

Original Research Article

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Genetic Diversity Studies in Tomato (*Solanum lycopersicum* L.) Under Protected Conditions

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ABSTRACT

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Forty tomato genotypes were evaluated in randomized block design with three replications at College of Agriculture, Vellayani, Kerala during October 2013 to April 2014. A wide range of variation was observed among the characters studied which have a great interest for polyhouse tomato breeding. Genetic divergence analysis was carried out using Mahalanobis D^2 statistics and the 40 tomato genotypes were grouped into eight clusters. Cluster I was the largest cluster with twenty four genotypes followed by cluster II with ten genotypes and all other clusters were solitary. The highest intracluster distance was noticed in cluster II followed by cluster I. The highest intercluster distance was observed between clusters VII and VIII, followed by clusters IV and VIII. Lycopene content and truss per plant had maximum contribution towards total divergence followed by fruit length, fruit weight and yield per plant.

Introduction

The aim of protected cultivation is to achieve independence of climate and weather and to allow crop production in areas where the natural environment limits or prohibits plant growth. In the present scenario of perpetual demand of vegetables and drastically shrinking land holdings in the country, it is the best drudgery less approach for better resource management. Tomato, (*Solanum lycopersicum* L.) the globally leading popular vegetable belonging to Solanaceae family is being extensively cultivated under protected

conditions and gives higher returns. India enjoys the second position in tomato production next to China, with a share of 11.50 % of world production. India has an area of 1.20 Mha, total production of 19.40 Mt and a productivity of 16.10 t ha⁻¹ for tomato. Being an important vegetable crop, there is a need to develop tomato varieties and hybrids suitable to specific agroecological conditions and also for specific end use. One of the present techniques of measuring genetic divergence is by Mahalanobis's D^2 statistic.

Hybridization between divergent parents is likely to produce wide variability and transgressive segregation with high heterotic effects. D^2 analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence, both at the inter- and intra-cluster levels. The progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. Therefore, genetically diverse genotypes per genotypes should be used in a hybridization programme to get superior recombinants.

Materials and Methods

The experimental material consisted of 40 tomato genotypes collected from various sources and were laid out in Randomized Block Design (RBD) with three replications at College of Agriculture, Vellayani, Kerala during October 2013 to April 2014. The experiment was conducted in saw toothed type naturally ventilated polyhouse of gutter height of 5m high, gutter slop of 2% and size 1000 m² (50 m x 20 m) located in Instructional farm, Vellayani. Transplanting was done at a spacing of 75 x 60 cm in raised beds. Data were recorded on various characters. Analysis of variance was done based on RBD as suggested by Panse and Sukhatme (1967) for each of the characters separately. Mahalanobis generalized distance (D^2) was used to determine the degree of divergence and the genotype were grouped into clusters following Tocher's method (Rao, 1952).

Results and Discussion

In the present study, 40 genotypes of tomato were subjected to D^2 analysis based on all the characters studied. The genotypes were

grouped into eight clusters on the basis of relative magnitude of D^2 values (Table 1). C. The grouping of genotypes into eight clusters indicated the presence of genetic diversity among the genotypes. These findings are in close conformity with those of Sharma *et al.* (2009), Basavaraj *et al.* (2010), Evgenidis *et al.* (2011), Thamir *et al.* (2014) and Dar *et al.* (2015).

Cluster I had the maximum number of genotypes (24), followed by cluster II (10) and other clusters had only one genotype. The composition of clusters of heterogenous geographic origin indicated that, the strains were distributed among the different clusters randomly irrespective of their geographical origin. This indicates the fact that there was no parallelism between genetic diversity and geographical divergence in the tomato crop. Similarly, Chernet *et al.* (2014) clustered 36 genotypes into six distinct clusters and Iqbal *et al.* (2014) grouped 47 tomato genotypes into five clusters. Wide genetic diversity was observed among the genotypes which were grouped into five clusters by Tocher's method based on D^2 values. (Meena and Bahadur, 2015).

The D^2 technique measures the forces of differentiation at two levels, namely intracluster and intercluster level and thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes. The intracluster distance shows divergence among the genotypes within a cluster, whereas the intercluster distance expresses relative divergence among the clusters. The average inter and intra cluster distances were estimated based on total D^2 values as given in table 2.

The intracluster distances seen to be lower than intercluster distances. Cluster II had the highest intracluster distance (20.46)

followed by cluster I (18.44). All the other clusters had zero intra cluster distance as they included only one genotype.

The highest intercluster distance was observed between clusters VII and VIII (56.42), followed by clusters IV and VIII

(50.05), clusters VII and VI (49.69) and clusters V and VIII (47.80). Cluster I had least proximity to clusters VII and VIII. Cluster II exhibited least proximity with clusters IV, VIII and VII. Cluster III had more distance with clusters VIII and VI.

