

GENETIC ANALYSIS FOR FRUIT YIELD AND ITS COMPONENT TRAITS IN TOMATO (*SOLANUM LYCOPERSICUM* L.) POPULATION

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Abstract: The present investigation was undertaken to study the genetics of fruit yield and yield components traits through generation mean analysis, which facilitates the idea about nature of gene action (Additive, Non-additive) as well as epistasis interaction involved in the expression of the trait. A six generations [Parents, F₁, backcrosses (B₁ and B₂) and F₂] of the five crosses of tomato, 1) GAT-4 × AVTOV 1002, 2) ATL-11-05 × AVTOV 1002, 3) GT-2 × AVTOV 1008, 4) AVTOV 1007 × AVTOV 1005/2 and 5) IIHR-329 × IIHR-335 were grown in compact family block design at the field of Main Vegetable Research Station, Anand Agricultural University, Anand. Both type of additive and non-additive gene effects found significant for majority of the yield contributing and biochemical traits in the studied five crosses. The magnitude of dominant gene effects was much higher than the additive gene effects in all the five crosses for yield contributing traits. This indicated predominant effect of dominance gene effects in the inheritance of yield and yield attributing traits involved in the expression of the traits. Contribution of duplicate type of epistasis, indicating complex inheritance pattern for the traits. Recurrent selection and bi-parental mating should be used for the improvement of the characters which shows the predominant dominant gene effect. However, complementary epistasis also found in some of cross combinations suggesting selection can be useful in subsequent generations for improvement of these characters.

Keywords: Additive, Bi-parental mating, *Solanum lycopersicum*, Tomato

INTRODUCTION

Vegetables are increasingly recognized as an essential food for nutritional security and beneficial for health of mankind. At present, the global value of fruit and vegetable production exceeds that of all food grains combined, owing to their nutritional as well as economic power. Among all the vegetable crops, tomato is at top among all economic crops in the world. It is one of the most important vegetable crops and now a commercially growing crop. It is widely grown all over tropical, sub-tropical and temperate regions of the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. Therefore, its cultivation is also a key economic activity for low-income farmers. The red pigment in tomato (lycopene) is now being considered as the “world’s most powerful natural antioxidant”. It may interfere with oxidative damage to DNA and lipoprotein and inhibits the oxidation of LDL cholesterol (Gester, 1997). Therefore, tomato is one of the most important “protective foods.”

Tomato (*Solanum lycopersicum* L.) belongs to nightshade family *Solanaceae* having diploid (2n=2x=24) chromosome number and are considered to have evolved primarily by genic change rather than large-scale chromosomal rearrangements (Anderson *et al.*, 2010). It has a genome size of 950 mb. Tomato ranks third in priority after potato and onion in India. India ranks second in the area (0.814 million ha) and production (19.197 million tonnes)

with the productivity of 24.93 metric tonnes per hectare in the world (Anon., 2019). In Gujarat, tomato is grown in 47.98 million ha with an annual production of 1382.00 metric tonnes and productivity of 29 metric tonnes per hectare, respectively (Anon., 2019).

The utmost goal of plant breeding programme is to develop best hybrids or improved cultivars superior to those already under the commercial cultivation. Considerable amount of important work has already been done in this crop, but great amount of information is still needed for the understanding of genetics of fruit yield, yield attributing traits and quality parameters of tomato crop, growing in middle Gujarat agro-climatic condition.

Genetic improvement depends primarily on the effectiveness of selection among progenies that differ in genetic value. Epistatic effects involving genic combinations of fixed and non-fixed genes are exhibit and contribute to the genotypic mean of population. Genetic analysis using generation mean analysis has been used to estimate the gene actions controlling the quantitative traits, and knowledge of additive, dominance and epistatic effect, which would benefit breeders in designing the most appropriate breeding approaches for developing a suitable and superior tomato variety. Total six number of generations of five different families were used to study the gene actions of morphological and biochemical traits such as fruit yield and its components to estimate the additive, dominant and epistatic effects of the fruit yield and quality traits in selected tomato population.

