Genetic divergence and breeding potential in cherry tomato {*Solanum lycopersicum* (L) var *cerasiforme* Mill}

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ABSTRACT

Genotypes, collected from various Indian research institutes, were cultivated in a randomized block design with three replications at Tamil Nadu Agricultural University, Coimbatore. Mahalanobis's D^2 analysis was employed to assess genetic divergence and the contribution of individual traits. The D^2 analysis grouped the genotypes into six clusters. Cluster I was the largest with 16 genotypes, followed by Cluster II (3) and Cluster V (2), while Clusters III, IV and VI each contained one genotype. Intra-cluster distances showed Cluster V (6.23), Cluster I (5.55) and Cluster II (4.90) as the most genetically diverse within themselves. Inter-cluster distances revealed the highest divergence between Cluster II and Cluster V (14.47), followed by Cluster I and Cluster V (14.24), indicating significant genetic dissimilarity for parental selection. Cluster mean analysis provided insights into trait performance. Yield per hectare was highest in Cluster IV (26.97 tonnes), followed by Cluster III (26.00 tonnes) and Cluster V (23.97 tonnes). Single fruit weight was notably highest in Cluster II (15.37 g). For quality traits, total soluble solids (6.19 °Brix), total sugars (2.04 mg/100 g) and lycopene (8.22 mg/100 g) were highest in Cluster IV. Total carotenoids (18.13 mg/100 g), total phenol (0.54 mg/100 g) and total antioxidant (1.94 µ mol AA/g) were highest in Cluster VI. These findings suggest that genotypes from highly divergent clusters, particularly Clusters IV, V, VI, III and I, could be effectively utilized in hybridization programmes to develop superior cherry tomato varieties combining high yield and enhanced quality.

Keywords: Cherry tomato; genetic diversity; plant breeding; genotype clustering; yield; quality traits

INTRODUCTION

Vegetables, with their vibrant array of colours, flavours, vitamins and minerals, are essential to a healthy daily diet, as Simarelli (2001) noted. Among them, the tomato (*Solanum lycopersicum* L) stands out as a globally popular and widely cultivated solanaceous crop. Its wild relatives are a treasure trove of genetic diversity, offering a vast range of variations in fruit quality characteristics like flavour, aroma, colour and texture (Miller and Tanksley 1990).

Cherry tomatoes {*Solanum lycopersicum* (L) var *cerasiforme* Mill} are particularly favoured as a table-purpose tomato, cherished for their small fruits consumed fresh or used as raw material for processed goods (Charlo et al 2007). They also hold significant industrial value for preparing products like tomolive and tomatina. Key desirable traits found in cherry tomatoes include disease resistance, favourable fruit abscission, high soluble solids content, ideal fruit size, excellent flavour, good texture, rich pigmentation and extended post-harvest quality (Kwon et al 2009). As promising wild relatives of *Solanum*, cherry tomatoes offer immense potential in breeding programmes due to their rich genetic diversity, which is crucial for selecting parental material and their wide geographic distribution (Medina and Lobo 2001). The success of any breeding programme hinges on choosing the right parents. Research shows that crossing genetically diverse parents often leads to superior and varied offspring. Genetic diversity is vital in plant breeding because distant genotypes or origins generally exhibit greater heterosis (hybrid vigour) than crosses between closely

related strains. In crop improvement, genetic variability among genotypes is a fundamental pre-requisite for developing new cultivars and selecting better segregants for various important economic traits (Buckseth et al 2012).

The importance of genetic diversity is evident in a species' ability to survive and adapt. Studies on genetic divergence have been instrumental in designing effective hybridization programmes for crop plants. These programmes aim to generate new variants with improved adaptation and yielding potential far beyond their parent types (Sekhar et al 2010). Understanding genetic divergence between cultivars or accessions before initiating any crossing programme allows breeders to focus their efforts on combinations most likely to produce highly heterotic outcomes, especially when considering various metric characters across a set of accessions. Mahalanobis's D^2 analysis has proven to be an effective tool for assessing genetic divergence among genotypes. Such analysis ultimately helps in selecting desirable parents for recombination breeding, leading to the development of superior hybrids or varieties. Against this background, this study aimed to investigate the genetic divergence of cherry tomato for yield and quality traits.

