Genetic Divergence Studies for Yield Component Traits in Genome-wide Association Mapping Panel of Tomato (*Solanum lycopersicum* L.)

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ABSTRACT: Genetic diversity is key factor for any crop improvement. Genetic diversity, its nature and its degree are useful for selecting desirable parents from a germplasm collection for development of superior hybrids and for successful breeding programme. In this study accessions of genome-wide association mapping panel of tomato were assessed for their genetic divergence using Mahalanobis D^2 statistics. Genetic divergence studies revealed considerable genetic diversity among 264 accessions of tomato for a set of eleven quantitative traits pertaining to the earliness, growth and yield *viz.,* plant height (cm), number of branches per plant, days taken to 50 % flowering, number of clusters per plant, number of fruits per cluster, number of fruits per plant, average fruit weight (g), number of locules per fruit, fruiting duration (days), fruit diameter (cm) and total yield per plant (kg). Analysed 264 tomato accessions grouped into 11 distinct clusters depending upon the similarities of their D^2 values following Tocher's method. Considerable diversity within and between 11 clusters was observed among the accessions. The characteristics such as average fruit weight, fruit diameter and number of locules per fruit were the potent factors in differentiating the accessions of tomato studied. The use of diverse genotypes from the clusters with high inter-cluster distance, such as cluster XI and VIII, XI and II and XI and VII in hybridization is expected to result in high heterosis and throw desirable transgressive segregants in the segregating generations that can form potential pre-breeding material for the improvement of tomato crop.

Keywords: Genetic divergence, Yield Component Traits, Genome-wide Association Mapping Panel Tomato.

INTRODUCTION

Tomato (*Lycopersicon esculenlum* Mill) also known as 'wolf apple' or 'vilayati bhaigan', belongs to the family Solanaceace. It is a native of Peru Equad or region (Rick, 1969). It is the most prominent fruit and vegetable grown during the summer season worldwide. It is regarded as the most significant vegetable crop after the potato due to its great yielding capacity, wider adaptability, and multiple usage. Tomatoes are consumed fresh as well as in processed form (Das *et al.,* 1998). Because of its unique nutritional value, tomatoes prioritise among the most important "protective foods" (Mehta*,* 2017), and regular consumption of tomatoes and tomato-based products has been linked to a lower risk of chronic human diseases like some cancers and cardiovascular diseases (Franceschi *et al.,* 1994); (Gerster, 1997). Problems like acidosis are quite common in our society leading to many ailments, aches and loss of calcium from the bones. These can be prevented by adding tomatoes to the diet as they have an alkali power (Anon., 2009).

Germplasm is considered the reservoir of variability for different characters (Vavilov, 1951). Characterization and evaluation of germplasm are the prerequisites for the utilization of available diversity in the crop improvement programme (Singh *et al.,* 2002; Rathi *et al.,* 2011). The breeding strategy in tomato involves assembling variable germplasm and selection of superior genotypes for utilizing them in the hybridization programme to develop a superior hybrids Banumathy *et al*. (2010). To achieve these targets, the collection of germplasm from indigenous and exotic sources is crucial and utilization of these genetic resources requires their proper and systematic evaluation to understand the genetic variability, heritability, genetic advance and character association with yield components. Genetic diversity is an important factor for any heritable improvement. Knowledge of genetic diversity, its nature and its degree are useful for selecting desirable parents from a germplasm for the successful breeding programme (Sarawg *et al.,* 2007; Prakash *et al.,* 2019). Considering

the above facts, the present studies had been planned with the objective to assess the extent of genetic diversity in available gene pool based on eleven quantitative traits

MATERIAL AND METHODS

A net of 264 tomato accessions comprising of diverse collections of tomato constituted in collaboration with ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi and UHS Bagalkot along with four checks of tomato (Arka Sourabh, Anagha, DMT2 and DMT4) were utilized for the present study. The germplasm lines were evaluated in an augmented block design with 5 blocks and four checks during *kharif*, 2019-20 and summer 2020-21 at College of Horticulture, Bengaluru, University of Horticultural Sciences, Bagalkot. In each block, 52 germplasm lines and four checks were grown and each germplasm line was grown in a single row of 3 m length. Row-to-row spacing of 60 cm and plant-to-plant spacing of 45 cm was maintained. All agronomic practices were performed as per the package of practices of UHS, Bagalkot and necessary prophylactic plant protection measures were carried out to safeguard the crop from pests and diseases.

