



Genetic Divergence Studies in Tomato Genotypes Grown under Low-Cost Polyhouse Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Assessment of genetic diversity was made for sixteen yields and yield contributing traits in twenty-one tomato genotypes using D^2 statistics. These genotypes were grouped into five clusters by the use of the Tocher method. Cluster I was the most significant, comprising 13 genotypes (Pusa Ruby, CLN2123A1 Red, PKM-1, IIHR-2042, Marglobe, EC 163605, Hawaii 7998, Palam Pink, EC 521038, Punjab Rakthak, EC 163383, Arka Abha and IIVR BT-10) followed by Cluster II with 5 genotypes (EC 163611, Punjab Sartaj, EC 160885, Punjab Barkha Bahar and Roma). Other Clusters (III, IV and V) were solitary ones (EC 249515, Kashi Chayan, DVRT-2). Cluster II recorded a maximum intra cluster distance of 3521.73 followed by cluster I (2796.45), whereas, cluster III, IV and V had zero intra cluster distance. The inter cluster D^2 value also ranged widely, with a minimum value of 4082.34 between cluster I and IV, indicating a close relationship among the genotypes included. The maximum inter cluster D^2 value (23102.20) between cluster II and V indicates high diversity among the genotypes in the clusters. Hence, maximum contribution towards divergence was observed by average fruit weight (14%) followed by fruit set percentage (12%), number of flowers per cluster (8%), fruit yield

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per plant (7%), number of fruits per truss (6 %) and total soluble solid content (6 %). Hence, due importance could be given to the selection of genotypes for further improvement based on these traits.

Keywords: Genetic diversity; D² analysis; hybridization; lycopene.

1. INTRODUCTION

Tomato is one of the important vegetable crops grown throughout the world because of their wider adaptability, high yielding potential, and suitability for a variety of cuisine in fresh and processed form. An increasing population with shrinkage of land per capita requires the development of high yielding varieties suitable for protected structures in the current era. However, keeping in view the poor economic status and fragmented land holdings of small and marginal farmers, low-cost polyhouse cultivation seems to be the more evident and viable option. Since tomato is the most preferred cash crop suited under polyhouse conditions, the need of the hour is to identify/develop suitable genotypes under low-cost poly house structures. An improvement in yield and quality in self-pollinated crops like tomatoes is normally achieved by selecting genotypes with desirable character combinations existing in nature or by hybridization. The selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme [1]. In general, the more diverse the parents, the more likely it is that the segregating generation will have high heterotic F₁s and a broad spectrum of variability. Genetic divergence is important in assessing diversity and establishing relationships among cultivated species, facilitating the development of conservation strategies, using genetic resources in breeding programmes, and studying crop evolution. Genetic divergence among the genotypes plays an essential role in the selection of parents having wider variability for different yield and yield attributing characters [2]. The plant breeder would benefit from information on nature and the degree of genetic divergence when selecting the right parents for the breeding programme. The current study attempted to assess genetic divergence using D² statistics and various clustering procedures, based on yield and yield attributing characters and to assess the relative contribution of different components to total divergence.

2. MATERIALS AND METHODS

Twenty-one tomato genotypes were raised during Rabi 2018-19 in the Experimental Farm,

Division of Vegetable Science & Floriculture, SKUAST, Jammu. The experiment was laid out in Augmented Randomized Block Design with three checks replicated once in every block. A spacing of 60 × 45 cm was adopted. The recommended packages of practices were followed. Three plants of each genotype were tagged and observations were recorded on sixteen yield and yield attributing characters plant height, number of branches per plant, days to 50 percent flowering, number of flowers per truss, number of fruits/truss, fruit set (%), number of truss/plant, average fruit weight, fruit polar diameter, fruit equatorial diameter, fruit shape index, number of fruits per plant, fruit yield per plant, pericarp thickness, total soluble solid content, and lycopene content. The genetic distance between the genotypes was worked out using Mahalanobis D² analysis and grouping of genotypes into clusters was done following the Tochers method [3].

3. RESULTS AND DISCUSSION

Genetic diversity data is used to identify promising diverse genotypes that could be used in future breeding programmes. Twenty one genotypes were grouped into five divergent clusters based on D² values (Table 1). Cluster I comprised 13 genotypes (Pusa Ruby, CLN2123A1 Red, PKM-1, IHR-2042, Marglobe, EC 163605, Hawaii 7998, Palam Pink, EC 521038, Punjab Rakthak, EC 163383, Arka Abha and IIVR BT-10) followed by Cluster II with five genotypes (EC 163611, Punjab Sartaj, EC 160885, Punjab Barkha Bahar and Roma). Other Clusters (II, IV and V) were solitary ones (EC 249515, Kashi Chayan, DVRT-2 respectively). The composition of clusters of heterogeneous geographic origin indicates that genotypes were distributed randomly among the different clusters regardless of their geographical origin. This demonstrates that there was no correlation between genetic diversity and geographical divergence in the tomato crop. The scattering of the genotypes from the same geographic region into different clusters may be due to genetic heterogeneity (different genes producing identical phenotypes), genetic architecture, and history of selection. Similar

findings were obtained by Gadekar et al. (1992) and Rai et al. [4] in tomatoes.