Table.1 Clustering Pattern of 40 Tomato Genotypes

Cluster number	Number of genotypes	Genotypes
I	24	LE 5, LE 6, LE 8, LE 10, LE 11, LE 12, LE 13, LE 15, LE 18, LE 20, LE 21, LE 22, LE 23, LE 25, LE 27, LE 28, LE 29, LE 30, LE 31, LE 32, LE 33, LE 36, LE 37 and LE 49
II	10	LE 4, LE 7, LE 14, LE 16, LE 17, LE 19, LE 26, LE 38, LE 39 and LE 54
III	1	LE 56
IV	1	LE 24
V	1	LE 3
VI	1	LE 53
VII	1	LE 1
VIII	1	LE 2

Table.2 Average Intra and Inter Cluster Distances (D2 values)

Clusters	I	II	III	IV	V	VI	VII	VIII
I	18.44	27.61	24.66	22.67	27.59	33.06	34.71	42.02
II		20.46	25.22	38.28	27.06	29.75	34.41	34.48
III			0.00	33.90	21.53	37.13	21.25	45.97
IV				0.00	33.32	40.43	38.30	50.05
V					0.00	40.31	19.64	47.80
VI						0.00	49.69	24.60
VII							0.00	56.42
VIII								0.00

Diagonal elements - intracluster values

Off diagonal elements – intercluster values

Table.3 Percent Contribution of Various Characters for Divergence in Tomato

Sl. No.	Characters	Times ranked 1 st	Contribution (%)
1	Plant height (m)	16	2.05
2	Height at flowering (cm)	20	2.56
3	Leaves preceding first inflorescence	5	0.64
4	Internodal length (cm)	11	1.41
5	Leaf length (cm)	6	0.77
6	Leaf width (cm)	4	0.51
7	Days to flowering	0	0.00
8	Days to fruitset	0	0.00
9	Flowers cluster ⁻¹	0	0.00
10	Inflorescence plant ⁻¹	1	0.13
11	Fruitset (%)	7	0.90
12	Pollen viability (%)	34	4.36
13	Truss plant ⁻¹	112	14.36
14	Fruits truss ⁻¹	37	4.74
15	Fruits plant ⁻¹	20	2.56
16	Fruit length (cm)	95	12.18
17	Fruit girth (cm)	46	5.90
18	Fruit weight (g)	88	11.28
19	Length breadth ratio	3	0.38
20	Yield plant ⁻¹ (g)	77	9.87
21	TSS (°Brix)	1	0.13
22	Beta carotene (mg 100g ⁻¹)	25	3.21
23	Lycopene (mg 100g ⁻¹)	159	20.38
24	Ascorbic acid (mg 100g ⁻¹)	13	1.67

The minimum intercluster distance was observed between clusters V and VII (19.64) indicating a close relationship among the genotypes included. Average inter and intra-cluster distances revealed that in general, inter-cluster distances were much higher than those of intracuster distances, suggesting homogeneous and heterogeneous nature of the genotypes lines within and between the clusters respectively. These results are in accordance with the findings of Mahesha *et al.* (2006), Sekhar *et al.* (2008), Reddy *et al.* (2013) and Meena and Bahadur (2015) in tomato.

Depending upon the breeding objective, the potential lines to be selected from different

clusters as parents in a hybridization program may be based on genetic distance. In accordance to the findings, Hazra *et al.* (2010) and Meena and Bahadur (2015) reported that the clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters.

The proportional contribution of characters towards the total D² statistics was different, which is represented in table 3. Lycopene content (20.38%) and truss per plant (14.36%) were the maximum contributors towards total divergence followed by fruit length (12.18%), fruit weight (11.28%) and

yield per plant (9.87%). Fruit girth (5.90%), fruits per truss (4.74%), pollen viability (4.36%), beta carotene (3.21%), fruits per plant (2.56%) and height at flowering (2.56%) were moderately contributing towards total divergence. These results indicated that the rest of the characters were not contributing much towards the total divergence.

In conclusion of the present study forty tomato genotypes 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 eight clusters. The clustering pattern indicated that the geographic diversity need not necessarily be related to genetic diversity. The present study including forty tomato genotypes under protected conditions revealed that cluster VII had superior performance for yield. For the quality characters of tomato clusters VI, VII and VIII were promising. Genotypes in these clusters are proposed for hybridization to get heterotic hybrids in F_1 generation and some promising transgressive segregants in F_2 generation. Therefore, selection of divergent parents based on cluster distance is recommended for getting good hybrids or segregants in tomato under protected conditions.

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