concentrate the soluble compounds[36]. The findings confirm that the biochemical diversity assessment can be efficiently utilized for the identification of superior genotypes, as well as the estimation of genetic relationships between diverse groups of tree tomato. Multi-elemental parameters showed greater degree of variation among different genotypes. The concentration of minerals in tree tomato fruits depends on soil fertility status, and climate conditions. The characterization of multi-elemental parameters of tree tomato fruits provides information about the fruit quality, both for its culinary and industrial uses[37]. Among genetic parameters, high range (>20%) of phenotypic coefficient of variation and genotypic coefficient of variation (PCV and GCV) was recorded in case of different biochemical traits[38]. It is observed that value for PCV was marginally higher than GCV for all the traits indicating less environmental influences on them[39]. Higher estimates of GCV and PCV indicated that the genetic variability among the genotypes was due to their genetic makeup. Thus, selection is effective based on quantitative traits alone. Estimation of heritability combined with genetic advance increases the intensity of selection in a breeding program. High heritability (>60%) and genetic advance as per cent of mean (>20%) was recorded in flavonoid and iron along with other biochemical and multi-elemental parameters indicated scope for improvement through direct selection pressure[40]. Correlation analysis revealed significant association of polar and equatorial diameter of fruit to average fruit weight. These components are major yield parameters to enhance fruit yield through direct selection. Almost all multi-elemental and few biochemical parameters were significantly correlated to each other indicated direct association of these traits may be useful in quality breeding. In our finding, genotypic correlation coefficient was higher than phenotypic correlation coefficient indicated that in these associations, there was inherited relationship between the traits[41]. Path coefficient analysis showed that average fruit weight had highest positive direct effect on iron content[42]. Average fruit weight may be taken as principal trait to enhance the iron content for quality breeding. In general, average fruit weight also significantly affects fruit yield per plant[43]. At both genotypic and phenotypic levels, the residual effect was very low (<0.5) in path analysis, signifying the inclusion of the maximum traits influencing the iron content in this analysis.

Conclusion

The results in the study showed significant genetic variability among the tree tomato genotypes grown at Sikkim and other north eastern Himalayan region. The genotypes such as STT-40, STT-110, STT-10, STT-130 and STT-140 of highly divergent clusters II and V, may be utilized in breeding programs. They can be used for development of high yielding F_1 hybrids with desirable quantitative traits through heterotic combination. STT-110 produced important fruit yield contributing traits *i.e.,* polar diameter, equatorial diameter and average fruit weight and may be utilized as breeding material for further analysis. STT-110 also produced higher value for zinc. Except zinc, other multi-elemental parameters were high in STT-40. These genotypes may be used in the breeding programs aimed for quality breeding. However, each biochemical parameter was high in different genotype or didn't follow a distinct pattern. Present study provides a scope for the selection of desirable parents for hybridization programs and other breeding analysis, such as trait-specific breeding in tree tomato.

Acknowledgement

Authors thank to the Department of Horticulture, Sikkim University for providing facilities for conducting this study. Authors duly acknowledge the farmers of concerned location for extending cooperation for sample collection.

Conflict of Interest

The author(s) declare that they have no competing interests.

Authors' Contributions

Conceptualization and editing: SKP, RK. Data analysis and software handling: AD; Interpretation of the data: NS.

References

1 Bohs L, Transfer of *Cyphomandra* (Solanaceae) and its species to *Solanum, Taxon*, 44 (4) (1995) 583-587.
2 Prohens J & Nuez F, The Tamarillo (*Cyphomandra betacea*), *Small fruits Review*, 2 (1) (2001) 43-68.
3 McCane J & Widdowson D A, Fruit and Nutrition Supplement, the composition of foods (5th edition Holland, Unwin and Buss, London), (1992), 74-87.
4 Romero-Rodriguez M A, Vazquez-Oderiz M L, Lopez-Hernandez J & Simal-Lozano J, Composition of babaco, feijoa, passionfruit and tamarillo produced in Galicia (north-west Spain), *Food Chem*, 49 (1) (1994) 23-27.
5 Vera de Rosso V & Mercadante A Z, HPLC-PDA-MS/MS of anthocyanins and carotenoid from dovyalis and tamarillo fruits, *J Agri Food Chem*, 55 (22) (2007) 9135-9141.
6 Rastogi S, Pandey M M & Rawat A K S, Phytochemical analysis, phenolic content and antioxidant properties of different parts of *Terminalia bellirica* (Gaertn.) Roxb.- A comparative study, *Indian J Tradit Know*, 17 (2) (2018) 370-375.