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MATERIAL AND METHODS

Population development

The breeding material for this study was developed from nine parents *viz.*, GAT-4, AVTOV 1002, ATL-11-05, GT-2, AVTOV 1008, AVTOV 1007, AVTOV 1005/2, IIHR-329 and IIHR-335, which were selected on the basis of their wide variation in morphological characters (Fruit size, shape and biochemical content) and geographical origin.

The first filial (F_1) and backcrosses generations (B_1 and B_2) were produced by hand-emasulation and pollination. The crossing and selfing procedure to obtain the desired evaluation material were done during the *rabi* season of the year 2017-18.

Experimental design

Six generations that included the parents, first filial, F_2 generation and backcross of five crosses were grown in the *rabi* season of 2018-19 for evaluation, in ratio of 1:1:1:4:2:2 in compact family block design with three replications. Field operations and other post transplanting operations were practiced in vogue on Main Vegetable Research Station, AAU, Anand both in nursery as well as in the field. Experimental field was fertilized at the rate of 100 N: 50 K_2O : 50 P_2O_5 Kg per hectare in the form of urea, DAP and Muriate of Potash.

Data collection and statistical analysis

Various observations for different fifteen morphological and biochemical traits under study were recorded on plants selected randomly from each experimental unit and each replication *i.e.*, Five plants in each P_1 , P_2 and F_1 , ten plants in each B_1 and B_2 and twenty plants in each F_2 . An individual observation of each generation of each family was considered for statistical analysis. All five families were evaluated for days to first flowering, plant height (cm), primary branches per plant, fruits per plant, fruit weight (g), fruit length (cm), fruit girth (cm), locules per fruit, pericarp thickness (mm), fruit yield per plant (kg), seeds per fruit, 1000 seed weight (g), total soluble solids ($^{\circ}$ brix), lycopene content (mg) and titrable acidity (%).

Analysis of variance

The differences between families were tested through Compact Family Block Design as reviewed by Panse and Sukhatme (1969), whereas differences among generations within each family was tested through Randomized Complete Block Design as suggested by Snedecor (1938) and reviewed by Panse and Sukhatme (1969).

Estimation of scaling test and gene action

The most important condition in analyzing gene effects is assessing the adequacy of the additive-dominance model using a scaling test. Four scales, *i.e.*, A, B, C and D, (Hayman and Mather, 1955) were estimated using following equations for their values and variances using mean values, $A = 2B_1 - P_1 - F_1$, $B = 2B_2 - P_2 - F_1$, $C = 4F_2 - 2F_1 - P_1 - P_2$ and $D = 2F_2 - B_1 - B_2$. The significance of any of the scaling test

indicated the presence of non-allelic interactions. The non-significance of all scales indicated the absence of non-allelic interaction. The adequacy of an additive-dominance model (Mather, 1949 and Hayman and Mather, 1955) later suggested the estimation of gene effects using the three-parameter model, whereas the non-adequacy of the model suggested the use of the six-parameter model. Joint scaling test of Cavalli (1952) also applied to test adequacy of 3 and 6-parameter model. When, this simple additive-dominance model failed to explain the variation in generation means, the six-parameter perfect fit solution advocated by Hayman (1958) was used to estimate main and interaction effects.

RESULTS AND DISCUSSION

Mean square values obtained from analysis of variance for all the studied fifteen traits are given in Table 1. The results indicated that most of the evaluated traits showed differences among the generations.

The analysis of variance revealed significant differences between all the families for days to first flowering, plant height, fruits per plant, fruit weight, fruit girth, locules per fruit, pericarp thickness, seeds per fruit, fruit yield per plant, total soluble solids and titrable acidity; whereas all the five families exhibited significant difference among the different six generations, except family III (for pericarp thickness and fruit yield per plant); family IV (for pericarp thickness and total soluble solids) and family V (for primary branches per plant, fruit length, fruit girth, pericarp thickness and titrable acidity).

