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Genetic Diversity of Tomato (*Solanum lycopersicum* L.) Genotypes through D^2 Analysis

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A B S T R A C T

Twenty four tomato genotypes were evaluated during June to September 2018 at Horticulture College and Research Institute, Periyakulam with an aid to estimate genetic diversity for 15 quantitative and qualitative characters. Using Mahalanobis D^2 statistics method, the 24 genotypes were grouped into three clusters, indicating the presence of diversity among the genotypes for different traits. The cluster III containing 17 genotypes followed by cluster II and I comprises of four and three genotypes respectively (Table 5). The highest intra-cluster distance was recorded in cluster III (60.00) and the maximum inter-cluster distance between cluster II and III (85.59), indicating the existence of wide genetic variability. On basis of cluster means for 15 different traits, cluster III recorded earlier flowering (18.35 days) and also registered the highest number of fruit per plant (24.53) and TSS (3.81º Brix). Cluster I recorded the highest fruit weight (57.98 g), plant height (95.98 cm), lycopene content (5.33 mg per 100 g) and ascorbic acid content (16.70 mg per 100 g). Cluster II registered maximum number of fruits per cluster (2.78) and yield per plant (1.29 kg) with high firmness of 5.43 lbf. Based on cluster mean analysis, the genotypes *viz*., PKM 1, ACC NO 65, ACC NO 71, EC 163599, EC 686543 and Arka Saurabh could be used in crop improvement programme in tomato for above-mentioned traits.

Introduction

Tomato (*Solanum lycopersicum* L.) a member of Solanaceae family, is one of the most important vegetable crops grown widely all over the world. It is often called poor man's orange, because of its high nutritive value. The cultivated tomato originated in the Peru-Ecuador-Bolivia area of the South American (Vavilov, 1951). Its ripe fruits are consumed

fresh as well as after cooking as a protective supplementary food and also utilized in the various value added durable products such as puree, paste, powder, ketchup, sauce and canned whole fruits, while the green unripe fruits are used for making pickles and chutney.

Tomato crop has wider adaptability, high yielding potential and multipurpose uses in fresh as well as processed food industries. It stands unique among vegetables because of its high nutritive values and innumerable uses (Vitamin A, C and Minerals). Its firmly ripened fruits are a source of lycopene (an antioxidant), ascorbic acid and beta-carotene. Lycopene is treasured for its anticancer attribute. It is reported to have properties as antiseptic and blood purifier. It acts as an antioxidant which is often colligated with carcinogenesis.

Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Furthermore, if an improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and breeding value of the available germplasm (Singh *et al.*, 2002). Evaluation of germplasm is of immense important in genetic improvement of the crop. It was also said that plant breeders use a much less diverse genetic pool than the overall available genetic diversity within the crop (Joshi *et al.*, 2012). Heterogeneous local population of the genus forms an important source of genetic variation (Zeven, 1998). For the selection of parents in hybridization, diversity among parents for the character of interest, estimation of genetic distance is most important as diverse plants are supposed to give high hybrid vigour (Harrington, 1940). Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts in a smaller number of hybrid combinations (Fuzzato *et al.,* 2002).

Among the various methods developed to study the genetic divergence in the genotypes, the Mahalanobis D^2 (Mahalanobis, 1936) is reliable and most frequently used. D^2 analysis is a useful tool to assess relative contribution of different components to the total divergence, both at the inter- and intra-cluster levels. Improvement in self-pollinated crops like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization (Meena *et al.,* 2013). Such studies are also useful in the selection of parents for hybridization to recover superior transgressive segregates. Considering the above facts, the research has been planned with the following objective to assess the extent of genetic diversity in the available germplasm based on fifteen traits comprising of qualitative and quantitative traits.

