

**MORPHOLOGICAL BASED GENETIC VARIABILITY ANALYSIS AND CLUSTERING OF TOMATO**Aina Yadav<sup>\*1</sup>, Neeraj Tandan<sup>1</sup> and Rajvir Singh<sup>2</sup><sup>1</sup>Department of Biotechnology, Shri Venkateshwara University, Gajraula (U.P.), India.<sup>2</sup>Department of Botany, K.K. Degree College, Etawah (U.P.), India.**\*Corresponding Author: Aina Yadav**

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**ABSTRACT**

19 tomato genotypes were used in this study and observations were taken for two seasons. Genetic parameters like range, mean, standard error, variance and standard deviation were calculated among 8 quantitative traits of tomato. Among 19 tomato genotypes plant height, days to 50% flowering, number of primary branches/plant, number of fruits/plant, number of locules/fruit, fruit length, fruit diameter and fruit weight ranged from 98.3-143.3 cm, 50.1-62.9 days, 5.9-13.6, 28.3-317.6, 3.3-7.1, 2.2-6.3 cm, 2.6-5.3 cm and 31.6-115.0 gm, respectively. Maximum variability was found in number of fruits/plant. Genetic dissimilarity coefficients for 19 tomato genotypes based on quantitative traits ranged from 0.019-0.994. Maximum dissimilarity coefficient value occurred between DVRT-2 vs PB-UPMA was 99.4% and minimum dissimilarity coefficient value occurred between EC-538158 vs EC-538423 was 1.9%. Clustering classified the 19 tomato genotypes into 5 distinct clusters *i.e.* cluster A, B, C, D and E. Therefore, these traits could be considered and exploited for selection purpose. This study was concluded that there is a wide genetic variability in the genotypes and the genotypes could be utilized for genetic improvement of tomato.

**KEYWORDS:** 19 tomato genotypes, study and observations.**INTRODUCTION**

Tomato (*Solanum lycopersicum* Mill.) is one of the most important vegetable crops around the world either outdoors or indoors and an excellent source of lycopene belongs to Solanaceae family also called Nightshades which includes more than three thousand species. In India, it ranks second among vegetables next to potato in terms of area and production. Tomato universally treated as 'Protective Food', is being extensively grown as annual plant. It is a rich source in minerals, vitamins and organic acids. Morphological, agronomic, as well as biochemical parameters have been widely used in the evaluation of tomato cultivars for genetic diversity, breeding value and yield potential (Dharmatti *et al.*, 2001; Mohanty and Pusti, 2001; Susic *et al.*, 2002; Parthasarathy *et al.*, 2002). The characterization will help in the identification of varieties and their future utilization for varietal improvement using conventional techniques of selection and hybridization. Collection, characterization and evaluation of crop germplasm are key steps towards selection of new varieties for direct production or for use in hybridization programmes (Osei *et al.*, 2009; Osei *et al.*, 2010; Osei *et al.*, 2014).

Knowledge of interrelationship between yield and its components is obvious for efficient selection of desirable plant type. Plant breeders are continuously endeavoring to improve the genetic potential of yield and quality traits of tomato crop so as to meet the demands of an ever-increasing population of the world. The approaches to make significant improvement in tomato production require information regarding nature and magnitude of genetic variation in quantitative traits and their interrelationships in the available germplasm, which are important pre-requisites for a systematic breeding program (Firas *et al.*, 2012). Researchers have emphasized on evaluation of genetic components such as coefficient of variation, heritability and expected genetic progress in the prediction of response quantitative characters to selection (Mohanty, 2002; Mohanty, 2003; Saeed *et al.*, 2007; Dar and Sharma, 2011; Mohamed *et al.*, 2012). The information obtained through clustering will support tomato breeders in identifying a limited number of extremely differentiated genotypes to be selected for further use in developing suitable variety/hybrids. The objective of this study was to evaluate the genetic variability and relationships of tomato based on morphological traits to improve tomato production.

**MATERIALS AND METHOD**

Seeds of 19 tomato genotypes were obtained from Department of Horticulture, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (UP) (Table-1). The genetic material was grown in pot for germination and growth at Scientific and Applied Research Centre, Meerut with standard agronomical practices and observations were taken for two seasons *viz.*, 2012-13 and 2013-14.