Estimation of scaling test

Significant values for individual scaling tests gave evident (Table 1) about the presence of non-allelic interactions for days to first flowering, plant height, primary branches per plant (except family V) and fruits per plant. Hence six parameter model was used to explain the magnitude and nature of gene action and types of epistasis for the expression of above said characters. It is evident by the estimates of generation mean that due to significant estimates of d (family I) and h (family I and II) for days to flowering indicated non additive genetic effects with duplicate type of epistasis were responsible for the inheritance of the character. Regarding non-allelic interactions, all three types of epistasis were found significant in family I (Table 1). Similar results were reported for early flowering by Devi *et al.* (2005). Non-allelic interactions were present in all families for days to first flowering were also reported by Rattan and Chadha (2009), Patel *et al.* (2010), Amin *et al.* (2017) and Rajan *et al.* (2019) in population of tomato. For plant height, the result of scaling tests (Table 2.1) divulged significant estimates of additive gene effects and the presence of non-allelic interaction in all the five families, with duplicate epistasis (except family I), which exhibited complex

inheritance pattern of the studied trait. The non-significant differences were observed among the generations of family V for primary branches per plants.

Table 1. Analysis of variance of generation means in five families of tomato for different characters

Source	Degree of freedom	Mean sum of square							
		Days to first flowering	Plant height	Primary branches per plant	Fruits per plant	Fruit weight	Fruit length	Fruit girth	
Analysis of variance between families									
Replications	2	0.450	228.64	0.0732	9.53	8.26	0.6774	0.177	
Families	4	865.68**	9033.3**	1.5732	6559**	2135.3**	1.952	24.12*	
Error	8	14.91	935.8	3.474	574.7	281.1	0.823	4.26	
Analysis of variance between generation within family									
Family I (GAT 4 × AVTOV 1002)									
Replications	2	0.031	331.18	0.112	0.204	1.22	0.088	0.75	
Generations	5	21.84**	3429.26**	19.26**	1962.3**	1008.1**	4.52**	8.17**	
Error	10	1.796	521.85	0.38	7.49	0.98	0.165	1.11	
Family II (ATL 11-05 × AVTOV 1002)									
Replications	2	0.50	145.08	0.178	17.34	5.26	0.1880	0.03	
Generations	5	58.60**	4417.52**	6.26**	1986.26**	2841**	2.11**	41.25**	
Error	10	1.488	169.314	0.077	15.04	4.97	0.155	0.16	
Family III (GT-2 × AVTOV 1008)									
Replications	2	0.99	37.27	0.151	8.53	3.20	0.0062	1.01	
Generations	5	40.47**	3039.09**	8.32**	550.1**	309.7**	1.19**	6.05**	
Error	10	0.672	49.079	0.69	13.49	8.15	0.288	0.84	
Family IV (AVTOV 1007 × AVTOV 1005/2)									
Replications	2	1.22	18.09	0.181	1.22	1.74	0.821	1.80	
Generations	5	56.55**	876.66**	7.93**	798.6**	43.53**	0.65**	0.93	
Error	10	0.881	15.40	0.57	28.79	1.79	0.141	0.507	
Family V (IIHR-329 × IIHR-335)									
Replications	2	0.13	50.76	0.050	71.54	1.33	1.16	0.033	
Generations	5	57.58**	2013.77**	10.65	4039.9**	428.25**	1.46	6.97	
Error	10	0.86	52.870	7.77	192.43	16.94	7.91	3.83	
Source	Degree of freedom	Mean sum of square							
		Locules per fruit	Pericarp thickness	Fruit yield per plant	Seeds per fruit	1000 seed weight	Total soluble solids	Lycopene content	Titrable Acidity
Analysis of variance between families									
Replications	2	0.099	0.3642	0.132	7.64	0.07	0.203	0.00022	0.0009
Families	4	2.664*	3.856**	25.51**	709.24**	0.63	5.12**	0.068	43.25**
Error	8	0.548	0.368	2.62	51.13	0.74	0.456	0.024	0.02
Analysis of variance between generation within family									
Family I (GAT 4 × AVTOV 1002)									
Replications	2	0.02	0.007	0.0033	4.02	0.03	0.03	0.000063	0.00018*
Generations	5	2.11**	0.706**	14.63**	256.01**	6.02**	1.19**	0.095**	0.001**