MATERIAL and METHODS

This research took place at the university orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. Twenty four cherry tomato genotypes were studied, gathered from various research institutes across India. These included: Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka: IIHR 2753, IIHR 2754, IIHR 2871, IIHR 2873 and IIHR 2876; Indian Agricultural Research Institute (IARI), New Delhi: Pusa Cherry Tomato 1; Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttar Pradesh: Pant Cherry Tomato 1; Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu: ATL-01-19, HAT 20, LE 13, LE 87, LE 89, LE 315, LE 338, LE 598, LE 887, LE 1223, PAV 2373, VGT 89, VGT 90, VGT 95, VR 35, VRCT 17 and VRCT 155. All genotypes were grown in a field experiment set up as a randomized block design with three replications. Data were collected on various growth, yield and quality traits. For this study, Mahalanobis's D^2 analysis was used to assess the genetic divergence among the 24 cherry tomato genotypes and to determine each character's contribution to the overall diversity. D^2 values, representing the uncorrelated values between any two uncorrelated genotypes, were calculated as described by Rao (1952). The D^2 values were then grouped into clusters using Tocher's method, also outlined by Rao (1952). Finally, the intra- and inter-cluster distances were calculated using the formula provided by Singh and Chaudhary (1979).

RESULTS and DISCUSSION

Genetic diversity among 24 cherry tomato genotypes was measured using the Mahalanobis D^2 statistics method (Mahalanobis 1936). The most important traits were subjected to this genetic divergence analysis. Based on the D^2 values, the genotypes were grouped into six clusters (Table 1). Cluster I was found to be the largest, comprising 16 genotypes, followed by clusters II and V, with 3 and 2 genotypes respectively. Clusters III, IV and VI each contained only one genotype.

The intra- and inter-cluster distances were examined (Table 2). Cluster V recorded the highest intra-cluster distance (6.23), followed by cluster I (5.55) and cluster II (4.90), which indicated considerable genetic divergence among the genotypes within these respective clusters. Clusters III, IV and VI, containing single genotypes, exhibited no intra-cluster distance. Inter-cluster distances revealed that the highest value (14.47) was observed between clusters II and V. This was followed by clusters I and V (14.24), V and VI (14.07), III and V (13.42) and IV and V (13.06), all of which indicated wide diversity between the genotypes belonging to these respective cluster pairs.

Genotypes from these highly divergent clusters can be utilized as parents in hybridization programmes to obtain superior heterotic hybrids from segregating populations. Conversely, clusters III and IV recorded the least inter-cluster distance, suggesting a closer relationship between the genotypes included in these clusters. Overall, inter-cluster distances were found to be much higher than intra-cluster distances, which signifies the homogeneous and heterogeneous nature of the genotypes within and between clusters respectively. Similar information on intra- and inter-cluster distances among genotypes has also been

Table 1. Clustering pattern of twenty four genotypes of cherry tomato based on D^2 analysis

Cluster	Number of genotypes	Genotypes
I	16	IIHR 2873, IIHR 2876, IIHR 2871, LE 887, LE 89, VGT 90, LE 338, LE 315, VGT 89, LE 598, VR 35, VGT 95, PAV 2373, LE 1223, VRCT 17, LE 87
II	3	ATL-01-19, HAT 20, VRCT 155
III	1	LE 13
IV	1	IIHR 2753
V	2	Pant Cherry Tomato 1, Pusa Cherry Tomato 1
VI	1	IIHR 2754

Table 2. Average intra- (bold) and inter-cluster D^2 values for clusters in twenty four cherry tomato genotypes

Cluster	I	II	III	IV	V	VI
I	**5.55**	7.05	6.81	7.59	14.24	8.05
II		**4.90**	7.75	8.25	14.47	8.88
III			**0.00**	5.91	13.42	7.42
IV				**0.00**	13.06	6.74
V					**6.23**	14.07
VI						**0.00**

reported in studies by Meena and Bahadur (2013) and Thapa et al (2014).

