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Genetic divergence for yield and yield attributes in tomato (*Solanum lycopersicum*)

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ABSTRACT

The research experiment was conducted to study genetic diversity for quantitative and qualitative traits in tomato (*Solanum lycopersicum* L.). The investigation was conducted during *rabi*, 2015-16 at Vegetable Research Farm, College of Horticulture, Rajendranagar, Hyderabad. Using Mahalanobis D^2 statistic, the 30 genotypes were grouped into eight clusters, indicating the presence of diversity for different traits. The cluster I had the highest number containing 19 genotypes followed by cluster II containing five genotypes. However, the cluster III, IV, V, VI, VII and VIII were solitary. The maximum intra-cluster distance was recorded within cluster II (64.36) and the maximum inter-cluster distance between cluster VII and VI (220.70), indicating the existence of wide genetic variability. Based on mean performances, cluster III registered maximum plant height (134.40 cm). The genotypes included in clusters I took less number of days to first flowering (28.60), cluster III took less number of days to 50% flowering (35.33) and cluster I took less number of days to fruit set (38.33). The cluster VII registered high number of fruits per plant (326.00) and high fruit yield per plant (1.54 kg). The genotypes included in clusters I had maximum average fruit weight (51.23 g). The cluster V registered high TSS (9.07 ^{o}Brix). The cluster I registered high content of ascorbic acid (32.38 mg/100g) and beta carotene (2.33 mg/100g). Hence, these characters can be utilized in breeding programme for enhancing their respective characters. Based on cluster mean analysis, the superior and genetically divergent genotypes can be used in crop improvement programme in tomato.

Key words: Genetic diversity, *Solanum lycopersicum,* Tomato, Yield, Yield attributes.

Tomato (*Solanum lycopersicum* L.) belongs to the family solanaceae and is native of Peru and Equador region (Rick 1969). Tomato is a typical day neutral plant and is mainly self-pollinated, but a certain percentage of cross-pollination also occurs. It is a warm season crop reasonably resistant to heat and drought and grows under wide range of soil and climatic conditions.

Tomato is one of the most important solanaceous vegetable crops grown widely all over the world. It is a very versatile vegetable for culinary purposes. Ripe fresh tomato fruit is consumed fresh as salads, consumed after cooking and utilized in the preparation of range of processed products such as puree, paste, powder, ketchup, sauce, soup and canned whole fruits. Unripe green fruits are used for preparation of pickles and chutney. Tomatoes are important source of lycopene (an antioxidant), ascorbic acid and beta carotene and valued for their colour and flavour.

Yield is a complex character controlled by large number of contributing characters and their interactions. A study of correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. For any effective selection programme, it would be desirable to consider the relative magnitude of association of various characters with yield.

Commercial F_1 hybrids are common in tomato and selection of new parents for higher heterosis is a continuous process. Generally diverse plants are expected to give high hybrid vigour (Harrington 1940). Hence, it necessitates the study of genetic divergence among the germplasm collection for identification of parents for further breeding programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. D^2 statistics developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. Such studies are also useful in selection of parents for hybridization to recover superior transgressive segregants and it can further result into release of improved open pollinated varieties for commercial cultivation. Considering the above facts, the research was planned with the objective to assess the extent of genetic diversity in the available germplasm based on fifteen traits

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comprising of qualitative and quantitative traits.

MATERIALS AND METHODS

The present investigation was carried out at Research Farm of the Department of Vegetable Science, College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad during *rabi*, 2015-16. The experimental materials comprised of thirty genotypes of tomato collected from different sources. The experiment was laid out in a Randomized Block Design with three replications accommodating 21 plants in each genotype. Seeds were transplanted at a spacing of 75×45 cm. All the recommended cultural practices were adopted for raising the crop successfully. The observations were recorded on five randomly selected plants per replication for each genotype on fifteen characters: plant height (cm), days to 50% flowering, average fruit weight (g), number of branches per plant, polar diameter (cm), equatorial diameter (cm), number of locules per fruit, number of flowers per cluster, fruit yield per plant (g), number of clusters per plant, number of fruits per plant, number of fruit per truss, total soluble solids (%), acidity (%) and ascorbic acid (mg/100 g). Mean across three replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis 1936) and genotypes were grouped into different clusters following Tocher's method. The 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.

