

Assessment of genetic diversity among tomato (*Solanum lycopersicum*) genotypes under salt-affected conditions

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ABSTRACT

The experiment was conducted in a randomized block design with 38 genotypes (including three checks) of tomato (*Solanum lycopersicum* L.), in three replications for thirteen quantitative traits. The analysis of variance showed that mean squares due to genotypes were significant for all the characters. Based on the Mahalanobis D² statistics, 38 genotypes were grouped into 15 clusters. The maximum number of genotypes (9) were grouped into Cluster I. The highest inter-cluster distance was observed between Cluster XI and Cluster VI, indicating that crossing genotypes from these two clusters is likely to produce highly heterotic and diverse segregants. Highest per cent contribution towards clustering of genotypes were observed in total soluble solids, followed by unmarketable fruit yield/plant, average fruit weight and equatorial diameter of fruits.

Key words: Cluster, Divergence, Distance, Salt-affected conditions, Genotypes, Variability

Tomato (*Solanum lycopersicum* L.), a member of family Solanaceae, is warm season, self-pollinated vegetable crop. It is grown all over the world with wider consumption both in raw or in processed forms (Jethava *et al.*, 2024; Kumar *et al.* 2024). The information on genetic diversity, its nature and degree are useful for selecting desirable parents from a germplasm for the successful breeding programme (Sarawg *et al.*, 2007; Prakash *et al.* (2019); Thakur *et al.* (2025). In general, genetically diverse parents are expected to produce hybrids with greater vigor and yield potential. Hence, it necessitates study of genetic divergence among existing varieties and germplasm collection for identification of parents for hybridization programme (Singh *et al.*, 2023; Neha *et al.*, 2025). D² statistics developed by (Mahalanobis 1936) provides a measure of magnitude for divergence between two genotypes. Keeping in view, present study was undertaken to assess their utility in developing heterotic combinations for commercial use.

MATERIALS AND METHODS

The experiment was conducted at Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar

(Kumarganj), Ayodhya, Uttar Pradesh, India, during rabi 2019. Thirty-eight genotypes including three checks (ArkaVikas, KashiAman and DVRT-2) were used in arandomized block design with three replications. Each genotype consisted of tworow spaced 60 cm apart with plant-to-plant spacing of 50 cm. The soil has high pH (8.5-10), concentrations of exchangeable sodium ion (>15%) and electrical conductivity (EC) less than 4 ds/cm. Observations were recorded for days to 50% flowering, plant height (cm), number of locules per fruit, pericarp thickness (mm), polar diameter of fruit (cm), equatorial diameter of fruit (cm), number of fruits per cluster, average fruit weight (g), number of fruits per plant, marketable fruit yield per plant (kg), unmarketable fruit yield per plant (kg), total fruit yield per plant (kg), and total soluble solids (°Brix). Mahalanobis D² statistics and genotypes were grouped into different clusters following Tochers method as described by (Rao 1952) and (Mahalanobis 1936).

RESULTS AND DISCUSSION

The 38 tomato genotypes were grouped into 15 distinct non-overlapping clusters (Table 1). Cluster I contained the highest number of genotypes (9), followed by Cluster III (5) and Cluster IV (4). Clusters II, V, VI, VII, VIII, IX, and X each included two genotypes, while Clusters XI to XV comprised a single genotype each. This indicated presence of considerable diversity in genotypes. The major clusters reveal genetic divergence analysis. Although the genotypes of same origin or geographic region were also found to be grouped simultaneously in the same cluster. The instance of grouping of genotypes of

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different origin or geographic region in the same cluster were frequently observed. Thus, there is no parallelism between genetic and geographic diversity.

The minimum intra-cluster distance (0.00) was found for cluster XI, XII, XIII, XIV, XV and maximum for cluster X (167.17), followed by cluster IX (148.68), cluster I (148.29), cluster III (138.85), cluster VIII (132.41) and cluster IV (124.24) (Table 2). The maximum inter-cluster distance was found between cluster XI to VI (1745.89), followed by cluster VI to V (1602.37), cluster XIII to V (1532.42), cluster XIII to XI (1452.04), cluster XIV to XIII (1284.15), cluster X to XI (1253.19), cluster VIII to V (1215.37), cluster XIV to XI (1192.74), cluster XV to II (1143.93), cluster XIV to II (1031.96), cluster XV to VI (1018.13), cluster XV to XIII (1007.25) and cluster IX to VI (957.58) were very high.

The minimum inter-cluster D^2 value was found in cluster XIV to V (191.73), followed by cluster XI to V (195.90), cluster XIII to IX (211.19), cluster XIV to IV (220.65), cluster XII to VII (221.65), cluster VIII to VI (237.18), cluster X to IV (243.89), cluster VII to II (244.77), cluster VII to IV (250.84), cluster V to IV (254.30), cluster XII to I (255.56), cluster VIII to I (258.31) and cluster IX to III (261.97).

