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## Study of Genetic Diversity in Cherry Tomato (*Solanum lycopersicum L. var. cerasiforme*) Genotypes for Various Quantitative and Qualitative Traits

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### ABSTRACT

The current investigation was led with 29 cherry tomato (*Solanum lycopersicum var cerasiforme L.*) "genotypes during the 2018 Kharif Experimental Field, Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Science and Technology, Kashmir, Shalimar Srinagar. The test was randomized to a randomized controlled preliminary (RCBD) with three reactions. Variety considers it uncovered that critical contrasts existed between the genotypes examined. Genotypes were characterized into four gatherings as indicated by Mahalanobis D2 measurements. Bunch II contained 12 genotypes followed by bunch I and IV containing six genotypes each, and bunch III had 5 genotypes. The centre bunch range (D2) was higher in bunch III (40.20), trailed by bunch II (25.25), bunch IV (25.00), and bunch I (16.55). The bury bunch range was more prominent than the inside group range, demonstrating a more elevated level of hereditary variety. In this way, could be utilized under a varietal hybridization program to get more beneficial genetic material. The most elevated commitment to variety was found in the hectare of organic product yield - 1 bookkeeping (29.86%), crop stature (19.26%), and the number of branches (13.86%). In absolute, they contributed 62.98%.

**Keywords:** cherry tomato, organic product, vegetable producers.

### INTRODUCTION

Cherry tomatoes (*Solanum lycopersicum L. var. cerasiforme*) are viewed as an assortment of developed tomato plants having a place with the Solanaceae family. Wild cherry tomatoes were first found throughout tropical America and afterward appropriated in tropical Asia and Africa [1]. The products of cherry tomatoes have a excellent appearance and delectable taste and are generally welcomed by buyers. Cherry tomatoes have fixed, whole, and solid development propensities with long racemes and numerous splendidly hued leafy foods and weighing somewhere in the range of 10 and 30 g [2]. Cherry tomatoes are impervious to illness and endure exceptionally high moistness, have a high dietary benefit (because of its high nutrient C substance), and present an entirely adaptable measure of organic product set-1 (15-50). Cherry tomatoes deliver little products of the soil flavors. These little tomatoes are generally new in huge business sectors, yet have incredible potential for development, introducing various flavors and colors and their adequacy [3]. Testing for germplasm is significant for plant hereditary turn of events. Hereditary variety examination assists with interpreting the genetic foundation and the quantity of germplasm generation. It has additionally been recommended that vegetable producers utilize a hereditary pool that is altogether not the same as the hereditary variations inside the harvest [4]. Inborn variety likewise permits ranchers to take out different guardians from lessening the accessible genetic stock and to zero in on fewer mixture mixes [5]. The D<sup>2</sup> computations created by [6] are a useful asset for assessing the greatness of contrasts between living individuals and are broadly used to

survey variety.

Furthermore, the decent commitment of the different yield components to the total separation utilizing Mahalanobis D<sup>2</sup> examination helps in recognizing the choice boundary to be used as a method for crop improvement.

### MATERIALS AND STRATEGIES

The flow study was led at Vegetable Experimental Farm, Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar (Jammu and Kashmir), Srinagar, during Kharif Season 2018. The test was led at Randomized Block Design with three Responses. Destinations of size 3 × 2 m (6 m<sup>2</sup>), contain one line of every genotype in every redundancy with spaces of 100 × 40 cm. 29 lines/genotypes of various cherry tomatoes, kept independently tried for diverse harvest and yield yields. This acknowledgment was recorded in twenty assortments of figuring and exactness, to be specific, plant stature (cm), number of branches, dates to early blossoming, number of blossoms bunch 1, natural product number gathering 1, normal organic product length (cm), normal natural product width (cm), Pericarp thickness (mm), Fruit yield number 1, Early natural product collect dates, Medium organic product weight (g), Fruit yield 1 (kg), Fruit yield 1 (q), Contents by - TSS (°Brix), Juice to mash proportion, 100 Seed weight (g), Ascorbic corrosive (mg100g<sup>-1</sup>), Acidity (% citrus extract), Lycopene content (mg100g<sup>-1</sup>) and Total carotenoids (mg100g<sup>-1</sup>). Cherry tomato transformation offers high potential for incorporation in reproducing programs, using their critical highlights for hereditary variety in parental choice, just as their wide geological variety [7]. An assortment of cutting edge genotypes with attractive qualities with high changeability can be remembered for a hybridization program to improve future yields. The information on hereditary variety is a significant factor in any fruitful turn of events, and its temperament and degree help in choosing alluring guardians in the germplasm for any effective reproducing program. A few multilateral-based order strategies have been proposed to suit their different purposes, the standard scope of [6], which involves a prime spot in plant propagation. It is a delicate and valuable asset for estimating the level of variety among natural individuals and to assess the simultaneous commitment of type to finish variety at the two degrees of inner and outside assortments.

