

## **Genetic divergence in tomato (*Lycopersicon esculentum* Mill.)**

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### **ABSTRACT**

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Sixty-seven tomato genotypes of different geographical origin were assessed to know the value and magnitude of genetic divergence using Mahalanobis  $D^2$  statistics. A wide genetic diversity was observed among the genotypes and was grouped into seven clusters. The clustering pattern indicated that the geographic diversity need not necessarily be related to genetic diversity. The maximum inter cluster distance was observed between cluster V and VI ( $D^2=243.700$ ), closely followed by cluster III and V ( $D^2=239.740$ ), cluster IV and V ( $D^2=222.521$ ), cluster IV and VII ( $D^2=211.82$ ), cluster VI and VII ( $D^2=209.086$ ) and cluster V and VII ( $D^2=207.860$ ). The cluster II revealed the least distance relationship with the cluster III ( $D^2=86.717$ ). Therefore, selection of divergent parents based on these cluster distance is recommended for getting good hybrids or segregants in tomato.

**Key words :** Genetic divergence,  $D^2$  analysis, Clustering pattern and Tomato

**T**omato is one of the most popular, widely grown and versatile vegetables grown in the world. Tomato can be consumed either in the form of fresh as salads, after cooking and utilized in the preparation of range of processed products such as puree, paste, ketchup, sauce, soup, pickles, chutney and canned whole fruits. Now a day's cultivation of commercial  $F_1$  hybrids are very common to achieve higher productivity, uniformity and good quality fruits and selection of newer parents for higher heterosis is thus a continuous process. Generally diverse parents are expected to give high hybrid vigour (Harrington, 1940). Mahalanobis  $D^2$  multivariate analysis (Mahalanobis, 1936) is one of the valuable tool for obtaining quantitative estimates of genetic divergence between biological populations. Further grouping of the genotypes based on Tochers method will be more useful in choosing suitable parents for heterosis breeding. Therefore, an attempt was made in the present investigation to examine the nature and magnitude of genetic divergence in tomato genotypes.

### **MATERIALS AND METHODS**

Sixty-seven genotypes collected from different sources were evaluated during 2002-2003 in the Department of Olericulture, Kittur Rani Channamma, College of Horticulture, Arabhavi. The crop was grown in a randomized block design with three replications at spacing of 75 x 60 cm. Five randomly chosen plants in each replication of each genotype were labelled and used for recording the observations. The data were subjected to multivariate analysis. The original mean values were transformed to normalize variables and all possible  $D^2$  values were calculated. The grouping of the genotypes

was done by using Tochers method as described by Rao (1952). The criterion used in clustering by this method is that genotypes belonging to the same cluster should show a smaller  $D^2$  value than those belonging to different clusters.

### **RESULTS AND DISCUSSION**

The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. After computing  $D^2$  values for all the possible pairs, sixty-seven genotypes were grouped into seven clusters, which indicated a large genetic diversity (Table 1). The cluster I was the largest with 44 genotypes followed by cluster II with 11 cluster IV with 7 and cluster III with 2 genotypes. The clusters V, VI and VII included only one genotype each. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence. Present result supported the findings of Dharmatti *et al.* (2001) and Parthasarathy and Aswath (2002). Intra-cluster distance (Table 2) revealed that, cluster IV with 7 numbers of genotypes showed maximum intra-cluster diversity ( $D^2=68.998$ ) followed by cluster I ( $D^2=61.060$ ) with 44 genotypes, cluster II ( $D^2=57.351$ ) with 11 genotypes and cluster III ( $D^2=23.327$ ) with 2 genotypes. The clusters V, VI and VII had no intra-cluster distance ( $D^2=0.000$ ) as they possessed single genotype in each. Based on distance between clusters, *i.e.*, inter-cluster distance, the maximum divergence was observed between cluster V and VI ( $D^2=243.700$ ), closely followed by cluster III and V ( $D^2=239.740$ ), cluster IV and V ( $D^2=222.521$ ), cluster IV and VII ( $D^2=211.820$ ), cluster VI and VII ( $D^2=209.086$ ) and cluster V and VII

**Table 1 : Classification of tomato genotypes into different clusters based on D<sup>2</sup> values**

Cluster No.	Number of genotypes	Name of the genotype			
I	44	KT 02	KT 03	KT 04	KT 06
		KT 07	KT 09	KT 12	KT 13
		KT 14	KT 16	KT 18	KT 19
		KT 20	KT 21	KT 22	KT 23
		KT 25	KT 26	KT 27	KT 28
		KT 29	KT 30	KT 31	KT 33
		KT 34	KT 35	KT 36	KT 37
		KT 38	KT 39	KT 40	KT 42
		KT 44	KT 46	KT 47	KT 53
		KT 55	KT 57	KT 59	
		Punjab Kesari	Arka Vikas		
		Arka Saurabh	Arka Meghali		
		Arka Abha			
		II	11	KT 01	KT 10
KT 24	KT 41			KT 54	KT 56
KT 60	Arka Alok			Arka Ashish	
III	02	KT 32	KT 43		
IV	07	KT 05	KT 08	KT 48	KT 50
		KT 51	KT 52	KT 58	
V	01	KT 45			
VI	01	KT 49			
VII	01	KT 11			

**Table 2 : Average intra- and inter-cluster D<sup>2</sup> values along with their 'D' values (in parenthesis) for 21 characters formed by 67 genotypes of tomato**

Cluster	I	II	III	IV	V	VI	VII
I	61.060	100.910	152.372	100.683	148.365	146.309	192.943
II		57.351	86.717	117.993	169.519	137.105	116.576
III			23.327	132.551	239.740	145.533	111.742
IV				68.998	222.521	106.005	211.820
V					0.000	243.700	207.860
VI						0.000	209.086
VII							0.000

Note: Diagonal values indicate intra-cluster distances.

