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Pushpendra Kumar

Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

CN Ram

Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

DK Gautam

Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

AM Choudhary

Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

AK Singh

Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

JK Yadav

Department of Plant Pathology, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

Shubham Yadav

Department of Horticulture, DR. R.M.L.A.U. Faizabad, Uttar Pradesh, India

Correspondence

Pushpendra Kumar Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

Genetic diversity for yield and quality attributing traits in tomato [(Solanum lycopersicon (Mill.) Wettsd.)]

Pushpendra Kumar, CN Ram, DK Gautam, AM Choudhary, AK Singh, JK Yadav and Shubham Yadav

Abstract

The present study was carried out during Rabi seasons of 2016-17 and 2017-18 at Main Experiment Station of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experimental materials of the study comprised of 54 treatments of tomato [40 F1's and 14 parental lines (10 lines viz., NDT-1, NDT-2, NDT-3, NDT-4, NDT-5, NDT-6, NDT-7, NDT-8, Azad T-6, Arka Saurabh and 4 testers viz., Pusa Ruby, Punjab Chhuhara, Arka Vikash and Arka Meghali]. The 14 parents were involved in a crossing programme to develop a line \times tester set (10 lines + 4 testers + 40 F₁'s). The experimental materials (40 F₁'s and 14 parental lines) were evaluated in Randomized Complete Block Design (RBD) with three replication having each experimental unit with spacing of 60 cm \times 50 cm with plot size of 1.2 m $\times 3.0$ m. The observations were recorded on eighteen characters, viz., days to 50 % flowering, days to first fruit set, days to first fruit harvest, plant height (cm), number of primary branches per plant, number of fruits per cluster, number of fruits per plant, fruit weight per plant (kg), average fruit weight (g), fruit length (cm), fruit girth (cm), number of locules per fruit, pericarp thickness (mm), total soluble solids (TSS), ascorbic acid (mg/100g fresh fruit) total fruit yield per plant (kg). Fifty four genotypes were grouped into 8 different non over lapping clusters. Maximum intra-cluster distance was found for cluster-VII in first year, cluster-V in second year and pooled followed by cluster-IV in both the years and pooled. The highest inter-cluster distance was observed between cluster-III and cluster-VI in first year and pooled, cluster-IV and cluster-VII in second year followed by cluster-VI and cluster-VII in both years and pooled. Maximum contribution in genetic divergence showed by plant height and minimum contribution showed by days to first fruit set and days to first fruit harvest. Thus, there exists ample variation for improvement after selection in the available germplasm of tomato.

Keywords: tomato [(Solanum lycopersicon (Mill.) Wettsd.)], genetic divergence and Mahalanobis D^2 analysis and segregating generation

Introduction

Tomato (*Solanum lycopersicon* (Mill.) Wettsd.), 2n=2x=24, a member of the family Solanaceae and the genus *Solanum*, is an herbaceous, annual and sometimes perennial in nature, prostrate and sexually propagated vegetable crop plant with bisexual flowers. The family Solanaceae once considered poisonous and inedible, has become one of the most popular and extensively consumed vegetable. There are four to eight flowers in each compound inflorescence. There is a light protective anther cone surrounding the stigma leading to self-pollination. Anthesis occurs at about 6-8 A.M. in summer and 9-11 A.M. in winter. Based on growth habit tomato plants are of two types, determinate and indeterminate. Determinate type tomato plants are bushy and inflorescences occur almost at every inter-node but in indeterminate type, inflorescences are formed after every 3 leaves and the terminal bud does not set fruits. Indeterminate type tomato varieties are suitable for the greenhouse cultivation.

It is originated in Peru Ecuador and Bolivia region of Andes in South America (Rick, 1969)^[14]. It is one of the most popular and widely cultivated vegetable throughout the world in open field conditions as well as protected conditions. Because of its economic importance the area under cultivation is increasing every year. India ranks third in terms of production after China and USA. In India, total area under tomato cultivation is 0.808 million hectares with production of 19.69 million tonnes and its productivity is 24.4 tonnes per hectare, whereas, the

UP have occupied an area 0.020 million hectares with production of 0.826 million tonnes and their productivity is 41.3 tonnes per hectare. In India the leading tomato growing states are, Karnataka, West Bengal, Maharashtra, Uttar Pradesh, Haryana, Punjab, Gujarat and Bihar. (Anonymous, 2016).

