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GENETIC DIVERGENCE STUDIES FOR FRUITS YIELD AND QUALITY COMPONENTS IN DIVERSE TOMATO (*SOLANUM LYCOPERSICUM* L.) GENOTYPES

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ABSTRACT

39 genotypes of tomato which were grouped into 9 clusters and exhibited no association between geographical and genetic divergence, the clusters I (12) and II (11) contained highest number of genotypes followed by clusters III (5) and V (4) groups. The maximum inter-cluster D^2 value was observed between the cluster III and V (80.36) and intra- cluster distance was higher in cluster II (26.75). Among the 21 characters average fruit weight (58.43%) contributed maximum per cent to the diversity followed by number of secondary branches (19.43), number of fruits plant^{-1}(11.61%). Cluster III show high mean values for number of seeds fruit^{-1} (120.89) and average fruit weight (61.60). Cluster IX show high mean values for secondary branches (17.33), fruit length (4.60), pericarp thickness (5.0), number of locules fruits^{-1}(4.0) and fruit diameter (5.80). Cluster V show high mean values for flower cluster^{-1} (6.90), Number of fruits cluster^{-1}(4.59), T.S.S. (8.13), fruits plant^{-1} (153.02) Cluster VI show high mean values for fruit yield plant^{-1}(3.57) and number of locules fruits^{-1}(4.0).Cluster VIII show high mean for days to first flowering (45.53), day to maturity (87.60) and days to 50% fruit setting (64.17),cluster IV show high mean values for only fruiting clusters plant^{-1} (42.10).

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INTRODUCTION

Tomato (*Solanum lycopersicum* L.) a member of family Solanaceae is one of the most important vegetable crops in India as well as in the world (Cheema and Dhaliwal, 2005; Kumar *et al.,* 2010; Kumar and Dudi, 2011; Osekita and Ademiluyi, 2014). It has a chromosome number of 2n = 24 (Rick, 1969).Tomato is native of West Coast of South America (Mexico and Peru) and was cultivated by Indians about 500 B.C. long before arrival of Spaniards (Tasisa *et al.*, 2012). Tomato is the most important vegetable crop next only to potato because of its wider adaptability, high yielding potential and multipurpose uses (Reddy *et al.*, 2013b). Tomato is grown as annual or short lived perennial herbaceous plants. It has a taproot, and the growth habit of the plant is determinate, semi-determinate and indeterminate. 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 (Kumar *et al.*, 2010). It is an important protective food because of its special nutritive value as it contains abundant and well balanced nutrition consisting of minerals, vitamins, dietary fiber, citric acid *etc.* (Thapa *et al.*, 2014). Ascorbic acid may play a key role in delaying the pathogenesis of a variety of degenerative diseases, such as cardiovascular disease, certain cancers, cataracts and it also prevents DNA mutation induced by oxidative stress (Marchioli *et al.*, 2001; Lutsenko *et al.*, 2002). Lycopene and â-carotene are the tomato carotenes which present the highest nutritional value (Tomlekova *et al.*, 2007; Glogovac *et al.*, 2010). Lycopene may alleviate chronic diseases such as cancer and coronary heart disease (Omoni and Aluko, 2005; Kun *et al.*, 2006). Looking at its commercial importance, there is utmost need to develop new varieties with higher yield, disease resistance, 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 (Lahbib *et al.*, 2012; Srivastava *et al.*, 2014). The greater is parental diversity, the greater is the chance of developing higher yielding breeding lines (Singh *et al.*, 2012). In India, major tomato producing states are Bihar, Karnataka, Uttar Pradesh, Orissa, Andhra Pradesh, Maharashtra and Madhya Pradesh. India occupied only area of 882.0 ('000 ha), production 18735.9 ('000 MT) and productivity 21.9 (MT/ha).In Madhya Pradesh, major producing districts are Ratlam, Indore, Khargone, Dhar, Jhabua. Madhya Pradesh alone produced 1937.37('000 MT) with area of 65.72 ('000 ha) and productivity 29.5 (MT/ha). (http://nhb.gov.in/).

Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the scale of hybridization activities and concentrate their efforts in a smaller number of combinations (Fuzzato *et al.*, 2002). Although tomato is a self pollinated crop, there is genetic diversity not only in the morphological features but also in the quality attributes. Among the various methods identified or developed to study the genetic divergence in the genotypes the Mahalanobis D^2 (Mahalanobis, 1936) is reliable and most frequently used. For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952). It is a

very useful technique of measuring genetic divergence (Meena and Bahadur, 2013; Sharma and Devi, 2013; Ramanjaneyulu *et al.*, 2014; Srivastava *et al.*, 2014). Further, grouping of the accessions based on Tocher's method will be more useful in choosing suitable parents for heterosis breeding (Prashanth *et al.*, 2008). 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 (Singh *et al.*, 2006a; Ara *et al.*, 2009).

Keeping in view the above facts present investigation was undertaken to its precision and versatility with an objective to study of genetic diversity in 39 tomato genotypes based on 21 traits, to help the breeders in selecting promising and genetically diverse parents for desired improvement in tomato germplasm.

MATERIALS AND METHODS

The present experiment was conducted at Vegetable Research Farm, College of Agriculture Rewa, JNKVV, Jabalpur (Madhya Pradesh). Under the study thirty nine tomato genotypes are presented in (Table 1) and these genotypes evaluated for different plant and fruit characters during *Rabi* 2010-2011. The experiment was laid out in a Randomized Block Design (RBD) with three replications to assess the value and magnitude of genetic divergence in tomato genotypes. Rewa is situated in the North, Eastern part of Madhya Pradesh, the climatic region comes under the semi-arid and subtropical having extreme winter and summer. It is situated at the latitude of 24°31 N, longitude 81°15 E altitude of 306 meter above the sea level. All the recommended agronomic package of practices were followed (like staking, earthing up, irrigation, weeding *etc.*), as recommended for commercial tomato production. Five randomly taken plants were used to record observations on quantitative and qualitative traits i.e., days to first flowering, days to 50% flowering, days to 50% fruit setting, days to 100% fruit setting, days to fruit maturity, number of flowers per cluster, number of fruits cluster^{-1}, number of fruiting clusters plant^{-1}, plant height (cm), number of primary branches, number of secondary branches, fruit length (cm), fruit diameter (cm), test weight (g), average fruit weight (g), T.S.S.(%), number of fruits plant^{-1}, pericarp thickness (mm), number of locules fruits^{-1}, fruit yield plant^{-1} (kg.), number of seeds fruit^{-1}.

The data collected were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT 9.1. Genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

By employing Mahalanobis generalized distance (D^2) statistics the genetic diversity among 39 genotypes was measured for all the genotypes the correlated unstandardized mean value(x) for 21 characters under consideration were transformed to the correlated standardized value(y).The D^2 value which being the sum of squares of differences for each Y values was calculated for all the combination. Based on the D^2 values the genotypes were grouped into 9 clusters (Table 2) using Tocher's method as given by Rao (1952) of clusters, studied the cluster I was the largest comprising of 12 genotypes followed by cluster II with 11 genotypes and cluster III with 5 genotypes, cluster V with 4 genotypes and cluster VII with 3 genotypes, remain four clusters (IV, VI, VII, IX) comprised of single genotypes each. The clustering pattern in the present study showed that accessions of different geographical areas were clubbed in one group indicating that there was no parallelism between genetic diversity and geographical origin. These results are similar to the findings of Mehta and Asati (2008), Singh *et al.* (2006b),Singh *et al.* (2008), Basavaraj *et al.*(2010), Kumar *et al.* (2010), Shashikanth *et al.* (2010); Kumar *et al.* (2013), Meena and Bahadur (2013). On the other view, 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

Table 1: Source and place of collection of tomato genotypes used in the present study