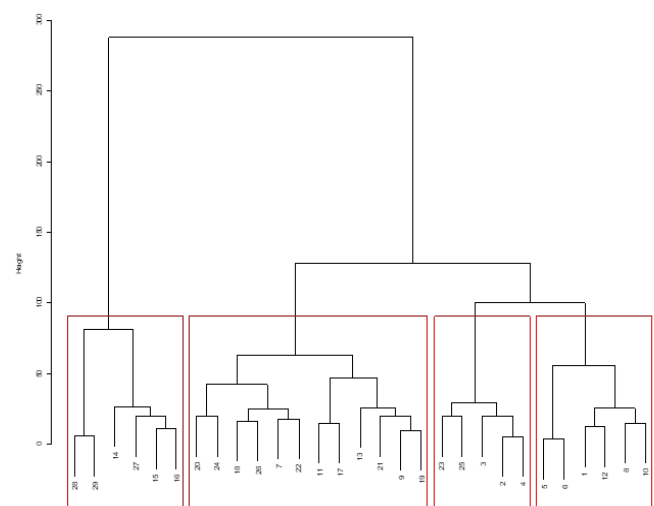
### RESULTS AND DISCUSSION

The heredity disparity was assessed for 29 genotypes of cherry tomato. In view of the exhibition of genotypes, 29 cherry tomato genotypes were gathered into four bunches (Table-1) according to Mahalanobis D<sup>2</sup>

examination utilizing Wards strategy. The dendrogram (Fig. 1) demonstrated that the most extreme number of genotypes fall in bunch Ii (12) trailed by group I and IV each containing six genotypes and group III comprised of 5 genotypes. Bunch I comprised of SK-CT-28, SK-CT-29, SK-CT-14, SK-CT-27, SK-CT-15, and SK-CT-16. The genotypes SK-CT-20, SK-CT-21, SK-CT-18, SK-CT-26, SK-CT-7, SK-CT-22, SK-CT-11, SK-CT-17, SK-CT-13, SK-CT-21, SK-CT-9 and SK-CT-19 were falling in bunch Ii. Group Iii comprised of SK-CT-23, SK-CT-25, SK-CT-3, SK-CT-2, and SK-CT-4. The bunch IV included SK-CT-5, SK-CT-6, SK-CT-1, SK-CT-12, SK-CT-8, and SK-CT-10. Comparative outcomes dependent on D<sup>2</sup> insights was likewise performed by [8-14].

**Table-1:** Distribution of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) genotypes into clusters based on D<sup>2</sup> Statistics

S. No.	Cluster	No. of genotypes in the cluster	Name of genotypes
1	I	6	SK-CT-28, SK-CT-29, SK-CT-14, SK-CT-27, SK-CT-15, SK-CT-16.
2	II	12	SK-CT-20, SK-CT-21, SK-CT-18, SK-CT-26, SK-CT-7, SK-CT-22, SK-CT-11, SK-CT-17, SK-CT-13, SK-CT-21, SK-CT-9, SK-CT-19
3	III	5	SK-CT-23, SK-CT-25, SK-CT-3, SK-CT-2, SK-CT-4
4	IV	6	SK-CT-5, SK-CT-6, SK-CT-1, SK-CT-12, SK-CT-8, SK-CT-10



