



Research Note

Genetic variability studies in cherry tomato [*Solanum lycopersicum* (L.) var. *cerasiforme* Mill.] for growth, yield and quality

E. Venkadeswaran^{1*}, P. Irene Vethamoni², T. Arumugam³, N. Manivannan⁴, S. Harish⁵, R. Sujatha⁶ and E. Alli Rani⁷

^{1,2,6}Horticultural College and Research Institute, Tamil Nadu Agricultural University,

^{3,7}Horticultural College and Research Institute, Periyakulam - 625604,

⁴Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore - 641 003,

⁵Agricultural College and Research Institute, Madurai - 625104, Tamil Nadu, India

*E-Mail: e.venkadeswaran@gmail.com

Abstract

The material of the present study consisted of twenty four genotypes of cherry tomato to study the genetic components for growth, yield and quality at university orchard, Tamil Nadu Agricultural University, Coimbatore, India. The genetic variability demonstrated that phenotypic coefficient of variation was higher contrasted with genotypic coefficient of variation for all the attributes in 24 genotypes. Even though PCV was more than GCV but the difference was very narrow suggesting that, there was less influence of environment. High estimations of heritability and genetic gain increase were displayed for plant height at final harvest, the number of primary branches plant⁻¹ at final harvest, inter nodal length of main stem, stem girth, the number of flowers cluster⁻¹, the number of flowering clusters plant⁻¹, the number of fruits cluster⁻¹, the number of fruit cluster plant⁻¹, days from fruit set to fruit maturity, per cent fruit set, the number of fruits plant⁻¹, fruit length, fruit girth, fruit width, the number of locules fruit⁻¹, fruit weight, the number of seeds fruit⁻¹, weight of seeds fruit⁻¹, weight of 1000 seeds, yield plant⁻¹, fruit firmness, pericarp thickness, shelf life of fruits, total soluble solids, total sugars, ascorbic acid, titrable acidity, lycopene, total carotenoids, total phenol and total antioxidant. Thus, the selection might be effective for improving these traits.

Keywords

Cerasiforme, Cherry tomato, Genetic advance, Genetic variability, Heritability

The most genetic diversity is found in the wild family members of tomato, which show fluctuation for quality attributes such as flavour, aroma, color, and texture (Miller and Tanksley, 1990). It is the most imperative warm-season fruit vegetable grown throughout the world (Anita Pedapati *et al.*, 2014). Cherry tomato [*Solanum lycopersicum* (L.) var. *cerasiforme* Mill.] is devoured as new vegetable and crude material for juice, ketchup, sauce, canned fruits, puree, paste, *etc.* The wild cherry tomato was first found throughout tropical and subtropical America and then propagated in the tropics of Asia and Africa (Gharezi *et al.*, 2012). Cherry tomatoes, one of the attractive wild *Solanum* types, offer great potential in breeding programs due to their valuable genetic diversity

characteristics for selecting parental material and their wide geographic range (Medina and Lobo, 2001). Cherry tomato growing is becoming particularly popular among upper segments of society (Vidyadhar *et al.*, 2015). Compared to standard tomatoes, they become popular in the retail chains and are sold at a premium. For the incorporation of desirable characters to maximize yield, the basic requirement is information on the nature and extent of genetic variability in a cherry tomato population for desirable characters and inter-trait relationships. With this background the study was aimed at to study the genetic components such as variability, heritability and genetic advance in cherry tomato for growth, yield and quality.

The field experiment was conducted in the University Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. Twenty four cherry tomato genotypes were collected from various research institutes across the country viz., Indian Institute of Horticultural Research, Bengaluru (IIHR 2753, IIHR 2754, IIHR 2871, IIHR 2873 and IIHR 2876), Indian Agricultural Research Institute, New Delhi (Pusa Cherry Tomato 1), Govind Ballabh Pant University of Agriculture

and Technology, Pantnagar (Pant Cherry Tomato 1) and Tamil Nadu Agricultural University, Coimbatore (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). The study has been designed in a randomized block with three replications. Thirty six characters of selected plants for each genotype replication were analyzed for variance (Panse and Sukhatme, 1957). Heritability in the broad sense was calculated and expressed in per cent by the

Table 1. Mean, range, variability, heritability and genetic advance as per cent of mean for growth, yield and quality traits of cherry tomato genotypes