Tomato is a short duration crop of about three to four months. It is a day neutral warm season crop reasonably resistant to heat and drought and grows under wide range of soil and climatic conditions. Though tomato is a self-pollinated crop, the unusual high heterosis observed in it, has been attributed to the fact that, originally tomato was a highly out crossing genus which has later evolved into a self-pollinated one (Rick, 1965)^[13] and edible part is botanically known as berry (Kalloo *et al.* 2001)^[6]. It is globally cultivated for its fleshy fruits and known as protective food. Under Indian condition, the fruits mainly consumed either as raw or in the preparation of sambar, chatni, pickles etc.

Tomato is also rich in medicinal value. The pulp and juice are digestible, mild aperients, a promoter of gastric secretion and blood purifier. It is reported to have antiseptic properties against intestinal infestations. In the present days, it is gaining more medicinal importance because of the antioxidant property of ascorbic acid and lycopene content. It is also an important source of β -carotene and valued for their colour and flavour. Thus, today it is one of the important raw materials for multimillion food industries. Tomatoes are also called as "Poor man's apple". In many countries it is considered as "poor man's orange" because of its attractive appearance and nutritive value (Singh et al. 2004) [15]. Apart from these, lycopene is valued for its anti-cancerous property (Tiwari et al. 2002) ^[18]. It acts as an antioxidant and scavenger of free radicals, which is often associated with carcinogenesis. Thus, lycopene has great beneficial effects on human health (Khachik et al. 1995)^[7].

Without regular infusion of genetic variability and selection in tomato, through hybridization it is not feasible to make advances in productivity and production. Various breeding techniques advocated considering the breeding behaviour of the crop. Heterosis breeding as a tool for genetic improvement in tomato has been advocated by several workers (Bhatt et al. 1999; Premalakshme et al. 2005; Fageria et al. 2001; Thakur et al. 2004 and Duhan et al. 2005) ^[2, 11, 4, 16, 3]. For obtaining high yield as well as quality fruits which are important for realizing economic gain. The commercial exploitation of hybrid vigour in tomato has received greater importance because of several advantages of hybrids over pure line varieties with response to marketable fruit yield and its component traits as well as resistance to biotic and abiotic stresses. That is why large number of commercial hybrids developed in the country in this crop. With increasing popularity of F₁ hybrids in tomato, it is imperative, to obtain such hybrids that have excellent qualities and yield coupled with resistance to diseases. Identification of high yielding and stable varieties and the development of F₁ hybrids will help the farmers to adopt variety/hybrid for successful commercial cultivation of tomatoes. In view of such an importance the tomato crop has gained, increasing the productivity per unit area by even lesser degree assumes greater significance. This increase in production assumes significance because the production of tomato is not sufficient to meet the requirement of fresh market and processing industries. Breeder can no longer depend upon use of basic stock of the breeding material unless there is a wide genetic diversity for the characters. Hence, selection of parents for hybridization could be more dependable as decided by the appropriate methods for genetic diversity. Nonhierarchical Euclidean analysis is a valuable tool for obtaining quantitative estimate of divergence between biological populations. In the process of formulating the tomato crop improvement programmes, understanding about the nature and degree of genetic divergence available in the germplasm plays pivotal role.

Material and Method

The present study was carried out during Rabi seasons of 2016-17 and 2017-18 at Main Experiment Station of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experimental materials of the study comprised of 54 treatments of tomato [40 F₁'s and 14 parental lines (10 lines viz., NDT-1, NDT-2, NDT-3, NDT-4, NDT-5, NDT-6, NDT-7, NDT-8, Azad T-6, Arka Saurabh and 4 testers viz., Pusa Ruby, Punjab Chhuhara, Arka Vikash and Arka Meghali]. The 14 parents were involved in a crossing programme to develop a line \times tester set (10 lines + 4 testers + 40 F₁'s). The experimental materials (40 F₁'s and 14 parental lines) were evaluated in Randomized Complete Block Design (RBD) with three replication having each experimental unit with spacing of $60 \text{cm} \times 50 \text{cm}$ with plot size of $1.2m \times 3.0m$. The observations were recorded on eighteen characters, viz., days to 50 % flowering, days to first fruit set, days to first fruit harvest, plant height (cm), number of primary branches per plant, number of fruits per cluster, number of fruits per plant, fruit weight per plant (kg), average fruit weight (g), fruit length (cm), fruit girth (cm), number of locules per fruit, pericarp thickness (mm), total soluble solids (TSS), ascorbic acid (mg/100g fresh fruit) total fruit yield per plant (kg). The genetic divergence of 54 genotypes of tomato was worked out using Mahalanobis (1928)^[8] D² statistics.

