To estimate the genetic divergence for tested genotypes of Tomato (*Lycopersicon esculentum* Mill)

Abstract

The present investigation was carried out at the Horticulture Research centre of the Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, U.P. (250 110) during *Kharif season*, 2020. The D^2 statistics was applied to assess the genetic divergence among 20 genotypes of tomato using Mahalonobis D^2 analysis. The experimental materials were planted in Randomized Block Design (RBD) with three replications. The analysis of variance revealed significant differences among the genotypes for all the characters under study. The genotypes were grouped into five different genetic clusters on the basis of genetic affinity or diversity. Cluster III comprised of highest 7 genotypes followed by Cluster I comprised of 4 genotypes, Cluster II also comprised of 4 genotypes, Cluster V comprised of 3 genotypes and Cluster IV comprised lowest number of 2 genotypes. The highest mean value was recorded in Cluster V for number of fruits per cluster, number of fruits per plant, fruit yield per plant (g), fruit yield /ha (q) and 1000 seed weight (g) followed by cluster II for harvest duration (days), average fruit weight (g) and number of seeds per fruits, Cluster III for number of primary branches, plant height (cm), Cluster I for number of clusters per plant and Cluster IV for number of locules per fruit respectively. The maximum intra cluster distance was found in cluster V and minimum intra cluster distance was recorded cluster IV. The highest inter-cluster distance was recorded between Cluster I and Cluster V and the minimum inter cluster D^2 distance was recorded between cluster I and Cluster IV. The highest contribution in the manifestation of genetic divergence was exhibited by number of fruits per cluster followed by number of primary branches, fruit yield per hectare, number of locules per fruit, plant height, harvest duration, number of clusters per plant, average fruit weight, number of fruits per plant, 1000 seeds weight, fruit yield per plant and lowest in number of seeds per fruit. So, breeding for the improvement of those characters have the possibility to develop superior hybrids in tomato.

Keywords: *Genetic Divergence, Intra and Inter cluster, Contribution, Tomato*

INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) is one of the most economically important vegetable crops belong to the family Solanaceae with diploid chromosome number 2n=24. Tomato has originated in the South American Andes. The wild species of tomato are native to the Andean region like Chile, Equador, Bolivia, Colombia and Peru. The most likely ancestor is the wild tomato *Lycopersicon esculentum* var. Cerasiforme like cherry tomato, which is indigenous throughout tropical and subtropical America.

The tomato is a good source of vitamins and minerals as compared to cereals, the pulp and juice are digestible and a mild promoter of gastric secretion and blood purifier. In India, it is grown as autumn-winter, winter and spring- summer crop in many parts but owing to high temperature and rains, tomato cannot be grown commercially in the North Indian plains from May to October. The mid- Hills of Himachal Pradesh are a leading supplier of fresh market tomatoes to the Northern markets of the country during rainy and autumn season fetching off-season prices to our growers.

Tomato is an annual fruit plant which can reach a height of over two metres. In South America, however, the same tomato plants can be harvested for several years in succession. The first fruit harvest is possible 45-55 days after flowering, or 90-120 days after sowing. The tomato fruit shape differs as per cultivar. The fruit colour ranges from yellow to red.

Vegetables are occupied most important place in crop diversity and play a key role in food nutrition and economic security of our country. India ranks second in the vegetable production after china. In India vegetables are grown largely on a commercial scale in an area of 10.10 Million hectare with production of 185.883 Metric tons and productivity of 18.40 Metric tons per hectare (Anonymous, 2018-19). Tomato is cultivated in India with 778 thousand hectares in area with production of 19397 thousand Metric tons (Anonymous 2018-19). The D^2 statistic measure divergence at two levels, namely, inter-cluster and intra-cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization programme (Mahalanobis 1936).