S. No	Genotypes	Source/Place of collection	S. No	Genotypes	Source/Place of collection
X_1	Nandi	UAS, Bangalore,	X_{21}	Dhanashree	MPKV,Rahuri,M.H.
X_2	Arka Meghali	IIHR, Bangalore	X_{22}	DT - 10	IARI, New Delhi
X_3	DVRT - 1	IIVR, Varanasi	X_{23}	DVRT - 2	IIVR, Varanasi
X_4	Salimar - 2	Srinagar, SEK-UAT	X_{24}	Vaibhav	UAS,Bangalore,
X_5	PKM - 1	Coimbatore, TNAU	X_{25}	Christmas Grape	Holland
X_6	Roma	IARI, New Delhi	X_{26}	Madan Tomato	NDUAT,Narendra nager ,Faizabad
X_7	GT - 2	GAU,Anand	X_{27}	F1 - Bhasker	Awedh seed company,Faizabad
X_8	CO - 3	Coimbatore, TNAU	X_{28}	Santury Research	Awedh seed company,Faizabad
X_9	T.L.B.R. - 3	UAS Dharwad	X_{29}	Ujvork Udham	Awedh seed company,Faizabad
X_{10}	Utkal Urvashi	OUAT,Bhubneshwar	X_{30}	MHT - 301	Ludhiana, PAU
X_{11}	H-88-78-1	UAS Dharwad	X_{31}	Mahalaxmi	Dharwad
X_{12}	Arka Saurabh	IIHR, Bangalore	X_{32}	MHT - 256	Ludhiana, PAU
X_{13}	Arka Vikas	IIHR, Bangalore	X_{33}	T - 99	JNKVV.Jabalpur(M.P.)
X_{14}	Shankarmit	UAS Dharwad	X_{34}	MST - 256	Dharwad
X_{15}	Utkal Raja	OUAT,Bhubneshwar	X_{35}	Bhagya	Dharwad
X_{16}	H-88-78-2	UAS Dharwad	X_{36}	H - 86	IIVR, Varanasi
X_{17}	Palam Pink	Palampur,H.P.	X_{37}	VS - 44	IIVR, Varanasi
X_{18}	Selection - 7	Hissar, CCH-HAU	X_{38}	VS - 312	IIVR, Varanasi
X_{19}	Arka Alok	IIHR, Bangalore	X_{39}	VS – 404	IIVR, Varanasi
X_{20}	Utkal Kumari	OUAT,Bhubneshwar			

Table 2: Grouping of tomato genotypes based on D ^{2} values

Cluster	Number of genotypes	Name of genotypes
I	12	Arka Meghali, DVRT -1, Salimar -2, PKM -1, GT-2, Arka Vikas, DT-10, DVRT-2, F_1-Bhasker, MHT-301, MST-256, VS -312 .
II	11	CO-3, Arka Saurabh, Shankarmit, Utkal Raja, Utkal Kumari Arka Alok, Dhanashree, Mahalaxmi, Bhagya, VS -44, and VS-404,
III	5	Palam Pink, Madan Tomato, Santury Research, H-86, T-99.
IV	1	Ujvork Udham.
V	4	Nandi, Roma, H-88-78-1, Christmas Grape.
VI	1	MHT-256.
VII	3	T.L.B.R.-3, Utkal Urvashi, H-88-78-2.
VIII	1	Vaibhav.
IX	1	Selection-7.

Table 3: Per cent contribution of 21 characters towards diversity in tomato genotypes

Characters	Per cent contribution	Order of contribution
Days to first flowering	0.00%	-
Days to 50% flowering	0.00%	-
Days to 50% fruit setting	0.00%	-
Days to 100% fruit setting	0.00%	-
Days to fruit maturity	0.00%	-
Number of flowers cluster^{-1}	0.00%	-
Number of fruits cluster^{-1}	0.00%	-
Number of fruiting cluster plant^{-1}	0.13%	-
Plant height(cm)	1.89%	V
Number of primary branches	1.08%	-
Number of secondary branches	19.43%	II
Fruit length(cm)	1.89%	V
Fruit Diameter (cm)	4.18%	IV
Test weight fruit^{-1} (g)	0.00%	-
Average Fruit weight (g)	58.43%	I
T.S.S. (%)	0.00%	-
Number of fruits plant^{-1}	11.61%	III
Pericarp thickness (mm)	0.54%	-
Number of locules fruits^{-1}	0.00%	-
Fruit yield plant^{-1} (kg)	0.13%	-
Number of seed fruit^{-1}	0.67%	-

