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Genetic Diversity in Tomato (*Solanum lycopersicum* L.) based on Quantitative Traits

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ABSTRACT

Present investigation was conducted at Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi, Uttar Pradesh state, India during 2014–15 to assess the genetic diversity among 66 accessions of tomato maintained at Institute of Agricultural Sciences, Banaras Hindu University. The techniques of principal component analysis and D^2 analysis were used for genetic diversity assessment. The analysis revealed significance of four principal components representing 70.12% of the total variability. Some of the important yield traits like average fruit weight, fruit yield plant^{-1} and number of locules fruit^{-1} were the most important traits in PC1 indicating that selection for diversity must be based on these traits. The correlation plot depicted that the traits plant height, number of fruits cluster^{-1} and number of fruits plant^{-1} were closely related to each other. Based on the scores of 1st and 2nd principal component, the genotypes were distributed in biplot. Most of the genotypes were congregated near the centre and revealed narrow genetic diversity existing among the germplasm accessions. The coordinates of the genotype EC 538380 indicated it as the most unique. The entries EC 538155, Pant T3, EC 521069, EC 538434 and EC 168283 were standing separate from the majority of entries. Cluster analysis also indicated congregation of most of the genotypes in one group. Overall, the study indicated limited genetic diversity in the test material.

KEYWORDS: Cluster, diversity, tomato, principal component analysis

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1. INTRODUCTION

Tomato (*Solanum lycopersicum* L.), a member of solanaceae family is the most important vegetable crops in terms of area, production, industrial values and contribution to human nutrition (Fentik, 2017). It offers nutritive benefits to the consumers, provides economic viability to farmers, and high profitability to the food industries. It supplies an excellent raw material for processing industries. Its peculiar sensorial properties capable of instant gratification of taste-buds, unique biochemical composition offering enormous health benefits on long term and extremely appealing colour in its products has made it immensely popular within a very short span of its domestication somewhere in 16th century (Guillaume and Causse, 2012). Very shortly after its domestication, it gained second position among vegetables and seventh in the list of important crop species worldwide (Kulus, 2018) on account of its amenability to grow under a range of diverse climatic zones and under different day-length regimes. Technological advances and development of modern varieties have led to efficient cultivation (Mata-Nicolas, 2020)

Tomato accounts for nearly 16% of world vegetable production (Anonymous, 2021a). India is the 2nd largest producer of tomato in terms of both area and production. In India, its cultivation has expanded unprecedentedly from an area of 0.29 million ha in the year 1991–92 to nearly 0.80 million ha in the year 2017–18 (Anonymous, 2018). It is a potential foreign exchange earner and during the year 2019–20, nearly 0.94 million metric tonnes of tomato worth 223 crore rupees were exported from India (Anonymous, 2021b, 2021).

Yield enhancement in tomato under Indian context is the prime objective as national yield levels are abysmally low (24.4 mt ha^{-1}), far below the world average of 37.1 mt ha^{-1} (Anonymous, 2018). This necessitates identification of superior lines from germplasm collections or development of efficient genotypes through hybridization of diverse lines in order to attain high degree of heterosis. Genetic diversity assessment becomes more important in tomato considering the initial narrow genetic diversity caused by domestication bottleneck which took place nearly 400 years ago in Europe (Bhattarai et al., 2016) followed by lopsided breeding of tomato extensively utilizing limited germplasm accessions particularly in Indian context by private industries (Patil et al., 2010).

Conventionally, genetic diversity is assessed using quantitative traits utilizing different multivariate techniques like D^2 analysis (Mahalanobis, 1936) and Principal Component Analysis (PCA). PCA has the advantage of reducing the dimensionality of a multivariate dataset while retaining as much information (Silva et al., 2009) and eliminating redundancy in data sets (Adams, 1977) by transforming a number of correlated variables into a smaller number of uncorrelated variables called principal components.