Materials and Methods

The present investigation was conducted during *Kharif season* of the year 2020 at Horticultural Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. The experimental material comprised of 20 diverse genotypes of tomato. Out of these, 20 genotypes (Table-1) were from Indian Institute of Vegetable Research, Varanasi Uttar Pradesh. The diverse genotypes of tomato were sown in well prepared field with using standard experimental design in Randomized block design (RBD) with three replications. The schedules of various cultural operations were carried out during the course of investigation according to need of crops. All agricultural practices and packaging were adopted to raise a tomato crop healthy. Seed were sown in lines in raised nursery bed having 1 meter width and 3.0-meter length which were 10 cm apart from each other and the depth was maintained at 0.5 cm. Transplanting of young seedlings from nursery to the main field was done after 25 days of sowing with 90x30 cm spacing. The observations were recorded from five randomly selected plants from each genotype and each replication. The reding was recorded for twelve characters *viz.*, number of primary branches, plant height (cm), number of fruits per cluster, number of clusters per plant, number of fruits per plant, number of locules per fruit, harvest duration (days), average fruit weight (g), fruit yield per plant (g), fruit yield per hectare (q), number of seeds per fruits and 1000 seed weight (g). The genetic divergence in twenty genotypes was estimated using **Mahalanobis** D^2 **statistic (1936)** following **Rao (1952).**

RESULT AND DISCUSSION

The estimates of genetic divergence among the twenty genotypes were done following the method of Mahalanobis D^2 statistic and as describe by **Rao (1952).** The group constellation was done following Tocher's method **(Rao, 1952).**

The cluster mean for twelve characters under study have been presented in Table-2. The result revealed that the number of primary branches were observed highest mean value for cluster III (4.95) followed by cluster II (4.67), Cluster V (4.67) and lowest cluster I (3.58). Plant height were observed highest mean value for cluster III (88.95) followed by cluster V (83.33), Cluster I (81.92), Cluster II (81.42) and lowest in cluster IV (62.83). Number of fruits per cluster were observed highest mean value for cluster V (5.17) followed by cluster III (4.71), Cluster IV (4.17), Cluster II (4.08) and lowest in cluster I (3.42). Number of clusters per plant were observed highest mean value for cluster I (9.67) followed by cluster V (9.44), Cluster II (6.33), Cluster IV (5.00) and lowest in cluster III (4.86). Number of fruits per plant were observed highest mean value for cluster V (51.11) followed by cluster I (30.75), Cluster II (26.67), Cluster III (24.14) and lowest in cluster IV (23.33). Number of locules per fruit were observed highest mean value for cluster IV (5.17) followed by cluster II (4.92), Cluster I (4.33), Cluster V (4.22) and lowest in cluster III (3.14). Harvest duration were observed highest mean value for cluster II (41.58) followed by cluster V (40.78), Cluster I (35.92), Cluster IV (32.00) and lowest in cluster III (31.57). Average fruit weight was observed highest mean value for cluster II (48.92) followed by cluster III (44.52), Cluster I (33.92), Cluster V (33.78) and lowest in cluster IV (30.50). Fruit yield per plant were observed highest mean value for cluster V (1573.11) followed by cluster II (1283.00), Cluster III (1061.19), Cluster I (1057.25) and lowest in cluster IV (718.33). Fruit yield per hectare were observed highest mean value for cluster V (530.13) followed by cluster II (426.16), Cluster III (350.22), Cluster I (348.86), and lowest in cluster IV (237.05). Number of seeds per fruit were observed highest mean value for cluster II (109.75) followed by cluster III (79.14), Cluster V (75.78), Cluster I (62.08), and lowest in cluster IV (50.67).1000 seeds weight was observed highest mean value for cluster V (3.41) followed by cluster II (2.24), Cluster IV (3.02), Cluster III (2.93) and lowest in cluster I (2.56). In heterosis breeding, genotypes of diverse cluster are known to play an important role of potential parents and when each genotype of different cluster are inter crossed, they are likely to produce very good heterotic combinations. Based on cluster analysis the selected genotypes expecting to bring the improvement in the germplasm and also serve as potential hybrids, as well as evaluation of genotypes for quality purpose. Thapa *et. al.,* (2014), Kiran, *et. al.,* (2017), Maurya *et. al.,* (2019), Anuradha *et. al.,* (2020), Kumar *et. al.,* (2021).

A total of 20 genotypes were grouped into five different genetic clusters on the basis of genetic affinity or diversity by **Tocher's** methods presented on Table-3.

