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Estimation of genetic diversity for yield related quantitative traits among genotypes of tomato [*Solanum lycopersicon* (Mill.) Wettsd.]

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Abstract

An experiment was conducted with 46 genotypes of tomato to worked-out the genetic divergence using Mahalanobis'sD^2 analysis during *Rabi* season 2014-15 at Main Experimental Station, Department of vegetable Science, N.D.U.A. & T., Kumarganj, Ayodhya. Based on the performance of different characters, all the genotypes were grouped into seven clusters. The maximum numbers of genotypes were accommodated in cluster VI. The maximum intra and inter cluster distance was found in cluster V (57.65) and between cluster II and VII (1109.44), respectively. On the basis of cluster mean of different characters studied, cluster II showed superiority in plant height, primary branches per plant, number of fruits per plant and T.S.S. (%), whereas cluster VII showed superiority in average fruit weight, fruit circumference, number of locules per fruit, fruit length and fruit yield per plant. The hybridization between cluster II and VII might give rise the different superior recombinants in segregating generations and as a consequence development of new promising genotypes through different breeding methods which may out yield a existing variety or may use as donor parent for improvement of other genotypes/varieties and also for the development of F$_1$ hybrids.

Keywords: Estimation, genetic diversity, quantitative traits, tomato

Introduction

Tomato (*Solanum lycopersicon* (Mill.) Wettsd.), 2n=2x=24 is one of the most versatile vegetable crop grown throughout the world because of its wider adaptability, high yielding potential and suitability for uses in fresh as well as processed food industries. Tomato is one of the most important "protective foods" because of its special nutritive value. 100 g of edible part of tomato fruit contains 93.1 % moisture, 3.6 g carbohydrate, 1.9 g protein, 0.1 g fat, 0.6 g minerals, 0.7 g fibre, 320 IU vitamin A. and 31.0 mg vitamin C (Ascorbic acid). The Veracruz-Puebla region of Mexico is the center of domestication of the cultivated tomato. From Mexico, tomato was taken to Italy, Spain, Portugal and other European countries, Africa and Middle East by the explorers in the 16th century. Tomato moved to the USA from northern Europe around 1781 where it was first grown by Thomas Jefferson in Virginia. Tomato is basically a self-pollinated crop, but a certain percentage of cross-pollination also occurs. Anthesis starts from 6.00 AM, continues up to 10.30 AM and anther dehiscence from 7.00 to 10.00 AM; dehiscence of anther is longitudinal. The optimum temperature for pollination is around 21°C. Generally diverse plants are expected to give high hybrid vigour (Harrington, 1940); hence, it necessitates the study of genetic divergence among the existing varieties and germplasm collection for identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme.

Materials and Methods

The experiment was laid out in Randomized Block Design with three replications to assess the performance of 46 genotypes of tomato. Seed were sown in nursery bed on 07 September 2014 and 25 days old healthy seedling were transplanted in the experimental field on 02 October,2014 in two row of 4.5 m length with inter and intra row spacing of60 cm x 45 cm respectively. Fertilizer @ 120kgN: 80kgP_2O_5: 50kg K_2O/ha were applied to the crop.

A light irrigation was given immediately after transplanting. All recommended cultural practices were followed to maintain good crop stand and growth of the plant. Observations were recorded on five randomly selected plants from each genotype in each replication and were summed up and divided by five to get mean values.

Table 1: Clustering pattern of forty six genotypes of tomato on the basis of Mahalanobis D^2 statistics

Cluster number	No. of genotypes	Genotypes
I	8	NDT-341, NDT-351, NDT-352, NDT-360, NDT-342, NDT-345,NDT-343,NDT-344
II	1	NDT-376
III	8	NDT-347, NDT-382, NDT-358, NDT-356, NDT-374, NDT-363,H-86 (C),NDT-359
IV	8	NDT-355, NDT-372, NDT-364, NDT-373, NDT-379, NDT-370, NDT-362,H-24(C)
V	7	NDT-371, NDT-378, NDT-375, NDT-377, NDT-380, NDT-381, NDT-368
VI	13	NDT-348, DVRT-2(C), NDT-354, NDT-365, NDT-353, NDT-349,NDT-361 NDT-366, NDT-369, NDT-367, NDT-357, NDT-350, NDT-346
VII	1	NDT-383