The mean data on yield and yield contributing traits were subjected to analysis of variance in augmented block design as per the standard statistical procedure (Federer, 1956). The genetic divergence was assessed following Mahalanobis D^2 statistics (Mahalanobis, 1936). The accessions of tomato were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952). The average inter and intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977). The contribution of different traits towards genetic divergence was computed using method given by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The genetic diversity for 264 accessions of tomato was assessed quantitatively for yield and yield related attributes by employing Mahalanobis D^2 statistics. Several authors also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D^2 statistics (Basavaraj *et al.,* 2010; Evgenidis *et al.,* 2011). Mahalanobis D^2 statistics was found to be a useful tool to assess the relative contribution of different characters to the total divergence both inter and intra-cluster levels Rao (1952). By following Tocher's method, tomato accessions were grouped into eleven clusters by treating estimated D^2 values as the square of the generalized distance. The distribution of entries into various clusters is given in Table 1.

Cluster I was the largest having 205 accessions followed by cluster IV (28), cluster II (22), cluster IX (2) and cluster III, V, VI, VII, VIII, IX and X had one accession each. Intra- and inter cluster average D^2 values are presented in Table 2. Genotypes usually did not cluster according to geographical distributions. This is in agreement with the results of Pramanick *et al.* (1992); Shashikanth *et al.* (2010); Pedapati *et al.,*

(2014); Dar *et al.* (2015); Maurya *et al.* (2019). There is no direct relationship between geographical distribution and genetic distance. Among the eleven clusters, cluster XI with one genotype showed maximum intra-cluster diversity (D^2 = 253.13) followed by cluster IV (D^2 = 197.68), cluster II (D^2 = 193.21) and cluster I (D^2 = 159.52). Cluster III, V, VI, VII, VIII, IX and X had only one genotype each and hence, the intra cluster distance was zero. Based on the distance between clusters, *i.e.,* inter-cluster distances, the maximum divergence was observed between clusters XI and VIII (D^2 = 2836.63) followed by clusters XI and II (D^2 =2831.30) and clusters XI and VII (D^2 = 2721.71). Cluster VII had the least inter-cluster distance (D^2 = 170.04) with cluster VI. This indicated a close relationship among the genotypes included in the clusters VII and VI. Average intra and inter cluster distances revealed that, in general, inter cluster distances were much higher than those of intra cluster distances, suggesting the homogeneous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Mahesha *et al.* (2006); Sekhar *et al.* (2008); Maurya *et al.* (2019) in tomato.

In general, the characters responsible for discrimination between populations can narrow down the problem of selecting divergent parents for breeding programme. These clusters have been formed based on the contribution of different characters to the divergence. Average fruit weight (23.03 %) contributed the maximum to the total genetic diversity among the accessions followed by fruit diameter (22.68 %), number of locules per fruit (11.98 %), number of fruits per plant (10.19 %). Similar findings were observed by Narolia and Reddy (2012); Mohanty and Prusti (2001); Spaldon and Kumar (2017); Kumar *et al.* (2021). De *et al.* (1988) opined that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization. The characters that predominantly contributed to divergence in this study also happen to be the main components of yield. The results of the present study point out a positive contribution of genetic divergence for yield components and this can be of considerable help in selecting yield and other economic traits.

The highest cluster mean for total yield per plant was observed in cluster IX (6.64 kg) followed by cluster V (6.09) and II (5.91). The inter-cluster distance observed between clusters X and IX (D^2 = 1054.30), clusters IX and II (D^2 = 1102.90) and clusters X and II (D^2 = 705.43) were comparatively high. Hence, the crosses between genotypes of these respective clusters may be tried to improve to the total yield per plant. The highest number of fruits per plant observed in genotypes of cluster XI (446.7) followed by cluster IX (285.4) and cluster IV (167.56). The inter-cluster distance observed between clusters X and IX (D^2 = 1054.30) and clusters XI and IX (D^2 = 762.31) were comparatively high. Hence, the crosses between genotypes of these respective clusters may be tried to improve yield per plant through number of fruits per plant.

For average fruit weight, the highest cluster mean was shown by the cluster II (72.4) followed by cluster VIII (70.66) and Cluster V (63.92). Inter-cluster distance between clusters VIII and V (D^2 = 369.79) and clusters V and II (D^2 = 323.64) were comparatively high. Hence, the crosses between the genotypes of these respective clusters can be tried for improvement of average fruit weight, which ultimately contributes to the total yield per plant. The lowest cluster mean for days taken to 50 per cent flowering was observed in the cluster XI (29.50) and also clusters III (30.00) and IV

(31.71) shown low cluster means. Inter-cluster distance between cluster XI and VI (D^2 = 2595.90) and cluster XI and III (D^2 = 2123.37) were comparatively high. Hence, hybridization between genotypes of these respective clusters would be attempted to enhance the earliness. The study also indicated that the character such as fruit diameter, number of fruits per cluster, number of clusters pre-plant should also be considered while selecting parents for hybridization as they are important contributors to genetic divergence.