Result and Discussion

The studies of genetic divergence among the 54 (10 lines, 4 testers and 40 F₁'s) genotypes of tomato were carried out by using Mahalanobis D². Fifty four genotypes were grouped into 8 different non over lapping clusters given in Table 1. In Y₁, cluster VII had highest number of genotypes followed by cluster IV, Cluster I, cluster V, cluster III and cluster IV, cluster VI and cluster VIII. In Y₂, cluster I had highest number of genotypes followed by cluster II and cluster III, Cluster V, cluster IV, cluster VI, cluster VII and cluster VIII. In over pooled, cluster IV and cluster V had highest number of genotypes followed by cluster III, Cluster II, cluster I, cluster VI, cluster VII and cluster VIII. The estimates of intra and inter-cluster distance represented by D² values had given in Table 2. The intra-cluster and inter-cluster D² value ranged indicate the selected breeding lines were highly divergent. In Y_1 , the highest intra-cluster distance was shown by cluster VII followed by cluster IV, cluster V, cluster III, cluster II, cluster I cluster VI while, the minimum intra-cluster distance was shown by cluster VIII it was pangenotypic. The maximum inter-cluster distance was observed between cluster III and cluster VI, followed by cluster VI and cluster VII, cluster IV and cluster VI, cluster V and cluster VI and cluster II and cluster VI while, the minimum inter-cluster distance was observed between cluster I and cluster VIII. In Y₂, the highest intra-cluster distance was shown by cluster V followed by cluster IV, cluster II, cluster III, cluster I and cluster VI while, the minimum intra-cluster distance was shown by cluster VII and cluster VIII it was pangenotypic. The maximum intercluster distance was observed between cluster VI and cluster VIII, followed by cluster VI and cluster VII, cluster II and cluster VI, cluster III and cluster VI and cluster V and cluster VI while, the minimum inter-cluster distance was observed between cluster II and cluster V. In over pooled, the highest intra-cluster distance was shown by cluster V followed by cluster IV, cluster III, cluster II, cluster VI and cluster I while, the minimum intra-cluster distance was shown by cluster VII and cluster VIII it was pangenotypic. The maximum intercluster distance was observed between cluster III and cluster VI, followed by cluster VI and cluster VII, cluster VI and cluster VIII, cluster IV and cluster VI and cluster II and cluster VI while, the minimum inter-cluster distance was observed between cluster VII and cluster VIII. The comparison of clusters means revealed considerable differences among the clusters of different quantitative and quality characters given in Table 3. In Y1, Cluster I showed high mean value for days to 50% flowring, days to first fruit set and days to first fruit harvest. Cluster II showed high mean value for number of fruits per cluster, fruit girth and pericarp thickness. Cluster III showed high mean value for plant height, number of primary branches per plant, number of locules per fruit and pericarp thickness. Cluster V showed high mean value for ascorbic acid. Cluster VI showed high mean value for number of fruits per plant and fruit weight per plant. Cluster VII showed high mean value for average fruit weight and fruit length. Cluster VIII showed high mean value for total soluble solids and total fruit yield per plant. In Y_2 , Cluster I showed high mean value for days to 50% flowring. Cluster III showed high mean value for pericarp thickness. Cluster IV showed high mean value for total fruit yield per plant. Cluster VI showed high mean value for number of fruits per plant and fruit weight per plant. Cluster VII showed high mean value for number of fruits per cluster average fruit weight, fruit length, fruit girth and total soluble solids. Cluster VIII showed high mean value for days to first fruit set, days to first fruit harvest, plant height, number of primary branches per plant, number of locules per fruit and ascorbic acid.