The cluster mean analysis, as presented in Table 3, revealed distinct performance variations among the cherry tomato genotypes grouped into different clusters across various growth, yield and quality traits. Regarding plant height at flowering, the highest cluster mean value was observed in Cluster IV (116.09 cm), followed by Cluster VI (111.81 cm) and Cluster V (110.15 cm). At final harvest, the highest plant height was recorded in Cluster V (264.04 cm), with Cluster IV (229.23 cm) and Cluster VI (201.25 cm) following. For number of primary branches per plant, Cluster III showed the highest mean at flowering (10.67), trailed by Cluster VI (10.40) and Cluster V (9.40). At final harvest, Cluster III again exhibited the highest mean (16.53 primary branches), followed by Cluster V (14.77) and Cluster VI (14.30). In terms of flowering phenology, the lowest mean value for days to first flowering was recorded in Cluster IV (27.53 days), followed closely by Cluster III (28.53 days). Analyzing floral and fruit set characteristics, the highest cluster mean value for number of flowers per cluster was found in Cluster V (48.17), with Cluster IV (8.73) and Cluster III (7.20) showing considerably lower means. The number of flower clusters (truss) per plant was highest in Cluster III (103.07), followed by Cluster IV (83.80) and Cluster VI (78.71). The number of fruits per cluster was highest in Cluster V (15.43), followed by Cluster IV (6.20) and Cluster III (5.40). Fruit set was highest in Cluster VI (83.93%), with Cluster III (75.93%) and Cluster IV (71.77%) also showing strong performance. The number of fruits per plant was notably highest in Cluster V (343.75), followed by Cluster IV (306.50). Concerning fruit quality and yield, the highest cluster mean value for single fruit weight was recorded in Cluster II (15.37 g), significantly higher than Cluster III (6.29 g), Cluster I (6.04 g) and Cluster IV (4.40 g). The lowest cluster mean for 1000-seed weight was observed in Cluster V (1.30 g), followed by Cluster VI (1.75 g) and Cluster III (1.89 g). Finally, the highest cluster mean value for yield per hectare was recorded in Cluster IV (26.97 tonnes), with Cluster III (26.00 tonnes) and Cluster V (23.97 tonnes) also demonstrating high yield potential.

Regarding fruit quality, the total soluble solids were highest in Cluster IV (6.19 °Brix), followed by Cluster III (6.15 °Brix) and Cluster V (6.13 °Brix). The highest total sugars were recorded in Cluster IV (2.04 mg/100 g), with Clusters III and V showing nearly identical levels (2.03 mg/100 g). Ascorbic acid content was lowest in Cluster VI (25.17 mg/100 g), followed

Table 3. Cluster mean for major growth, yield and quality traits of twenty four cherry tomato genotypes

Character	Cluster					
	I	II	III	IV	V	VI
Plant height at flowering (cm)	80.24	67.51	101.99	116.09	110.15	111.81
Plant height at final harvest (cm)	141.93	160.61	148.27	229.23	264.04	201.25
Number of primary branches/plant at flowering	8.35	6.33	10.67	8.40	9.40	10.40
Number of primary branches/plant at final harvest	10.06	8.78	16.53	12.27	14.77	14.30
Days to first flowering	35.81	39.07	28.53	27.53	33.23	42.80
Number of flowers/cluster	5.39	4.89	7.20	8.73	48.17	5.80
Number of flowering clusters (truss)/plant	69.04	47.18	103.07	83.80	44.94	78.71
Number of fruits/cluster	3.87	3.13	5.40	6.20	15.43	4.93
Number of fruit clusters/plant	43.74	24.40	38.35	49.44	22.64	50.89
Per cent fruit set	71.63	65.23	75.93	71.77	32.67	83.93
Number of fruits/plant	169.94	76.30	207.10	306.50	343.75	250.90
Fruit weight (g)	6.04	15.37	6.29	4.40	3.49	4.20
1000-seed weight (g)	1.90	2.78	1.89	2.48	1.30	1.75
Yield (tonnes/ha)	20.18	23.48	26.00	26.97	23.97	21.08
Total soluble solids (°Brix)	5.46	5.11	6.15	6.19	6.13	6.01
Total sugars (mg/100 g)	1.80	1.69	2.03	2.04	2.03	1.99
Ascorbic acid (mg/100 g)	35.12	41.67	28.55	28.45	27.99	25.17
Titrable acidity (%)	0.21	0.24	0.15	0.16	0.10	0.16
Lycopene (mg/100 g)	5.84	5.26	7.73	8.22	8.17	8.17
Total carotenoids (mg/100 g)	7.89	7.98	10.05	12.88	11.23	18.13
Total phenol (mg/100 g)	0.46	0.47	0.53	0.47	0.51	0.54
Total antioxidant (µ mol AA/g)	0.84	0.86	1.08	1.38	1.21	1.94