Error	10	0.05	0.02	0.52	2.323	0.062	0.01	0.000063	0.00003
Family II (ATL 11-05 × AVTOV 1002)									
Replications	2	0.06	0.04	0.011	1.54	0.11	0.06	0.00009	0.0045**
Generations	5	2.37**	2.75**	6.46**	73.49**	2.69**	0.84**	0.16**	0.02**
Error	10	0.05	0.02	0.166	0.43	0.06	0.02	0.00005	0.00003
Family III (GT-2 × AVTOV 1008)									
Replications	2	0.22*	0.01	0.62	0.07	0.13	0.12*	0.00014	0.00012*
Generations	5	1.29**	0.20	1.06	59.27**	0.75**	0.579**	0.02**	0.0093**
Error	10	0.04	0.06	0.33	0.52	0.07	0.01	0.000046	0.00002
Family IV (AVTOV 1007 × AVTOV 1005/2)									
Replications	2	0.47	0.06	0.312	2.78	0.07*	0.027	0.000079	0.00028**
Generations	5	1.72**	1.08	5.53**	126.89**	1.09**	0.773	0.09**	0.15**
Error	10	0.25	0.90	0.56	1.590	0.015	0.2342	0.00012	0.00003
Family V (IIHR-329 × IIHR-335)									
Replications	2	0.75**	0.234	0.025	2.04	0.03	0.005*	0.00004	0.00008
Generations	5	0.5528**	0.773	11.91**	320.14**	1.21**	4.01**	0.03**	0.1506
Error	10	0.060	0.512	0.186	1.083	0.015	0.0012	0.00230	0.00004

Note: * and ** indicate significance at 5 % and 1% levels of significance, respectively

Significant additive gene action with additive × dominant and dominant × dominant genic interaction was observed for primary branches per plant with complementary epistasis. This suggests improvement by selection method in particular trait. For fruits per plant (Table 1), all the estimates of six parameter model found significant in family I, III, IV and family V; however, the involvement of duplicate epistasis observed in family II, III, IV and V, where the estimates of dominance and dominance × dominance gene interaction had opposite signs. Similar outcome was reported by Patel *et al.* (2010) and Amin *et al.* (2017).

Significant estimates of additive gene effect in all the five families and dominant gene effect in family I, II and family III for fruit weight suggested the preponderance of additive and non-additive gene action for the expression of the trait. Duplicate type of epistasis was present in all the families except family I (Table 2). The results of family I, II and III for fruit weight showed similarity with the result obtained by Thainukulet *et al.* (2017), Kaushik and Dhaliwal (2018) and Rajan *et al.* (2019). The non-significant differences were observed among the generations for fruit length in family V and fruit girth in family IV and V. Significant values of individual scaling tests indicated the presence of epistasis for fruit length and fruit girth, suggesting six parameter model was used to estimate the magnitude of non-allelic interactions. Prominent additive and additive × dominant gene effect found significant for all the five families for fruit length (family I, II, III and IV) and fruit girth (Family I, II and III). Genetic analysis for locules per fruit exhibited the significant values of χ^2 tests of joint scaling test not supported the outcome

of simple scaling test for family V, indicated absence of inter-allelic interactions. This lack of congruence may be due to differential fertility and viability of individuals of different segregating generations or may be due to sampling error. Involvement of significant estimates of additive and dominant gene action with additive × additive, additive × dominance and dominance × dominance types of epistasis for family II, III and IV (Table 2).

For the pericarp thickness, the non-significant differences were observed among the generations of family III, IV and V (Table 3). Involvement of significant estimates of additive genetic effects in its inheritance, in addition, additive × additive gene interaction was found predominant in family I; however additive × dominant and dominant × dominant genic interactions found predominant in family II with duplicate epistasis, suggests complex inheritance pattern of the character under study. The similar results also obtained by Kaushik and Dhaliwal (2018) and Rajan *et al.* (2018) for pericarp thickness of tomato.