**Fig-1:** Dendrogram dividing the cherry tomato genotypes into four clusters by wards method.

1-SK-CT-01, 2- SK-CT-02, 3-SK-CT-03, 4-SK-CT-04, 5-SK-CT-05, 6-SK-CT-06, 7-SK-CT-07, 8-SK-CT-08, 9-SK-CT-09, 10-SK-CT-10, 11-SK-CT-11, 12- SK-CT-12, 13- SK-CT-13, 14-SK-CT-14, 15-SK-CT-15, 16-SK-CT-16, 17-SK-CT-17 18- SK-CT-18, 19- SK-CT-19, 20-SK-CT-20, 21-SK-CT-21, 22-SK-CT-22, 23-SK-CT-23, 24-SK-CT-24, 25- SK-CT-25, 26-SK-CT-26, 27-SK-CT-27, 28-SK-CT-28, 29-SK-CT-29.

The average intra and entomb group separation (D2) values in (Table-2) uncovered that bunch Iii had the most noteworthy intra bunch separation (D2) estimation of 40.20, followed by bunch II (25.25), group IV (25.00) and group I (16.55). The higher estimations of intra bunch separation show more prominent hereditary variety among individuals from the group. At the same time the most minor intra group separation demonstrates restricted hereditary dissimilarity. The bury group separation among various bunches shows that qualities bunch I and II are most different, having greatest entomb group separation of (116.54) trailed by group I and IV (95.68), group I and III (78.83), group II and III (59.26) and bunch III and IV (46.97). Comparable outcomes were accounted for by [15, 8, 10, 11, 12, 14, 16].

Bunch mean in regard of twenty quantitative and subjective characters of 29 genotypes were introduced in (Table-3a and b). From the examination of table, it was seen that the most noteworthy bunch mean for plant stature (135.32), number of branches (28.11) least number of locules organic product 1(2.00), juice mash proportion (1.77) and complete carotenoids (1.36) were recorded in group I; most elevated group mean for normal organic product length (3.15), normal organic product width (3.04), pericarp thickness (3.04), 100 seed weight (0.88) and least bunch mean for quite a long time to initially organic product gathering (75.71) were seen in group II; most noteworthy group mean for number of blossoms bunch 1 (7.97), ascorbic corrosive (38.12) and least bunch mean for quite a long time to first blooming (24.68) were seen in bunch III. The most elevated bunch mean for number of natural products group 1(6.92), organic product weight (15.81), organic product yield plot-1 (8.47), organic product yield hectare-1(141.18), TSS (6.63), Tritrable acidity (0.65) and lycopene (0.94) were seen in group IV. Consequently, the characteristics indicating high commitment towards hereditary uniqueness can be refined by choosing the genotypes from those bunches having most significant group implies for the individual qualities, which this way relies on the target of the rearing project. In this manner, the choice of genotypes having high bunch mean qualities for a specific attribute can be used in hybridization program. Selection of genotypes dependent on bunch mean for the better abuse of hereditary potential was

likewise announced by [17, 13, 9,14].

The percent commitments of the qualities towards complete hereditary dissimilarity in (Table-4) uncovered that natural product yield hectare-1 was the fundamental factor adding to uniqueness representing (29.86%) trailed by plant stature (19.26%), number of branches (13.86%), normal natural product weight (9.4%), normal organic product length (5.24%), organic product yield plot-1 (4.43%), pericarp thickness (2.96%), number of organic products bunch 1 (2.32%), TSS content (2.02%), lycopene content (2.00%), number of blossoms group 1 (1.46), days to first blooming (1.32%), all-out carotenoids (1.23%), normal organic product width and (1.20%) and ascorbic corrosive (1.00%). Minimal commitment towards dissimilarity was from 100 seed weight (0.21%) trailed by days to initially natural product collecting (0.35%), juice to mash proportion (0.51%), number of locules organic product 1 (0.52%), and tritrable sharpness (0.85%). The qualities contributing most extreme towards the difference should be given extraordinary accentuation for choosing the groups to be picked for hybridization and the resulting choice of the guardians from the bunches be founded on there as such execution. In cherry tomato, top-level input from qualities towards dissimilarity has been accounted for to be diverse for various arrangements of materials utilized in experimentation relying on the genotypes under examination by [10, 18, 8, 13].