Genetic diversity assessment is pivotal to germplasm maintenance and its utilization. The significance of phenotypic data in genetic diversity assessment has been highlighted by Marefatzadeh-Khame et al. (2021). Assessment of genetic diversity is also important for broadening the breeding pools, utilization of heterosis and selection of parental lines (Yousef et al., 2018). Genetic diversity becomes important in present-day context of sustainable yield in changing climatic scenario (Ebert, 2020; Renna et al., 2019). Several reports are available deciphering degree of genetic divergence in tomato germplasm collections (Bhattarai et al., 2018). It is desirable to assess the genetic diversity in new collections containing more number of genotypes representing diverse eco-geographical collections. Furthermore, it is essential to confirm the previous results using new accessions and at other locations. In this context, present investigation aimed at assessing genetic diversity among 66 accessions of tomato germplasm maintained at Institute of Agricultural Sciences, Banaras Hindu University.

2. MATERIALS AND METHODS

2.1. Experimental site and environment

Present investigation was conducted at Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi during 2014–15. The experimental site represented eastern part of Uttar Pradesh and is located in the middle Ganges valley at 25°19'59"N latitude, 83°00'00"E longitude and at elevation of nearly 77 m above mean sea level. The location has characteristic humid subtropical climate with large variations between summer and winter temperatures. Average annual rainfall is 1110 mm.

2.2. Experimental material and experimentation

The experimental material comprised of 66 germplasm accessions collected from different parts of world, and being maintained at Institute of Agricultural sciences, BHU, Varanasi. The germplasm accessions included released varieties, improved genotypes, Indian landraces and exotic lines. The nursery was raised in mid of August-2014. Proper care was taken to ensure raising of healthy seedlings. The 25-day-old seedlings were transplanted in the main field. The experiment was laid out in Randomized Complete Block design with three replications. An inter-row and inter-plant spacing of 60 and 40 cm was maintained. All the recommended package of practices was followed.

2.3. Data collection and analysis

Data were recorded from five randomly selected plants for nine yield traits viz., days to 50% flowering, plant height,

number of primary branches plant^{-1}, number of fruits cluster^{-1}, number of fruits plant^{-1}, average fruit weight, number of locules fruit^{-1}, number of seeds fruit^{-1} and fruit yield plant^{-1}. Principal Component Analysis (PCA) was performed using XLSTAT (Free version). Cluster analysis was performed using D^2 statistics which employed Euclidean distance by Ward's method for grouping of genotypes into different clusters.

3. RESULTS AND DISCUSSION

3.1. Principal component analysis (PCA)

Prior to PCA, data were tested for normality and the data not following normal trend (number of fruits cluster^{-1}, number of fruits plant^{-1} and number of seeds fruit^{-1}) were transformed as per Box & Cox (1964). The mean performances of all the genotypes are listed in Table 1.