In over pooled, Cluster I showed high mean value for days to 50% flowring, days to first fruit set and days to first fruit harvest and total fruit yield per plant. Cluster II showed high mean value for fruit girth. Cluster III showed high mean value for plant height, number of primary.

Table 1: Clustering pattern of fifty four genotypes of tomato on the basis of Mahalanobis 'D²' statistics over two years and Pooled

Cluster number	Years	No. of genotypes	Genotypes
	\mathbf{Y}_1	8	NDT-3×Punjab Chhuhara, NDT-3×Arka Vikas, Arka Saurabh, NDT-2×Arka Vikas, Arka Saurabh×Arka Meghali, NDT-2×Arka Meghali, NDT-3×Arka Meghali, Punjab Chhuhara
Ι	Y ₂	12	NDT-3×Punjab Chhuhara, NDT-3×Arka Vikas, Arka Saurabh, Arka Saurabh×Arka Meghali, NDT-2×Arka Vikas, NDT-2×Arka Meghali, Punjab Chhuhara, NDT-3×Arka Meghali, NDT-8, Arka Saurabh×Punjab Chhuhara, Arka Saurabh×Arka Vikas, NDT-
	-		1×Punjab Chhuhara
	Pooled	3	NDT-3×Punjab Chhuhara, NDT-3×Arka Vikas, Arka Saurabh
	Y1	4	NDT-8×Punjab Chhuhara, NDT-8×Arka Vikas, NDT-2×Punjab Chhuhara, Arka Saura×Punjab Chhuhara
Π	\mathbf{Y}_2	11	Azad T-6×Punjab Chhuhara, Azad T-6×Arka Vikas, Azad T-6×Arka Meghali, NDT-1, NDT-4×Arka Vikas, NDT-6×Pusa Ruby, Pusa Ruby, NDT-8×Pusa Ruby, NDT-7×Pusa Ruby, NDT-4×Punjab Chhuhara, NDT-4×Arka Meghali
	Pooled	4	NDT-8×Punjab Chhuhara, NDT-8×Arka Vikas, NDT-2×Punjab Chhuhara, Arka Saurabh×Punjab Chhuhara
	Y ₁	4	Azad T-6×Punjab Chhuhara, Azad T-6×Arka Vikas, Azad T-6×Arka Meghali, Azad T-6×Pusa Ruby
III	Y ₂	11	NDT-8×Punjab Chhuhara, NDT-8×Arka Vikas, NDT-2×Punjab Chhuhara, NDT-8×Arka Meghali, NDT-6×Arka Meghali, NDT-6×Arka Vikas, NDT-7×Punjab Chhuhara, NDT-3, NDT-6×Punjab Chhuhara, NDT-7×Arka Meghali
	Pooled	5	Azad T-6×Punjab Chhuhara, Azad T-6×Arka Vikas, Azad T-6×Arka Meghali, Azad T-6×Pusa Ruby, NDT-1
IV	\mathbf{Y}_1	12	NDT-4×Arka Meghali, Pusa Ruby, NDT-6×Pusa Ruby, NDT-4×Punjab Chhuhara, NDT-1×Pusa Ruby, NDT-7×Pusa Ruby, NDT-8×Pusa Ruby, NDT-4×Arka Vikas, NDT-4, NDT-5, NDT-4×Pusa Ruby, NDT-2×Pusa Ruby
	Y ₂	7	NDT-2. Arka Vikas, NDT-1×Arka Vikas, NDT-2×Pusa Ruby, Arka Meghali, NDT-1×Arka Meghali, Azad T-6
			NDT-4×Arka Meghali, Pusa Ruby, NDT-6×Pusa Ruby, NDT-4×Punjab Chhuhara, NDT-1×Pusa Ruby, NDT-7×Pusa Ruby, NDT-
	Pooled	19	8×Pusa Ruby, NDT-4×Arka Vikas, NDT-4×Pusa Ruby, NDT-5×Arka Meghali, NDT-5×Punjab Chhuhara, NDT-5×Arka Vikas,
			NDT-5×Pusa Ruby, NDT-5, NDT-4, Azad T-6, NDT-2×Pusa Ruby, NDT-1×Punjab Chhuhara, NDT-3×Pusa Ruby
	Y ₁	5	NDT-5×Punjab Chhuhara, NDT-5×Arka Vikas, NDT-5×Arka Meghali, NDT-5×Pusa Ruby, Azad T-6
¥7	\mathbf{Y}_2	9	NDT-5×Arka Vikas, NDT-5×Arka Meghali, NDT-5×Punjab Chhuhara, NDT-5×Pusa Ruby, NDT-4×Pusa Ruby, NDT-1×Pusa Ruby, NDT-5, NDT-4, NDT-3×Pusa Ruby
v	Pooled	19	NDT-2×Arka Vikas, Arka Saurabh×Arka Meghali, NDT-2×Arka Meghali, NDT-3×Arka Meghali, Punjab Chhuhara, Arka Saurabh×Arka Vikas, NDT-6×Punjab Chhuhara, NDT-8, NDT-7×Arka Meghali, NDT-7×Punjab Chhuhara, NDT-3, NDT-1×Arka Vikas, Arka Vikas, Arka Meghali, NDT-6×Arka Meghali, NDT-6×Arka Vikas, NDT-7×Arka Vikas, NDT-8×Arka Meghali, NDT-2
	Y1	2	NDT-6, NDT-7
VI	Y ₂	2	NDT-6, NDT-7
	Pooled	2	NDT-6, NDT-7
VII	Y1	18	NDT-6×Arka Vikas, NDT-7×Arka Vikas, NDT-6×Arka Meghali, NDT-7×Punjab Chhuhara, NDT-3, NDT-6×Punjab Chhuhara, NDT-7×Arka Meghali, Arka Saurabh×Arka Vikas, NDT-1×Punjab Chhuhara, NDT-1×Arka Vikas, NDT-8×Arka Meghali, NDT-2, Arka Vikas, NDT-1, NDT-1×Arka Meghali, Arka Meghali, NDT-3×Pusa Ruby, Arka Saurabh×Pusa Ruby
v 11	Y ₂	1	Arka Saurabh×Pusa Ruby
	Pooled	1	Arka Saurabh×Pusa Ruby
<u> </u>	Y ₁	1	NDT-8
VIII	Y ₂	1	Azad T-6×Pusa Ruby
	Pooled	1	NDT-1×Arka Meghali