Table 2: Intra and inter clusters D^2 values for seven clusters in tomato

Cluster number	I	II	III	IV	V	VI	VII
I	52.988	480.318	106.796	159.182	122.53	221.732	322.938
II		0.000	695.08	793.676	592.022	962.945	1109.440
III			54.414	74.866	94.942	144.962	208.456
IV				37.808	73.162	73.775	193.536
V					57.657	114.187	254.365
VI						51.664	188.943
VII							0.000

Table 3: Intra-cluster group means for thirteen characters in tomato

Clusters	Days to 50% flowering	Plant height (cm)	Primary branches/ plant	No of fruits perplant	Days to First fruit harvest	Average fruit weight (g)	Fruit circumference (cm)	Pericarp thickness (cm)	No of locules per fruits	TSS (%)	Fruit Length (cm)	Harvesting duration	Fruit yield per plant (kg)
I	63.167	109.067	3.321	42.570	80.167	45.125	13.604	0.375	3.500	6.066	6.547	21.750	1.941
II	61.000	141.933	4.733	83.803	78.333	29.333	12.733	0.387	3.133	7.113	6.733	20.333	2.487
III	62.125	87.887	3.408	39.878	81.417	46.500	16.596	0.401	4.392	6.012	7.602	20.875	1.879
IV	60.833	74.800	3.588	42.454	78.333	44.750	15.139	0.408	4.142	5.671	6.881	21.167	1.907
V	60.619	87.162	3.667	49.592	78.238	40.810	14.210	0.510	3.390	5.675	7.252	20.714	2.043
VI	62.615	69.677	2.862	40.025	81.385	46.154	13.370	0.418	2.954	5.704	6.695	23.692	1.868
VII	62.333	85.267	2.867	37.527	80.667	66.667	17.067	0.467	4.733	6.387	7.967	22.333	2.513

Result and Discussion

The 46 genotypes were grouped into 7 different non-overlapping clusters (Table-1). Cluster VI had highest number of genotypes (13) followed by cluster I (8), cluster III (8), cluster IV (8) and cluster V (7) whereas cluster II and Cluster VII had presented only one entry in each groups. The minimum inter-cluster distance was recorded between clusters IV and cluster V (73.16). The minimum intra-cluster distance (0.00) was found for cluster II and cluster VII, and maximum (57.65) was recorded for cluster V. The maximum inter-cluster distance was observed between clusters II to cluster VII (1109.44) while, inter-cluster values between clusters II to cluster VI (962.94), clusters II to cluster V (592.02), clusters II to cluster IV (793.67), cluster II to cluster III (695.08) and cluster II to cluster II (480.31) were high. The minimum inter-cluster distance was recorded between clusters IV and cluster V (73.16).

Cluster I showed maximum mean value for days to 50 per cent flowering (63.16). Cluster II showed maximum mean values for plant height (141.93 cm), primary branches/ plant (4.73), no of fruits per plant (83.80) and TSS (7.11). Cluster III showed maximum mean values for days to first fruit harvest (81.41). Cluster V showed maximum mean values for pericarp thickness (0.51 cm). Cluster IV showed maximum mean value only for harvesting duration (23.69 days). Cluster VII showed maximum mean value for average fruit weight (66.66 g), fruit circumference (17.06 cm), no of locules per fruits (4.73), fruit length (7.96 cm), fruit yield per plant (kg) (2.51). Cluster IV do not showed maximum value for any character but it had showed minimum mean values for TSS (5.67 %). Cluster I showed minimum mean value for pericarp thickness (0.37 cm) and fruit length (6.54 cm). Cluster II showed minimum mean values for average fruit weight (29.33 g), fruit circumference (12.73 cm) and harvesting duration (20.33 days). Cluster V showed minimum mean values for days to 50 per cent flowering (60.61 days), days to first fruit harvest (78.23 days).

The maximum inter-cluster distances suggested that members of these two clusters are genetically very diverse to each other. The higher inter-cluster distance indicated greater genetic diversity between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

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