Morphological data of ten plants for each genotypes were recorded for the different traits as follow:

- 1. Plant height (cm):** Plant height was measured in centimeters from the ground level to the tip of the plant on 70th day after transplanting.
- 2. Days to 50% flowering:** The number of days taken from date of transplanting to the date at which 50% of the total number of plants flowered in each treatment.
- 3. Number of primary branches:** Number of branches per plant was counted at the time of harvest.
- 4. Number of fruits/plant:** Total number of fruits harvested from all the pickings was pooled and average number of fruits per plant was calculated.
- 5. Number of locules/fruit:** Fruits was cut crosswise and numbers of locules were counted.
- 6. Fruit length (cm):** Randomly selected ten fruits per plant were used to determine fruit length by vernier calipers and expressed in centimeters.
- 7. Fruit diameter (cm):** Randomly selected ten fruits per plant were used to determine fruit diameter by vernier calipers and expressed in centimeters.
- 8. Fruit weight (gm):** Weight of randomly selected fruit from each genotype was weighed in gram using weighing machine after harvesting.

Two season (2012-13 and 2013-14) pooled quantitative data for plant height (cm), days to 50% flowering, number of primary branches, number of fruits/plant, number of locules/fruit, fruit length (cm), fruit diameter (cm) and fruit weight (gm) were analyzed using simple statistics to calculate the genetic parameters like Range, Mean, Standard error, Variance and Standard deviation for 8 quantitative traits of 19 tomato genotypes using statistical package PAST version 2.03 (Hammer *et al.*, 2001). The pooled data for quantitative traits were used to construct a dendrogram showing the relationships among 19 tomato genotypes using computer software NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System) version 2.2. Finally, the data were subjected to cluster analysis using the NTSYSpc version 2.2 (Rohlf, 2000).

## RESULTS AND DISCUSSION

### Morphological traits and their mean performance

The mean performance and range for 8 quantitative traits of tomato genotypes is presented in Table-2. Plant height of 19 tomato genotypes ranged from 98.3 cm (Anigoor lata) to 143.3 cm (DVRT-1 and PB-UPMA) and the

mean was 128.34 cm. Days to 50% flowering ranged from 50.1 days (Anigoor lata) to 62.9 days (PB-UPMA) and the mean was 55.89 days. Number of primary branches varied from 5.9 (EC-538423) to 13.6 (PB-UPMA) and the mean was 9.01. Number of fruits per plant of 19 tomato genotypes ranged from 28.3 (DVRT-2) to 317.6 (PB-UPMA) and the mean was 148.67. The number of locules per fruit ranged from 3.3 (EC-538155) to 7.1 (FLA-7421) and the mean was 5.63 locules per fruit. Among the 19 tomato genotypes, the minimum and maximum fruit length was recorded in EC-538155 (2.2 cm) and Anigoor lata (6.3 cm), respectively and mean was 4.41 cm. Fruit diameter ranged from 2.6 cm (EC-538405) to 5.3 cm (Anigoor lata) and the mean was 3.48 cm. The highest fruit weight of 115.0 gm was obtained in PDT-3-1-1 and the lowest was 31.6 gm in BT-12. The mean of fruit weight was 58.54 gm. Among 19 tomato genotypes, PB-UPMA showed maximum values for plant height, days to 50% flowering, number of primary branches and number of fruits per plant. Anigoor lata showed minimum values for plant height and days to 50% flowering. Similar results also reported by Kumar *et al.* (2013 & 2014), Sharma *et al.* (2014), Taiana *et al.* (2015).

The range of variability was highest for number of fruits per plant (28.3-317.6), followed by plant height (98.3-143.3), fruit weight (31.6-115), days to 50% flowering (50.1-62.9), number of primary branches (5.9-13.6), number of locules per fruit (3.3-7.1), fruit length (2.2-6.3) and fruit diameter (2.6-5.3). The highest variance recorded for number of fruits per plant (6316.78), followed by fruit weight (759.84), plant height (180.75), days to 50% flowering (17.19), whereas the lowest variance were estimated for fruit diameter (0.65), followed by number of locules per fruit (1.15), fruit length (1.51), number of primary branches (5.09). High variance was observed for most of the traits indicating more contribution of genetic component for the total variation. Variance revealed the presence of considerable amount of genetic variability for yield and its components studied in all the environments. Therefore, these traits (Table-2) could be considered and exploited for selection purpose. These results were in accordance of the results obtained by Bernousi *et al.* (2011), Manna and Paul (2012), Naik (2012), Patel *et al.* (2013), Agrawal *et al.* (2014), Khapte and jansirani (2014), Prajapati *et al.* (2015).

