



## Variability, heritability and genetic advance in tomato genotypes

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### ABSTRACT

The present study was undertaken to explore the characters highly responsible for yield of tomato. Genotypic variability, heritability and genetic advance for yield and yield contributing characters were studied for 18 tomato genotypes and data were recorded on plant height at maturity, number of branches per plant, days to 50 percent flowering, number of fruits per cluster, number of fruits per plant, average fruit weight, number of locule per fruit and fruit yield per plant. The experimental results revealed that the phenotypic variation was high as compared to genotypic variation for all the traits studied and maximum for yield per plant, average fruit weight and plant height. High PCV, GCV and genetic advance was observed for yield per plant, number of fruits per plant and number of locules per fruit indicating the additive genetic effect. Phenotypic selection for their improvement could be achieved by simple selection.

**Key words:** Genetic advance, Heritability, Tomato, Variability.

### INTRODUCTION

Tomato (*Lycopersicon esculentum*L) is an annual crop belonging to the family Solanaceae, which consists of approximately 100 genera and 2500 species, including several other plants of agronomic importance such as potato, eggplant, pepper, and tobacco (Olmstead *et al.*, 2008). The annual production of tomato was more than 145.5 million tons, harvested from over 4.3 million hectares with an average yield of 336 kg ha<sup>-1</sup> (FAO, 2012). Throughout evolution, domestication and dispersion to different parts of the world, the genetic base of tomato was strongly narrowed, resulting in the loss of alleles of interest for breeding necessitating the importance of developing high yielding varieties. The basic tool to bring genetic improvement in a crop is to utilise the available genetic variability. If the variability with the population is largely due to the genetic cause with least environment effect, the probability of obtaining superior genotype is so visible. Yield improvement in tomato is a polygenic character and it is associated with agronomic, morphologic and physiologic traits. Hence direct selection is often misleading. The progress of breeding in such a population is primarily contributed by magnitude, nature of interaction of genotype, and environmental variation emphasising the importance to partition the observed variability into heritable and non-heritable traits with suitable genetic parameters such as heritability, genetic advance etc. The genotypic and phenotypic co-efficient of variation are useful in detecting amount of variability present in the genotypes whereas heritability and genetic advance would help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Patel *et al.*, 2013).

Hence the present study was undertaken to explore the characters highly responsible for yield of tomato by estimating variability, heritability, genetic advance and also to find out superior hybrids, and potential genotypes for further breeding programs.

### MATERIALS AND METHODS

Eighteen tomato germplasm accessions (LE 6, LE 14, LE 115, LE 7, LE 3, LE 104, LE 105, LE 23, LE 10, LE 355, LE 13, LE 118, LE 116, LE 19, LE 15, LE 11, LE 22 and LE 150) were collected from Horticulture College and Research Institute, Tamil Nadu Agricultural University, Coimbatore (TNAU). Field experiments were conducted during 2016-2017 with 18 genotypes in randomized block design (RBD) with three replications in which 21 days old seedlings were transplanted in two rows of 5m length with a spacing of 45 x 90 cm. All the recommended agronomic and plant protection techniques were adopted. In each genotype, Ten plants were selected for recording various observations *viz.*, plant height (cm), number of branches per plant, days to 50% flowering, number of fruits per cluster, number of fruits per plant, average fruit weight (g), number of locules per fruit and fruit yield per plant(g).

Plant height was measured just before last harvesting in centimeters from the ground level to the top of the primary branch on 10 random plants from the middle of the plot, data was averaged and expressed in cm plant<sup>-1</sup>. Total number of branches in each plant was recorded and expressed as number of branches. Number of days taken from sowing to 50 per cent flowering in each genotype was recorded and the mean value was expressed as days to 50% flowering. Number of fruits per cluster was counted at the time of first

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harvest on ten random plants. The number of fruits was counted at each harvest and cumulative total of all the harvest were taken together as number of fruits per plant. The data were recorded on ten randomly selected plants in a plot and averaged. Average fruit weight was measured in gram. The data were recorded on ten randomly selected fruits in a plot and averaged. The number of locules was counted after cutting the fruit transversely and counting the locules isolated by septae. The data were recorded on ten randomly selected fruits in a plot and averaged. Fruit yield per plant was recorded from randomly selected plants from each replication and average was calculated.