Y1=2016-17 and Y2=2017-18

Table 2: Intra and inter clusters D² values for eight clusters in tomato over two years and Pooled

	Years	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
	Y1	24.16	56.89	233.36	112.43	163.56	279.73	87.65	39.49
Cluster I	Y2	28.78	118.84	71.66	76.56	131.96	267.88	181.04	275.22
	Pooled	7.72	33.31	91.96	53.97	32.46	168.95	86.09	48.57
Cluster II	Y1		24.42	232.49	150.44	216.49	457.15	79.03	98.87
Cluster II	Y2		43.29	105.54	96.64	68.63	555.01	75.60	69.95

	Pooled	13.44	92.72	77.79	34.10	266.39	104.41	80.82
Cluster III	Y1		29.65	91.43	80.11	763.35	168.38	276.99
	Y2		42.96	98.83	173.07	488.76	167.51	230.30
	Pooled		21.41	49.98	87.62	418.45	39.48	62.56
	Y1			43.82	72.54	502.55	109.75	154.17
Cluster IV	Y ₂			46.50	135.36	404.37	78.57	194.73
	Pooled			29.76	67.35	272.17	64.36	62.78
	Y1				42.72	488.57	176.06	165.55
Cluster V	Y ₂				50.28	444.31	123.39	103.77
	Pooled				33.43	246.88	88.78	65.07
	Y1					15.78	507.11	184.21
Cluster VI	Y ₂					16.31	645.17	833.19
	Pooled					9.78	392.08	279.21
	Y1						75.03	133.25
Cluster VII	Y ₂						0.00	80.95
	Pooled						0.00	25.08
Cluster VIII	Y1							0.00
	Y_2							0.00
	Pooled							0.00

