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## Estimation of gene action involved in inheritance of yield and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

**Gaurav Singh, GC Yadav, Angad Singh, Devraj Singh and Manjeet Kumar**

**Abstract**

The present investigation entitled "Estimation of gene action involved in inheritance of yield and yield attributing traits in Tomato (*Solanum lycopersicum* L.)" was conducted during *Rabi* seasons of 2017-18 (E<sub>1</sub>) and 2018-19 (E<sub>2</sub>) to study the, nature and magnitude of gene action using diallel mating design at the Main Experiment Station (MES) of the Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) India. Ten diverse parents of tomato were crossed in a diallel fashion (excluding reciprocals) for generating experimental material. All the ten parents and their 45 hybrids were grown in Randomized Block design with three replications. Observations were recorded on the 16 characters *viz.*, Days to 50 per cent flowering, Days to first fruit harvest, Plant height (cm), Number of primary branches per plant, Number of fruits per cluster, Number of fruits per plant, Average fruit weight (g), Pericarp thickness (mm), Number of locules per fruit, Fruit length (cm), Fruit diameter (cm), Marketable fruit yield per plant (kg), Total fruit yield per plant (kg), Total soluble solids (%), Titrable acidity (%), Ascorbic acid content (mg/100 g fresh fruit). The data were analyzed to fulfil the following objectives to estimate gene action for yield and its component traits. Analysis of variance revealed significant differences for the parents, F<sub>1</sub>'s and parents vs. F<sub>1</sub>'s for all the characters indicating wide variation except fruit circumference in both years and fruit length in Y<sub>1</sub>. Both additive and dominance variance were found important in the inheritance of most of the traits, whereas dominance variance were more prominent than the additive variance. Mean degree of dominance showed over dominance for the most of the traits.

**Keywords:** Tomato, gene action, additive, non additive, yield

**Introduction**

Tomato (*Solanum lycopersicum* L.) is one of the most popular solanaceous vegetable crop, having chromosome number  $2n=2x=24$ . Tomato universally treated as "Protective Food" is being extensively grown as annual plant all over the world. Tomato is a warm season crop reasonably resistant to heat, drought and grows under wide range of soil and climatic conditions. It is an herbaceous, annual to perennial, prostrate and sexually propagated plant, mostly grown as annual plant. Flowers are normally perfect; there are four to eight flowers in each compound inflorescence. There is a light protective anther cone surrounding the stigma leading to self-pollination. Anthesis occurs from 7:00-8:00AM and dehiscence from 9:00-11:00AM. It is a day neutral plant and mainly self-pollinated but a certain percentage of cross-pollination also occurs. Tomato is an herbaceous sprawling plant growing up to 1-3 m in height with weak woody stem. The flowers are yellow in colour and the fruits of cultivated varieties vary in size from cherry tomatoes, about 1-2 cm in size to tomatoes, about 10 cm or more in diameter. Most cultivars produce red fruits when ripe. The plants have taproot system and two types of growth habit, determinate & indeterminate. Fruits bearing of different types. Determinate or bush types bear a full crop at once and top off at a specific height. They are often good choices for container growing and determinate types are preferred by commercial growers who wish to harvest a whole field at one time, or home growers which are interested in canning. Indeterminate cultivars develop into vines that never top off and continue producing until killed by frost they are preferred by home growers who wish ripe fruit throughout the season. As an intermediate form, there are plants sometimes known as "vigorous determinate" or "semi-determinate"; these top off like determinates but produce a second crop after the initial crop. Many, if not all, heirloom tomatoes are indeterminate. There is an urgent need to initiate multiple cross breeding programme to satisfy dominance hypothesis with accumulation of maximum number of favorable dominant alleles. One possible way to achieve is to use the potential F<sub>1</sub> possessing all the consumer's requirements to

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develop double cross hybrids. Once, double cross hybrids are produced, they could be utilized for recovering transgressive segregants for further development of potential varieties or used directly. Tomato being most important to growers, consumers and to the processing industry, there is pressing need to increase its productivity to fulfill the increasing demand. Although, a lot of genetic studies have been done in tomato and as a consequence a large number of varieties/hybrids have been developed. However, there is still lack of adequate information for a very strong improvement programme to increase area and quality specific varieties. Development of hybrids with extreme earliness, quality, uniformity and adaptability to adverse conditions, is easily possible in tomato because it is a self-pollinated crop.