**Analysis of variance:** The mean and variances were analyzed based on the formula given by Singh and Chaudhary (1977). The analysis of variance (ANOVA) for all characters was carried out separately and presented in Table 1. The values of mean, range and coefficient of variance were presented in Table 2. Heritability was estimated as per the procedure presented by Burton and De Vane (1953), Johnson *et al.* (1955) and Hanson *et al.* (1956). Genetic advance at 5 per cent selection intensity was worked out. The value of 'k' was taken as 2.06 assuming 5 percent selection intensity. In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed.

$$\text{Genetic advance as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

**RESULTS AND DISCUSSION**

**Genetic variability:** The mean performance of 18 genotypes for eight characters exhibited a wide range of variations and the mean performances were observed for all the traits (Table 1). Analysis of variance was carried on various yield and yield contributing traits for studying the variation. Variance due to genotypes were highly significant for all the characters studied, indicating that the genotypes selected for the present study were genetically different. The estimation of these variances showed that genotypic variations contributed maximum to the phenotypic variations for all the traits studied (Table 3). The analysis of variance revealed significant mean square estimates for all the characters indicating sufficient genetic difference among the genotypes. The variation in the genotypes would be helpful in the development of superior varieties in further breeding programme.

The phenotypic variance ranged from 12.12 to 35.24 and the lowest variance was recorded for days to 50 per cent flowering and maximum was recorded for number of fruits per plant followed by fruit yield per plant and number of locules per fruit (Table 3). The genotypic coefficient of variance (GCV) ranged from 11.95 to 35.06. High GCV was observed for number of fruits per plant followed by fruit yield per plant and number of locules per fruit whereas the lowest GCV was recorded in days to 50% flowering (Table 3).

The investigation revealed that the phenotypic variation was high as compared to genotypic variation for all the traits studied indicating the influence of environment and it was found maximum for fruit yield per plant, average fruit weight and plant height. These results are in agreement

**Table 1:** Analysis of variance for eight characters in tomato genotypes.

Source	df	Mean sun of square							
		Plant height	Number of branches per plant	Days to 50% flowering	Number of fruits per cluster	Number of fruits per plant	Average fruit weight	Number of locules per fruit	Fruit yield per plant
Replication	2	0.52	0.01	0.61	0.01	1.75	1.86	0.01	2.14
Genotype	17	398.81**	8.51**	47.38**	2.94**	144.68**	862.93**	4.49**	94654.25**
Error	34	1.35	0.03	0.42	0.01	4.97	5.36	0.02	14572.11

\*\*Significant at 1 per cent level

**Table 2:** Descriptive statistics for yield and yield component traits in tomato genotypes.

Traits	Mean	Range		Standard error	Coefficient of Variance
		Minimum	Maximum		
Plant height (cm)	94.98	82.52	121.42	0.67	1.22
Number of branches per plant	8.48	6.56	12.52	0.11	2.30
Days to 50% flowering	33.08	27.00	38.25	0.37	1.96
Number of fruits per cluster	4.78	3.21	6.58	0.08	2.90
Number of fruits per plant	62.39	30.34	100.86	1.28	3.57
Average fruit weight (g)	65.82	46.41	103.52	1.33	3.51
Number of locules per fruit	4.44	2.56	6.60	0.08	3.26
Fruit yield per plant (kg)	1915.74	970.00	2883.33	69.69	6.30