Table 1: Mean performances of tomato germplasm lines

Sl. No.	Entry	DF (50%)	PH (cm)	NPB/ Pl	Fr/Cl	No. Fr/Pl	AFW (g)	No. Seeds/ Fr	No. Loc/ Fr	FY/Pl (Kg)
1.	EC 620578	55.0	93.9	3.6	3.8 (1.22)	34.9 (0.771)	39.7	76.7 (2.92)	2.40	1.38
2.	EC 521087	45.3	105.0	4.2	4.5 (1.38)	63.4 (0.776)	36.0	62.3 (2.84)	3.13	2.28
3.	EC 520061	39.0	69.3	4.8	4.2 (1.30)	29.7 (0.769)	35.0	84.7 (2.96)	2.67	1.04
4.	EC 20510	44.0	75.1	3.0	3.6 (1.17)	37.7 (0.772)	38.7	51.7 (2.75)	2.00	1.45
5.	EC 620541	42.3	59.0	6.6	3.4 (1.13)	36.0 (0.772)	53.0	59.7 (2.81)	3.57	1.91
6.	EC 531803	46.3	96.3	5.4	3.9 (1.25)	32.3 (0.771)	43.7	66.3 (2.86)	3.07	1.41
7.	Nandi	40.3	78.3	5.8	6.1 (1.61)	37.0 (0.772)	49.0	52.3 (2.75)	3.83	1.86
8.	EC 528374	47.3	92.3	4.4	4.5 (1.38)	57.0 (0.775)	31.7	50.3 (2.73)	3.13	1.82
9.	EC 538156	43.3	60.0	3.9	4.1 (1.28)	49.7 (0.774)	27.0	68.7 (2.88)	2.77	1.34
10.	EC 620530	46.0	53.0	4.6	2.9 (1.00)	37.8 (0.772)	58.3	72.3 (2.90)	3.87	2.21
11.	Kashi Sharad	36.7	105.0	3.8	2.6 (0.91)	28.3 (0.769)	72.0	62.3 (2.83)	3.00	2.04
12.	EC 620536	55.0	83.0	5.3	4.0 (1.26)	46.0 (0.774)	55.7	93.3 (3.01)	3.00	2.56
13.	EC 538411	38.3	87.0	5.1	3.8 (1.22)	27.0 (0.768)	51.3	103.3 (3.04)	3.00	1.37
14.	EC 620538	41.7	69.7	4.9	3.9 (1.24)	23.5 (0.766)	41.5	117.7 (3.10)	2.50	0.98
15.	EC 605694	42.3	81.7	3.8	4.1 (1.29)	27.3 (0.768)	30.6	52.7 (2.76)	2.20	0.84
16.	CLN 2116	42.7	75.0	5.1	3.2 (1.07)	28.7 (0.769)	31.3	105.3 (3.06)	3.63	0.90
17.	EC 538434	46.3	70.8	5.3	4.1 (1.28)	42.5 (0.773	62.5	204.7 (3.31)	5.00	2.62
18.	EC 538380	35.3	103.3	6.7	6.7 (1.69)	116 (0.778)	1.2	32.0 (2.51)	2.00	0.14
19.	EC 620419	39.0	70.3	4.4	6.4 (1.66)	29.0 (0.769)	47.3	77.3 (2.93)	1.83	1.37
20.	EC 168283	40.0	71.0	5.9	6.3 (1.64)	47.0 (0.774)	29.3	78.3 (2.93)	2.33	1.37
21.	EC 538155	55.7	57.7	2.0	4.2 (1.31)	25.0 (0.767)	32.7	61.3 (2.82)	2.87	0.82
22.	EC 521069	42.0	73.3	4.1	6.7 (1.69)	47.3 (0.774)	20.3	94.0 (3.01)	2.00	0.96
23.	EC 620438	43.3	82.0	3.8	4.4 (1.35)	30.0 (0.769	68.0	86.7 (2.97)	2.00	2.04
24.	BS 24-2	41.3	98.2	5.7	4.5 (1.37)	40.0 (0.773)	40.2	90.0 (2.99)	3.50	1.61
25.	EC 538440	46.0	83.7	3.7	5.3 (1.51)	29.3 (0.769)	30.2	70.3 (2.88)	2.83	0.89
26.	PS 1	42.0	67.0	4.7	4.2 (1.31)	32.8 (0.771)	43.7	96.7 (3.02)	2.87	1.44
27.	BS 31-3	35.7	66.3	4.6	4.5 (1.37)	52.5 (0.775)	50.7	48.7 (2.72)	5.60	2.58
28.	BS 18-7	49.0	87.0	3.3	4.8 (1.42)	31.3 (0.770)	35.3	75.7 (2.92)	3.67	1.10
29.	Columbia	44.0	76.2	5.4	4.7 (1.40)	33.3 (0.771)	38.0	84.0 (2.96)	3.67	1.27
30.	BS 2-5	43.3	74.9	3.3	3.1 (1.05)	32.7 (0.771)	38.3	47.7 (2.71)	3.93	1.25
31.	Pant-T-3	46.3	46.2	3.7	3.1 (1.06)	31.7 (0.770	55.0	41.7 (2.64)	4.30	1.75
32.	H 24	50.7	68.1	3.8	3.7 (1.20)	32.5 (0.771)	43.3	56.7 (2.79)	3.73	1.41

Table 1: Continue...