Six parameter models were enough to describe the heredity pattern of fruit yield per plant since scaling tests and χ^2 estimates were found a significant for family I, II, IV and V indicated the presence of epistasis (Table 3). Therefore, six parameter model was used to estimate the non-allelic interactions along with their magnitude; however, family III exhibited non-significant difference between the six generations. Result showed that additive and dominance genes were controlling the mechanism of inheritance of fruit yield due to significant additive and dominance estimate in family I and family IV with duplicate epistasis, while family II showed

significant estimates of additive × dominant genetic interaction. Estimates of additive gene effect and dominance × dominance interactions found significant for family V. Zdravkovic *et al.* (2011) and Chi (2017) also reported higher estimates of non-additive gene action comparable to additive gene actions responsible for fruit yield per plant. The

prevailing type of non-allelic interaction involved in the inheritance of the trait was additive × dominance and additive × additive, also recorded by Patel *et al.* (2010), Shankar *et al.* (2013), Shalaby (2013), Dagade and Dhaduk (2016), Amin *et al.* (2017) and Kaushik and Dhaliwal (2018) for fruit yield per plant.

Table 2. Estimates of simple scaling test and gene effects for days to first flowering, plant height, primary branches per plant and fruits per plant

Family	Scaling Test				χ^2 at 3 d.f.	Gene effect								Gene action		
						Three parameter Model			Six Parameter Model							
	A	B	C	D		M	d	h	m	D	H	I	j		l	
Days to first flowering																
I	8.00**	10.27**	15.27**	-1.50	33.51**	-	-	-	45.48**	-2.80**	2.07**	3.00**	-1.13**	-	21.26**	D
II	-7.87**	-8.93**	-7.33**	4.73**	42.37**	-	-	-	38.53**	-0.39	-18.60**	-9.47**	0.53	26.26**	D	
III	-6.40**	-1.33	-13.87**	-3.07*	41.82**	-	-	-	35.06**	0.39	-0.53	6.13*	-2.53**	1.59	D	
IV	-7.26**	-4.60**	-11.93**	-0.03	42.32**	-	-	-	42.56**	0.23	-9.29	0.06	-1.33	11.79**	D	
V	-5.73**	2.00	-11.86**	-4.06**	63.37**	-	-	-	34.70**	1.40	1.86	8.13**	-3.86**	-4.40	D	
Plant height																
I	50.46**	-85.05**	24.96	29.77**	41.82**	-	-	-	196.5**	46.40**	12.64	-59.55**	67.75**	94.13*	C	
II	41.73*	-41.20*	94.86**	47.16**	20.97**	-	-	-	189.01**	36.73**	-3.73**	-94.33**	41.46**	93.79	D	
III	-41.13	-76.20**	57.06	87.20**	479.9**	-	-	-	173.3**	30.90**	-107.9**	-174.4**	17.53	291.7**	D	
IV	40.93**	-16.32**	62.38**	18.88**	41.78**	-	-	-	135.4**	32.25**	-8.88	-37.77*	28.63**	13.16	D	
V	-25.26	-6.50	36.97	34.37*	61.78**	-	-	-	175.6**	-	-28.31	-68.74*	-9.37	100.5*	D	
Primary branches per plant																
I	-2.79	-6.86	-9.84	-0.09	55.48**	-	-	-	11.71**	3.94**	4.59**	0.19	2.04**	9.47**	C	
II	1.83	-1.52	3.65	1.67	13.89**	-	-	-	13.10*	1.350	0.028	-3.34	1.68*	3.04	C	
III	-2.82*	-6.28**	-6.68**	1.21	36.03*	-	-	-	11.93**	2.59**	0.25	-2.43	1.73*	11.53**	C	
IV	-0.11	-5.74**	-0.51	1.17	25.10*	-	-	-	12.42**	3.55**	0.26	-2.34	2.82**	8.21*	C	
V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Fruits per plant																
I	-29.06*	-112.6*	-	-22.76**	526.51**	-	-	-	32.31**	27.39**	77.18**	45.52**	41.77**	96.15**	C	
II	32.20	-62.58**	70.89	50.64	21.22**	-	-	-	98.63**	63.66**	-123.0*	-101.2	47.39*	131.6	D	
III	-11.80	-57.59**	-27.046	21.17**	75.38**	-	-	-	68.74**	28.37**	-49.92**	-42.34**	22.89**	111.7**	D	
IV	-47.35**	-76.26**	-56.11**	33.75**	111.9**	-	-	-	50.16**	19.44**	-59.00**	-67.50**	14.45*	191.1**	D	
V	-	-	9.17**	134.98**	320.1**	-	-	-	123.7**	-	-238.5**	-269.9**	24.63*	530.7**	D	

