

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.709.186>

Estimation of Genetic Variability for Yield and Yield Related Traits in Tomato (*Solanum lycopersicum* L.) under Polyhouse Condition

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ABSTRACT

Keywords

GCV, Genetic variability, Genetic advance, Heritability, PCV, Tomato

Article Info

Accepted:

10 August 2018

Available Online:

10 September 2018

The present investigation was carried out on thirty six genotypes of tomato for genetic variability assessment. The analysis of variance revealed that significant genetic differences were present among the tomato genotypes for all the traits studied. High GCV and PCV estimates were observed for number of fruits per plant, average fruit weight, fruit yield per hectare, fruit yield per plant, number of flowers per cluster and number of fruits per cluster. Number of fruits per plant recorded maximum heritability followed by average fruit weight, number of flowers per cluster, number of fruits per cluster, fruit length, days to first fruit ripening, fruit yield per plant, fruit yield per hectare, fruit width, 100 seed weight and days to first fruit set. High estimates of genetic advance as percentage of mean was observed for number of fruits per plant, average fruit weight, fruit yield per hectare, fruit yield per plant, number of flowers per cluster, number of fruits per cluster, fruit length, fruit width, 100 seed weight, fruit shape index and internodal length. Therefore, selection for these characters in segregating generations based on phenotypic performance would likely be more effective for further improvement in tomato.

Introduction

Tomato (*Solanum lycopersicum* L.) is an important vegetable of Solanaceae family having chromosome number $2n=2x=24$. It has originated from wild form in the Peru-Ecuador-Bolivia region of the Andes, South America (Rick, 1969) and is grown in almost every corner of the world (Roberston and Labate, 2007). It is one of the most popular and widely grown vegetable in the world ranking second in importance to potato in many countries. Tomato is one of the most

highly praised vegetables consumed widely. It is a major source of vitamins, minerals and organic acids. There are various types of flavouring compounds found in the fruits, which enrich the taste. India have diverse agroclimatic conditions, the protected vegetable cultivation technology can be utilized for year round and off-season production of high value low volume vegetable crops, production of virus free high quality seedlings, quality hybrid seed production and as a tool for disease resistance breeding programmes. Among vegetables,

tomato is the first crop grown in polyhouse worldwide. Demand for tomatoes is usually strong due to the vine-ripe nature and general overall high level of eating quality. Selection of the most suitable cultivar is a pre-requisite for successful tomato cultivation in a greenhouse. The important characteristics related to cultivars include high fruit yield, high number of fruits, good shelf life, high TSS, disease resistance and freedom from cracking and green shoulder. Consumer's preference with respect to size, shape and colour of the variety also plays an important role in varietal selection.

The efficiency of selection largely depends upon the magnitude of variability present in the breeding population. Hence, knowledge of variability present in the gene pool of a crop species is essential to start a judicious breeding programme. Earlier variability used to be assessed by visual observation. Now biometrical methods are available for systematic assessment of genetic variability. Keeping this in view, the present investigation was aimed at assessing the genetic variability among thirty six genotypes of tomato.

Materials and Methods

The experiment was conducted at Vegetable Research Centre (V.R.C.), Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand during the year 2017-18. This university is situated in the foot hills of Shivalik range of Himalayas in the narrow belt called 'Tarai'. Geographically, it is situated at an altitude of 243.84m above mean sea level, and between 29.50° North latitude and 79.30° East longitude. The climate of the region is broadly humid subtropical with cool winter and hot dry summer. The soil of experimental field was sandy-loam with adequate drainage and optimum water holding capacity. The experimental material for this study consists of 36 genotypes of tomato.

Five competitive plants from each entry in each replication were randomly selected before flowering and tagged for the purpose of recording observations on different quantitative traits and their average values were used in the statistical analysis. The genotypes were studied for fifteen yield related traits *viz.*, days to 50 per cent flowering, days to first fruit set, days to first fruit ripening, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, internodal length (cm), average fruit weight (g), fruit length (cm), fruit width (cm), fruit shape index, plant height (cm), 100 seed weight (g), fruit yield per plant (kg) and fruit yield per hectare (t/ha). The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications according to procedure given by Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

The broad sense heritability (h^2_{bs}) was estimated by following the procedure suggested by Weber and Moorthy (1952). Genetic advance as per cent of mean was categorized as low, moderate and high as given by Johnson *et al.*, (1955).

Results and Discussion

Mean data of fifteen yield related traits were subjected to Analysis of variance (ANOVA) for Randomized Block Design (RBD) is presented in Table 1. The mean sum of square due to treatments was found highly significant for all yield related traits under study at 1% and 5% level of significance, which indicated that considerable amount of variability were present in the genotypes included in the study. Hence, there is ample scope for selection of promising genotypes in breeding programme for yield related traits. Similar results with

respect to analysis of variance also reported by Narolia *et al.*, (2012), Agarwal *et al.*, (2014), Reddy *et al.*, (2014), Singh *et al.*, (2014), Prajapati *et al.*, (2015), Kumar and Singh (2016), Kumar *et al.*, (2017a) and Kumar *et al.*, (2017b).