The genetic divergence between genotypes was estimated using Mahalanobis's D^2 statistics (1936). The distance D from the sample was computed using the formula.

$D^2p = d^1 S^{-1} d$

where, D^2p, Square of distance considering 'p' variables d = Vector observed differences of the mean values of all the characters (x_{i1}- x_{i2}); S^{-1}, inverse of variance and covariance matrix.

All the genotypes used were clustered into different groups following Tocher's method (Rao 1952). The intra and inter-distance were also computed. The criterion used in clustering to the same cluster should at least on the average, show a smaller D^2 values than those belonging to different clusters.

The device suggested by Tocher (Rao 1952) was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so on. The permissible increase in D^2 value shown by a population to the nearest population. If at any stage increase in average D^2 value exceeded the average of already included, because of the addition of new genotypes, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

Based on D^2 values, average intra and inter cluster distances were calculated as per Euclidean method.

The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1985). Square of intra cluster distance = ΣDi^2 / n

where, ΣDi^2, sum of distance between all possible combinations; n, Number of all possible combinations.

The average inter cluster distances were calculated by the formula (Singh and Chaudhary 1985).

Square of inter cluster distance = $\Sigma Di^2 / n_i n_j$

where, ΣDi^2, sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study; n_i, Number of entries in cluster i; n_j, Number of entries in cluster j.

The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1985). In all the combination, each character is ranked on the basis of di, $y_i^j - y_i^k$ values.

where, di = mean deviation, y_i^j; mean value of the j^{th} genotype for the i^{th} character and y_i^k, mean value of the k^{th} genotype for the i^{th} character.

Rank 'I' is given to the highest mean difference and rank 'p' is given to the lowest mean difference where, P is the total number of characters.

Finally, number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

RESULTS AND DISCUSSION

Clustering

Clustering of genotypes under study is presented in Fig 1. Based on D^2 values, the 30 genotypes were grouped into eight highly divergent clusters (Table 1). Some of genotypes were so divergent in all the characters; hence each single genotype formed a separate cluster. Thus six clusters viz. III (EC-620408), IV (EC-640288), V (EC-801747), VI (EC-801755), VII (EC-011309) and VIII (EC-801737) were solitary with one genotype in each cluster.

The remaining two clusters were having maximum number of genotypes. Cluster I was biggest with 19 genotypes viz. (EC-801753, EC-801754, EC-620288, EC-631325, EC-620639, EC-620775, EC-654286, EC-654289, EC-631406, EC-631407, EC-631415, EC-636482, EC-631410, EC-620563, EC-620414, EC-620494, EC-631396, Arka vikas (C) and Pusa ruby(C) followed by cluster II with 5 genotypes viz. (EC-801741, EC-801751, EC-620642, EC-567305, EC-010326 (Table 1). In clustering pattern, there was no parallelism between geographical distribution of genotypes and genetic divergence. Therefore, geographical diversity could not be related to genetic diversity in the material investigated. This was in agreement with results of Mahesha *et al*. (2006), Reddy *et al*. (2013) and Khaidem *et al.* (2014). Mostly, breeding progenies incorporate genes from multiple sources, resulting in casting off the basic geographical identity of the genotype (Meena *et al.* 2015).