Table 3. Estimates of simple scaling test and gene effects for fruit weight, fruit length, fruit girth and locules per fruit

Family	Scaling Test				χ^2 at 3 d.f.	Gene effect								Gene action	
						Three parameter Model			Six Parameter Model						
	A	B	C	D		M	d	h	m	D	H	I	j		l
Fruit weight															
I	-11.39	-	-	-10.08	90.85**	-	-	-	25.52**	20.06**	64.90**	20.16	17.99**	38.59	C

		47.38**	78.94**														
II	101.36**	54.51**	37.48	-	59.2**	91.09**	-	-	-	58.07**	23.92**	169.4**	118.3**	23.42**	-	274.2**	D
III	33.91**	-	-10.48	-11.12	58.10**	-	-	-	37.07**	26.06**	36.23**	22.23	28.03**	-	-	33.99**	D
IV	1.2	-8.74**	8.42	7.98**	16.14**	-	-	-	34.81**	4.21*	-7.24	-15.95**	4.97*	-	23.50**	D	
V	-37.68**	0.87	-10.54	13.13*	85.26**	-	-	-	45.35**	-	-2.52	-26.26*	-	-	63.07**	D	
Fruit length																	
I	0.74	-1.49*	1.6	1.17**	141.67**	-	-	-	9.2**	1.22**	0.69	-2.35**	1.11**	3.09*	-	-	C
II	1.49	-2.98**	-2.29*	-0.4	23.82**	-	-	-	8.59**	2.25**	1.94	0.8	2.24**	0.69	-	-	C
III	1.2*	-0.8	0.01	-0.2	89.41**	-	-	-	9.38**	0.68*	1.85	0.39	1.0**	-0.79	-	-	D
IV	1.03	-0.75	1.17	0.44	8.63*	-	-	-	9.61**	0.76*	0.07	-0.88	0.89*	0.59	-	-	C
V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Fruit girth																	
I	7.41**	-0.81	7.26**	0.33	53.2**	-	-	-	18.03**	3.91**	0.32	-0.67	4.11**	-5.93	-	-	D
II	-7.0**	0.25	4.76	5.76**	99.88**	-	-	-	16.28**	-6.21**	-4.77	-11.51**	-3.62**	18.26**	-	-	D
III	2.86**	-6.55**	-3.03	0.33	85.96**	-	-	-	15.76**	3.93**	1.67	-0.65	4.7**	4.34	-	-	C
IV	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Locules per fruit																	
I	0.73*	-0.8*	0.87	0.47	0.15	-	-	-	4.18**	0.37	1.13	-0.93	0.77**	1.00	-	-	C
II	-2.87**	-2.07	1.00	2.97**	88.51**	-	-	-	4.45**	-0.53*	-4.2**	-5.93**	-0.40	10.86**	-	-	D
III	-0.53	2.33**	0.47	-0.67*	49.82**	-	-	-	2.88**	-1.63**	2.07**	1.33**	-1.43**	-3.13**	-	-	D
IV	-2.07**	-2.4**	-5.87**	-0.7**	105.5**	-	-	-	2.8**	-0.37*	1.8**	1.4**	0.17	3.07**	-	-	C
V	-0.93**	-0.27	-0.47	0.37	7.47	-	-	-	3.83**	-0.03	0.3	-0.73	-0.33	1.93	-	-	C

Table 4. Estimates of simple scaling test and gene effects for pericarp thickness, fruit yield per plant, seeds per fruit and 1000 seed weight