**Table 3:** Genetic parameters for various traits in tomato genotypes.

Trait	GCV (%)	PCV (%)	Heritability ( $h_2$ )	GAM (%)
Plant height	12.12	12.18	98.99	24.83
Number of branches per plant	19.80	19.94	98.66	40.52
Days to 50% flowering	11.95	12.12	97.37	24.30
Number of fruits per cluster	20.67	20.87	98.06	42.16
Number of fruits per plant	35.06	35.24	98.97	71.85
Average fruit weight	25.68	25.92	98.16	52.41
Number of locules per fruit	27.52	27.71	98.61	56.29
Fruit yield per plant	29.09	29.77	95.52	58.58

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation

$h_2$ %= heritability (broad sense) GA=Genetic advance, GAM= Genetic advance as percent mean.

with the observations of Golani *et al.* (2007) and Henareh (2015). Sajjan (2016) evaluated 300  $F_6$  recombinant inbred lines and observed that the genotypes exhibited a wide range of variability and phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied. Mehedi Hasan *et al.* (2016) used 30 tomato (*Lycopersicon esculentum* L.) genotypes to study genetic variability for yield and yield-contributing traits and found existence of high degree of variation among the genotypes for the studied traits. They also found that yield contributing traits recorded higher phenotypic co-efficient of variation when compared to genotypic co-efficient of variation indicating considerable environmental influences on them.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found higher for number of fruits plant<sup>-1</sup>, average fruit weight, yield per plant and number of locules per fruit, which suggested prevalence of greater phenotypic and genotypic variability among the accessions. Wide difference between GCV and PCV for number of branches per plant and days to 50 per cent flowering implied its susceptibility to environmental fluctuation. In the present study, highest estimates of GCV and PCV were recorded for fruit yield per plant. Pinnamwar and Dhatt (2017) estimated combining ability for different characters by crossing 3 male sterile lines and 32 testers and found that two lines, 30A and 97A, and six testers, CT-1201, CT-1202, CT-1204, CT-1205, CT-1207, CT-1217 as good general combiners.

**Heritability and genetic advance:** Genetic variability may be due to additive, dominance and epistatic gene action. In the present study, the broad sense heritability estimates were high for all the traits of interest and it ranged from 95.52 to 98.99. High heritability was recorded for all the traits and the maximum heritability was recorded in plant height, followed by number of fruits per plant, number of branches per plant, number of locules per fruit, average fruit weight and number of fruits per cluster respectively whereas lower heritability was recorded for fruit yield per plant respectively

(Table 3). Such high values of heritability for plant height, number of branches per plant, average fruit weight, number of fruits per plant and number of fruits per cluster implies that it may be due to environment influence and selection based on phenotypic performance would be reliable. In traits with high heritability, genotypic variance is more than environmental variance and these characters could be considered and exploited for selection in earlier generations. Whereas, in the traits with low heritability, influence of environmental factors is strong for their expression and genotype selection based on these characters may be postponed to the later generations.

High genetic advance was observed for number of fruits per plant, fruit yield per plant, number of locules per fruit and average fruit weight. These results are in close conformity with that of Golani *et al.* (2007) and Xavier Flemin *et al.* (2016). Singh (2009) and Ara (2009) also reported high heritability and genetic advance as per cent of mean (GAM) for plant height, number of branches per plant, average fruit weight, number of locules per fruit, number of fruits per plant and fruit yield per plant, indicating predominance of additive gene action for these characters. These traits maybe controlled by additive gene action. High heritability with low genetic advance was reported for plant height, days to 50 % flowering, number of branches per plant and number of fruits per plant which implies that it is controlled by non-additive gene action.

## CONCLUSION

The information generated from this study can be exploited for further breeding programme in tomato. High heritability (> 75 %) coupled with high genetic advance has been recorded for plant height, number of branches per plant, average fruit weight, number of locules per fruit, number of fruits per plant and fruit yield per plant. These traits which exhibited high heritability in broad sense and high genetic advance as percent mean are largely governed by additive gene action and hence there is further scope for effective improvement through selection.

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