Lower inter-cluster values between clusters suggested that genotypes of the clusters were not much genetically diverse from each other, while higher inter-cluster distance indicated more genetic divergence between genotypes of those clusters. These results are in close conformation with those of Naveen *et al.* (2018), Kiran *et al.* (2020), Limbaniet *al.* (2020), Yadav *et al.* (2020).

The cluster means for different traits indicated considerable differences between clusters. The entire cluster from cluster I to cluster XV had average mean performance for most of the characters, exhibiting extreme cluster mean values for none of the characters (Table 3). Cluster V to XV had in general medium mean performance for most of the characters, showing extreme cluster means for none of the characters.

Cluster V showed maximum mean value (5.22) for pericarp thickness, cluster VI maximum mean value (7.08) for total soluble solids. Cluster X showed maximum mean values (23.95) for number of fruits/plant and (124.23) for unmarketable fruit yield/plant. Cluster XI showed maximum mean values (89.10) for plant height and (6.16) for locules/fruit. Cluster XII showed maximum mean value (4.72) for fruits/clusters. Cluster XIV showed maximum mean value (50.56) for days to 50% flowering. Cluster XV showed maximum mean values (7.65) for polar diameter of fruit, equatorial diameter of fruit (8.68), average fruit weight (90.63), marketable fruit yield/plant (1478.14) and total fruit yield per plant (1550.13). Cluster VII had not showed maximum mean value for any character but it had showed minimum mean values (4.16) for polar diameter of fruit and total soluble solids (5.48).

Cluster XII showed minimum mean values (4.99) for equatorial diameter of fruit, average fruit weight (32.83), number of fruits per plant (11.61), marketable fruit yield/plant (423.39), unmarketable fruit yield/plant (32.12) and total fruit yield/plant (455.51). Cluster XIII showed minimum mean values for days to 50% flowering (38.65),

Table 1: Clustering pattern of 30 genotypes of tomato on the basis of Mahalanobis' D^2 statistics

Cluster number	No. of genotypes	Genotypes
I.	9	NDT-3, DVRT-2, NDT-5-2, ArkaVikas, 12345, 2013/TODVAR-1, WT, 2013/TODVAR-5, S5Xndt-3-2-1-1-1
II.	2	NDT-8, 2015/TODINDVAR-1
III.	5	NDT-5-3-1-1, WT-1-1, 2012/TLCVRes.-7-1, WT-1-2, KashiAman
IV.	4	NDT-3-1-2, S5XNDT-3-2-1-1, 2013/TODVAR-2-2-1-1, NDTH-11W-17-1-3
V.	2	NDT-2-1-1, NDTH-11W-22-1-1-2
VI.	2	NDT-5-3-1-2, NDTH-11W-22-1-2-1
VII.	2	NDT-5-1-2-1, S5XNDT-3-2-1-1-2
VIII.	2	NDT-2-3, NDT-5-1-2-2
IX.	2	UtkalKumari, NDT-2-1
X.	2	NDT-3-1-1, S5XNDT-3-2-2-1
XI.	1	NDTH-11W-22-1-2-2
XII.	1	2013-TODVAR/-2-2-2
XIII.	1	Local collection-1
XIV.	1	NDTH-11W-8-2-1
XV.	1	3535

Table 2: Average on intra and inter- clusters D² values for 15 clusters in tomato

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I.	148.29	364.37	274.17	352.61	711.77	371.36	279.63	258.31	352.92	552.34	743.04	255.56	326.30	571.53	546.71
II.		59.22	748.49	539.14	893.98	745.92	244.77	569.62	795.34	334.00	696.17	483.16	556.27	1031.96	1143.93
III.			138.85	292.78	610.64	524.35	408.98	307.25	261.97	719.50	789.75	278.39	567.19	342.27	484.55
IV.				124.24	254.30	933.14	250.84	598.06	243.89	473.75	286.76	324.59	925.75	220.65	528.46
V.					86.08	1602.37	461.69	1215.37	364.55	655.81	195.90	567.72	1532.42	191.73	694.81
VI.						106.52	827.70	237.18	957.58	1253.19	1745.89	566.71	302.48	1192.74	1018.13
VII.							107.35	511.26	388.53	319.64	450.98	221.65	623.92	456.84	830.34
VIII.								132.41	601.31	768.08	1249.29	409.56	211.19	876.80	751.57
IX.									148.68	606.63	455.73	431.32	792.53	298.62	286.86
X.										167.17	366.07	718.18	783.38	904.60	993.88
XI.											0.00	781.13	1452.04	487.63	833.98
XII.												0.00	621.39	321.04	870.36
XIII.													0.00	1284.15	1007.25
XIV.														0.00	664.58
XV.															0.00