**Table-2:** Average intra cluster (Diagonal) and inter cluster (Above Diagonal) distance values in cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*)

S. No.	Cluster	I	II	III	IV
1	I	<b>16.55</b>	116.54	78.83	95.68
2	II		<b>25.25</b>	59.26	44.48
3	III			<b>40.20</b>	46.97
4	IV				<b>25.00</b>

### CONCLUSION

In the present study twenty-nine cherry tomato genotypes were assessed to know the value and magnitude of genetic divergence using Mahalanobis D<sup>2</sup> statistics and revealed that significant divergence existed among them. The genotypes were grouped into 4 clusters with maximum number of genotypes in cluster II (12) followed by cluster I and IV, each containing 6 genotypes and cluster III containing five genotypes. Custer IV had superior performance for yield. For the quality characters of cherry tomato clusters I and IV were promising. So the genotypes in these clusters can be used for the development of

superior segregants with high yield potential along with better quality traits.

**Table-3a:** Cluster means for various growth, maturity, yield attributing and quality characters in different clusters of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) genotypes

S. No.	Cluster	Plant height (cm)	Number of branches	Days to first flowering	Number of flowers cluster <sup>-1</sup>	Number of fruits cluster <sup>-1</sup>	Average fruit length (cm)	Average fruit width (cm)	Pericarp thickness (mm)	Number of locules fruit <sup>-1</sup>	Days to first fruit harvesting	Average fruit weight (g)	Fruit yield plot <sup>-1</sup>	Fruit yield ha <sup>-1</sup>
1	I	135.32	28.11	24.97	7.76	6.24	1.84	1.64	1.64	2.00	79.32	4.23	1.72	28.70
2	II	95.39	22.47	27.47	6.80	4.71	3.15	3.04	3.04	3.04	75.71	11.39	1.79	29.83
3	III	115.78	25.81	24.68	7.97	6.60	2.10	1.95	1.95	2.35	77.80	8.09	3.98	66.43
4	IV	113.65	23.56	29.46	7.69	6.92	2.69	2.23	2.23	2.35	80.40	15.81	8.47	141.18

**Table-3b:** Cluster means for various quality characters in different clusters of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) genotypes

S. No.	Cluster	TSS (°Brix)	Juice pulp ratio	100 seed weight (g)	Ascorbic acid (mg100g <sup>-1</sup> )	Titrable acidity (% citric acid)	Lycopene (mg100g <sup>-1</sup> )	Total carotenoids (mg100g <sup>-1</sup> )
1	I	5.94	1.77	0.77	36.82	0.45	0.79	1.36
2	II	2.80	1.30	0.88	26.18	0.44	0.44	0.56
3	III	5.40	1.50	0.74	38.12	0.54	0.90	1.13
4	IV	6.63	1.39	0.81	36.27	0.65	0.94	0.13

**Table-4:** Percent contribution of individual traits towards total genetic divergence

S. No.	Traits	% contribution towards total divergence
1	Plant height (cm)	19.26
2	Number of branches	13.86
3	Days to first flowering	1.32
4	Number of flowers cluster <sup>-1</sup>	1.46
5	Number of fruits cluster <sup>-1</sup>	2.32
6	Average fruit length (cm)	5.24
7	Average fruit width (cm)	1.20
8	Pericarp thickness (mm)	2.96
9	Number of locules fruit <sup>-1</sup>	0.52
10	Days to first fruit harvesting	0.35
11	Average fruit weight (g)	9.4
12	Fruit yield plot <sup>-1</sup> (kg)	4.43
13	Fruit yield hectare <sup>-1</sup> (q)	29.86
14	TSS content (°Brix)	2.02
15	Juice to pulp ratio	0.51
16	100 Seed weight (g)	0.21
17	Ascorbic acid (mg100g <sup>-1</sup> )	1.00
18	Titrable acidity (% citric acid)	0.85
19	Lycopene content (mg100g <sup>-1</sup> )	2.00
20	Total Carotenoids (mg100g <sup>-1</sup> )	1.23