Sl. No.	Entry	DF (50%)	PH (cm)	NPB/ Pl	Fr/Cl	No. Fr/Pl	AFW (g)	No. Seeds/ Fr	No. Loc/ Fr	FY/Pl (Kg)
33.	H 86	44.0	81.7	5.3	3.7 (1.20)	35.0 (0.772)	70.7	66.3 (2.86)	3.80	2.47
34.	EC 538423	47.7	68.7	3.5	5.5 (1.52)	38.0 (0.771)	46.7	75.7 (2.91)	2.33	1.77
35.	Punjab Upma	54.0	56.5	5.2	3.9 (1.26)	35.0 (0.771)	44.3	55.0 (2.77)	2.57	1.55
36.	Kajela	45.3	66.6	5.0	3.3 (1.11)	34.3 (0.772)	38.7	55.3 (2.78)	2.83	1.26
37.	DT 2	43.3	68.2	5.4	4.4 (1. 35)	35.7 (0.769)	44.3	139.0 (3.16)	3.27	1.58
38.	DVRT 1-2	43.7	62.6	4.8	4.3 (1.33)	28.3 (0.770)	37.7	51.7 (2.75)	3.50	1.07
39.	DT 10	44.3	72.1	4.3	3.7 (1.20)	31.0 (0.773)	42.0	83.7 (2.96)	3.77	1.30
40.	HT 4	46.3	78.0	4.9	5.4 (1.52)	42.7 (0.771)	38.0	65.7 (2.85)	2.93	1.75
41.	TLC 1	36.7	66.3	4.7	2.5 (0.86)	33.3 (0.774)	30.0	71.7 (2.90)	3.53	1.00
42.	T- Local	54.0	60.3	4.0	3.9 (1.25)	45.0 (0.771)	33.0	120.0 (3.10)	4.03	1.49
43.	Selection7	46.0	78.4	5.3	4.0 (1.27)	32.3 (0.774)	73.0	93.7 (3.01)	4.83	2.36
44.	NDT 3	44.7	64.4	5.0	3.2 (1.07)	45.3 (0.771)	39.3	52.7 (2.76)	3.17	1.78
45.	NDTVR60	47.7	83.9	4.5	4.5 (1.37)	34.7 (0.771)	37.7	65.0 (2.85)	2.50	1.31
46.	VR 20	42.3	92.8	4.0	5.2 (1.49)	35.3 (0.769)	39.7	79.3 (2.94)	2.00	1.40
47.	Angurlata	44.0	85.0	3.9	5.1 (1.47)	28.3 (0.769)	47.7	59.0 (2.81)	3.13	1.35
48.	Azad T-5	46.7	71.3	4.3	4.6 (1.39)	32.0 (0.770)	68.3	97.7 (3.03)	3.00	1.94
49.	Flawery	43.7	70.3	5.2	4.6 (1.39)	43.7 (0.773)	49.0	122.7 (3.12)	2.93	2.08
50.	Superbug	45.0	73.4	3.3	3.4 (1.12)	30.3 (0.770)	32.7	63.7 (2.84)	2.10	0.99
51.	GT	37.7	63.7	5.4	4.2 (1.31)	28.0 (0.769)	44.7	56.3 (2.78)	3.47	1.22
52.	FLA 7171	52.0	76.0	4.8	3.3 (1.11)	32.7 (0.771)	61.7	106.7 (3.06)	4.50	1.85
53.	CO 3	43.7	79.3	4.6	3.3 (1.10)	24.0 (0.766)	64.3	66.0 (2.86)	3.80	1.54
54.	Arka Vikas	46.7	76.7	4.7	4.3 (1.33)	27.3 (0.768)	56.3	113.7 (3.09)	2.87	1.54
55.	Kashi Amrit	46.0	100.3	4.9	6.1 (1.61)	42.3 (0.773)	35.7	87.3 (2.98)	3.87	1.51
56.	NDT 8	50.0	61.0	5.6	5.6 (1.54)	32.7 (0.771)	52.7	64.0 (2.85)	2.97	1.74
57.	PM 1	44.7	65.0	4.1	3.8 (1.22)	32.7 (0.771)	48.0	51.3 (2.74)	3.97	1.55
58.	H 88-78-1	39.3	78.3	4.7	4.1 (1.29)	37.7 (0.772)	41.3	103.3 (3.05)	3.67	1.55
59.	Swarna Naveen	45.3	71.5	3.5	4.3 (1.32)	24.3 (0.767)	34.7	76.0 (2.92)	3.40	0.85
60.	Floradel	47.3	73.0	4.7	3.7 (1.21)	53.6 (0.775)	58.7	77.0 (2.92)	3.97	3.15
61.	Feb-04	52.7	71.8	5.6	4.1 (1.29)	25.0 (0.767)	32.3	67.0 (2.87)	3.53	0.81
62.	Kashi Anupam	41.7	64.3	4.3	4.1 (1.29)	49.3 (0.774)	24.7	37.7 (2.59)	2.50	1.23
63.	Pusa Sadabahar	49.7	52.6	2.3	4.0 (1.28)	42.7 (0.773)	30.7	67.3 (2.86)	2.67	1.27
64.	Shalimar 2	39.0	72.7	3.5	3.6 (1.18)	33.7 (0.771)	33.7	67.3 (2.86)	2.80	1.12
65.	BT 120	49.0	84.0	4.7	4.1 (1.28)	26.0 (0.768)	49.1	86.7 (2.98)	3.67	1.25
66.	NDTVR73	46.0	87.3	3.6	4.3 (1.33)	32.0 (0.77)	30.3	65.0 (2.85)	3.83	0.94
					λ= -0.125	λ=-1.283		λ=-0.196		