by Cluster V (27.99 mg/100 g) and Cluster IV (28.45 mg/100 g). The lowest cluster mean value for titratable acidity was observed in Cluster V (0.10%), followed by Cluster III (0.15%). For pigments, the highest cluster mean value for lycopene was recorded in Cluster IV (8.22 mg/100 g), with Clusters V and VI also showing high levels (8.17 mg/100 g). Total carotenoids content was found to be highest in Cluster VI (18.13 mg/100 g), followed by Cluster IV (12.88 mg/100 g) and Cluster V (11.23 mg/100 g). The total phenol content in leaves was highest in Cluster VI (0.54 mg/100 g), followed by Cluster III (0.53 mg/100 g) and Cluster V (0.51 mg/100 g). The highest total antioxidant content was recorded in Cluster VI (1.94 µ mol AA/g), mirroring Cluster IV (1.38 µ mol AA/g), with Cluster V having a lower value (1.21 µ mol AA/g).

The inferences drawn from inter-cluster distances can be utilized for selecting genetically diverse and superior genotypes. Inter-crossing genotypes from these diverse clusters is expected to result in a wide array of variability, facilitating effective selection for desirable traits. To enhance both yield and quality, genotypes from Clusters IV, V, VI, III and I may be involved in future breeding programmes to achieve combined improvements. These findings are consistent with previous studies by Meena and Bahadur (2013), Srivastava et al (2014), Thapa et al (2014) and Dar et al (2015).

CONCLUSION

This study successfully assessed the genetic divergence among 24 cherry tomato genotypes, providing valuable insights for future breeding programmes. The application of Mahalanobis D^2 statistics effectively grouped the genotypes into six distinct clusters, with Cluster I being the largest. The analysis of intra- and inter-cluster distances confirmed significant genetic variability both within and between the identified clusters, underscoring the rich genetic resources available. Specifically, the high inter-cluster distances, particularly between Cluster II and Cluster V (14.47), indicate the presence of wide genetic divergence. This finding is crucial as crossing genotypes from such highly divergent clusters is expected to maximize heterosis and generate a broad spectrum of variability, thereby, increasing the

probability of selecting superior segregants with improved traits. Furthermore, the cluster mean analysis provided detailed information on the performance of each cluster across various growth, yield and quality parameters. Clusters IV, V and III consistently showed high values for economically important traits such as yield per hectare (eg Cluster IV at 26.97 tonnes), total soluble solids (Cluster IV at 6.19 °Brix) and key phytochemicals like lycopene (Cluster IV at 8.22 mg/ 100 g) and total carotenoids (Cluster VI at 18.13 mg/ 100 g). Cluster II was notable for high single fruit weight (15.37 g). Therefore, it is concluded that genotypes from genetically diverse clusters, particularly combinations involving Clusters IV, V, VI, III and I, should be strategically utilized as parental lines in future hybridization programmes. This approach is anticipated to facilitate the effective selection of progeny that combines desirable yield characteristics with enhanced nutritional and processing quality, ultimately leading to the development of superior cherry tomato varieties.

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