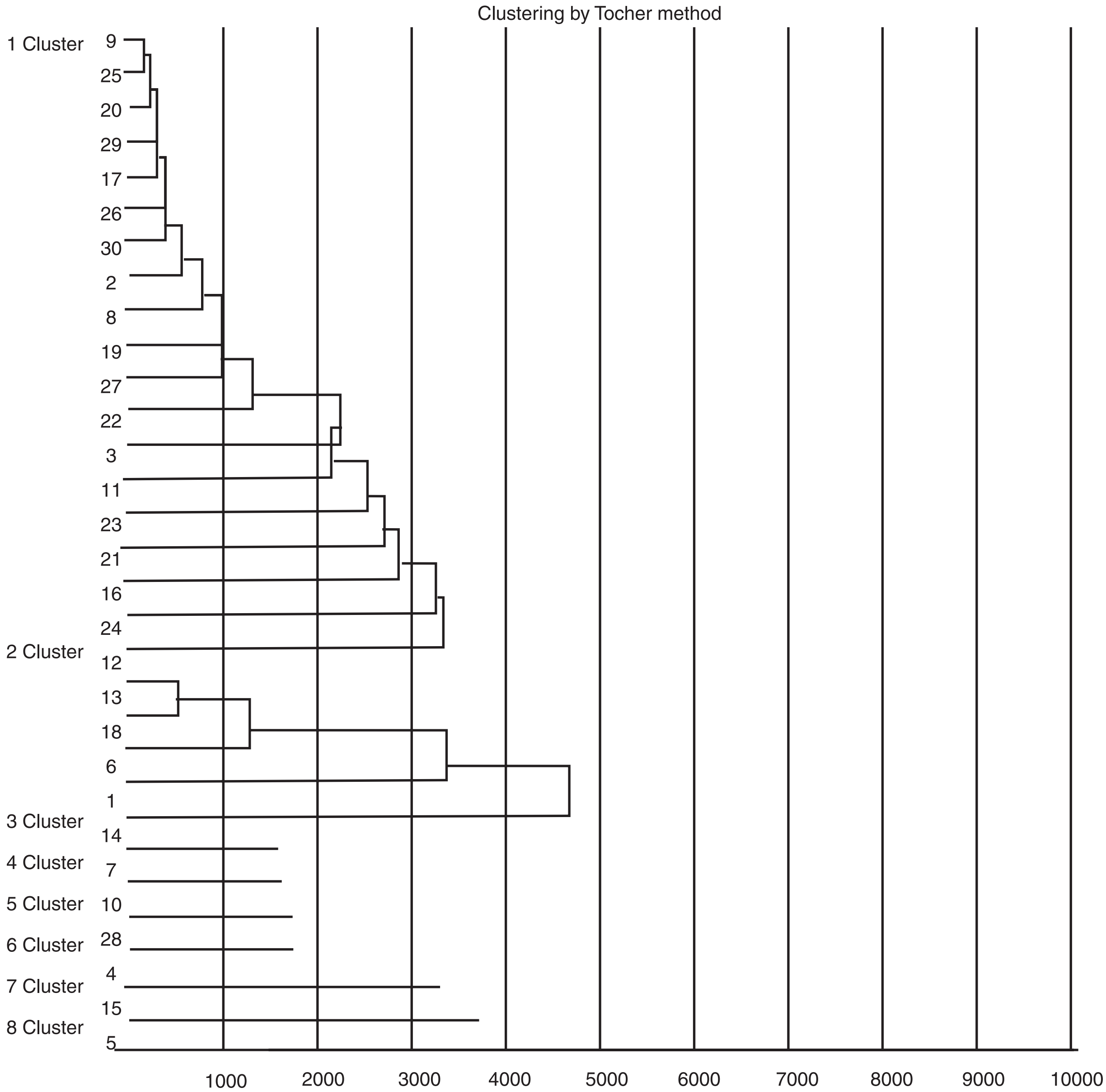

Fig 1 Dendrogram showing clustering pattern for divergence of tomato genotypes.

The intra-cluster distances indicates the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters (Table 2). The intra cluster D^2 values ranged from 0.00 (Cluster III, IV, V, VI, VII and VIII) to 64.36 (Cluster II). The cluster II had the maximum D^2 value (64.36) followed by Cluster I (46.55). The inter cluster distance was minimum between cluster VI and IV (41.93) indicating close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance was observed between clusters VII and VI (220.70) followed by between clusters VII and IV (206.28) indicating wider genetic diversity among the genotypes included in these groups. Cluster VII followed by the VI is the most diverse as all other clusters showed maximum inter cluster distance from it.