Table 4: Average Intra and Inter cluster D^2 values of tomato genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	23.22	42.05	64.05	27.25	35.93	37.07	30.87	34.78	31.61
II		26.75	38.23	33.85	60.33	30.61	47.22	33.99	40.19
III			26.10	50.72	80.36	38.59	72.58	45.95	52.38
IV				0.00	36.78	17.90	40.18	23.43	22.21
V					22.76	47.55	44.26	45.88	44.72
VI						0.00	51.37	22.29	23.17
VII							23.35	43.65	48.88
VIII								0.00	29.97
IX									0.00

for different characters under selection. This could be due to selection or genetic drift, which helps in creating more diversity rather than genetic distance. Hence, selection of genotypes for hybridization to generate diverse new gene combinations should be based on genetic diversity rather than geographic diversity. This finding is in conformity with the findings of Ganesh *et al.* (2007), Pawar *et al.* (2013) and Vidhya *et al.* (2014). Similarly, Gonçalves *et al.* (2009) grouped 40 tomato accessions into 5 diverse clusters; Yashavantakumar *et al.* (2009) grouped 70 tomato genotypes into 7 clusters, Ghosh *et al.* (2009) clustered 40 genotypes into 6 clusters; Meena and Bahadur (2013) Classify 30 tomato germplasms into 6 clusters. Chernet *et al.* (2014) clustered 36genotypes into 6 distinct clusters; Iqbal *et al.* (2014) grouped 47 tomato genotypes into 5 clusters.

Per cent contribution of 21 characters toward diversity in tomato genotypes were presented in (Table 3), out of twenty one characters under studied it is resulted that, average fruit weight (58.43%) contributed maximum per cent to the diversity followed by number of secondary branches (19.43), number of fruits plant^{-1}(11.61%), fruit diameter (4.18%), number of seeds fruit^{-1}(0.67%), pericarp thickness (0.54%) and number

of fruiting clusters plant^{-1}(0.13%), fruit yield plant^{-1}(0.13%) each. Singh *et al*. (2008) and Reddy *et al*. (2013a) were also observed such maximum contribution for fruit weight to total divergence of tomato genotypes. De *et al*. (1988) opined that traits contributing maximum towards the D^2 values needed to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for crossing.

The inter cluster D^2 values are given in (Table 4) and the nearest and farthest cluster from each cluster based on D^2 values is given in (Table 5). The inter cluster D^2 values were maximum (80.36) between the cluster III and cluster V. Revealing considerable genetic divergence among the accessions of this cluster and was due to both natural and artificial selection forces among the accessions Rathi *et al*., (2011).The minimum distance observed between cluster IV and VI (17.90) indicated close relationship among the genotypes included. Cluster III was the most diverse as many other clusters maximum inter cluster distance with it. The intra cluster D^2 values are given in (Table 4). The intra cluster D^2 values distance was observed in clusters I, II, IIII, V and VII, whereas, reaming cluster comprised only one genotypes each. The intra cluster distance was higher in cluster II (26.75) followed by cluster II (26.10) and lowest in cluster V (22.76). Indicated that the accessions belonging to these groups were genetically most diverse and the accessions included in these clusters can be used as a parent in hybridization program to get higher heterotic hybrids from the segregating population. Similar results were revealed by Mehta and Asati (2008), Meena and Bahadur (2013) and Vidhya *et al*. (2014).

The crop improvement, crossing among genotypes with outstanding mean performance was suggested by Kumar *et al*. (2013), and the reliable conformity for this can be known on the basis of cluster means. The cluster mean of twenty one different characters (Table 6) were compared and indicated considerable differences between clusters for all the characters studied. Cluster I show high mean values with primary branches (8.45) Cluster III show high mean values for number of seeds fruit^{-1} (120.89) and average fruit weight (61.60). Cluster IX show high mean values for secondary branches (17.33), fruit length (4.60), pericarp thickness (5.0), number of locules fruits^{-1}(4.0) and fruit diameter (5.80). Cluster V show high mean values for flower per cluster (6.90), Number of fruits cluster^{-1}(4.59), T.S.S. (8.13), fruits plant^{-1} (153.02) Cluster VI show high mean values for fruit yield plant^{-1} (3.57) and number of locules fruits^{-1}(4.0).Cluster VIII show high mean for days to first flowering (45.53), day to maturity (87.60), days to 50%