The values in parenthesis are Box-Cox transformed value; DF (50%): Days to 50% flowering; PH: Plant height; NPB/ Pl: Number of primary branches plant^{-1}; No. Fr/Cl: Number of fruits cluster^{-1}; No. Fr/Pl: Number of fruits plant^{-1}; AFW: Average Fruit Weight; No. Loc./Fr: Number of locules fruit^{-1}; No. seeds/Fr: Number of seeds fruit^{-1}; FY/Pl: Fruit yield plant^{-1}

In PCA, eigen values are of prime importance, as they determine how many PCs to be retained for further analysis and interpretation. As a convention, those PCs with eigen value more than 1.0 are retained and considered significant PCs. These PCs have higher contribution towards genetic diversity and the traits associated with these components have larger impact on genetic diversity pattern. The PCA revealed cumulative variability of 70.12% (Table 2, Figure 1) by the first four significant axes. The eigen value of first principal component equaled 2.46 and represented 27.29% of total variability. The 2nd principal component had eigen value of 1.57 and represented 17.43% of total variability. Similarly, third and fourth principal component had eigen value of 1.22 and 1.07, respectively and represented 13.50 % and 11.91% of total variability respectively.

Table 2: Eigen values and PC scores for different traits

Principal components	PC1	PC2	PC3	PC4
Eigen value	2.46	1.57	1.22	1.07
Variability (%)	27.29	17.43	13.50	11.91
Cumulative %	27.29	44.71	58.21	70.12
PC scores				
Days to 50% flowering	0.14	-0.35	-0.08	0.75
Plant height (cm)	-0.12	0.39	-0.41	-0.07
No. of primary branches plant^{-1}	0.10	0.62	0.13	-0.11
No. of fruits cluster^{-1}	-0.29	0.38	-0.31	0.36
No. of fruits plant^{-1}	-0.15	0.36	0.54	0.47
Average fruit weight	0.56	0.04	-0.15	-0.10
No. of seeds fruit^{-1}	0.28	0.10	-0.53	0.20
No. of locules fruit^{-1}	0.43	0.08	0.34	-0.03
Fruit yield plant^{-1}	0.52	0.22	0.05	0.16