Table 1: Classification of tomato accessions into different clusters based on D^2 value.

Clusters	Number of individuals	Individuals
Cluster-I	205	Ageta-32, Angoorlata, ArkaAbha, Arka Alok, Arka Meghali, Arka Vikas, Avinash-2-2-1, Azad T-2, Azad T-5, B-4-1, B-7-2, Bhillai, BTH-9 M, C-1-4, C-3-2, C-4-1, C-8-1, C-10-2, C-11-1, C-11-2, C-11-3, C-20-1, C-20-2, C-26-1, CH-155, CLN-2026, CLN-1621, CLN-2366, D-1-1, D-2-2-1, D-3-2, D-5-1, DARL-66, Dhrubya, DT-10, DVRT-2, E-4-3, EC-13904, EC-273966, EC-381263, EC-381554, EC-501577, EC-501580, EC-501582, EC-501583, EC-519730, EC-520059, EC-520071, EC-520075, EC-521039, EC-521078, EC-538404, EC-538405, EC-538408, EC-538419, EC-538423, EC-538439, EC-538440, EC-538441, EC-538455, EC-552141, EC-560340, EC-605695, EC-605696, EC-620362, EC-620366, EC-620370, EC-620373, EC-620375, EC-620383, EC-620386, EC-620398, EC-620401, EC-620406, EC-620409, EC-620410, EC-620411, EC-620419, EC-620421, EC-620438, EC-620444, EC-620446, EC-620455, EC-620456, EC-620469, EC-620470, EC-620474, EC-620476, EC-620480, EC-620486, EC-620500, EC-620502, EC-620514, EC-620519, EC-620530, EC-620533, EC-620540, EC-620556, EC-620568, EC-620575, EC-620598, EC-625644, EC-625645, EC-625651, EC-625652, EC -625660, F-5020, F-6050-1, F-6059, F-7012, F-7025, FEB.-02, FEB.-04, Fla-7171, Fla -7421, Flora-Dade, G-4-5, G-5-4, G-6-3, GT-1, GT-2, GT-3, H-88-78-1, H-88-78-2, H-88-78-3, H-88-78-4, H-88-78-5, Hawai, Hisar Anmol, Hisar Arun (Sel-7), I-4-4, IC-373378, IC-427766, IC-447708, IC-469626, IIHR-2202, INDAM-2102, INDAM-2103, INDAM-2103-1, INDAM-2103-1-1, INDAM-2103-4, INDAM-2103-6, Sun-Cherry, Kashi Vishesh, Kashi Amrit, Kashi Anupam, Kajla, Kalyanpur Type-1, LA-3772, LA-3957, LA-3997, M-1-4, M-3-2, Monte Favet, N-2-2, N-2-3, Nandhi, NDT-8, NDT-4, NDTVR-60, NDTVR-73, NF37SB-8, Palam Pink, Pant T-3, Pant T-5, Parul, Pb-Chhuhara, Pb.Upma, Persia Bed, PDVT-14, PKM-1, PS-1, Pusa-120, Punjab Barkha Bahar-2, Pusa Hybrid-2, Roma, Sanjeevani, Sankranti, Sel-18, Sioux, Solan Gola, SolanVajr, Sun-Cherry, Swarna Naveen, Swarna Vaibhav, TLBR-6, TLH-17, TLH-27, TLH-30, Tripura Local, Utkal Pragyan, Utkal Raja, VRT-32-1, VRT-101A, WIR-5032, 97/384, 97/753, 15 SB, Rio Grande, S. Lalima, Pallavi, Punjab Keshri, V. Pragyan, DMT1 and DMT2
Cluster-II	22	IIHR-01, Mukthi, Pusa Ruby, Prestige, WIR-13717, PDT-3-1, Kashi Sharad, Pusa Gaurav, DMT4, F-6022, INDAM-2103-6-1, EC-620403, Utkal Urvashi, EC-528372, NDT-1, DMT3, Money Maker, EC-501575, INDAM-2103-6-4, C-9-2, DVRT-1 and Hisar Lalit
Cluster-III	1	EC-521056
Cluster-IV	28	EC-529080, Switzerland, EC-605694, EC-570028, EC-6202041, EC-520046, CLN-2116, EC-538155, F-7028, EC-538138, EC-317-6-1, EC-501574, Kashmiriya, WIR-3957, EC-526139, EC-501576, CHRT-4, EC-520074, EC-620413, EC-620464, BL-1208, EC-528374, WIR-13706, Jawahar-99, Co-3, WIR-13708, EC-529083 and F-6009
Cluster-V	1	EC-2791
Cluster-VI	1	97/754 (Kewalo)
Cluster-VII	1	Anagha
Cluster-VIII	1	Arka Sourabh
Cluster-IX	1	EC-620374
Cluster-X	1	EC-520061
Cluster-XI	2	EC-520078 and EC-538380