7 Jain A K & Tiwari P, Nutritional value of some traditional edible plants used by tribal communities during emergency with reference to Central India, *Indian J Tradit Know*, 11 (1) (2012) 51-57.

8 Bamaniya B S, Shree S, Verma R B, Kumar R & Verma R K, Polygenic variations and character association studies in garlic, *Curr J Appl Sci Tech,* 31 (3) (2018) 1-8.

9 Sharma S, Kour R, Kumar K & Prasad H, Genetic variability in strawberry (*Fragaria x ananassa* Duch.) cultivars assessed by morphological traits and EST-SSR markers of *Rubus ellipticus*, *Indian J Biotech*, 20 (2021) 81-90.

10 Rao C R, Advances Statistical Methods in Biometrical Research, (John Wiley and Sons Inc., New York), (1952), 236-272.

11 Rangana S, Manual of Analysis of Fruits and Vegetables Products, (Tata McGraw Hill Co. Pvt. Ltd., New Delhi), (1976), 77.

12 AOAC, Official Methods of Analysis, (17th edition, Association of Official 28 Agricultural Chemists, Washington D.C.), 1995.

13 Thimmaiah S K, Standard Methods of Biochemical Analysis. (Kalyani Publishers, Kolkata, India), (1999) 287-288.

14 Lowry O H, Rosebrough N J, Farr A L & Randall R J, Protein measurement with the Folin Phenol Reagent, *J Biological Chem*, 193 (1951) 265-275.

15 Swain T & Hillis W E, The phenolic constituents of *Prunus domestica* I - The quantitative analysis of phenolic constituents, *J Sci Food Agri*, 10 (1959) 63-68.

16 Nehal N, Mann S & Gupta R K, Nutritional and phytochemical evaluation of *A. lividus* L. syn. *Amaranthus blitum* subsp. *Oleraceus* (L.) Costea leaves. *Indian J Tradit Know*, 15 (4) (2016) 669-674.

17 Ajai A I, Ochigbo S S, Abdullahi Z & Anigboro P I, Determination of trace metals and essential minerals in selected fruit juices in Minna, Nigeria, *Int J Food Sci*, 2014 (2014) 462931.

18 Mahalanobis P C, On the generalized distance in statistics, Proceedings of National Academic Science (India), 2 (1936) 79-85.

19 Burton G W & De Vane E H, Estimating heritability in tall fescue (*Festuca arundinancea*) from replicated clonal materials, *Agronomy J,* 45 (1953) 478-481.

20 Johnson H W, Robinson H F & Comstock R E, Estimation of genetic and environmental variability in Soyabean, *Agronomy J,* 47 (1955) 314-318.

21 Lush J L, Genetic variability for quantitative and qualitative characters in brinjal (*Solanum melongena* L.), *African J Agri Res*, 8 (39) (1949) 4956-4959.

22 Al-Jibouri H A, Miller P A & Robison H F, Genotype and environmental variances and covariances in an upland cotton cross of inter-specific origin, *Agronomy J,* 50 (1958) 633-636.

23 Wright S, Correlation and causation, *J Agri Res*, 20 (1921) 557-585.

24 Dewey D R & Lu K H, Correlation and path analysis of components of crested wheat grass seed production, *Agronomy J,* 51 (1959) 515-518.

25 Rathi S, Kumar R, Munshi A D & Verma M, Breeding potential of brinjal genotypes using D^2 analysis, *Indian J Hort,* 68 (3) (2011) 328-331.

26 Hussain S, Behera P P, Choudhury M R & Sarma R N, Morphological characterisation of rice accessions of semi deep water ecology, *Indian J Tradit Know*, 22 (1) (2023) 7-16.

27 Jin L, Zhao L, Wang Y, Zhou R, Song L, *et al.*, Genetic diversity of 324 cultivated tomato germplasm resources using agronomic traits and InDel markers, *Euphytica*, 215 (2019) 69.

28 Debnath A, Kumar R, Prasad S K, Sharma N & Kushwah J K, Multivariate analysis for genetic diversity estimation among tomato (*Solanum lycopersicum* L.) Genotypes, *Eco Env Cons,* 26 (3) (2020) 1208-1211.