### Genetic dissimilarity matrix and cluster analysis

The genetic dissimilarity coefficients for the 19 tomato genotypes based on quantitative traits ranged from 0.019 to 0.994 (Table-3). The highest dissimilarity coefficient value occurred between DVRT-2 vs PB-UPMA was 99.4% and the lowest dissimilarity coefficient value occurred between EC-538158 vs EC-538423 was 1.9%. A dendrogram was constructed by clustering of 19 genotypes of tomato are shown in Figure-1. The resulting dendrogram classified the 19 tomato genotypes into 5 distinct clusters i.e. cluster A, B, C, D and E comprising

of 5, 3, 3, 2 and 2 tomato genotypes, respectively (Table.4).

Cluster A grouped into two subclusters *viz*; A-1 and A-2. Subcluster A-1 consisted of only 2 genotypes namely PB Chhuhara and EC-538450, which showed the dissimilarity coefficient value of 0.046. Subcluster A-2 consisted of 3 genotypes namely EC-538158, EC-538423 and EC-538405. In Subcluster A-2, the maximum dissimilarity coefficient occurred between EC-538158 vs EC-538405 with a value of 0.041 and the minimum dissimilarity coefficient occurred between EC-538158 vs EC-538423 with a value of 0.019. In the clustering, out of 19 tomato genotypes; only one genotypes (DVRT-2) was isolated at the top of clustering and three genotypes were isolated at the end of cluster A (Anigoor lata, EC-538155 and PDT-3-1-1). Cluster B consisted of 3 genotypes namely PB Keshri, IIHR-1 and DVRT-1. In this cluster, the maximum dissimilarity coefficient occurred between PB Keshri vs DVRT-1 with a value of 0.069 and the minimum dissimilarity coefficient occurred between PB Keshri vs IIHR-1 with a value of 0.055. Cluster C

consisted of 3 genotypes namely FED-2, BT-12 and H-86. In this cluster, the maximum dissimilarity coefficient occurred between FED-2 vs H-86 with a value of 0.128 and the minimum dissimilarity coefficient occurred between FED-2 vs BT-12 with a value of 0.023. Cluster D consisted of only two tomato genotypes FLA-7421 and VR-1, which showed the dissimilarity coefficient value of 0.106. Cluster E consisted of only two tomato cultivars/genotypes VRT-2 and PB-UPMA, which showed the dissimilarity coefficient value of 0.177.

Dendrogram was prepared to evaluate similarity/dissimilarity between tomato genotypes and all obtained data showed that the collected genotypes have a huge variation. Similar results have also been reported by Shashikanth *et al.* (2010), Sharma *et al.* (2013), Chernet *et al.* (2014), Henareh *et al.* (2015), Rashid *et al.* (2016). Based on the present investigation it was recommended that crosses are made in breeding programs between PB Chhuhara and DVRT-1. This evaluation could support breeders to choose and identify genotypes with desirable character for addition in tomato breeding programs.

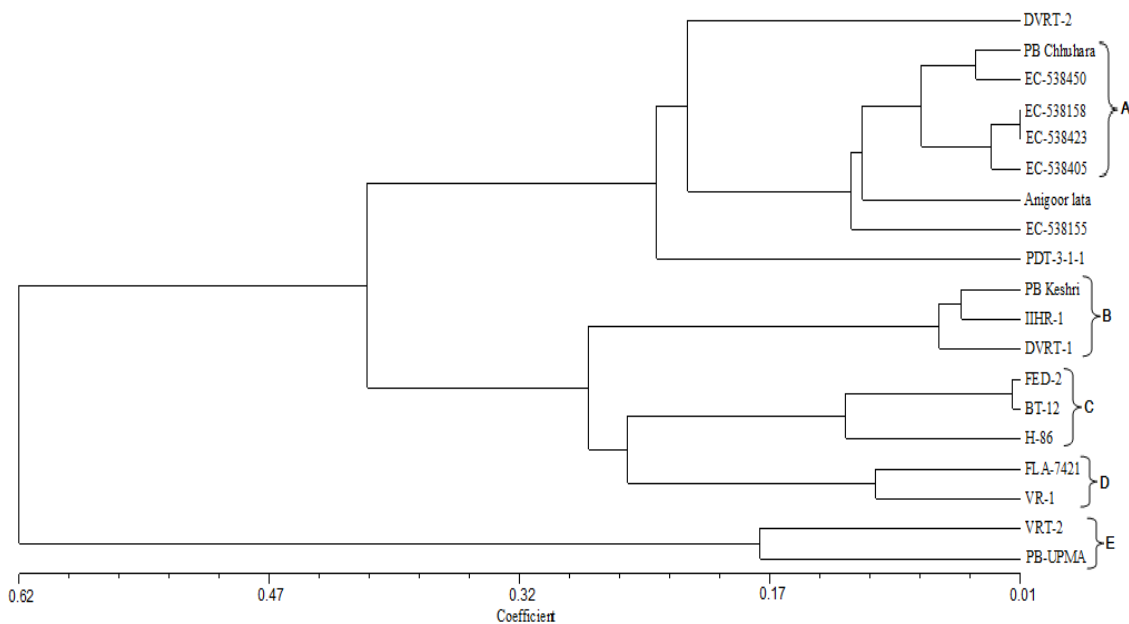


Figure 1: UPGMA based cluster analysis of 19 tomato using morphological traits.