Cluster III comprised of highest 7 genotypes *viz*, VRT-51, VRT-19, VRT-50, VRT-30, VRT-1, VRT-34 and VRT-16-1. Cluster I comprised of 4 genotypes *viz,* Sel-7, VRT-06, ToLCV-41 and ToLCV-16. Cluster II also comprised of 4 genotypes *viz,* Pusa Ruby, VRT-13, Kashi Anupam and H-24. Cluster IV comprised lowest number of 2 genotypes *viz,* Kashi Hemant and VRT-2 (p.c). Cluster V comprised of 3 genotypes *viz,* VRT-67, Kashi Amarit and ToLCV-28.

It was concluded that in general, there was parallelism between genetic and geographical diversity. The view point has been supported by the work Mehta and Asati (2008), Sharma *et. al.,* (2010), Mulge *et al.* (2012), Reddy *et. al.,* (2013), Kiran, *et. al.,* (2017), Maurya *et. al.,* (2019), Anuradha *et. al.,* (2020), Kumar *et. al.,* (2021).

The average inter and intra- cluster D^2 values are presented in Table-4. The maximum intra cluster distance was found in cluster V (2.55) followed by cluster II (2.44), cluster I (2.16), cluster III (2.14) and minimum intra cluster distance was recorded cluster IV (1.92).

The maximum inter cluster D^2 distance (6.024) was recorded between Cluster I and Cluster V and the minimum inter cluster D^2 distance (3.134) was recorded between cluster II and Cluster III. The selection of parents based on large inter-cluster and intra-cluster distances for hybridization work gives a range of useful combinations. Similar results were also earlier reported Sharma *et. al.,* (2010), Narolia and Reddy (2012), Reddy *et. al.*, (2013), Pedapati *et. al.,* (2014), Thapa *et. al.,* (2014), Kiran, *et. al.,* (2017), Mourya *et. al.*, (2019), Anuradha *et. al.,* (2020), Kumar *et. al.,* (2021).

The contribution of various characters under study toward the expression of genetic divergence as presented in Table-5. The result showed that number of fruits per cluster had maximum contribution (12.05) followed by number of primary branches (11.70), fruit yield per hectare (11.07), number of locules per fruit (9.72), plant height (8.58), harvest duration (8.54), number of clusters per plant (8.33), average fruit weight (6.92), number of fruits per plant (6.64), 1000 seeds weight (5.70), fruit yield per plant (5.44) and number of seeds per fruit (5.31). It ensues from the present study that genotypes showing greater contribution towards genetic diversity in tomato may be considered for utilization in crossing program, irrespective of geographical considerations. Rai *et. al.,* (1998), Buckseth *et. al.,* (2012), Ayush *et. al*., (2012), Alam *et. al.,* (2019), Maurya *et. al.,* (2019), Anuradha *et. al.,* (2020) and Kumar *et. al.*, (2021).

CONCLUSION

The objective of the experiment, it is concluded that the genotypes were grouped into five clusters. Cluster III comprised highest genotypes followed by Cluster I, Cluster II, Cluster V and Cluster IV. So, the cross combinations cluster IV and Cluster III are recommended for developing progeny with high vigour and desirable characters in tomato The highest mean value was recorded in Cluster V, Cluster II, Cluster III, Cluster I and Cluster IV respectively. The maximum intra cluster distance was found in cluster V and minimum intra cluster distance was recorded cluster IV. The highest inter- cluster distance was recorded between Cluster I and Cluster V and the minimum inter cluster D^2 distance was recorded between cluster I and Cluster IV. The character highest number of fruits per cluster contributed maximum divergence. selection of divergent genotypes and use in crossing programme would give greater chances of obtaining high heterosis and high genetic variability for quantitative and other desirable traits in segregating generations to develop high yielding cultivars in tomato.

REFERENCES

Alam MS, Huda MN, Rahman MS, Azad AKM, Rahman MM, Molla MM. Character association and path analysis of tomato (*Solanum lycopersicum* L.). *Journal of Bioscience and Agriculture Research.* 2019;22(01): 1815-1822.

Anonymous. Department of Agriculture, Cooperation and Farmers Welfare.2018-19.

