

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

Comment [ah1]: Suggest to change the title into : Assessment of genetic divergence in tomato (*Lycopersicon esculentum*) genotypes

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 Mahalanobis D^2 analysis. The experimental materials were planted in Randomized Block Design (RBD) with three replications. The analysis of variance revealed significant differences ($p > 0.05$) 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.

Comment [ah2]: What is this? Coordinate?

Comment [ah3]: Maybe can used the standard universal season?

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

Comment [ah4]: Revise this sentence - Findings in this study

Comment [ah5]: Alphabetical order

INTRODUCTION

Comment [ah6]: Suggested to revise back this session. Author need to state what is the problem with tomato? And why this study was conducted? What are the current situation with cultivation of tomato that need this study to carried out?

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.

Comment [ah7]: Any reference?

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.

Comment [ah8]: Ref?

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-

Comment [ah9]: Find other reference

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cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization programme (Mahalanobis 1936).

Comment [ah11]: What is your objective?

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Materials and Methods

Comment [ah13]: Suggested to describe the method into subtopic:
1. plant material
2. cultivation/growth condition
3. Assessment of plant growth
5. statistical analysis

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 obtained 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).

Comment [ah14]: Based on which standard cultivation method?

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).

Comment [ah15]: Revise back this sentences? what author want to state? Similar study?

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).

Comment [ah16]: Author need to explain or describe 1st the differences between the 20 genotypes choose. Based on what? Geography or diversity or local varieties or ?

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)].

Comment [ah17]: Need to explain what happened in their study. And relate with your findings

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).

Comment [ah18]: ?????

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

Comment [ah19]: Revise!

Comment [ah20]: Based on what?????

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.

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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

Comment [ah21]: Maybe u can explain what is the differences with the genotypes?

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