Table 1: List of tomato genotypes.

S. No.	Genotypes	S. No.	Genotypes
1.	DVRT-2	11.	H-86
2.	PB Chhuhara	12.	FLA-7421
3.	EC-538158	13.	EC-538155
4.	Anigoor lata	14.	IIHR-1
5.	PDT-3-1-1	15.	DVRT-1
6.	EC-538450	16.	EC-538423
7.	PB Keshri	17.	VRT-2
8.	FED-2	18.	VR-1
9.	BT-12	19.	PB-UPMA
10.	EC-538405		

**Table 2: Range, mean, standard error, variance and standard deviation for 8 quantitative traits in 19 tomato genotypes.**

Traits	Range		Mean	Std. error	Variance	Stand. dev
	Minimum	Maximum				
Plant height (cm)	98.3	143.3	128.34	3.08	180.75	13.45
Days to 50% flowering	50.1	62.9	55.89	0.95	17.19	4.14
Number of primary branches	5.9	13.6	9.01	0.52	5.09	2.26
Number of fruits/plant	28.3	317.6	148.67	18.23	6316.78	79.47
Number of locules/fruit	3.3	7.1	5.63	0.25	1.15	1.07
Fruit length (cm)	2.2	6.3	4.41	0.28	1.51	1.23
Fruit diameter (cm)	2.6	5.3	3.48	0.18	0.65	0.81
Fruit weight (gm)	31.6	115.0	58.54	6.32	759.84	27.56

**Table 4: Distribution of 19 tomato genotypes into different clusters.**

S. No.	Cluster number	Number of tomato genotypes	Genotypes
1.	A	5	PB Chuhara, EC-538450, EC-538158, EC-538423 and EC-538405
2.	B	3	PB Keshri, IIHR-1 and DVRT-1
3.	C	3	FED-2, BT-12 and H-86
4.	D	2	FLA-7421 and VR-1
5.	E	2	VRT-2 and PB-UPMA

Table 3: Genetic dissimilarity coefficient of 19 Tomato genotypes derived from quantitative traits.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.000																		
2	0.206	0.000																	
3	0.256	0.084	0.000																
4	0.217	0.144	0.105	0.000															
5	0.334	0.246	0.223	0.242	0.000														
6	0.214	0.046	0.072	0.130	0.201	0.000													
7	0.646	0.456	0.411	0.488	0.385	0.434	0.000												
8	0.498	0.295	0.266	0.358	0.401	0.303	0.289	0.000											
9	0.483	0.281	0.251	0.342	0.398	0.291	0.307	0.023	0.000										
10	0.239	0.074	0.041	0.101	0.257	0.083	0.443	0.274	0.257	0.000									
11	0.394	0.193	0.196	0.296	0.337	0.208	0.345	0.128	0.121	0.201	0.000								
12	0.754	0.549	0.524	0.618	0.602	0.552	0.300	0.267	0.288	0.537	0.362	0.000							
13	0.166	0.099	0.134	0.146	0.189	0.074	0.485	0.374	0.363	0.141	0.274	0.618	0.000						
14	0.628	0.433	0.391	0.475	0.389	0.416	0.055	0.245	0.264	0.420	0.306	0.259	0.470	0.000					
15	0.597	0.409	0.371	0.454	0.341	0.387	0.069	0.268	0.285	0.404	0.301	0.311	0.434	0.067	0.000				
16	0.248	0.083	0.019	0.093	0.231	0.074	0.424	0.275	0.259	0.031	0.205	0.534	0.133	0.404	0.385	0.000			
17	0.918	0.713	0.677	0.762	0.762	0.717	0.424	0.420	0.437	0.689	0.534	0.194	0.786	0.396	0.458	0.686	0.000		
18	0.651	0.445	0.426	0.522	0.512	0.451	0.265	0.175	0.196	0.438	0.258	0.106	0.517	0.218	0.258	0.436	0.292	0.000	
19	0.994	0.818	0.789	0.881	0.840	0.818	0.476	0.537	0.557	0.805	0.634	0.273	0.883	0.457	0.509	0.800	0.177	0.376	0.000



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