Effectiveness of any selection programme depends upon the existence of genetic variability present within the population. The assessment of genetic variability present in a given crop population can be determined by using the biometrical components such as range, variance, coefficient of variation, standard error and heritability.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are the best criteria to measure available variability. Heritability of a character is important in determining its response to selection. Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an effective breeding program.

Assessment of variability parameters revealed that there is lot of variation present among the genotypes studied. In general, the value of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters.

Similar results were also reported in tomato by Premalakshmi *et al.*, (2014), Rai *et al.*, (2016), Kumar *et al.*, (2017a) and Kumar *et al.*, (2017b).

Data presented in Table 2 revealed that high GCV and PCV estimates were observed for many traits *viz.*, number of fruits per plant (97.64 and 98.98%), average fruit weight

(40.64 and 41.31%), fruit yield per hectare (34.76 and 36.65%), fruit yield per plant (34.75 and 36.64%), number of flowers per cluster (30.37 and 31.17%) and number of fruits per cluster (26.74 and 27.60%). Moderate to high GCV and PCV was observed in fruit length (19.99 and 20.74%) and fruit width (19.60 and 21.17%).

Moderate to high GCV and PCV for these traits clearly indicate ample scope for yield improvement in tomato through selection due to the presence of sufficient variability genotypes studied. The GCV and PCV were low for days to first fruit ripening (6.64 and 6.94%), days to first fruit set (7.80 and 8.98%) and days to 50 per cent flowering (9.59 and 11.62%) whereas, moderate for fruit shape index (15.02 and 18.20%), 100 seed weight (13.82 and 14.97%) internodal length (13.64 and 16.11%) and plant height (12.01 and 15.99%).

The results of the present investigation agreed with the finding of Islam *et al.*, (2012), Saleem *et al.*, (2013), Singh *et al.*, (2014), Pujer *et al.*, (2015), Kumar and Singh (2016), Kumar *et al.*, (2017b) and Kaushal *et al.*, (2017).

Broad sense heritability estimates ranged from 56.37 per cent (Plant height) to 97.31 per cent (Number of fruits per plant) (Table 2).

Number of fruits per plant recorded maximum heritability (97.31%) followed by average fruit weight (96.80%), number of flowers per cluster (94.95%), number of fruits per cluster (93.86%), fruit length (92.89%), days to first fruit ripening (91.51%), fruit yield per plant (89.97%), fruit yield per hectare (89.97%), fruit width (85.72%), 100 seed weight (85.26%) and days to first fruit set (75.57%). The heritability estimates for these traits indicate that these characters are least influenced by the environment.

Table.1 Analysis of variance for fifteen yield related traits in tomato

S. N.	Characters	Mean sum of squares		
		Replication	Genotype	Error
		df	2	35
1	Days to 50 per cent flowering	24.482	40.012**	5.415
2	Days to first fruit set	25.817	48.642**	4.732
3	Days to first fruit ripening	0.190	96.107**	2.882
4	Number of flowers per cluster	0.889	44.451**	0.775
5	Number of fruits per cluster	0.073	12.547**	0.268
6	Number of fruits per plant	60.911	8,771.391**	79.967
7	Internodal length	0.126	7.068**	0.821
8	Average fruit weight	168.874	3,880.309**	42.306
9	Fruit length	0.108	2.774**	0.069
10	Fruit width	0.116	2.490**	0.131
11	Fruit shape index	0.021	0.089**	0.012
12	Plant height	577.632	8,026.012**	1,646.279
13	100 seed weight	0.0005	0.0076**	0.0004
14	Fruit yield per plant	0.0005	5.051**	0.181
15	Fruit yield per hectare	0.833	6,255.634**	224.116

* Significant at 5% level of probability

** Significant at 1% level of probability

Table.2 Estimation of genetic components and other genetic parameters for different yield related traits in tomato