Family	Scaling Test				χ^2 at 3 d.f.	Gene effect										Gene action
						Three parameter Model			Six Parameter Model							
	A	B	C	D		M	d	h	m	d	H	I	j	l		
Pericarp thickness																
I	0.9**	0.13	2.37**	0.67*	22.34**	-	-	-	5.36**	0.55**	-0.47	-1.33*	0.38	0.3	-	D
II	-4.01**	1.65**	-2.21**	0.08	225.9**	-	-	-	4.04**	-2.78**	-0.54	-0.16	-2.83**	2.53*	-	D
III	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IV	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Fruit yield per plant																
I	1.49	-6.34**	-12.12**	-3.64	212.81**	-	-	-	4.80**	1.74**	10.96**	7.28**	3.91**	-2.43	-	D
II	-3.72	-0.37	-4.07**	0.01	14.51**	-	-	-	6.18**	-0.09	2.79	-0.02	-1.68**	4.11	-	C
III	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IV	6.27**	1.88*	2.95	-2.6**	44.37**	-	-	-	7.33**	2.76**	4.85**	5.2**	2.2**	-13.35**	-	D
V	-3.23**	-1.59	-2.45	1.18	12.91**	-	-	-	9.44**	-2.72**	1.21	-2.37	-0.82	7.18**	-	C
Seeds per fruit																

I	-31.07**	-13.27**	-21.13**	11.60**	251.47**	-	-	-	64.88**	0.3	-7.13*	-23.19**	-8.9**	67.53**	D
II	-0.93	15.27**	-10.53**	-12.43**	253.2**	-	-	-	52.36**	-7.37**	33.93**	24.86**	-8.01**	-39.2**	D
III	12.0**	1.40	21.33**	3.97**	109.8**	-	-	-	57.23**	8.23**	-3.73	-7.93**	5.3**	-5.47	C
IV	-0.87	4.47*	11.13**	3.77	10.19*	-	-	-	55.68**	0.47	8.13	-7.53	-2.67	3.93	C
V	-24.07**	-29.33**	-16.87**	18.27**	287.0**	-	-	-	68.35**	-4.17**	-14.99**	-36.53**	2.63*	89.93**	D
1000 seed weight															
I	-0.60*	-3.18**	-3.95**	-0.09	135.5**	-	-	-	3.98**	-0.01	3.26**	0.17	1.29**	3.60**	C
II	-0.10*	1.15*	4.78**	2.32**	65.14**	-	-	-	4.92**	-1.2**	-6.69**	-4.63**	-1.07**	4.48**	D
III	1.58*	1.39*	0.19	-1.39**	18.05**	-	-	-	4.30**	-0.4	2.57**	2.78**	0.09	-5.74**	D
IV	-0.78	-2.02**	-5.18**	-1.19**	61.85**	-	-	-	3.25**	0.15	2.69**	2.38**	0.62**	0.42	C
V	-1.45**	1.01*	2.29**	1.37**	36.47**	-	-	-	4.81**	-1.48**	-3.58**	-2.73**	-1.23**	3.18*	D

Table 5. Estimates of simple scaling test and gene effects for total soluble solids, lycopene content and titrable acidity

					Three parameter Model			Six Parameter Model								
	A	B	C	D	M	d	h	m	d	h	i	j	l			
Total soluble solids																
I	-1.38**	-2.8**	-2.73**	0.72**	174.91**	-	-	-	5.02**	0.15	-	1.45**	-1.45**	0.71**	5.62**	D
II	2.23**	0.27	-0.85	-1.68**	34.66**	-	-	-	4.1**	1.01**	3.84**	3.35**	0.98**	-5.85**	D	
III	-1.97**	-0.38	-1.96**	0.19	79.71**	-	-	-	4.24**	-0.36**	0.15	-0.39	-0.79**	2.74**	C	
IV	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
V	-1.45**	2.67**	3.23**	1.01**	759.8**	-	-	-	4.5**	-1.87**	0.30	2.02**	-2.06**	0.8*	C	
Lycopene content																
I	0.38**	-0.72**	-0.43**	-0.04	143.31**	-	-	-	0.38**	0.35**	0.21	0.09	0.55**	0.25	C	
II	0.99**	0.41**	-0.41**	-0.90**	222.4**	-	-	-	0.14**	0.35**	1.87**	1.81**	0.29**	-3.21**	D	
III	-0.02	-0.05	-0.002	0.03	1.49	0.22**	0.06**	0.21**	-	-	-	-	-	-	-	
IV	0.62**	-0.01	0.09	-0.21**	100.7**	-	-	-	0.45**	0.21**	0.71**	0.43**	0.36**	-0.95**	D	
V	0.16**	-0.13**	-0.1	-0.06	34.24**	-	-	-	0.38**	0.01	0.28**	0.13	0.14**	-0.16	D	
Titrable Acidity																
I	-0.14**	-0.10**	0.1*	0.17**	70.73**	-	-	-	0.34**	-0.04**	-	0.43**	-0.34**	-0.02	0.58**	D
II	0.16**	-0.28**	-0.39**	-0.13**	819.5**	-	-	-	0.28**	0.22**	0.38**	0.26**	0.22**	-0.14**	D	
III	0.14**	0.25**	0.43**	0.02	370.8**	-	-	-	0.31**	-0.05**	-0.07	-0.05	-0.06**	-0.34**	C	
IV	0.6**	0.64**	1.48**	0.12	350.6**	-	-	-	0.77**	-0.21**	-0.44	-0.24	-0.02	-0.99**	C	
V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