29 De Sousa, S R, Costa M F, Filho C H A M, Vasconcelos L F L, De Arau´jo A S F, *et al.*, Assessment of the phenotypic diversity in natural populations of *Annona coriacea* Mart.: implications for breeding, *Genet Resour Crop Evol*, 69 (2022) 1121-1135.

30 Kumar R, Kumar R, Prasad B D, Kumar J & Bamaniya B S, Genetic diversity of bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] genotypes of Eastern India through agro-morphological traits and ISSR markers: implication for future breeding, *Genet Resour Crop Evol*, (2023), https://doi.org/10.1007/s10722-023-01670-0.

31 Marefatzadeh-Khameneh M, Fabriki-Ourang S, Sorkhilalehloo B, Abbasi-Kohpalekani J &Ahmadi J, Genetic diversity in tomato (*Solanum lycopersicum* L.) germplasm using fruit variation implemented by tomato analyzer software based on high throughput phenotyping, *Genet Resour Crop Evol*, 68 (2021) 2611-2625.

32 Acosta-Quezada P, Raigon Jimenez M D, Riofrio-Cuenca T, Garcia Martinez M D, Plazas Avila MDLO, *et al.*, Diversity for chemical composition in a collection of different varietal types of tree tomato (*Solanum betaceum* Cav.), an Andean exotic fruit, *Food Chem,* 169 (2015) 327-335.

33 EL-Mansy A B, El-Moneim D A, ALshamrani S M, Safhi F A, Abdein M A, *et al.*, Genetic diversity analysis of tomato (*Solanum lycopersicum* L.) with morphological, cytological, and molecular markers under heat stress, *Horticulturae*, 7 (2021) 65.

34 Acosta-Quezada P G, Martinez-Laborde J B & Prohens, J, Variation among tree tomato (*Solanum betaceum* Cav.) accessions from different cultivar groups: implications for conservation of genetic resources and breeding, *Genet Resour Crop Evo,* 58 (6) (2011) 943-960.

35 Schouten H J, Tikunov1 Y, Verkerke W, Finkers R, Bovy A, *et al.*, Breeding has increased the diversity of cultivated tomato in the Netherlands, *Front Plant Sci*, 10 (2019) 1606.

36 Dutta S K, Chatterjee D, Sarkar D, Singh S B & Boopathi T, *et al.,* Common bean (*Phaseolus vulgaris* L., Fabaceae), landraces of *Lushai* hills in India: Nutrients and antioxidants source for the farmers, *Indian J Tradit Know*, 15 (2) (2016) 313-320.

37 Meza N & Manzano M, Characteristics of tree tomato (*Cyphomandra betaceae* [Cav] Sendtn) fruits based in aril coloration, at the Venezuelan Andes Zone, *Revista UDO Agricola,* 9 (2) (2009) 289-294.

38 Manna M & Paul A, Studies on genetic variability and characters association of fruit quality parameters in tomato, *Hort Flora Res Spectrum*. 2 (1) (2012) 110-116.

39 Kumar R, Kumar R, Prasad B D, Solankey S S, Kumar J, *et al.*, Genetic variation study using morphological and DNA marker-based genotyping in bottle Gourd (*Lagenaria siceraria* (Mol.) Standl.), *Currt J Appl Sci Tech*, 31 (2) (2018) 1-10.

40 Buckseth T, Sharma K M & Thakur K S, Genetic diversity and path analysis in tomato (*Solanum lycopersicum* L.), *Veg Sci*, 39 (2) (2012) 221-223.

41 Dar R A, Sharma J P, Gupta R K & Chopra S, Studies on correlation and path analysis for yield and physico chemical traits in tomato (*Lycopersicon esculentum* Mill.), *Vegetos*, 24 (2) (2011) 136-141.

42 Rani IC, Muthuvel I & Veeraragavathatham D, Correlation and path coefficient for yield components and quality traits in tomato (*Solanum lycopersicum* L.), *Agri Sci Digest*, 30 (1) (2010) 11-14.

43 Manna M & Paul A, Path analysis between fruit yield and some yield components in tomato (*Lycopersicon esculeutum* Mill), *Hort Flora Res Spectrum*, 3 (1) (2012) 215-219.