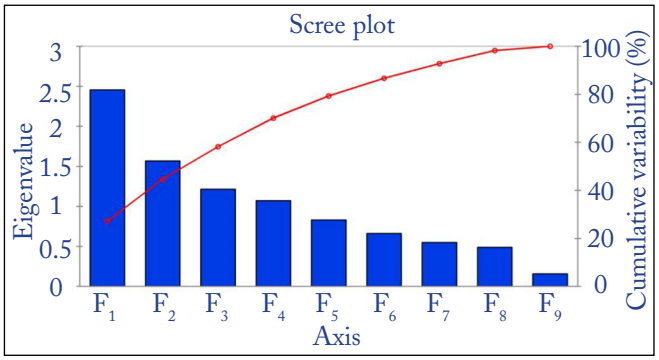

Figure 1: Scree plot depicting eigen values for different PCs

Present study is in agreement with the reports of Bhattarai et al. (2016) who reported nearly 71% contribution towards total variability by first three PCs. Henareh et al. (2015) found significance of 1st three PCs revealing 71.6% of total variability. Other studies reported more number of PCs with eigen value >1.0 and contributing 73.86% of total variability (Mukul et al., 2022; Ziaf et al., 2016). The study by Chernet et al. (2014b) revealed exceedingly higher eigen values and six PCs with eigen value more than 1.0. This may be on account of more number of traits (24) for germplasm characterization.

Principal component analysis assumes important role in choosing traits for breeding efficient genotypes. The characters with largest value (≈1.0) in the first principal component have significant impact on variability of genotypes (Chahal and Gosal, 2002). Hence, the traits having higher values in PC1 were identified. The PC scores revealed that average fruit weight contributed maximum to the variation followed by fruit yield plant^{-1} and number of locules fruit^{-1} for PC1. Three traits *viz.*, plant height, number of fruits cluster^{-1} and number of fruits plant^{-1} contributed negatively to variability. This is in coherence to the reports of Chernet et al. (2014b) who reported many yield traits associated with PC1. Other studies (Cebolla-Cornejo et al., 2013) also reported fruit size associated with first principal component. In contrast, Bhattarai et al. (2016) reported linkage of PC1 with other traits like leaf type and days to maturity as the major traits determining the clustering pattern. Sinha et al. (2021) indicated contribution of different traits in total variability in different principal components. The difference in pattern may be attributed to the constitution of germplasm collection.

The correlation plot (Figure 2) depicted that the traits plant height, number of fruits cluster^{-1} and number of fruits plant^{-1} were closely correlated to each other. Days to 50% flowering was negatively correlated to number of primary branches plant^{-1}. The correlation between the traits namely number of seeds fruit^{-1}, number of locules fruit^{-1} and average fruit weight may not be sufficiently explained based on only two axes being close to centre.

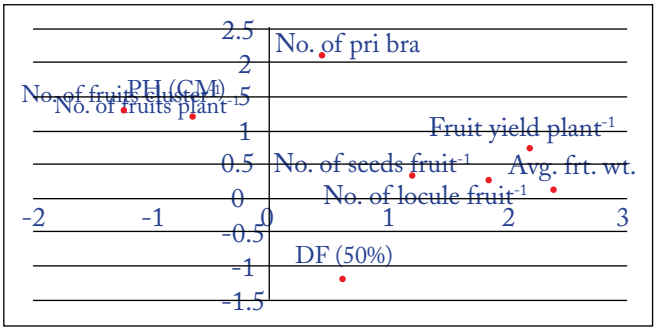

Figure 2: Correlation plot depicting correlation between different traits

Based on above criteria of PC1 and PC2, dispersion of genotypes was plotted in biplot (Figure 3). The co-ordinates of the genotype revealed that the accession EC 538380 was