Y1=2016-17 and Y2=2017-18

Table 3: Intra-cluster group mean for 16 clusters in tomato over two years and pooled

Cluster	¥7	Days to 50%	Days to first	Days to first	Plant height	Number of primary	Number of fruits	Number of	Fruit weight
number	rears	flowering	fruit set	fruit harvest	(cm)	branches per plant	per cluster	fruit per plant	per plant (kg)
Ι	Y1	30.51	37.79	61.61	80.68	3.29	5.04	44.85	1.36
	Y ₂	33.58	38.81	62.51	82.57	3.76	5.76	45.70	1.30
	Pooled	32.97	38.67	62.83	84.69	3.81	5.03	47.15	1.21
	Y1	29.49	36.94	60.87	69.66	3.55	5.76	36.21	0.96
II	Y ₂	32.57	37.85	61.66	124.71	4.08	5.96	35.01	0.96
	Pooled	31.11	37.56	61.50	70.29	3.78	5.97	36.84	0.96
	Y1	29.49	37.33	60.95	135.18	4.08	5.25	29.33	0.72
III	Y ₂	32.86	38.41	62.29	80.34	4.09	5.84	34.80	0.90
	Pooled	31.13	37.71	61.41	133.04	4.23	5.67	30.76	0.71
IV	Y1	29.03	36.19	60.06	123.94	3.52	5.43	38.39	1.21
	Y ₂	32.35	37.48	61.18	99.71	4.01	6.04	44.09	0.86
	Pooled	30.74	37.08	60.89	124.86	3.77	5.69	39.97	1.25
	Y1	29.38	36.69	60.37	132.91	3.49	5.27	39.49	1.32
V	Y ₂	32.20	37.82	61.61	134.74	4.04	5.77	42.28	1.40
	Pooled	31.50	37.90	61.59	83.63	3.64	5.56	39.77	1.06
	Y1	30.23	37.66	61.39	67.25	3.44	5.52	70.08	2.80
VI	Y ₂	33.44	38.91	62.65	68.51	3.91	6.03	71.34	2.71
	Pooled	31.83	38.28	62.03	67.88	3.67	5.77	70.71	2.76
	Y1	29.55	37.01	60.72	92.14	3.48	5.46	37.56	0.90
VII	Y ₂	32.97	39.03	62.60	131.75	3.16	6.44	37.39	0.65
	Pooled	31.14	38.41	61.97	129.45	2.93	6.19	36.76	0.64
	Y1	29.91	37.43	61.01	79.03	3.39	5.70	51.23	1.38
VIII	Y ₂	33.40	39.30	63.18	160.02	4.46	6.04	29.03	0.72
	Pooled	28.67	35.26	58.79	110.43	3.26	5.59	44.52	0.79

Table 3: contd....

Cluster number	Years	Average fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Number of locules per fruit	Pericarp thickness (mm)	Total soluble solid (TSS)	Ascorbic acid (mg/100 g fresh fruit)	Total fruit yield per plant (kg)
	Y1	33.43	6.68	12.48	4.07	4.59	5.90	35.78	2.81
Ι	Y ₂	35.53	7.31	14.15	4.57	4.91	6.11	36.79	3.11
	Pooled	39.12	7.61	13.80	3.83	4.79	5.69	38.69	3.19
	Y1	38.03	6.54	13.49	4.18	4.95	5.22	36.81	2.62
II	Y2	37.80	7.25	13.94	4.84	4.89	5.80	43.96	2.86
	Pooled	38.66	6.81	14.10	4.35	5.15	5.41	37.17	2.79
	Y1	41.19	6.83	12.45	4.70	4.54	5.60	54.13	2.46
III	Y2	38.99	7.30	14.10	4.69	5.21	5.67	34.95	2.70
	Pooled	43.71	7.15	13.28	4.90	4.94	5.86	52.54	2.70
	Y1	32.25	6.78	12.91	4.45	4.29	5.30	36.04	2.53
IV	Y ₂	52.43	7.71	14.08	4.97	5.10	6.04	41.67	3.41
	Pooled	32.50	6.92	13.42	4.39	4.65	5.55	41.36	2.64
	Y1	30.23	6.32	12.67	4.04	4.84	5.42	55.32	2.19
V	Y ₂	30.10	7.11	14.06	4.30	4.80	5.76	45.62	2.69
	Pooled	39.63	7.08	13.36	4.61	4.82	5.83	34.73	2.79
VI	Y1	25.21	6.35	11.98	4.31	4.29	5.55	41.36	2.76

