SHORT COMMUNICATION

D^2 Analysis for Fruit Yield and Quality Components in Tomato (*Lycopersicon esculentum* Mill.)

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Forty-nine tomato genotypes collected from different parts of Jammu region, Indian Institute for Vegetable Research, Varanasi and National Bureau of Plant Genetic Resources, New Delhi, India were studied using Mahalanobis D^2 Statistics to elucidate the genetic divergence for fruit yield, quality and their contributing characters. The genotypes were grouped into ten clusters by Toucher's method. The cluster I contained highest number of genotypes (13) followed by cluster VII (8), cluster III (7) and cluster IV (7). The cluster IX and X consisted of one genotype each. The intra cluster distance was highest in cluster IV (D=14.90) which accommodated promising genotypes namely RCMT-2, Pant T-8, and CTS-05-35-3 (SPS) having large, round, red fruits with good yield potential. Cluster VI (D=13.81) and cluster VIII (D=13.09) ranked second and third. Sufficient variation in these clusters indicates scope of genetic improvement through hybridization of genotypes available with in the cluster. Lowest intra-cluster distance was observed in cluster IX and X (D=0.00). Highest inter-cluster distance was observed between cluster IX and X (D=68.99) followed by cluster III and X (D=66.29). Sufficient genetic distance was also observed between the clusters V and III, IX and V and VI and IX. The genotypes which fall in diverse clusters namely PAU 2374, 127-1 Sel., VR 35, PAU 2372, Tomato 169, VR 415, Punjab Chuhara, RCMT 1, Pant T-10; DT-2 and CTS-05-16, KS 229, ATL-02-39 and VTG 85, with high inter-cluster distance may be utilized in heterosis as well as in recombination breeding programme to develop heterotic hybrids. Cluster mean analysis indicated cluster II, IV, V and IX accommodated tall genotypes while clusters II, V and X were characterized by higher number of fruits per plant. Pericarp thickness was maximum in cluster III, IV and II. Total soluble solids which is a processing trait was available in genotypes belonging to cluster II and X. Cluster X gave the highest gross yield as well as marketable yield followed by cluster V and II. The genotypes in cluster II, V and X could serve as direct source for development of high yielding open pollinated varieties.

Key Words: Divergence, Genotype clustering, Tomato, Yield

Tomato (*Lycopersicon esculentum* Mill.) is one of the most important vegetable crops in India as well as around the world. It finds a very important role in every kitchen with enormous role in food and nutritional security. It also has a very important and significant position in the post harvest industry. Going by its commercial importance, there is utmost need to develop newer varieties/genotypes/hybrids with disease resistance, heat tolerant and processing traits. For this purpose the breeders choose genetically distant parents, genetic diversity plays an important role in breeding vegetables, because hybrids derived from the lines of diverse origin display more heterosis than those between closely related strains. 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 identified/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 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. Keeping these points in mind, the present study was undertaken to know the magnitude of diversity in the available germplasm for yield and quality components and to identify the diverse parents so as to develop the heterotic crosses.

The present investigation was undertaken in the experimental farm of the Division of Vegetable Science and Floriculture, FOA, Chatha, SKUAST (J&K), India, during February-May, 2008. The research farm is situated at 33°55' North latitude and 74°58' East longitude at an elevation of 332 m above mean sea level. The place

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** Author for Correspondence: E-mail: sharmavsf@yahoo.co.in* experiences cool winters and very hot summers with average rainfall. Agroclimatically, the location represents Zone IV of the state of Jammu & Kashmir, India, and is characterised by humid, tropical climate.

The experimental material comprising of forty-nine tomato genotypes collected from different parts of Jammu region by Indian Institute for Vegetable Research, Varanasi and National Bureau of Plant Genetic Resources, New Delhi, and maintained in the Division of Vegetable Science and Floriculture, SKUAST (J&K), were grown in randomized block design with three replications during 2008. The seedlings were transplanted on 26th February, 2008 and were spaced at 75 cm row to row and 45 cm plant to plant. There were 15 plants in each entry/replication. All the recommended cultural practices were followed to raise a healthy crop. Data was recorded on 7 randomly selected plants per entry per replication for various horticultural characters namely total number of fruits per plant, average fruit weight (g), gross yield (g), marketable yield (g), marketable number of fruits per plant, plant height (cm) and 5 randomly selected fruits were taken per entry per replication for quality characters namely fruit shape index, pericarp thickness (mm), number of locules per fruit and total soluble solids (%). The data was analysed as per method given by Mahalanobis (1936). Criteria Toucher (Rao, 1952) was used for determining the groups and clustering was done accordingly. Average inter- and intra-cluster distances were estimated as per method given by Singh and Chaudhary (1985).

Forty-nine genotypes were grouped into 10 clusters on the basis of D^2 values, indicating adequate genetic diversity for selecting superior and diverse parents which can be exploited for any breeding programme. The perusal of data (Table 1) depicted that cluster I had the maximum number of genotypes (13) followed by cluster VII with 8 genotypes and cluster III and cluster IV with 7 genotypes in each cluster. The clustering pattern indicated that there was no association between genetic diversity and geographical diversity. These results are similar to the findings of Peter and Rai (1976), Rai *et al.* (1998), Joshi and Kohli (2003) and Singh *et al.* (2008). On the other hand, the genotypes that originated in one region had been distributed into different clusters, indicating that genotypes with same geographic origin could have under gone change for different characters under selection. This could be due to selection pressure, genetic drift and introduction, which help in creating more diversity rather than genetic distance.