(D<sup>2</sup>=207.860). The cluster II revealed the least distance relationship with the cluster III (D<sup>2</sup>=86.717).

For crop improvement in chilli, intercrossing among genotypes with outstanding mean performance was suggested by Roy and Sharma (1996). For plant height at 60 DAT, the highest cluster means (Table 3) was shown by cluster VI, followed by cluster VII, cluster IV and cluster II and cluster V. The highest inter-cluster distance was observed between cluster VI and V (D<sup>2</sup>=243.700), followed by cluster IV and V (D<sup>2</sup>=222.521), cluster VII and IV (D<sup>2</sup>=211.820) and cluster VI and VII (D<sup>2</sup>=209.086). Therefore, crosses between the genotypes belonging to these respective clusters may be tried to isolate genotypes with tall plants, which ultimately help in increasing the branches, flowers, fruit set and finally the yield as revealed by correlation studies (Mala and Vadivel, 1999). For days to first flowering, days to fifty per cent flowering, days to first fruit set and days to first fruit maturity, the lowest cluster mean was observed in cluster

VI followed by cluster V and cluster IV. The inter-cluster distance between cluster VI and V (D<sup>2</sup>=243.700) was comparatively high. Therefore, the crosses between the genotypes KT 49 (cluster VI) and KT 45 (cluster V) may be tried to improve earliness characters.

Average fruit weight, fruit volume, number of fruits per plant, early yield and per cent fruit set are the major yield contributing traits in tomato. For average fruit weight and fruit volume, the highest cluster means was shown by cluster V followed by cluster VII, cluster II and cluster I. The inter-cluster distance between the cluster V and VII (D<sup>2</sup>=207.860) and cluster VII and cluster I (D<sup>2</sup>=192.943) was comparatively high. For number of fruits per plant, the highest cluster means was shown by the cluster VI, followed by cluster IV. The inter-cluster distance between cluster VI and IV (D<sup>2</sup>=106.005) was high. For per cent fruit set, the highest cluster mean was shown by cluster VII, followed by cluster IV, cluster V and cluster II. The inter-cluster distance between cluster

**Table 3 : The mean values of 21 characters for 7 clusters in tomato**

Sr. No.	Character	Cluster						
		I	II	III	IV	V	VI	VII
1.	Days to first flowering	28.30	27.78	29.00	27.71	26.67	19.33	28.67
2.	Days to 50 per cent flowering	30.87	30.06	31.66	29.66	29.00	21.33	31.00
3.	Days to first fruit set	35.02	34.60	35.67	34.38	33.33	26.67	36.33
4.	Days to first fruit maturity	69.47	68.93	69.33	68.09	66.67	58.67	69.00
5.	Plant height at 60 DAT (cm)	59.77	63.95	59.47	64.29	61.80	81.67	66.07
6.	Number of primary branches at 90 DAT	10.66	10.81	12.03	11.23	10.20	13.67	11.20
7.	Number of flowers per cluster	5.75	5.54	5.43	6.27	4.93	6.13	6.27
8.	Pericarp thickness (cm)	0.57	0.54	0.58	0.36	0.63	0.32	0.44
9.	Number of locules per fruit	3.25	4.25	3.97	3.27	3.40	3.47	4.73
10.	TSS (°Brix)	4.00	4.23	4.00	4.31	3.77	4.13	4.18
11.	Acidity (%)	0.40	0.39	0.33	0.42	0.36	0.45	0.43
12.	Ascorbic acid (mg/100 g)	16.09	16.28	21.40	14.59	17.06	9.37	22.85
13.	Lycopene (mg/100 g)	9.86	12.24	7.40	9.19	12.67	12.93	10.51
14.	Average fruit weight (g)	92.09	97.25	57.71	36.98	210.40	43.00	140.13
15.	Fruit volume (cc)	72.65	76.18	43.67	25.85	150.00	36.00	106.00
16.	Number of seeds per fruit	74.78	157.15	213.33	95.19	63.00	127.00	253.33
17.	Per cent fruit set	76.70	79.06	77.66	80.80	79.67	77.31	80.93
18.	Number of fruits per cluster	4.42	4.35	4.20	5.06	3.93	4.73	5.07
19.	Number of fruits per plant	34.89	39.87	34.80	73.67	28.93	145.47	33.27
20.	Early yield per plant (kg)	1.13	1.30	0.92	0.70	1.30	1.42	1.03
21.	Total yield per plant (kg)	2.51	2.89	2.10	1.54	2.67	2.91	2.30

DAT = Days after transplanting

IV and V ( $D^2=222.521$ ) followed by cluster VII and IV ( $D^2=211.820$ ) and cluster VII and V ( $D^2=207.860$ ) was high. For early and total yield, the highest cluster means was shown by cluster VI followed by cluster II, cluster V and cluster I. The inter-cluster distance between cluster VI and V ( $D^2=243.700$ ) and cluster II and V ( $D^2=169.519$ ) were comparatively high. Hence, crosses can be made between the genotypes of these respective clusters for yield improvement.

For lycopene content, the highest cluster mean was shown by cluster VI followed by cluster V and cluster II. Inter-cluster distance between cluster VI and V ( $D^2=243.700$ ) was comparatively high and hence, the hybridisation programme may be employed between the genotypes of these clusters to improve lycopene content, which is a potential anti-oxidant used to counter cancer diseases. Similar results also reported by Das *et al.* (1998).

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