Cluster I displayed least intra cluster distance denoting the similarity of genotypes. While maximum intra cluster distance was recorded in cluster II and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters. Therefore, hybridization programme between the genotypes belonging to cluster II and of clusters VII may be undertaken for getting good segregants. Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Hence, selection for divergent parents based on the characters will be useful for heterosis breeding in tomato. Similar results were reported in tomato by Rai *et al.* (1998), Parthasarathy and Aswath (2002), Karasava *et al.*

Table 1 Cluster classification of 30 genotypes of tomato

Cluster	No. of genotypes	Genotypes
I	19	EC-801753, EC-801754, EC-620288, EC-631325, EC-620639, EC-620775, EC-654286, EC-654289, EC-631406, EC-631407, EC-631415, EC-636482, EC-631410, EC-620563, EC-620414, EC-620494, EC-631396, Arka Vikas (C), Pusa Ruby (C)
II	5	EC-801741, EC-801751, EC-620642, EC-567305, EC-010326
III	1	EC-620408
IV	1	EC-640288
V	1	EC-801747
VI	1	EC-801755
VII	1	EC-011309
VIII	1	EC-801737

(2005), Mahesha *et al.* (2006), Chopra *et al.* (2008), Nandan Mehta and Asati (2008), Sekhar *et al.* (2008), Shashikanth *et al*. (2010), Khaidem *et al*. (2014), Meena and Bahadur (2015) and Sunil Prajapati *et al.* (2015).

Cluster means of characters

The cluster mean for the fifteen characters studied in tomato genotypes revealed considerable differences among all the clusters (Table 3). From the present data, it was evident that plant height was highest in cluster III (134.40 cm) and lowest in cluster VI (40.27 cm). Maximum number of branches was recorded in cluster VIII (27.87).

The cluster III had the early days to first flowering (29.00 days) followed by cluster I (32.30 days). The cluster III had the early days to 50% flowering (35.33 days) followed by cluster IV (37.00 days). The cluster III had the early days to fruit setting (39.33 days) followed by cluster I (43.58 days).

Number of fruits per plant was maximum in cluster VII (326.00). Average fruit weight was highest recorded in cluster IV (40.73 g). Fruit yield per plant was highest in cluster VII (1.54 kg).

The genotypes of cluster V had maximum TSS value (9.07 ^{o}Brix). The acidity content was highest in cluster II (0.51%). The genotypes of cluster V had maximum TSS:acid ratio (37.83). Ascorbic acid content was maximum in cluster VI (25.66 mg/100g of fruit). Lycopene content was maximum in cluster VI (4.27 mg/100g of fruit). Beta carotene content was highest in cluster III (2.32 mg/100g of fruit) and lowest in cluster IV (0.19) and cluster VII (1.17 mg/100g of fruit). It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character. The potential lines are 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.

Relative contribution of different characters towards divergence

The relative contribution of the character towards total divergence always hints on the variability associated with that character. More is the relative contribution; maximum is the possibility of exploitation of that character in crop improvement. On verification of relative contribution of each character towards divergence (Table 4), it was observed that plant height contributed maximum (42.07%) towards divergence followed by number of fruits per plant (24.37%), lycopene (13.79%), days to fruit set (8.74%), TSS (3.45%), titrable acidity, TSS: Acid ratio, ascorbic acid (1.84%), days to first flowering (1.61%) and average fruit weight (0.46%). The remaining characters viz., number of branches per plant, days to 50 per cent flowering, fruit yield per plant, fruit yield per hectare and beta carotene did not contribute to the total divergence. These characters are less variable from genotype to genotype and their inheritance to next generation is almost nil. Therefore, these characters should not be given importance in selection of genotypes for breeding. Whereas, due weightage should be given to plant height, number of fruits per plant and lycopene, while germplasm is selected for further improvement. The quality character lycopene should be considered for development of high lycopene tomatoes. The genotypes with characters contributing more towards divergence can be included in breeding programmes for further improvement as they show rich amount variability.

From the present study, it is concluded that the maximum intra-cluster distance was shown by cluster II. The maximum inter cluster distance was observed between

Table 2 Average intra (bold) and inter-cluster D^2 values for eight clusters in 30 genotypes of tomato

Cluster	I	II	III	IV	V	VI	VII	VIII
I	46.55	106.97	88.26	77.79	70.84	97.37	164.19	82.54
II		64.36	115.91	140.28	90.24	154.86	87.94	99.03
III			0	150.56	73.96	172.18	145.33	130.97
IV				0	114.90	41.93	206.28	89.29
V					0	139.67	142.46	69.84
VI						0	220.70	103.00
VII							0	164.61
VIII								0