Anonymous. Horticultural Statistics at a Glance, 2018. Ministry of Agriculture and Farmers Welfare, Department of Agriculture, Co-operation and Farmers Welfare (Horticulture Statistics Division), Govt of India, New Delhi.2018.

Anuradha B, Saidaiahk P, Reddy R, Sudini H, Geeth A. Genetic divergence for yield and yield attributes in tomato (*Solanum lycopersicum* L.). *Green Farming.* 2020;11(4&5):293-298.

Asati BS, Rai N, Singh AK. Genetic parameters study for yield and quality traits in tomato. *Asian Journal of Horticulture.* 2008;3: 222-225.

Ayush AF, Serhan M, Shareef, Naseer A, Kutma MH. Study of genetic parameters and character interrelationship of yield and some yield components in tomato (*Solanum lycopersicon* L.). *International Journal of Genetics.* 2012; 2:29-33.

Buckseth T, Sharma MK, Thakur KS. Genetic Diversity and Path analysis in tomato (*Solanum lycopersicon* L. *Vegetable Science.* 2012; 39:221-223.

Kiran ML, Mishra HN, Mishra A, Nandi A, Tripathy P, Senapati N, Pradhan K. Genetic Divergence and Cluster Analysis in Tomato (*Solanum lycopersicum* L.). *Environment & Ecology*. 2017;35 (4B):3167—3171.

Kumar J, Dixit PS, Yadav L, Kumar M, Singh BP, Tomar S. Studies about genetic divergence in 40 genotypes of Tomato (*Solanum lycopersicum* L.). *Journal of Pharmacognosy and Phytochemistry*. 2021;10(1): 2290-2292

Mahalanobis PC. On the generalized distance in statistics. *Proceedings of the National Academy of Sciences, India.* 1936;**2**: 49-55.

Maurya S, Singh AK, Singh SK, Kumawat OP. Study of Genetic Divergence in Tomato (*Solanum lycopersicum* L.). *Int. J. Curr. Microbiol. App. Sci.* 2019;8(8): 2429-2436.

Mulge R, Mahendrasekhar P, Prasanth SJ. Prediction oh heterosis based on genetic divergence in tomato. *Indian Journal of Horticulture.* 2012;69(4): 530-535.

Narolia RK, Reddy RVSK. Genetic divergence studies in tomato (*Lycopersicon esculentum* Mill.). *Crop Research Hisar*. 2012;44(1/2): 125-128.

Pedapati A, Reddy RVSK, Bahu JD, Kumar SS, Sunil N. Genetic divergence analysis in tomato (*Solanum Lycopersicon* L). *Electronic Journal of Plant Breeding.* 2014; 5:517-525.

Rai N, Rajput YS, Kumar S. Genetic diversity in tomato using a non-hierarchial clustering approach. Vegetable Science. 1998;25(2): 133-135.

Rao CR. Advance Statistical Methods in Biometrical Research (Ist Edn). John Willey and Sons, New York. 1952.

Reddy BR, Begum H, Sunil N, Reddy TM. Genetic divergence studies in exotic collections of tomato (*Solanam Lycopersicum* L.). *International Journal of Agricultural Sciences.* 2013;9: 588-592.

Sharma JP, Singh AK, Rattan P, Kumar S, Kumar S. D^2 clustering of exotic germplasm of tomato (*Solanum Lycoperstcum* L.) for genetic improvement. *Mysore Journal of Agricultural Sciences*. 2010;45: 48-52.

Thapa RP, Jha AK, Deka BC, Reddy ANK, Verma VK, Yadav RK. Genetic divergence in tomato grown in subtropical mid-hills of Meghalaya. *Indian Journal of Horticulture.* 2014;71(1): 123-125.