Materials and Methods

The present study was conducted at western block, Department of Vegetable Crops, Horticulture College and Research Institute, Periyakulam during June-September 2018. The experimental materials comprised of twenty-four genotypes (Table 1) of tomato collected from different sources. The experiment was laid out in a randomized block design with two replications in the plot size of 8 m^2 accommodating 22 plants in each genotype with the spacing of 60 x 45 cm. The genotypes studied are PKM 1, ACC NO 65, ACC NO 71, ACC NO 78, ACC NO 79, ACC NO 80, ACC NO 84, ACC NO 88, ACC NO 90EC 6488, EC 10326, EC 12689, EC 16786, EC 16788, EC 163599, EC 164336, EC 164607, EC 608409, EC 608450, EC 570021, EC 677068, EC 686543, EC 808348 and Arka Saurabh. The observation were recorded on

five randomly selected plants per replication for each genotype on fifteen traits *viz*., plant height, days to 1st flowering, days to 50% flowering, average fruit weight, fruit length, fruit diameter, number of branches per plant, number of locules per fruit, number of fruits per cluster, fruit yield per plant, number of fruits per plant, lycopene content, total soluble solids, firmness and ascorbic acid content. Mean across two replications were calculated for each traits and the analysis of variation was carried out. Mahalanobis D^2statistics were worked for clustering the genotypes (Mahalanobis, 1936). Inter and intra cluster distances were worked out as per method suggested by Murty and Arunachalam (1967) to find actual divergence within and between the clusters.

Results and Discussion

Based on the D^2 values all the genotypes were grouped into three clusters, signalling the presence of diversity for different traits. The cluster III had the highest number of genotypes (17) followed by cluster II (4) and cluster I (3). In perusal of the Table 2 the intra-cluster distances indicates the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters. The highest intra-cluster distance was recorded within cluster III (60.0) followed by cluster II (47.60) and cluster I (39.39). The maximum inter-cluster distance was observed between cluster II and III (85.59) followed by cluster I and II (82.57) and cluster I and III (49.22).

These results suggest maximum divergence between genotypes of cluster II with genotypes of cluster III, indicating the fact that the genotypes when used in hybridisation programme produce superior segregants. The information obtained from inter-cluster distances may be used to select genetically diverse and superior genotypes. The genotypes possessing maximum genetic divergence is expected that more heterotic F_1 and most promising segregants in segregating generations. Inter crossing of divergent groups would lead to greater opportunity for crossing over, which may release hidden variability (Kumar *et al.,* 2010). The minimum inter-cluster distance was observed between cluster I and III (49.22). In general, less intra-cluster distance than inter cluster distance suggested homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively (Pawar *et al.,* 2013). The minimum intra cluster was observed in cluster I (39.39) showed all the three genotypes had less variability between them than cluster II (47.60) and cluster III (60.00).

Contribution of characters towards divergence

The diversity among 24 genotypes was measured by employing D^2 statistics. The contributions of each trait towards total genetic diversity are presented in Table 3. The traits, fruit yield per plant (50.00), plant height (28.27), and ascorbic acid content (15.58) contributed high percentage for divergence. Thus, these characters may be given high emphasis while selecting the lines for hybridization programme to generate large variability and will provide immense scope for the improvement of yield through selection. The same has been suggested by Kumar *et al.,* (2010). Other characters like fruit diameter (2.17%), firmness (1.81%), number of fruits per cluster (1.09%), lycopene content (0.72%) and TSS (0.32%) contributed very little percentage for divergence.

Cluster mean analysis

Table 4 demonstrates the mean values for fifteen characters in three clusters, which vary in their value differently from each other.

Table.1 List of germplasm lines and standard released varieties included in the study

S. No	Genotype	S. No	Genotype
1	PKM 1	13	EC 16786
2	ACC NO 65	14	EC 16788
3	ACC NO 71	15	EC 163599
4	ACC NO 78	16	EC 164336
5	ACC NO 79	17	EC 164607
6	ACC NO 80	18	EC 608409
7	ACC NO 84	19	EC 608450
8	ACC NO 88	20	EC 570021
9	ACC NO 90	21	EC 677068
10	EC 6488	22	EC 686543
11	EC 10326	23	EC 808348
12	EC 12689	24	Arka Saurabh

