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## Study of genetic variability for yield and its contributing characters in tomato (*Solanum lycopersicum* L.) under polyhouse condition

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#### Abstract

The present investigation was conducted on thirty six genotypes including hybrids of tomato for study of genetic variability for yield and its contributing traits. The analysis of variance (ANOVA) exhibited significant genotypic variance among the genotypes/hybrids for all the 12 characters were studied. High GCV and PCV estimates were observed for number of fruit per cluster, number of flower per cluster, average fruit weight, number of fruits per plant, fruits yield per plant and fruit yield per hectare. The characters number of fruits per plant recorded highest heritability followed by average fruit weight, number of flowers per cluster, number of fruits per cluster, fruit length, fruit yield per plant, fruit yield per hectare, fruit width and days of first fruit set. The high magnitude of genetic advance as per cent of mean was recorded for average fruit weight, number of fruits per plant, fruit yield per hectare, fruit yield per plant, number of flowers per cluster, number of fruit per plant, fruit length and fruit weight. Therefore selection for these characters in segregating generation based phenotypic performance would be more effective for further improvement of yield and its contributing traits in tomato.

**Keywords:** Tomato genetic variability, heritability, genetic advance

#### Introduction

Tomato ( $2n=24$ ) is an important vegetable of the world and now commonly used in all households. It contains red color pigment called lycopene (a carotenoid formed during ripening) and its presence in plasma has been related in reducing prostate cancer (Giovannucci *et al.*, 1999) [5]. It is being grown on 4.8 m ha area in world with annual production of 182.3 mt (Anonymous 2017) [2]. In northern plain of India, productivity of main season crop is relatively poor when compared with other productive regions since growing period coincides with harsh summer, uneven rains and heavy incidence of diseases and insect-pests. Therefore, evaluation of germplasm is imperative to understand the genetic background and breeding value for genetic improvement of tomato. Genetic variability is primary requirement for development of suitable varieties or hybrids for various horticultural traits. The phenotypic expression of the plant characters is mainly controlled by the genetic makeup of the plant and environment. The genetic variance of quantitative traits is composed of additive variance (heritable); non-additive variance (non-heritable); dominance and epistasis (non-allelic interaction). Therefore, it becomes important to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation besides heritability and genetic advance. Genetic advance can be used to predict the efficiency of selection. The information on heritability in conjunction with genetic advance is needed for effective selection (Johnson *et al.* 1955) [7].

#### 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 twelve 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)<sup>[16]</sup>. Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953)<sup>[4]</sup> 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)<sup>[26]</sup>. Genetic advance as per cent of mean was categorized as low, moderate and high as given by Johnson *et al.*, (1955)<sup>[7]</sup>.

### Results and Discussion

Mean data of twelve 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 sample 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)<sup>[15]</sup>, Agarwal *et al.*, (2014)<sup>[1]</sup>, Reddy *et al.*, (2014)<sup>[21]</sup>, Singh *et al.*, (2014)<sup>[25]</sup>, Prajapati *et al.*, (2015), Kumar and Singh (2016)<sup>[11]</sup>, Kumar *et al.*, (2017a)<sup>[12]</sup> and Kumar *et al.*, (2017b)<sup>[9]</sup>.

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 variance, standard error and heritability.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variance (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)<sup>[18]</sup>, Rai *et al.*, (2016)<sup>[20]</sup>, Kumar *et al.*, (2017a)<sup>[12]</sup> and Kumar *et al.*, (2017b)<sup>[9]</sup>.

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 studies. 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)<sup>[6]</sup>, Saleem *et al.*, (2013)<sup>[24]</sup>, Singh *et al.*, (2014)<sup>[25]</sup>, Pujer *et al.*, (2015)<sup>[19]</sup>, Kumar and Singh (2016)<sup>[11]</sup>, Kumar *et al.*, (2017b)<sup>[9]</sup> and Kaushal *et al.*, (2017)<sup>[8]</sup>.

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 (87.72%), 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. 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)<sup>[7]</sup>.

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), <sup>[1]</sup> Mukul *et al.*, (2014) <sup>[13]</sup>, Premalakshmi *et al.*, (2014) <sup>[18]</sup>, Kumar *et al.*, (2016) <sup>[10]</sup>, Nalla *et al.*, (2016) <sup>[14]</sup>, Rai *et al.*, (2016) <sup>[20]</sup>, Kumar *et al.*, (2017a) <sup>[12]</sup> and Kaushal *et al.*, (2017) <sup>[8]</sup>. 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.

**Table 1:** Analysis of variance for twelve yield and its contributing traits in tomato

S.N	Characters	df	Mean sum of squares		
			Replication	Genotype	Error
			2	35	70
1.	Days to 50 per cent flowering		24.48	40.01**	5.41
2.	Days to first fruit set		25.81	48.64**	4.73
3.	Days to first fruit ripening		0.19	96.10**	2.88
4.	Number of flowers per cluster		0.88	44.45**	0.77
5.	Number of fruits per cluster		0.07	12.54**	0.26
6.	Number of fruits per plant		60.91	8,771.39**	79.96
7.	Average fruit weight		168.87	3,880.30**	42.30
8.	Fruit length		0.10	2.77**	0.06
9.	Fruit width		0.11	2.49**	0.13
10.	Plant height		577.63	8,026.01**	1,646.27
11.	Fruit yield per plant		0.06	5.05**	0.18
12.	Fruit yield per hectare		0.83	6,255.63*	224.11

\*Significant at 5% level of probability

\*\* Significant at 1% level of probability

**Table 2:** Estimation of genetic components and other parameters for yield and it's contributing 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	29.33-44.67	34.43	9.50	11.62	6.37	65.05	16.29
2.	Days to first fruit set	43.00-57.47	49.03	7.80	8.93	4.34	75.57	13.97
3.	Days to first fruit ripening	68.20-95.13	84.01	6.63	6.94	2.02	89.51	13.08
4.	Number of flowers per cluster	7.67-26.40	12.56	30.37	31.17	7.01	94.95	60.96
5.	Number of fruits per cluster	5.47-14.80	7.57	26.74	27.63	6.74	93.86	53.36
6.	Number of fruits per plant	27.39-350.73	55.12	97.64	98.98	16.22	95.31	197.43
7.	Average fruit weight	9.90-158.93	88.00	40.64	41.31	7.39	93.80	81.38
8.	Fruit length	2.11-6.50	4.75	19.90	20.73	5.43	92.89	40.68
9.	Fruit width	1.83-6.35	4.52	19.60	21.17	8.10	85.72	37.39
10.	Plant height	236.13-448.67	380.05	12.01	15.98	10.56	56.37	18.57
11.	Fruit yield per plant	1.34-6.50	3.67	34.78	36.64	11.50	87.97	68.90
12.	Fruit yield per hectare	47.27-239.37	127.00	34.76	36.60	11.61	85.97	67.92

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