### Material and Methods

The present investigation entitled "Study on gene action involved in inheritance of yield and yield attributing traits in Tomato (*Solanum lycopersicum* L.)" was conducted during Rabi seasons of 2017-18 (E<sub>1</sub>) and 2018-19 (E<sub>2</sub>) to study the nature and magnitude of gene action using diallel mating design at the Main Experiment Station (MES) of the Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) India. The knowledge of the nature and magnitude of gene effects controlling inheritance of characters related to productivity would add in the choice of efficient breeding methods and thus accelerate the pace of its genetic improvement and also breaking the yield barriers. The diallel cross techniques was investigated by many researchers such as Sprague and Tatum (1942), Griffing (1956b)<sup>[8]</sup> and Jinks *et al.* (1969), who discussed the theory of diallel crosses and gave the procedure for estimating certain genetic parameters in term of gene models in varying degrees of complexity. A diallel cross is a set of all possible matings between several genotypes, which may be individuals, clones, homozygous lines, etc. Such crosses are used to estimate general and specific combining abilities of lines and crosses respectively. For 'n' inbred lines, the possible F<sub>1</sub>'s are n(n-1)/2, which are to be tested in a suitably replicated randomized design. With facilities available for testing a limited number of crosses, a diallel cross therefore will be possible only when n is relatively small. The selected parental lines namely NDT-Sel-1, NDT-Sel-2, NDT-Sel-3, NDT-Sel-5, NDT-Sel-6, NDT-Sel-8, NDT-Sel-9, Narendra Tomato-7, NDT-Sel-10 and Narendra Tomato-4 were crossed in the all possible combinations, excluding reciprocals, during the Rabi season of 2016-17. These 45 F<sub>1</sub>s along with their parents were evaluated for the study of heterosis, combining ability, gene action, heritability and genetic advance for 18 fruit yield and quality attributing traits. The ten diverse parental line selected their characteristics and crossed in diallel mating design as suggested by Griffing (1956b)<sup>[8]</sup> to produce 45 hybrids in Rabi season of 2016-17 and evaluated during Rabi season of 2017-18 and 2018-19. The experiment laid out in randomized block design with three replication and 55 treatment including 10 parents. The observation were recorded yield and its contributing traits in tomato, Days to 50 per cent flowering, Days to first fruit harvest, Plant height (cm), Number of primary branches per plant, Number of fruits per cluster,

Number of fruits per plant, Average fruit weight (g), Pericarp thickness (mm), Number of locules per fruit, Fruit length (cm), Fruit diameter (cm), Marketable fruit yield per plant (kg), Total fruit yield per plant (kg), Total soluble solids (%), Titrable acidity (%), Ascorbic acid content (mg/100 g fresh fruit).

### Result and Discussion

The number of groups of genes that control the character ( $\hat{h}^2/\hat{H}_2$ ) and exhibit dominance was -0.01 and -0.01 in E<sub>1</sub> and E<sub>2</sub>, respectively. The 'r' values were positive and very low in E<sub>1</sub> and positive in E<sub>2</sub> which showed excess of dominant genes during both the seasons (E<sub>1</sub>, E<sub>2</sub>). The values of t<sup>2</sup> and (1-b/SEb) for days to 50% flowering were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E<sub>1</sub>, E<sub>2</sub>). For Days to first fruit harvest The value of proportion of genes +/- ( $\hat{H}_2/4\hat{H}_1$ )<sup>1/2</sup> were found 0.22 and 0.22 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. For plant height the number of gene groups that control the character ( $\hat{h}^2/\hat{H}_2$ ) and exhibit dominance was 0.00 and 0.01 in E<sub>1</sub> and E<sub>2</sub>, respectively. The 'r' values were positive in both E<sub>1</sub> and E<sub>2</sub> which showed excess of dominant genes during both the seasons (E<sub>1</sub>, E<sub>2</sub>). Primary branches of plant were found 0.21 and 0.21 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. For Fruits per plant the value of proportion of genes +/- ( $\hat{H}_2/4\hat{H}_1$ )<sup>1/2</sup> were found 0.21 and 0.21 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. Average fruit weight (g) were found 0.19 and 0.19 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. For Pericarp thickness (cm) value of proportion of genes +/- ( $\hat{H}_2/4\hat{H}_1$ )<sup>1/2</sup> were found 0.23 and 0.23 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. Locules per fruit were found 0.20 and 0.22 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. For Fruits per cluster value of proportion of genes +/- ( $\hat{H}_2/4\hat{H}_1$ )<sup>1/2</sup> were found 0.19 and 0.19 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The values of t<sup>2</sup> and (1-b/SEb) for length of fruits were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E<sub>1</sub>, E<sub>2</sub>). Diameter of fruits revealed of proportion of genes +/- ( $\hat{H}_2/4\hat{H}_1$ )<sup>1/2</sup> were found 0.21 and 0.21 in E<sub>1</sub>, and E<sub>2</sub> respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. These above findings are similar to that of Rani and Veeraragavathatham (2010)<sup>[10]</sup>, Dutta *et al.*, (2013)<sup>[7]</sup>, Amaefula *et al.* (2014)<sup>[3]</sup>, Shankar *et al.*, (2014)<sup>[13]</sup>, Shepa *et al.*, (2014)<sup>[17]</sup>, Yadav *et al.*, (2017)<sup>[19]</sup>.