Table.2 Inter and intra cluster distances for different clusters

Cluster	I	II	III
I	39.39	82.57	49.22
II		47.60	85.59
III			60.00

Table.3 Contribution of 15 traits towards total genetic diversity

Traits	No. of first rank	% contribution
Days to 1st flowering (days)	0	0.00
Days to 50 % flowering (days)	0	0.00
Number of primary branches	0	0.00
Fruit weight (cm)	0	0.00
Fruit length (cm)	0	0.00
Fruit diameter (cm)	6	2.17
Plant height (cm)	78	28.27
Number of fruits per cluster	3	1.09
Number of locules per fruit	0	0.00
Firmness (lbf)	5	1.81
TSS (º Brix)	1	0.36
Lycopene content (mg per 100g)	2	0.72
Ascorbic acid content (mg per 100g)	43	15.58
Number of fruits per plant	0	0.00
Yield per plant	138	50.00
Total	276	100.00

Table.4 Cluster means for different traits in different cluster group's

Traits	Cluster		
	I	II	III
Days to 1st flowering (days)	22.33	21.12	18.35
Days to 50 % flowering (days)	30.50	29.12	29.85
Number of primary branches	6.83	5.02	5.40
Fruit weight (cm)	57.98	52.12	44.84
Fruit length (cm)	3.45	3.59	4.04
Fruit diameter (cm)	4.10	4.54	4.26
Plant height (cm)	95.98	54.91	90.24
Number of fruits per cluster	2.54	2.78	2.77
Number of locules per fruit	3.83	2.94	2.96
Firmness (lbf)	4.58	5.43	4.17
TSS (º Brix)	3.80	3.37	3.81
Lycopene content (mg per 100g)	5.33	3.45	3.75
Ascorbic acid content (mg per 100g)	16.70	13.60	12.77
Number of fruits per plant	23.72	24.01	24.53
Yield per plant	1.15	1.29	1.28

Table.5 Clusters and members of each cluster

Cluster No	Members
Cluster 1	PKM 1, ACC NO 90 and EC 16786
Cluster 2	ACC NO 65, ACC NO 71, EC 10326 and EC 677068
Cluster 3	ACC NO 78, ACC NO 79, ACC NO 80, ACC NO 84, ACC NO 88, EC 6488, EC 12689, EC 16788, EC 163599, EC 164336, EC 164607, EC 608409, EC 608450, EC 570021, EC 686543, EC 808348 and Arka Saurabh

Cluster I

The genotypes belonging to cluster I showed highest values for traits like number of primary branches (6.83), fruit weight (57.98 g), plant height (95.98 cm), number of locules per fruit (3.83), lycopene content (5.33 mg per 100g) and ascorbic acid content (16.70 mg per 100g) followed by cluster III (Table 5).

Which indicates that the genotypes included in these clusters could effectively be used for the crop improvement programme for increasing qualitative characteristics.

Cluster II

The genotypes belonging to cluster II were recorded for earlier to reach 50% flowering (29.12 days) and the highest fruit diameter (4.54), firmness (5.43 lbf) and per plant yield (1.29 kg). Among four genotypes any one could effectively be utilized as one of the parent to develop high yielding hybrids.

Cluster III

The genotypes belonging to cluster III were earlier to reach flowering (18.35 days) and

recorded highest fruit length (4.04 cm), Total soluble solids (3.81º Brix), number of fruits per plant (24.53) and per plat yield (1.28 kg) which indicates that the genotypes included in these clusters could effectively be used for thecrop improvement programme for their respective characters.

It was suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character. The potential lines were picked out from different clusters and used as parents in a hybridization programme. The choice should based on genetic distance and depending upon the objective of the breeding programme.

Many workers have observed that more diverse parents within its overall limits of fitness, the greater were the chances of heterotic expression in F_1's and a broad spectrum of variability in segregating generations (Arunachalam, 1981). While choosing parents for hybridisation programme, clustering pattern could be employed that would likely to render the maximum possible variability for various economic characters (Hazra *et al.,* 2010) and Kumar *et al.,* (2010). Moreover, it would be effective to intercross genotypes belonging to more diverse clusters like cluster II and III and cluster I and II to create wide spectrum of variability and to produce transgressive segregates for tomato.

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