The intra and inter cluster distances represent an index of genetic diversity among the clusters (Table 2). The cluster II had a maximum intra cluster distance of 3521.73 followed by cluster I (2796.45), whereas cluster II, IV and V had zero intra cluster distance. The inter cluster D^2 value also ranged widely, with a minimum value of 4082.34 between cluster I and IV indicating a close relationship among the genotypes included. The maximum inter cluster D^2 value (23102.20) between cluster II and V indicates high diversity among the genotypes in the clusters. Thus, the genotypes belonging to cluster II and cluster V may be selected in a hybridization program to get good segregant. Similar findings have been observed by Jogi et al., (2008), Meena and Bahadur [5], Dar et al., [6], Kumar et al., [7], Hossain et al., [8] and Spaldon and Kumar [9].

The cluster mean data for various traits in tomato genotypes is presented in Table 3. Cluster I

revealed the maximum mean value for number of branches/plant and lycopene content. Cluster II revealed maximum values for plant height, number of truss/plant and fruit polar diameter. Cluster III had the maximum mean value for number of fruits/truss, fruit set (%), number of fruits/plant and fruit equatorial diameter. Cluster IV recorded maximum mean values for days to 50% flowering and number of flowers/cluster, while cluster V had maximum mean values for average fruit weight, fruit pericarp thickness, total soluble solid content, and fruit yield per vine. Similar findings were observed by Jogi et al. (2008), Meena and Bahadur [5], Dar et al. [6], Kumar et al. [7], Hossain et al. [8] and Spaldon and Kumar [9]. The percent contribution of characters towards total divergence was assessed (Table 4). The maximum contribution towards divergence was observed by average fruit weight (14%) followed by fruit set percentage (12%), number of flowers per cluster (8%), fruit yield/plant (7%), number of fruits per truss (6 %) and TSS (6%). Hence, these characters could be given due importance for the selection of genotypes for further improvement.

Table 1. Clustering pattern of twenty one tomato genotypes

Clusters	No. of genotypes	Cluster members
Cluster I	13	Pusa Ruby, CLN 2123A1 Red, PKM-1, IIHR 2042, Marglobe, EC 163605, Hawaii 7998, Palam Pink, EC 521038, Punjab Rakthak, EC 163383, Arka Abha and IIVR BT-10
Cluster II	5	EC 163611, Punjab Sartaj, EC 160885, Punjab Barkha Bahar and Roma
Cluster III	1	EC 249515
Cluster IV	1	Kashi Chayan
Cluster V	1	DVRT-2

Table 2. Average intra and inter-cluster D^2 values for tomato genotypes

	Cluster Distance				
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2796.45	9489.86	5256.23	4082.34	6241.45
Cluster II		3521.73	18795.9	10917	23102.2
Cluster III			0.00	11316.3	5810.33
Cluster IV				0.00	4667.51
Cluster V					0.00

Table 3. Mean values of clusters for various traits in tomato genotypes

Cluster Means	Plant height (cm)	Days to fifty percent flowering	Number of branches per plant	Number of flowers per cluster	Number of fruits per truss	Fruit set (%)	Number of truss per plant	Number of fruits per plant	Average fruit weight (g)	Fruit polar diameter (cm)	Fruit equatorial diameter (cm)	Fruit shape index	Fruit pericarp thickness (mm)	Total soluble solids (°B)	Lycopene (mg/100 g)	Fruit yield per plant (kg)
Cluster I	134.63	48.12	6.44	8.19	4.11	55.71	20.44	40.84	43.81	3.29	3.79	0.87	3.85	4.21	1.99	1.73
Cluster II	214.92	49.46	5.53	6.41	3.44	54.00	22.94	47.85	27.16	3.48	3.64	0.94	3.58	3.86	0.98	1.10
Cluster III	88.10	48.93	5.18	5.22	4.63	88.69	21.30	56.19	22.32	3.30	4.40	0.75	3.87	4.13	0.26	1.25
Cluster IV	145.20	58.92	4.08	8.31	3.25	39.10	15.02	16.11	84.20	1.80	2.30	0.78	3.98	2.63	0.86	1.35
Cluster V	83.00	54.20	4.10	3.32	2.17	65.36	18.50	22.18	85.83	2.80	3.78	0.74	5.28	4.60	0.61	1.90

Table 4. Percentage Contribution of different traits towards diversity in tomato genotypes

SI.No.	Source	Percentage contribution	Times rankedfirst
1	Plant height (cm)	5.00	11
2	Days to fifty percent flowering	3.00	6
3	No. of branches/plant	6.00	13
4	No. of flowers/cluster	8.00	17
5	No. of fruits/truss	6.00	13
6	Fruit set (%)	12.00	25
7	No. of truss/plant	5.00	11
8	No. of fruits/plant	3.00	6
9	Average fruit weight (g)	14.00	29
10	Fruit polar diameter (cm)	6.00	13
11	Fruit equatorial diameter (cm)	7.00	15
12	Fruit shape index	6.00	13
13	Fruit pericarp thickness (mm)	4.00	8
14	Total soluble solids (°B)	6.00	13
15	Lycopene content (mg/100g)	2.00	4
16	Fruit yield/plant (kg)	7.00	15

4. CONCLUSION

It is concluded that the genotypes belonging to cluster II and cluster V are highly divergent hence can be selected in hybridization program. The selection of parents for hybridization should not be based solely on geographical diversity but should be based on both geographical origin and genetic divergence.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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