Table 1. Clustering pattern of 49 genotypes of tomato based on D^2 statistics

Clusters	Number of genotypes	Name of genotypes and serial number
I	13	HADT-294, VTG 90, CO 3, CTS-06-02, NDT 9, VTG 106, RUCH-1-1 Sel., CO 3-1 Sel., NTH-2003-1 Sel., ARTH-3 Sel., CTS-05-30-2 Sel., CTS-06-19, Improved Shalimar
II	2	CTS-05-35-2 (SPS), Pant T-7
III	7	VR 35, PAU 2372, Tomato 169, VR 415, Punjab Chuhara, RCMT 1, Pant T-10
IV	7	ATL-01-19, PAU 2371, Arka Vikas, Local 2707, CTS-05-35-3 (SPS), Pant T-8, RCMT 2
V	2	CTS-05-16-1 Sel., DT-2
VI	3	KS 229, ATL-02-39, VTG 85
VII	8	ARTH-3-1, 127-1 Sel., CTS-05-16-2-1 Sel., CTS-05-16-1-2 Sel., EC 521041, KS 227, VTG 86, VR 20
VIII	5	EC 538151-3 Sel., CTS-05-24-1 Sel., EC 538151-2 Sel., EC 251581-1 Sel., JTP-02-07
IX	1	PAU 2374127-1
X	1	Sel.

The intra- and inter-cluster values (Table 2) showed that cluster IV recorded maximum intra-cluster distance (14.90) followed by cluster VI (13.81) and cluster VIII (13.09), revealing considerable genetic divergence among

Table 2. Average intra (bold) and inter cluster distance values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**(12.24)**	38.75	22.66	18.77	54.55	45.34	27.36	35.62	29.74	62.30
II		**(11.11)**	44.75	34.12	39.29	26.17	28.02	19.28	48.76	49.74
III			**(11.20)**	29.42	59.07	50.69	35.52	42.21	19.39	66.29
IV				**(14.90)**	51.23	41.29	19.95	30.30	35.14	59.41
V					**(10.36)**	30.43	47.20	41.33	62.12	30.52
VI						**(13.81)**	36.16	28.08	54.21	42.82
VII							**(12.60)**	22.81	40.40	55.99
VIII								**(13.09)**	46.39	51.16
IX									**(00.00)**	68.99
X										**(00.00)**

Table 3. Cluster mean for different quantitative characters in 49 diverse genotypes of tomato (*Lycopersicon esculentum*)

Characters Cluster	Total number of fruits	Average fruit weight	Gross yield	Marketable yield	Marketable number of fruits/plant	Plant height	Fruit shape Index	Pericarp thickness	Number of locules/ fruit	Total soluble solids
I	28.00	37.96	1045.56	894.35	24.05	79.46	0.91	0.47	3.19	4.28
II	116.80	18.72	1959.50	2076.80	124.75	133.00	0.82	0.53	3.00	5.88
III	18.60	36.23	643.80	574.71	16.71	84.50	1.09	0.56	2.50	4.49
IV	42.60	37.94	1323.56	1109.25	35.38	95.14	0.88	0.56	3.29	4.21
V	160.50	22.24	3318.50	2807.53	137.25	110.00	0.94	0.43	3.00	4.53
VI	59.70	45.18	2619.57	2216.35	50.67	69.00	1.02	0.48	2.33	4.42
VII	48.40	35.99	16.11.39	1383.57	41.71	77.63	0.88	0.41	2.94	4.68
VIII	68.70	34.30	2005.95	1721.90	58.60	75.90	1.09	0.44	3.20	4.56
IX	11.50	35.50	407.05	283.20	8.00	95.00	0.92	0.40	3.00	3.40
X	147.30	28.69	4158.34	3208.04	113.33	77.50	0.90	0.35	2.50	5.40

the genotypes of the cluster. The parents within the cluster can be chosen for hybridisation programme. The relative distance of each cluster from other cluster *i.e.*, inter-cluster distance showed greater divergence between cluster IX and cluster X *i.e.*, D = 68.99 followed by cluster III and cluster X (D = 66.29) and cluster I and cluster X (D = 62.30), indicating greater diversity between genotypes belonging to respective pairs of cluster. The cluster I and cluster IV had the least genetic distance *i.e.*, D = 18.77.

The cluster means of genotypes (Table 3) revealed considerable genetic differences between the groups. Cluster II, for plant height (133.00) and total soluble solids (5.88); cluster III [VR 35, PAU 2372, Tomato 169, and cluster VIII for fruit shape index (1.09) and pericarp thickness (0.56); cluster IV [ATL-01-19, PAU 2371, Arka Vikas, Local 2707, CTS-05-35-3 (SPS), Pant T-8, RCMT 2], for pericarp thickness (0.56) and number of locules/fruit (3.29); cluster V [CTS-05-16-1 Sel., DT-2], for total number of fruits per plant (160.50) and marketable number of fruits/plant (137.25) and cluster X [127-1 Sel.], for gross yield (4158.34) and marketable yield (3208.04) registered highest mean values for two characters each. Remaining characters were low in performance.

The inferences drawn from inter-cluster distances may be used to select genetically diverse and superior genotypes. Intercrossing of genotypes from these diverse clusters may result in wide array of variability for having effective selection for these characters. These results are in accordance with Singh and Singh (1976) and Singh *et al.* (2008). Intercrossing of divergent groups would lead to greater opportunity for crossing over, which may release hidden variability by breaking linkage (Thoday, 1969). Hence, these genotypes might be used in single as well as multiple crossing programmes for development of promising hybrids. On the basis of mean value for economic traits and placement in distantly located clusters, the varieties RCMT-1, Pant T-10, DT-2 and Selection-127-1 are suitable both as open-pollinated varieties and as parents to be used in hybridization programme.

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