Table-1. List of cultivars and their sources

S. No.	No. of germplasm	Source	S. No.	No. of germplasm	Source
T_1	Pusa Ruby	**IARI, New Delhi**	**T_{11}**	VRT-13	**IIVR, Varanasi**
T_2	Kashi Hemant	**IIVR, Varanasi**	**T_{12}**	Kashi Anupam	**IIVR, Varanasi**
T_3	VRT-51	**IIVR, Varanasi**	**T_{13}**	VRT-2 (p.c)	**IIVR, Varanasi**
T_4	VRT-67	**IIVR, Varanasi**	**T_{14}**	VRT-34	**IIVR, Varanasi**
T_5	Sel.-7	**IIVR, Varanasi**	**T_{15}**	Kashi Amrit	**IIVR, Varanasi**
T_6	VRT-19	**IIVR, Varanasi**	**T_{16}**	VRT-16-1	**IIVR, Varanasi**
T_7	VRT-06	**IIVR, Varanasi**	**T_{17}**	ToLCV-28	**IIVR, Varanasi**
T_8	VRT-50	**IIVR, Varanasi**	**T_{18}**	ToLCV-41	**IIVR, Varanasi**
T_9	VRT-30	**IIVR, Varanasi**	**T_{19}**	H-24	**IIVR, Varanasi**
T_{10}	VRT-1	**IIVR, Varanasi**	**T_{20}**	ToLCV-16	**IIVR, Varanasi**

Table-2. Cluster mean for 12 characters in Tomato

Characters		Number of primary branches	Plant height (cm)	Number of fruits per cluster	Number of clusters per plant	Number of fruits per plant	Number of locules per fruit	Harvest duration (days)	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield /ha (q)	Number of seeds per fruits	1000 seed weight (g)
Cluster I	**Mean**	3.58	81.92	3.42	9.67	30.75	4.33	35.92	33.92	1057.25	348.86	62.08	2.56
	± SE	0.92	14.77	0.57	1.52	6.32	1.05	1.77	3.40	232.45	76.67	6.42	0.10
Cluster II	**Mean**	4.67	81.42	4.08	6.33	26.67	4.92	41.58	48.92	1283.00	426.16	109.75	3.24
	± SE	0.72	12.83	0.74	1.36	5.29	1.29	4.77	4.01	181.96	61.74	16.20	0.65
Cluster III	**Mean**	4.95	88.95	4.71	4.86	24.14	3.14	31.57	44.52	1061.19	350.22	79.14	2.93
	± SE	0.68	8.85	0.49	0.79	3.09	0.72	5.08	5.57	102.39	33.79	20.91	0.56
Cluster IV	**Mean**	4.17	62.83	4.17	5.00	23.33	5.17	32.00	30.50	718.33	237.05	50.67	3.02
	± SE	0.24	4.01	0.24	1.41	5.66	2.59	1.41	2.59	234.29	77.32	7.07	0.49
Cluster V	**Mean**	4.67	83.33	5.17	9.44	51.11	4.22	40.78	33.78	1573.11	530.13	75.78	3.41
	± SE	0.67	5.00	0.76	1.35	14.50	0.77	4.43	11.94	309.14	84.26	26.50	0.27

Table-3. Number of genotypes in each cluster in Tomato

Clusters	Number of genotypes	Name of genotypes
I	**4**	Sel-7, VRT-06, ToLCV-41 and ToLCV-16
II	**4**	Pusa Ruby, VRT-13, Kashi Anupam and H-24
III	**7**	VRT-51, VRT-19, VRT-50, VRT-30, VRT-1, VRT-34 and VRT-16-1
IV	**2**	Kashi Hemant and VRT-2 (p.c)
V	**3**	VRT-67, Kashi Amarit and ToLCV-28

Table-4. Inter and intra distances in Tomato

Clusters	I	II	III	IV	V
I	**2.161**				
II	3.906	**2.445**			
III	3.739	3.134	**2.147**		
IV	3.573	4.865	3.900	**1.925**	
V	4.478	3.953	4.694	6.024	**2.552**

Table-5. Contribution of various characters towards total genetic divergence

S. No.	Characters	Contribution %
1.	Number of primary branches	11.70
2.	Plant height (cm)	8.58
3.	Number of fruits per cluster	12.05
4.	Number of clusters per plant	8.33
5.	Number of fruits per plant	6.64
6.	Number of locules per fruit	9.72
7.	Harvest duration (days)	8.54
8.	Average fruit weight (g)	6.92
9.	Fruit yield per plant (g)	5.44
10.	Fruit yield /ha (q)	11.07
11.	Number of seeds /fruits	5.31
12.	1000 seed weight (g)	5.70