Table 2: Average intra-and inter-cluster D^2 values for 11 yield contributing traits formed by tomato accessions.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	159.52	351.56	275.23	456.25	278.22	266.34	269.29	353.44	885.66	502.66	2346.43
II		193.21	744.74	883.87	323.64	712.89	476.99	333.43	1102.90	705.43	2831.30
III			0.00	294.47	398.00	192.65	457.96	634.03	921.73	338.93	2123.37
IV				197.68	619.01	521.67	674.44	843.90	489.74	502.21	1245.38
V					0.00	321.84	298.25	369.79	935.75	663.06	2574.55
VI						0.00	170.04	516.20	1151.25	859.08	2595.90
VII							0.00	268.96	1259.54	984.70	2721.71
VIII								0.00	1260.25	834.05	2836.63
IX									0.00	1054.30	762.31
X										0.00	2171.56
XI											253.13

Table 3: Relative per cent contribution of different characters to divergence in tomato.

Sr. No.	Character or source	Times ranked first	Per cent contribution
1.	Plant height (cm)	784	2.26%
2.	Number of branches per plant	2373	6.84%
3.	Days taken to 50 % flowering	100	0.29%
4.	Number of clusters per plant	2161	6.22%
5.	Number of fruits per cluster	3333	9.60%
6.	Number of fruits per plant	3538	10.19%
7.	Average fruit weight (g)	7994	23.03%
8.	Number of locules per fruit	4160	11.98%
9.	Fruiting duration (days)	1114	3.21%
10.	Fruit diameter (cm)	7873	22.68%
11.	Total yield per plant (kg)	1286	3.70%
Total			100

Table 4: Mean values of yield contributing traits for nine clusters in tomato.

Sr. No.	Characters	Clusters										
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1.	Plant height (cm)	97.3	98.17	110.64	102.7	114.36	120.08	141.43	85.83	90.02	111.39	108.27
2.	Number of branches per plant	6.62	6.81	6.4	7.87	9.7	7	8.5	10.77	6.3	8.9	8.4
3.	Days taken to 50 % flowering	32.67	32.1	30	31.71	33	31.5	31.55	38.4	33.5	33	29.5
4.	Number of clusters per plant	20.72	20.98	15.9	32.09	18.97	17.4	14.39	17.03	55	18.2	52.55
5.	Number of fruits per cluster	4.64	3.96	6.13	7.41	3.43	3.37	4.04	4.16	5.29	8.47	9.51
6.	Number of fruits per plant	71.29	74.23	67.2	167.56	71.6	45.8	50.69	36.13	285.4	85.4	446.7
7.	Average fruit weight (g)	34.22	72.4	12.65	13.83	63.92	16.23	40.04	70.66	27.01	33.65	7.54
8.	Number of locules per fruit	3.69	3.93	4.2	3.62	3.6	2.9	3	3	3.1	6.2	3.15
9.	Fruiting duration (days)	79.96	82.3	90	82.23	77	78.5	78.65	93.22	88	87.5	90
10.	Fruit diameter (cm)	4.01	5.78	1.34	1.98	2.37	1.67	3.72	4.53	2.62	3.58	1.11
11.	Total yield per plant (kg)	3.48	5.91	2.68	3.19	6.09	1.42	2.21	2.58	6.64	4.54	3.55

CONCLUSION

Among the various methods identified/developed to study the genetic divergence in the genotypes, Mahalanobis D^2 (Mahalanobis, 1936) is reliable and the most frequently used. 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. Thus, from the present investigation it can be concluded that genotypes of cluster XI and VIII, XI and II and XI and VII are complementary for maximum traits and could be selected for hybridization to develop promising F_1 hybrids or transgressive segregants in succeeding generations. To improve maximum yield per plant, clusters IX, V and II are an ideal combination for three way cross or their derivatives for future selection.

Conflict of Interest. None.

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