Sl. No.	Traits	Mean	Range		Variability (per cent)		Heritability (h ²) (per cent)	Genetic advance as per cent of mean
			Min.	Max.	PCV	GCV		
1	Plant height at flowering (cm)	84.86	61.75	116.09	22.09	14.95	45.82	20.85
2	Plant height at final harvest (cm)	163.36	116.91	266.22	28.73	27.80	93.64	55.41
3	Number of primary branches plant ⁻¹ at flowering	8.37	5.67	11.07	23.80	13.23	30.89	15.15
4	Number of primary branches plant ⁻¹ at final harvest	10.83	7.53	16.53	24.84	23.92	92.78	47.47
5	Days to first flowering	35.65	26.40	50.60	19.06	13.53	50.39	19.79
6	Node at which first flowering cluster (truss) appears	12.54	9.67	15.13	12.00	8.23	46.99	11.62
7	Inter nodal length of main stem (cm)	2.61	2.01	3.69	15.92	15.11	90.05	29.53
8	Stem girth (cm)	3.53	2.91	5.64	18.09	17.33	91.75	34.19
9	Number of flowers cluster ⁻¹	9.17	4.20	51.20	21.52	20.43	90.14	39.96
10	Number of flowering clusters (truss) plant ⁻¹	66.74	35.87	103.07	26.24	25.60	95.25	51.48
11	Number of fruits cluster ⁻¹	4.95	2.93	17.07	21.51	20.42	90.12	39.94
12	Number of fruit clusters plant ⁻¹	39.87	19.14	59.21	26.44	25.57	93.51	50.93
13	Days from fruit set to fruit maturity	29.94	26.67	35.93	8.31	8.22	97.62	16.72
14	Per cent fruit set	68.28	31.20	83.94	18.63	18.11	94.48	36.27
15	Number of fruits plant ⁻¹	183.33	73.20	360.80	41.32	40.98	98.38	83.73
16	Fruit length (cm)	3.90	2.95	5.14	14.27	13.48	89.25	26.23
17	Fruit girth (cm)	7.21	5.19	10.05	17.01	15.94	87.75	30.76
18	Fruit width (cm)	1.24	0.97	3.03	32.42	31.90	96.81	64.66
19	Number of locules fruit ⁻¹	2.55	2.00	3.07	15.41	14.12	83.99	26.66
20	Fruit weight (g)	6.86	3.28	15.96	53.58	53.33	99.04	109.32
21	Number of seeds fruit ⁻¹	42.34	8.39	96.90	60.39	60.32	99.77	124.11
22	Weight of seeds fruit ⁻¹ (g)	0.09	0.01	0.27	81.17	81.04	99.68	166.67
23	Weight of 1000 seeds (g)	1.98	1.27	2.81	20.46	20.32	98.64	41.58
24	Yield plant ⁻¹ (g)	1073.61	612.45	1572.36	25.26	24.22	91.96	47.85
26	Fruit firmness (kg sq. cm ⁻¹)	1.06	0.76	1.65	19.65	17.52	79.46	32.16
27	Pericarp thickness (mm)	1.61	1.13	2.22	20.20	18.75	86.17	35.86
28	Shelf life of fruits (days)	27.10	23.00	32.50	10.46	10.15	94.11	20.28
29	Total soluble solids (°Brix)	5.55	4.72	6.19	8.41	8.12	93.10	16.13
30	Total sugars (mg 100 g ⁻¹)	1.83	1.56	2.05	8.37	8.09	93.39	16.11
31	Ascorbic acid (mg 100 g ⁻¹)	34.38	25.17	45.19	20.45	20.26	98.17	41.36
32	Titrate acidity (per cent)	0.20	0.10	0.34	40.02	38.43	92.24	76.03
33	Lycopene (mg 100 g ⁻¹)	6.24	3.62	8.22	20.19	20.05	98.61	41.01
34	Total carotenoids (mg 100 g ⁻¹)	8.90	6.48	18.13	28.69	28.56	99.12	58.57
35	Total phenol (mg 100 g ⁻¹)	0.47	0.37	0.54	12.63	11.15	77.98	20.29
36	Total antioxidant (µ mol. AA g ⁻¹)	0.95	0.69	1.94	29.05	28.54	96.57	57.78

method defined by Lush (1940). The method proposed by Johnson *et al.* (1955) was used to estimate genetic advance. Phenotypic and genotypic coefficient of variations was calculated based on the method advocated by Burton (1952).

The efficiency of selection depends on the nature and extent of genetic variability and degree of transmissibility of desirable characters. The phenotypic coefficient of variation was observed to be highest compared to genotypic coefficient of variation for all the traits under study (**Table 1**). Even though phenotypic coefficient of variation was more than genotypic coefficient of variation, the difference was very narrow suggesting the less influence of environment on expression of these traits. The maximum value of genotypic coefficient of variation and phenotypic coefficient of variation (more than 20 per cent) occurred for plant height at final harvest, the number of primary branches plant⁻¹ at final harvest, the number of flowers cluster⁻¹, the number of flower clusters (truss) plant⁻¹, the number of fruits cluster⁻¹, the number of fruit clusters plant⁻¹, the number of fruits plant⁻¹, fruit width, fruit weight, the number of seeds fruit⁻¹, weight of seeds fruit⁻¹, weight of 1000 seeds, yield plant⁻¹, ascorbic acid, titrable acidity, lycopene, total carotenoids and total antioxidant which suggested a higher phenotypic as well as genotypic variation among the genotypes and their responsiveness of these traits for further improvement with selection. A high degree of disparity between PCV and GCV was observed for plant height at flowering, the number of primary branches plant⁻¹ at flowering, days to first flowering and node at which first flowering cluster (truss) appears depicting their susceptibility to environmental fluctuations. Close correspondence between PCV and GCV for remaining characters implied their relative resistance to environmental variation. These likewise depicted genetic factors were responsible for the expression of these characters and selection could be made successfully based on phenotypic performance and these results were in consonance with Rathod (2014).