Table 3 Mean values of clusters for fifteen characters in 30 tomato genotypes

Cluster	Plant height (cm)	No. of branches/ plant	Days to first flowering	Days to 50 per cent flowering	Days to fruit set	No. of fruits/ plant	Average fruit weight (g)	Fruit yield/plant (kg)	Fruit yield/ha (t)	TSS (ºBrix)	Titrable acidity (%)	TSS: Acid ratio	Ascorbic acid (mg/100g of fruit)	Lycopene (mg/100g)	Beta carotene (mg/100g)
I	87.50	16.23	32.30	39.79	43.58	28.77	37.63	1.07	39.55	4.61	0.30	16.73	22.25	3.24	1.59
II	87.13	21.07	38.96	52.20	61.60	196.44	3.22	0.63	23.60	6.89	0.51	15.24	21.90	0.56	1.29
III	134.40	21.13	29.00	35.33	39.33	35.17	28.88	1.01	37.57	4.10	0.37	10.98	25.19	3.50	2.32
IV	52.47	8.47	32.53	37.00	49.53	15.13	40.73	0.62	22.83	7.13	0.19	36.91	24.59	3.91	1.92
V	103.37	19.73	42.47	50.67	57.70	42.40	3.96	0.16	6.21	9.07	0.24	37.83	21.65	0.00	1.32
VI	40.27	9.20	35.60	42.33	45.13	18.13	33.41	0.60	22.41	3.80	0.39	9.83	25.66	4.27	2.11
VII	101.20	19.20	39.47	46.00	57.17	326.00	4.73	1.54	57.15	5.93	0.50	11.79	24.45	0.00	1.17
VIII	71.33	27.87	48.40	64.67	74.20	50.67	2.02	0.10	3.80	7.00	0.26	26.94	19.95	0.00	1.20

cluster VII and VI followed by between clusters VII and IV. Therefore, the genotypes belonging to cluster VII and of clusters VI and IV to create wide spectrum of variability and produce transgressive segregates for tomato. Plant height, number of branches per plant, average fruit weight, number of fruits per plant, yield per plant, TSS and ascorbic acid content were major contributors to the genetic divergence in the germplasm. The genotype EC- 636482, EC-631410 and EC-620563 can be used for improving average fruit weight as well as fruit yield per plant. Quality parameters like TSS can be improved by using genotype viz., EC-801747 and EC-010326 as donor parents. Acidity can be improved by using genotypes EC-567305 and EC-620563 as donor parents. Similarly, EC-620639 and EC-801753 were identified for improving ascorbic acid. The genotype EC-801753 can be used for improving lycopene content and genotypes EC-620639 and EC-620408 can be used for improving beta carotene content.

Based on the country of origin, the exotic collections from USA and China are highly divergent. Three genotypes each from America and China have represented independent clusters. Hence, the due importance should be given to exotic cultivars to use as one of the parents and indigenous cultivars as counter parent to develop maximum heterotic potential hybrids as they are genetically so diverse in terms of quality, yield and yield attributing characters. The present study clearly demonstrated that there is sufficient amount of genetic diversity among and between exotic and indigenous tomato genotypes. The divergent genotypes identified will definitely useful to transgress /transfer the desirable genes for yield and quality traits into Indian tomatoes.

From the study, it can be interpreted that sufficient diversity was observed among the genotypes. Genotypes imported from USA were highly divergent from those of

Table 4 Per cent contribution of different characters towards diversity in tomato genotypes

Character	Times ranked 1st	Per cent contribution
Plant height (cm)	183	42.07
Number of branches per plant	0	0.00
Days to first flowering	7	1.61
Days to 50 per cent flowering	0	0.00
Days to fruit set	38	8.74
No. of fruits per plant	106	24.37
Average fruit weight (g)	2	0.46
Fruit yield per plant (kg)	0	0.00
Fruit yield per ha (t)	0	0.00
Total soluble solids (º Brix)	15	3.45
Titrable acidity (%)	8	1.84
TSS: Acid ratio	8	1.84
Ascorbic acid (mg/100g of fruit)	8	1.84
Lycopene (mg/100g)	60	13.79
Beta carotene (mg/100g)	0	0.00

China and India. Three genotypes each of USA and China origin were so divergent and represented separate clusters. Results of the study are highly useful for the selection of the superior and genetically divergent genotypes for tomato improvement. Emphasis should be given to exotic cultivars to include as one of the parents to realize maximum hybrid vigour.

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