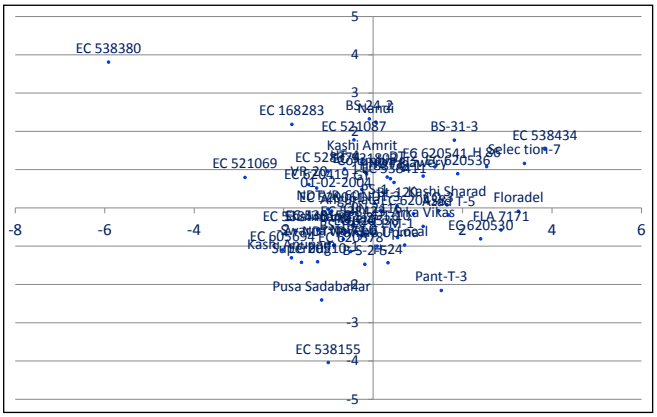

Figure 3: Dispersion of genotypes in Bi-plot

the most unique and had high negative values for traits associated with PC1 and high positive values for PC2. As the PC1 was associated with fruit weight, number of locules fruit^{-1} and fruit yield plant^{-1}, the genotype EC 538380 represented lower values for these traits. This genotype recorded high number of primary branches plant^{-1} and high number of fruits cluster^{-1} as high correlation of these traits with PC2. The co-ordinates of the genotype EC 538155 represented that the genotype had lesser number of primary branches plant^{-1} and lesser number of fruits cluster^{-1}. The genotype Pant T3 also had lesser number of primary branches plant^{-1} and lesser number of fruits cluster^{-1}. The genotype EC 538434, Selection 7, BS 31-3, H 86 *etc.* had positive values for both set of traits. Majority of the genotypes were congregated near the centre.

3.2. Cluster analysis

D^2 statistics is the most preferable tool for developing dendrogram based on intra- and inter-cluster distances among genotypes. It is regarded as a reliable strategy for categorization and choice of parents for breeding purposes (Feng-Mei et al., 2006). The significance of χ^2 test applied to 'V' statistic indicated considerable difference between the means of nine traits under study. Hence, further analysis was carried out for estimating D^2 values to study genetic divergence. Distribution of genotypes into different clusters by Ward's method in tomato is presented in Figure 4.

All the 66 tomato accessions were grouped into five different clusters based on the inter-genetic distances. Cluster-I constituted maximum number of genotypes (55) followed by cluster-II consisting of eight genotypes. Three clusters (Cluster-III, IV and V) had only one genotype. Most of the genotypes were clustered together revealing genetic.

relatedness revealing narrow genetic diversity in the germplasm collection. Three clusters were solitary with only one genotype in each group. The issue of narrow genetic base in tomato has been raised in earlier studies involving Indian tomato genotypes (Patil et al., 2010). Though the