**Table 1:** Estimates of components of variation and their related statistics in 10 × 10 diallel crosses of tomato over two seasons (E<sub>1</sub>, E<sub>2</sub>)

Components of variation and related statistics	Seasons	Days to 50% flowering	Days to first fruit harvest	Plant height (cm)	Primary branches per plant	Fruits per plant	Average fruit weight (g)	Pericarp thickness (cm)	Locules per fruit	Fruits per cluster
$\hat{D}$ (Additive effect)	E <sub>1</sub>	7.88*±0.24	1.11*±0.04	1.58±130.54	5.03±9.94	191.35±994.56	85.99*±9.56	35.60*±0.05	0.02±0.39	0.00±0.02
	E <sub>2</sub>	8.16*±0.26	1.16*±0.05	1.74±143.92	5.05±10.95	195.01±1095.46	96.09*±1.46	39.27*±0.06	0.03±0.43	0.00±0.02
$\hat{H}_1$	E <sub>1</sub>	2.61*±0.48	2.36*±0.10	22.73±33.81	10.72±21.16	512.80±283.48	183.04*±28.38	75.77*±0.11	0.00±0.10	0.00±0.04

	E <sub>2</sub>	2.73*±0.53	2.46*±0.11	22.81±37.30	10.75±23.32	569.47±306.63	204.53*±30.66	83.59*±0.12	0.00±0.11	0.00±0.04
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	E <sub>1</sub>	3.04*±0.41	2.00*±0.08	20.49±29.31	9.11±17.98	479.58*±217.05	155.56*±21.75	64.40*±0.09	0.00±0.08	0.00±0.03
	E <sub>2</sub>	3.18*±0.46	2.09*±0.09	20.45±32.32	9.13±19.82	530.88*±232.93	173.83*±23.30	71.04*±0.11	0.00±0.09	0.00±0.04
$\hat{F}$ (Mean Fr over arrays)	E <sub>1</sub>	-0.06±0.17	2.56*±0.10	1.21±33.20	11.62±22.94	36.34±269.18	198.41*±26.18	82.14*±0.12	0.00±0.07	0.00±0.04
	E <sub>2</sub>	-0.11±0.19	2.67*±0.12	1.52±36.69	11.65±25.28	30.95±312.32	221.70*±31.24	90.61*±0.14	0.00±0.07	0.00±0.05
$\hat{h}^2$	E <sub>1</sub>	-0.05±0.01	1.34*±0.05	-0.62±2.64	6.10±17.98	2.80±17.10	104.13*±19.10	43.10*±0.06	0.00±0.01	0.00±0.02
	E <sub>2</sub>	-0.04±0.01	1.40*±0.06	-0.53±2.87	6.11	6.66±16.22	116.35*±10.26	47.55*±0.07	0.00±0.02	0.00±0.02
$\hat{E}$ (Environmental component)	E <sub>1</sub>	1.16*±0.02	0.33*±0.01	3.41*±0.17	1.51±2.99	7.07±5.22	25.92*±5.22	10.73*±0.01	0.00±0.00	0.00±0.00
	E <sub>2</sub>	1.20*±0.02	0.35±0.16	3.41*±0.18	1.52±3.30	7.96±6.54	28.97*±5.25	11.84*±0.01	0.00±0.00	0.00±0.00
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	E <sub>1</sub>	0.57	3.79	1.63	1.42	0.50	0.53	0.40	0.36	0.75
	E <sub>2</sub>	0.57	3.62	1.70	1.42	0.50	0.52	0.40	0.38	0.75
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	E <sub>1</sub>	0.29	0.22	0.23	0.21	0.21	0.19	0.23	0.20	0.19
	E <sub>2</sub>	0.29	0.22	0.23	0.21	0.21	0.19	0.23	0.22	0.19
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E <sub>1</sub>	0.98	1.22	1.12	1.70	1.66	1.67	1.31	1.23	1.21
	E <sub>2</sub>	0.97	1.27	1.09	1.70	1.66	1.73	1.36	1.24	1.21
$\hat{h}^2/\hat{H}_1$ (Number of gene groups)	E <sub>1</sub>	-0.01	-0.03	0.00	0.02	0.09	0.07	-0.02	0.19	0.10
	E <sub>2</sub>	-0.01	-0.02	0.01	0.03	0.08	0.07	-0.01	0.07	0.10
r (Correlation coefficient)	E <sub>1</sub>	0.03	-0.53	0.47	0.42	0.83	0.84	0.73	0.50	-0.07
	E <sub>2</sub>	0.22	-0.53	0.45	0.42	0.83	0.84	0.72	0.46	-0.06
t <sup>2</sup>	E <sub>1</sub>	8.24	30.83	3.59	0.07	0.01	0.18	0.25	0.04	3.95
	E <sub>2</sub>	8.37	30.08	3.96	0.06	0.01	0.16	0.22	0.72	3.89
(1-b/SEb)	E <sub>1</sub>	0.09	-0.14	0.27	0.46	0.85	0.77	0.65	0.54	-0.03
	E <sub>2</sub>	0.09	-0.15	0.25	0.46	0.85	0.78	0.64	0.60	-0.03