The heritability in broad sense was found to be ranged from 30.89 per cent (number of primary branches plant⁻¹ at flowering) to 99.77 per cent (number of seeds fruit⁻¹). Higher values of heritability (more than 60 per cent) was observed for plant height at final harvest, the number of primary branches plant⁻¹ at final harvest, inter nodal length of main stem, stem girth, the number of flowers cluster⁻¹, the number of flower clusters plant⁻¹, the number of fruits cluster⁻¹, the number of fruit clusters plant⁻¹, days from fruit set to fruit maturity, per cent fruit set, the number of fruits plant⁻¹, fruit length, fruit girth, fruit width, the number of locules fruit⁻¹, fruit weight, the number of seeds fruit⁻¹, weight of seeds fruit⁻¹, weight of 1000 seeds, yield plant⁻¹, fruit firmness, pericarp thickness, shelf life of fruits, total soluble solids, total sugars, ascorbic acid, titrable acidity, lycopene, total carotenoids, total phenol and total antioxidant. Such high estimations of heritability for all

the traits outlined were least affected by the environment. Further plant height at flowering, the number of primary branches plant⁻¹ at flowering, days to first flowering and node at which first flower cluster appears recorded moderate heritability (30-60 per cent).

The genetic advance as per cent of mean (GAM) *i.e.*, genetic gain was ranged from 11.62 (node at which first flowering cluster appears) to 166.7 (weight of seeds fruit⁻¹). Higher estimates of the genetic advance as per cent of mean (more than 20 per cent) was observed for the characters *viz.*, plant height at flowering, plant height at final harvest, the number of primary branches plant⁻¹ at final harvest, inter nodal length of main stem, stem girth, the number of flowers cluster⁻¹, the number of flower clusters (truss) plant⁻¹, the number of fruits cluster⁻¹, the number of fruit clusters plant⁻¹, per cent fruit set, fruit length, fruit girth, the number of locules fruit⁻¹, weight of 1000 seeds, yield plant⁻¹, fruit firmness, pericarp thickness, shelf life of fruits, ascorbic acid, lycopene, total carotenoids, total phenol and total antioxidant which explained that they could be improved to a large extent. Whereas, the number of primary branches plant⁻¹ at flowering, days to first flowering, node at which first flowering cluster appears, days from fruit set to fruit maturity, total soluble solids and total sugars showed a moderate genetic advance. These results were found to be in consonance with the results of Samadia *et al.* (2006) for plant height, Kumar *et al.* (2006) for the number of primary branches plant⁻¹, Mehta and Asati (2008) and Pemba Sherpa *et al.* (2014) for days to first flowering, Mohanty (2003) for the number of flowers cluster⁻¹ and the number of flower clusters (truss) plant⁻¹, Chernet (2013) for per cent fruit set, Kumar *et al.* (2013) for the number of fruits cluster⁻¹ and the number of fruits plant⁻¹, Dufera (2013) for fruit length and fruit girth, Dar and Sharma (2011) for fruit weight, Rathod (2014) for yield plant⁻¹ and the number of locules fruit⁻¹, Kumar *et al.* (2013) for weight of seeds fruit⁻¹, Shokat *et al.* (2013) for fruit firmness, Saini *et al.* (2013) for pericarp thickness, Reddy *et al.* (2013) for shelf life of fruits, Nadeem *et al.* (2013) for total soluble solids, Rathod (2014) for titrable acidity, ascorbic acid, lycopene, total carotenoids and total sugars.

In this manner, the characters showing a high heritability accompanied with high value of genetic advance as per cent of mean demonstrated that the most probable heritability may be because of additive gene action and simple selection or pure line selection followed by hybridization with selection in earlier generations might be effective for improving these traits in cherry tomato. Low heritability accompanied with low genetic advance demonstrated that these traits were profoundly affected by environment and selection would be inadequate and consequently these characters could be improved by hybridization only. These results were in similarity with the studies of Senugupta *et al.* (2009) and Shokat *et al.* (2013).

High values of heritability associated with moderate to high GCV and genetic gain were exhibited for plant height at final harvest, the number of primary branches plant⁻¹ at final harvest, inter nodal length of main stem, stem girth, the number of flowers cluster⁻¹, the number of flowering clusters plant⁻¹, the number of fruits cluster⁻¹, the number of fruit cluster plant⁻¹, days from fruit set to fruit maturity, per cent fruit set, the number of fruits plant⁻¹, fruit length, fruit girth, fruit width, the number of locules fruit⁻¹, fruit weight, the number of seeds fruit⁻¹, weight of seeds fruit⁻¹, weight of 1000 seeds, yield plant⁻¹, fruit firmness, pericarp thickness, shelf life of fruits, total soluble solids, total sugars, ascorbic acid, titrable acidity, lycopene, total carotenoids, total phenol and total antioxidant. Thus, the selection might be effective for improving these traits.

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