S.N.	Characters	Range	General Mean	GCV	PCV	ECV	Heritability (%)	GA as % of mean
1	Days to 50 per cent flowering	30.33-43.67	35.43	9.59	11.62	6.57	68.05	16.29
2	Days to first fruit set	43.00-57.47	49.03	7.80	8.98	4.44	75.57	13.97
3	Days to first fruit ripening	68.20-95.13	84.01	6.64	6.94	2.02	91.51	13.08
4	No. of flowers per cluster	7.67-26.40	12.56	30.37	31.17	7.01	94.95	60.96
5	No. of fruits per cluster	5.47-14.80	7.57	26.74	27.60	6.84	93.86	53.36
6	No. of fruits per plant	27.39-355.73	55.12	97.64	98.98	16.22	97.31	198.43
7	Internodal length	7.80-13.40	10.58	13.64	16.11	8.56	71.72	23.80
8	Average fruit weight	9.90-159.93	88.00	40.64	41.31	7.39	96.80	82.38
9	Fruit length	2.11-6.55	4.75	19.99	20.74	5.53	92.89	39.68
10	Fruit width	1.83-6.35	4.52	19.60	21.17	8.00	85.72	37.39
11	Fruit shape index	0.86-1.66	1.07	15.02	18.20	10.27	68.14	25.55
12	Plant height	236.13-448.67	384.05	12.01	15.99	10.56	56.37	18.57
13	100 seed weight	0.13-0.42	0.35	13.82	14.97	5.75	85.26	26.29
14	Fruit yield per plant	1.34-6.83	3.67	34.75	36.64	11.60	89.97	67.90
15	Fruit yield per hectare	47.27-240.37	129.00	34.76	36.65	11.61	89.97	67.92

Internodal length (71.72%), fruit shape index (68.14%), days to 50 per cent flowering (68.05%) and plant height (56.37%) exhibited moderate level of heritability. However, low heritability (<50%) was not observed for any character. Low to moderate estimates of broad sense heritability indicates that these characters are highly influenced by environmental effects and the genetic improvement through selection in these traits is difficult due to masking effect of environment on the genotypic effects.

High estimates of genetic advance as percentage of mean (>20%) was observed for most of the characters under study *viz.*, number of fruits per plant (198.43%), average fruit weight (82.38%), fruit yield per hectare (67.92%), fruit yield per plant (67.90), number of flowers per cluster (60.96%), number of fruits per cluster (53.36%), fruit length (39.68%), fruit width (37.39%), 100 seed weight (26.29%), fruit shape index (25.55%) and internodal length (23.80%). High estimates of genetic advance as percentage of mean indicated that the preponderance of additive genetic effects in expression of these characters. Therefore, selection for these characters in segregating generations based on phenotypic performance would likely be more effective.

Moderate level of genetic advance as percentage of mean (10-20%) were observed for plant height (18.57%), days to 50 per cent flowering (16.29%), days to first fruit set (13.97%) and days to first fruit ripening (13.08%).

High heritability does not always mean high genetic advance. For yield improvement, selection of superior parents possessing better heritability and genetic advance for yield contributing traits is an essential prerequisite. Heritability in conjunction with genetic advance determines the best picture of the

amount of progress to be expected from selection and also the selection method to improve a character (Johnson *et al.*, 1955).

Based on the underlying facts, the traits under study were categorized into four different groups as per the analysis: First group included majority of the characters under study exhibited high estimates of broad sense heritability and high estimates of genetic advance as percentage of mean *viz.* number of flowers per cluster, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length, fruit width, 100 seed weight, fruit yield per plant and fruit yield per hectare.

High heritability and high genetic advance estimates for these characters indicated that these traits were less affected by environmental factors. This strongly indicated the preponderance of additive gene action involved in the expression of these characters and hence, there exists an ample scope for the improvement of concerned traits through direct selection. The second group of traits included days to first fruit set and days to first fruit ripening, which had high heritability estimates coupled with moderate genetic advance as per cent of mean. The third group consisted internodal length and fruit shape index which had moderate heritability coupled with high genetic advance. The fourth group included days to 50 per cent flowering and plant height which had moderate heritability estimates coupled with moderate genetic advance as per cent of mean.

For different characters, similar results were also observed by various researchers like Agarwal *et al.*, (2014), Mukul *et al.*, (2014), Premalakshmi *et al.*, (2014), Kumar *et al.*, (2016), Nalla *et al.*, (2016), Rai *et al.*, (2016), Kumar *et al.*, (2017a) and Kaushal *et al.*, (2017).

Thus, based on the findings of present investigation, it can be concluded that sufficient quantum of genetic variability was generated involving diverse genotypes of tomato, which indicates the existence of considerable scope for the improvement of these genotypes through selection and hybridization. Furthermore, moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except characters related to earliness which indicated predominant additive gene action thus these traits has ample scope for the improvement of concerned traits through selection.

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How to cite this article:

Ankit Panchbhaiya, Dinesh Kumar Singh, Priyanka Verma and Sanganamoni Mallesh. 2018. Estimation of Genetic Variability for Yield and Yield Related Traits in Tomato (*Solanum lycopersicum* L.) under Polyhouse Condition. *Int.J.Curr.Microbiol.App.Sci*. 7(09): 1553-1559. doi: <https://doi.org/10.20546/ijemas.2018.709.186>