Table 3: Intra-cluster group means for 13 characters in tomato

Character	Days to 50% flowering	Plant height	Locules per fruit	Pericarp thickness	Polar diameter	Equatorial diameter	Fruits Per cluster	Average Fruit weight	Numbers of fruits Per plant	Marketable yield Per plant	Unmarketable yield Per plant	Total fruit yield per plant	TSS
	44.02	64.04	4.51	4.27	5.39	6.06	3.68	56.40	16.34	886.22	67.10	953.32	6.45
	39.19	71.62	5.25	4.85	4.64	5.60	4.57	43.71	22.89	934.68	117.94	1052.61	6.39
	45.59	70.31	3.80	3.75	6.33	6.14	3.55	57.38	13.85	748.16	45.96	794.12	6.02
	46.04	86.85	5.43	4.12	6.20	6.93	3.81	64.42	14.60	889.33	79.51	968.84	5.83
	47.38	84.44	5.09	5.22**	6.55	7.22	4.67	79.88	18.75	1385.57	77.18	1462.76	5.64
	47.20	70.75	4.31	5.01	5.45	5.50	3.02	45.87	16.80	734.38	44.40	778.78	7.08**
	41.48	66.82	4.85	3.77	4.16*	5.24	3.67	35.97	21.74	724.58	70.70	795.27	5.48*
	45.49	58.43	4.94	2.62	5.96	6.32	4.19	44.25	17.23	708.32	62.99	771.30	6.59
	43.95	60.28	3.39	3.64	6.60	7.28	4.02	78.10	14.20	1022.97	70.11	1093.08	6.05
	41.41	61.93	5.75	2.28	5.44	5.56	4.20	56.28	23.95**	1233.37	124.23**	1357.60	5.81
	42.66	89.10**	6.16**	3.39	6.40	7.16	4.36	87.19	15.42	1315.29	120.59	1435.88	5.81
	41.50	63.60	5.64	5.05	4.74	4.99*	4.72**	32.83*	11.61*	423.39*	32.12*	455.51*	5.65
	38.65*	45.53*	2.79*	1.95*	4.91	5.29	3.83	46.27	17.66	586.70	66.39	1053.58	6.88
	50.56**	86.90	5.57	4.10	6.34	7.01	4.49	68.95	14.88	990.25	35.22	1025.47	5.60
	40.69	57.17	4.86	4.91	7.65**	8.68**	2.85*	90.63**	17.27	1478.14**	71.99	1550.13**	6.72

plant height (45.53), locules per fruit (2.79) and pericarp thickness (1.95). Cluster XV showed minimum mean value for fruits/cluster (2.85). These results are in close conformation with those of Rojalin *et al.* (2015), Yadav *et al.* (2020) and Srinivasulu *et al.* (2020).

The highest contribution to genetic divergence among genotypes was observed for total soluble solids (25.30%), followed by unmarketable fruit yield per plant (16.63%), average fruit weight (9.88%), equatorial fruit diameter (9.44%), and polar fruit diameter (8.25%). The remaining traits like plant height (7.12%), total

fruit yield per plant (6.36%), marketable fruit yield per plant (5.40%), pericarp thickness (5.14%), number of fruits per cluster (3.97%), locules per fruit (1.69%), and days to 50% flowering (0.83%) showed comparatively low contribution to total divergence (Table 4). These findings are in close agreement with the results of Jogi *et al.* (2018), Dhyani *et al.* (2019), Prabakaran *et al.* (2019), and Kiran *et al.* (2020). The crosses between entries separated by large inter-cluster distance and having high cluster mean values for one or other character will be helpful in improvement of tomato.

Table 4. Per cent contribution of 13 characters towards total genetic divergence in tomato

Character	Contribution (%)
Days to 50% flowering	0.831
Plant height	7.115
Locules per fruit	1.687
Pericarp thickness	5.140
Polar diameter	8.251
Equatorial diameter	9.444
Fruit per cluster	3.969
Average fruit weight	9.876
Fruit per plant	0.000
Marketable fruit yield per plant	5.399
Unmarketable fruit yield per plant	16.628
Total fruit yield per plant	6.361
TSS	25.298

CONCLUSION

The formation of distinct clusters with considerable inter-cluster distances indicates the presence of substantial genetic variability, offering greater opportunities for heterosis breeding and selection. The maximum inter-cluster distance was observed between Cluster XI and Cluster VI, suggesting that crossing genotypes from these clusters is likely to generate highly heterotic hybrids and diverse segregating populations.

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