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	Y2	26.47	6.89	13.19	4.68	4.70	5.94	42.91	3.08
	Pooled	25.84	6.62	12.59	4.49	4.50	5.75	42.13	2.92
	Y1	43.49	7.03	13.07	4.39	4.60	5.44	32.77	2.61
VII	Y2	57.94	7.72	14.22	4.66	4.70	6.31	40.69	3.22
	Pooled	57.31	7.45	13.62	4.48	4.50	6.12	34.58	3.04
	Y1	37.23	6.50	12.16	3.77	4.49	6.12	47.13	2.98
VIII	Y2	40.59	7.36	14.01	5.36	5.10	5.65	51.61	2.94
	Pooled	56.71	7.41	13.68	4.95	4.14	5.18	42.37	2.82

Y₁=2016-17 and Y₂=2017-18

Table 4: Per cent contribution of 16 characters towards total genetic
divergence in tomato over two years and pooled

Contribution (%)					
Y ₁	Y ₂	Pooled			
0.01	0.01	0.07			
0.01	0.01	0.01			
0.01	0.01	0.01			
42.42	46.96	44.03			
0.01	0.01	0.01			
0.49	0.63	0.70			
24.60	24.11	26.83			
2.10	1.89	1.89			
12.51	12.30	14.26			
0.49	0.77	0.84			
0.70	0.84	0.84			
3.14	2.66	2.87			
1.19	1.26	1.12			
0.91	0.84	1.05			
11.25	7.62	5.38			
0.21	0.14	0.14			
	$\begin{tabular}{ c c c c } \hline Cont \\ \hline Y_1 \\ 0.01 \\ 0.01 \\ 0.01 \\ 42.42 \\ 0.01 \\ 0.49 \\ 24.60 \\ 2.10 \\ 12.51 \\ 0.49 \\ 0.70 \\ 3.14 \\ 1.19 \\ 0.91 \\ 11.25 \\ 0.21 \\ \end{tabular}$	$\begin{tabular}{ c c c } \hline Contribution \\ \hline Y_1 & Y_2 \\ \hline 0.01 & 0.01 \\ 0.01 & 0.01 \\ 0.01 & 0.01 \\ 42.42 & 46.96 \\ 0.01 & 0.01 \\ 0.49 & 0.63 \\ 24.60 & 24.11 \\ 2.10 & 1.89 \\ 12.51 & 12.30 \\ 0.49 & 0.77 \\ 0.70 & 0.84 \\ 3.14 & 2.66 \\ 1.19 & 1.26 \\ 0.91 & 0.84 \\ 11.25 & 7.62 \\ 0.21 & 0.14 \\ \hline \end{tabular}$			

Y1=2016-17 and Y2=2017-18

Branches per plant and ascorbic acid. Cluster VI showed high mean value for number of fruits per plant and fruit weight per plant. Cluster VII showed high mean value for number of fruits per cluster, average fruit weight, fruit length and total soluble solids. Cluster VIII showed high mean value for number of locules per fruit. The results are in conformity with findings of earlier researchers *vs.*, Mahesha *et al.* (2006) ^[9], Jogi *et al.* (2008) ^[5], Mehta and Asati (2008) ^[10], Rana and Singh (2010) ^[12] and Thapa *et al.* (2014) ^[17].

In Y_1 , highest per cent contribution towards total genetic divergence given in Table 4 was exhibited by plant height followed by number of fruits per plant, average fruit weight and ascorbic acid. Rest of the characters exhibited low contribution towards total genetic divergence.

In Y_2 , highest per cent contribution towards total genetic divergence was exhibited by plant height followed by number of fruits per plant and average fruit weight. Rest of the characters exhibited low contribution towards total genetic divergence. In over pooled, highest per cent contribution towards total genetic divergence was exhibited by plant height followed by number of fruits per plant and average fruit weight. Rest of the characters exhibited low contribution towards total genetic divergence.

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