\*, \*\* Significant at 5 per cent and 1 per cent probability levels, respectively

## Count...

Components of variation and related statistics	Seasons	Length of fruits (cm)	Diameter of fruits (cm)	Marketable fruit yield per plant (kg)	Total fruit yield per plant (kg)	Total soluble solids (%)	Titration acidity (%)	Ascorbic acid content (mg/100g)
$\hat{D}$ (Additive effect)	E <sub>1</sub>	0.64±0.57	0.02±0.02	0.60*±0.23	0.07±0.14	2.38*±0.00	0.14*±0.00	0.58±5.99
	E <sub>2</sub>	0.66±0.63	0.02±0.02	0.66*±0.23	0.08±0.14	2.63*±0.00	0.16*±0.00	0.63±6.10
$\hat{H}_1$ (Dominance effect)	E <sub>1</sub>	0.08±0.13	0.05±0.05	0.34±0.69	0.15±0.30	0.90*±0.01	0.31*±0.00	0.11±0.69
	E <sub>2</sub>	0.10±0.14	0.06±0.05	0.38±0.69	0.17±0.31	1.01*±0.01	0.35*±0.00	0.13±0.74
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	E <sub>1</sub>	0.06±0.12	0.04±0.04	0.26±0.54	0.13±0.25	0.76*±0.01	0.27*±0.00	0.10±0.39
	E <sub>2</sub>	0.08±0.13	0.05±0.04	0.29±0.54	0.14 ±0.26	0.85*±0.01	0.29*±0.00	0.10±0.43
$\hat{F}$ (Mean Fr over arrays)	E <sub>1</sub>	0.04±0.06	0.05±0.05	0.08*±0.04	0.17±0.33	0.45*±0.00	0.34*±0.00	0.04±0.50
	E <sub>2</sub>	0.05±0.07	0.06±0.05	0.10*±0.03	0.18±0.33	0.51*±0.00	0.38*±0.00	0.04±0.53
$\hat{h}^2$	E <sub>1</sub>	0.01*±0.007	0.02±0.02	0.02±0.08	0.08±0.17	0.23*±0.00	0.18*±0.00	-0.00±0.12
	E <sub>2</sub>	0.00±0.00	0.03±0.03	0.03±0.08	0.09±0.17	0.25*±0.00	0.19*±0.00	0.00±0.13
$\hat{E}$ (Environmental component)	E <sub>1</sub>	0.01*±0.005	0.00±0.00	0.02±0.04	0.02±0.04	0.08*±0.00	0.04±0.00	0.03±0.41
	E <sub>2</sub>	0.02*±0.00	0.00±0.00	0.02±0.05	0.02±0.04	0.08*±0.00	0.05*±0.00	0.04±0.43
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	E <sub>1</sub>	0.61	0.54	0.52	0.47	1.72	1.52	0.34
	E <sub>2</sub>	0.62	0.45	0.52	0.47	1.73	1.46	0.35
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	E <sub>1</sub>	0.21	0.21	0.20	0.23	0.19	0.21	0.14
	E <sub>2</sub>	0.21	0.21	0.20	0.23	0.19	0.21	0.14
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E <sub>1</sub>	1.36	1.17	1.41	0.78	1.12	1.12	0.78
	E <sub>2</sub>	1.37	1.17	1.40	0.78	1.09	1.11	0.77
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	E <sub>1</sub>	0.30	-0.07	0.9	0.03	0.15	0.13	0.31
	E <sub>2</sub>	0.30	-0.07	0.20	0.03	0.15	0.15	0.30
R (Correlation coefficient)	E <sub>1</sub>	0.88	0.75	0.88	0.89	0.55	0.74	0.96
	E <sub>2</sub>	0.88	0.75	0.88	0.90	0.55	0.75	0.96
t <sup>2</sup>	E <sub>1</sub>	0.52	0.65	0.09	7.22	3.10	11.88	0.56
	E <sub>2</sub>	0.52	0.64	0.08	7.19	15.08	10.02	0.56
(1-b/SEb)	E <sub>1</sub>	0.78	0.62	0.93	0.60	0.20	0.35	1.03
	E <sub>2</sub>	0.78	0.62	0.92	0.60	0.20	0.38	1.03

\*, \*\* Significant at 5 per cent and 1 per cent probability levels, respectively

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