## REFERENCES

- [1] Gharezi, M., Joshi N and Indires K. M. 2012. Physico-chemical and sensory characteristics of different cultivars of cherry tomato. *Mysore Journal of Agricultural Science* 46(3): 610-613.
- [2] Prema, G., Indires K. M and Santhosha, H. M. 2011. Evaluation of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) genotypes for growth, yield and quality traits. *Asian Journal of Horticulture* 6(1): 181-184.
- [3] Maciel, G.M., Fernandes, M., Melo, O.D. and Oliveira, C.S. 2016. *Potencial agrônomo de híbridos de minitomate com hábito de crescimento determinado e indeterminado. Horticultura Brasileira* 34: 144-148.
- [4] Joshi, B. K., Gardner, R. G. and Dilip, R. P. 2012. Diversity analysis of tomato cultivars based on coefficient of parentage and RAPD molecular markers. *Journal of Crop Improvement*, 26: 177-196.
- [5] Fuzzato, S. R., Ferreira D. F., Ramalho, P. M. A and Ribeiro (2002). Genetic divergence and its relationship with diallel crossing in maize crop. *Ciencia-e-Agrotecnologia* 26:22-32.
- [6] Mahalanobis, P.C. 1936. On the generalized distance in statistics. In: *Proc. Nat. Inst. Sci. Indi.*, 2:49-55.
- [7] Medina, C.I and M. Lobo. 2001. Variabilidad morfológica en el tomate pajarito (*Lycopersicon esculentum* var. *cerasiforme*), precursor del tomate cultivado. *Revista Corpoica* 3(2): 39-50.

- [8] Kumar, P. A., Reddy, K. R., Reddy, R. V. S. K., Pandravada, S. R and Saidaiah, P. 2016. Genetic divergence studies in tomato genotypes. *The Bioscan* 11(4) : 3071-3074.
- [9] Sharma, H. R., Sharma, D. and Thakur, A. K. 2006. Analysis of genetic divergence in tomato (*Lycopersicon esculentum* Mill.). *Journal of Horticultural Science*, 1(1): 52-54.
- [10] Ullah, M. Z., Hassan, L., Singha, T. and Patwary, A. K. 2015. Genetic divergence in tomato lines (*Solanum lycopersicum* L.). *Journal of Bangladesh Agricultural University* 13(1):61-64.
- [11] Lekshmi, S. L and Celine, V. A. 2016. Genetic diversity studies in tomato (*Solanum lycopersicum* L.) under protected conditions. *International Journal of Current Microbiology and Applied Sciences* 5(4):212-217.
- [12] Kumar, N., Bhardwaj, M. L., Sharma, A and Kumar, N. 2017. Assessment of genetic divergence in tomato (*Solanum lycopersicum* L.) through clustering and principal component analysis under mid hills conditions of Himachal Pradesh, India. *International Journal of Current Microbiology and Applied Sciences* 6 (5): 1811-1819.
- [13] Patel, P., Kumar, U., Thakur, G. and Maurya, P.K. 2017. Assessment of genetic diversity through D<sup>2</sup> analysis in tomato (*Solanum lycopersicum* L.). *Bulletin of Environment, Pharmacology and Life Sciences* 6(1): 219-224.
- [14] Spaldon, S. and Kumar, S. 2018. Genetic divergence studies for quantitative and quality traits in tomato (*Solanum lycopersicum* L.). *International Journal of Environment, Agriculture and Biotechnology* 2(3):2456-1878.
- [15] Chernet, S., Below, D and Abay, F. 2014. Genetic diversity studies for quantitative traits of tomato (*Solanum lycopersicum* L.) genotypes in Western Tigray, Northern Ethiopia. *Journal of Plant Breeding and Crop Science* 6(9): 105-113.
- [16] Babu, M.R., Reddy, R.V.S.K., Reddy, K. R., Saidaiah, P and Rani, A. S. 2018. Studies on genetic diversity in tomato (*Solanum lycopersicum* L.). *Journal of Pharmacognosy and Phytochemistry* 1: 13-17.
- [17] Dar, R.A., Sharma, J.P and Mushtaq, A. 2015. Genetic diversity among some productive genotypes of tomato (*Lycopersicon esculentum* Mill.). *African Journal of Biotechnology* 14(22):1846-1853.
- [18] Jogi, M., Lingaiah, H.B., Indires, K.M., Singh, T.H., Samuel, D.K. and Ramachandra R.K. 2018. Genetic divergence studies in tomato (*Solanum lycopersicum* L.). *International Journal of Current Microbiology and Applied Sciences* 7(9): 2231-2237.