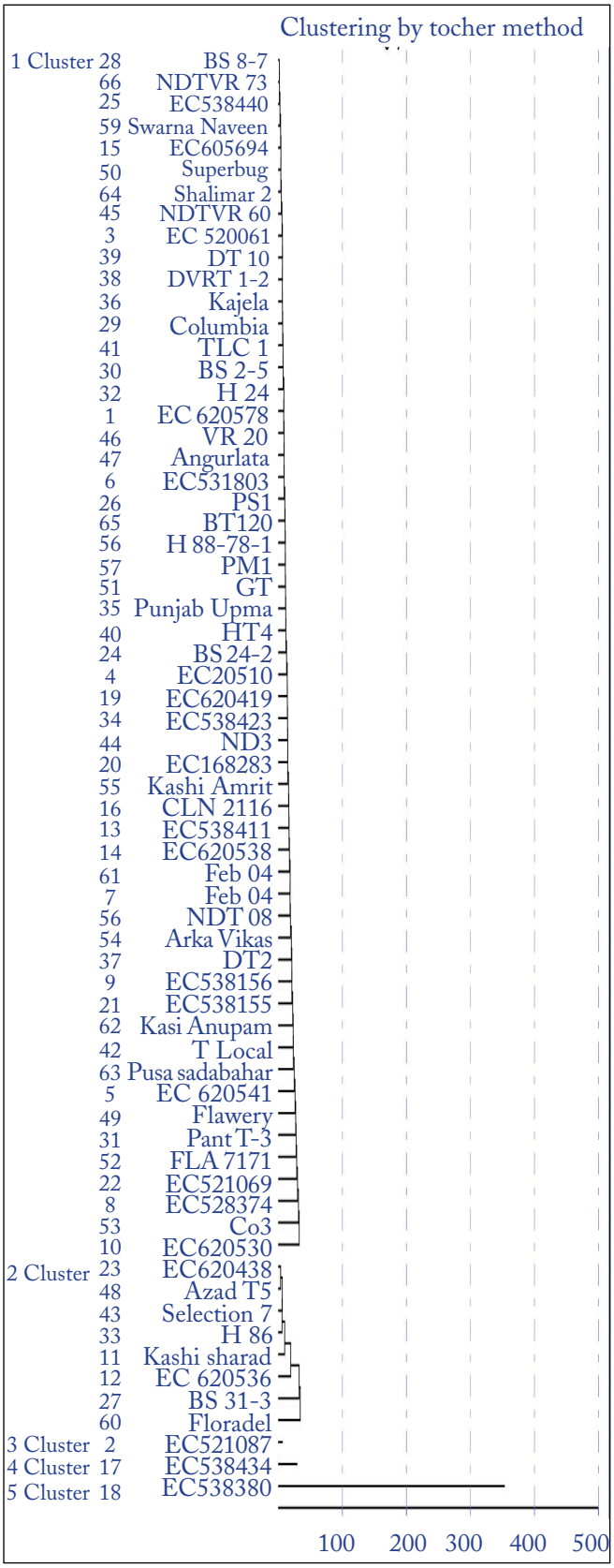

Figure 4: Dendrogram depicting clustering of genotypes based on D^2 analysis

tested genotypes in the present study represented exotic lines and different locations of India, the cluster analysis revealed only limited variability. Thus, the study refutes the general thinking of geographical diversity corroborating genetic diversity. Accordingly, limited genetic progress may be realized with existing accessions. The results emphasize the need of broadening of genetic base in the germplasm collection in order to attain genetic improvement. The accession EC 538380 was shown to be the most distinct entry by both PCA and D^2 analysis. The entry EC 538380 is characterized by more number of primary branches, more number of fruits cluster^{-1} and more number of fruits plant^{-1}. However, this entry suffers from the limitation of extremely small fruit. Hence, this genotype may be used in back crosses to enhance the number of primary branches and fruits though there are chances of linkage drag of smaller fruits. Clustering pattern of genotypes into different clusters has been reported earlier (Chernet et al., 2014a; Ullah et al., 2015). Clusters with single entry were observed in present study. These genotypes are of particular importance due to various unique characters possessed by them (Ullah et al., 2015).) Differential clustering pattern obtained in different studies may be suggestive of inherent variability in the germplasm pool under investigation, environmental influences on the expression of different traits and genotype-environment interaction. Prevoius studies also reported sufficiently high diversity in tomato germplasm (Basavaraj et al., 2010; Evgenidis et al., 2011). In previous studies (Henareh et al., 2015; Herison et al., 2018), five clusters were obtained with 97 genotypes in Iran and 27 genotypes in Indonesia, respectively.

4. CONCLUSION

The PCA indicated that selection for diversity was based on traits like average fruit weight, fruit yield plant^{-1} and number of locules fruit^{-1}. The correlation plot indicated association between plant height, number of primary branches plant^{-1} and number of fruits cluster^{-1}. The entry EC 538380 was the most distinct genotype. Cluster analysis categorized the 66 tomato accessions into five groups with uneven distribution of genotypes. Both PCA and cluster analysis indicated limited genetic diversity among 66 tomato accessions.

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