Table 5: the nearest and farthest clusters from each cluster between D^2 values in tomato genotypes

Cluster	Nearest cluster with D^2 values	farthest cluster with D^2 values
I	IV(27.25)	III(64.20)
II	V(30.61)	V(60.33)
III	II(38.23)	V(80.36)
IV	VI(17.90)	III(50.72)
V	I(35.93)	III()80.36
VI	IV(17.90)	VII(51.31)
VII	I(30.87)	III(72.58)
VIII	VI(22.29)	III(45.95)
IX	IV(22.21)	III(52.38)

Table 6: Cluster means for twenty one characters of tomato genotypes

SV	DFFL	DFFG	DFFS	DHFS	DFMY	NFGCL	NFTCL	FTGCL	PLGT	NPBR	NSBR	FLTH	FDI	TWT	AFWT	TSS	NFTCL	PCTH	NLFR	FYPL	NSDF
I	43.20	54.45	61.82	74.43	82.84	6.33	3.63	27.87	68.89	8.45	13.14	4.06	4.42	2.29	22.16	7.18	74.10	4.42	3.56	1.72	48.22
II	42.90	53.43	61.28	74.45	82.65	6.10	3.48	27.41	63.15	6.27	11.95	3.79	4.60	2.45	46.36	6.62	62.18	4.36	3.12	2.88	71.80
III	42.90	54.34	61.58	74.85	83.50	5.91	3.31	25.26	70.66	6.27	15.43	4.01	4.68	2.41	61.80	7.20	49.61	4.20	3.27	3.06	120.89
IV	42.33	54.20	61.40	74.77	83.83	5.40	3.40	42.10	50.47	5.57	14.60	4.20	3.70	2.37	30.30	7.60	102.60	4.00	3.00	3.57	101.27
V	41.52	53.44	60.59	72.86	82.73	6.94	4.59	34.97	85.41	7.13	14.91	3.51	2.98	2.21	13.28	8.13	153.02	3.25	2.83	1.90	78.69
VI	45.00	53.50	61.47	75.33	83.80	6.93	4.13	34.63	59.8	6.37	16.37	3.50	4.20	2.47	40.57	7.50	96.47	4.00	4.00	3.53	83.93
VII	43.93	53.08	60.08	73.48	81.44	5.92	3.80	15.19	52.77	5.98	8.90	3.83	3.43	2.42	20.93	7.72	65.16	4.33	3.00	1.21	63.63
VIII	45.53	56.40	64.17	79.27	87.60	5.73	2.90	27.90	72.47	4.40	15.50	2.20	2.70	2.40	33.83	6.57	56.10	4.00	4.00	1.93	120.73
IX	42.37	51.57	59.67	75.03	84.60	6.53	3.53	30.80	52.53	4.80	17.33	4.60	5.80	2.50	27.50	7.57	70.20	5.00	4.00	1.84	56.73

DFFS – Days to first flowering, DFFG- days to 50% flowering, DFFS- days to 50% fruit setting, NFGCL- Number of flower per cluster, NFTCL- number of fruits per cluster, FTGCL- number of fruiting per cluster, NSBR – number of secondary branches, FLTH- Fruit length, FDI- fruit diameter, TWT- test weight, NFTPL- number of fruits per plants, PCTH- pericarp thickness, NLFR- Number of locules/fruits, DHFS- days to 100% fruit setting, DFMY- days to fruit maturity, NPBPR- number of primary branches, TSS- total soluble solid, PLGT- plant height, FYPL – fruit yield/plant, AFWT- average fruit weight, NSDF- number of seeds per fruits.

Table 7: Diversity of qualitative traits in thirty nine tomato genotypes

S. No.	Genotype	Leaf type	Stem pubescence	Fruit shape	Stem type	Leaf/foliage cover	Immature fruits skin color
X_1	Nandi	Hirusetum	Medium	Oval	Round	Good	Light Green
X_2	Arka Meghali	Regular	dense	Flat round	Angular	Dense	Light Green
X_3	DVRT-1	Potato leaf	Low	Flat round	Angular	Poor	Dark Green
X_4	Salimar-2	Hirusetum	Medium	Round	Angular	Poor	Light Green
X_5	RKM-1	Hirusetum	Low	Round	Round	Dense	Dark Green
X_6	Roma	Angular	Medium	Round	Round	Dense	Light Green
X_7	GT-2	Regular	Medium	cylindrical	Round	Dense	Light Green
X_8	CO-3	Small/Narrow	Medium	Slightly flattened	Round	Good	Dark Green
X_9	TLBR-3	Small/Narrow	Medium	Round	Round	Low	Light Green
X_{10}	Utkal Urvarshi	Angular	Medium	Oval	Round	Poor	Light Green
X_{11}	H-88-78-1	Regular	dense	Round	Angular	Poor	Light Green
X_{12}	Arka Saurabh	Hirusetum	dense	Round	Angular	Good	Light Green
X_{13}	Arka Vikas	Hirusetum	Medium	Flat round	Angular	Good	Light Green
X_{14}	Shankarmit	Hirusetum	dense	Round	Angular	Dense	Dark Green
X_{15}	Utkal Raja	Hirusetum	dense	Round	Angular	Poor	Light Green
X_{16}	H-88/-78-2	Regular	dense	Round	Angular	Poor	Light Green
X_{17}	Palam Pink	Hirusetum	dense	Round	Angular	Dense	Dark Green
X_{18}	Selection-7	Hirusetum	Medium	Oval	Round	Poor	Dark Green
X_{19}	Arka Alok	Angular	Medium	Round	Round	Dense	Light Green
X_{20}	Utkal Kumari	Angular	dense	Slightly flattened	Angular	Dense	Light Green
X_{21}	Dhanashree	Angular	Medium	Round	Round	Dense	Light Green
X_{22}	DT-10	Paruvianum	dense	Round	Angular	Moderate	Dark Green
X_{23}	DVRT-2	Small/Narrow	Medium	cylindrical	Angular	Poor	Light Green
X_{24}	Vaibhav	Hirusetum	Medium	Heart shaped	Round	Dense	Light Green
X_{25}	Grape Crimson	Hirusetum	dense	Round	Angular	Poor	Dark Green
X_{26}	Madan Tamato	Regular	dense	Flat round	Angular	Dense	Light Green
X_{27}	F1-Bhasker	Hirusetum	dense	Flat round	Round	Dense	Light Green
X_{28}	Santury	Hirusetum	dense	Round	Angular	Dense	Light Green
X_{29}	Ujvork Udham	Hirusetum	dense	Round	Angular	Dense	Dark Green
X_{30}	MHT-301	Potato leaf	dense	Slightly flattened	Angular	Dense	Light Green
X_{31}	Mahalaxmi	Potato leaf	dense	Round	Round	Dense	Dark Green
X_{32}	MHT-256	Hirusetum	dense	Round	Angular	Dense	Light Green
X_{33}	T-99	Small/Narrow	Low	Flat round	Angular	Poor	Light Green
X_{34}	MST-256	Small/Narrow	dense	Flat round	Round	Dense	Light Green
X_{35}	Bhagya	Hirusetum	dense	Round	Round	Dense	Dark Green
X_{36}	H- 86	Hirusetum	dense	Round	Round	Dense	Light Green
X_{37}	VS - 44	Regular	dense	Slightly flattened	Angular	Poor	Light Green
X_{38}	VS - 312	Hirusetum	dense	Round	Round	Poor	Light Green
X_{39}	VS - 404	Angular	dense	cylindrical	Round	Dense	Dark Green

fruit setting (64.17), days to 100% fruit setting(79.27) and number of locules fruits^{-1}(4.0) and cluster IV show high mean values for only fruiting clusters plant^{-1} (42.10). On the basis of breeding objective, the potential lines to be selected from different clusters as parents in a hybridization program may be based on genetic distance. In accordance to the findings, Hazra *et al.* (2010) reported that the clustering pattern could be utilized in selecting parents for cross combinations likely to generate the highest possible variability for various important traits. Diversity of qualitative traits in 39 tomato genotypes is presented in (Table 7).

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