Note: ‘-’ indicates non-significant values for scaling tests and/or ANOVA for particular character of particular family, C-Complementary and D-Duplicate gene action.

Estimates of scaling test and chi-square test found significant for seeds per fruit and 1000 seed weight giving idea about presence of inter allelic interactions and failure of additive-dominance model in all five families. (Table 2.3). The genetic parameter viz., m, d, h, i, j and l were found significant which showed contribution in the expression of the trait in the family II and V for seeds per fruit and 1000 seed weight with duplicate epistasis. Significant estimates

of additive genetic effect and all three types of epistasis; however, significant values of dominant and all three types of epistasis indicated importance of additive and non-additive gene actions for family I and family III in the expression of the traits. Because of comparable environmental difference or difference in fertility and viability, there was a non-significant estimate for all the six parameters except mean value for family IV for

seeds per fruit.(Table 3). The similar finding also reported by Rajanet *al.* (2018) and Bhalala (2018) for seeds per fruit and 1000 seed weight.

All the five families exhibited an inadequate additive dominance model, suggesting presence of non-allelic interaction for total soluble solids. Significant additive (family II, III, IV and V), dominance (family I and II) and additive \times additive [i] type epistasis interactions were observed for all the family except family III. However, significant values for additive \times dominance epistasis was reported for all the families except family IV; and dominance \times dominance [I] type of epistasis exhibited by all the families, indicated involvement of predominant additive gene action and dominance \times dominance [I] type epistasis were in the expression of this trait. In addition, Family I, II and IV indicated duplicate types of epistasis interaction in the inheritance of the trait (Table 4).The investigation suggested that single breeding approach cannot be used to improve this character; predominant non-fixable gene effects indicated that there may be much scope of heterosis breeding and recurrent selection for the improvement of this character. The present investigation has an outcome in accordance to the results of Hamada *et al.* (2016), Kumar and Srivastava (2017) and it was also correlated with the result of Somraj *et al.* (2017), Triveni *et al.* (2017), Kaushik and Dhaliwal (2018) and Rajanet *al.* (2018) for total soluble solids.

Adequacy of additive dominance model was exhibited for lycopene content in family III, by non-significant values of individual scaling tests and it was confirmed by joint scaling test. Family III exhibited significant estimates of dominance and additive genetic component in the involvement in the expression of this trait. Family II and IV exhibited significant magnitude of dominance and additive gene effects, as well as prominent effects of all three types [i, j and l] of epistasis interactions, while family I expressed significant additive genetic effect and additive \times dominance type of epistasis interaction. Significant values for dominance and additive \times dominance epistasis interaction was found for family V (Table 4).The role of dominance gene action and comparable additive gene action were also noticed by Kumar and Srivastava (2017), Triveni *et al.* (2017), Somraj *et al.* (2017) and Kaushik and Dhaliwal (2018) for the lycopene content.

Significant and positive magnitude of individual scaling tests was suggesting the inadequacy of additive-dominance model and presence of epistasis interaction for the titrable acidity in family I, II, III and family IV. Significant estimates of all six-parameters observed in family I and family II. Significant estimates of additive genetic effect as well as additive \times dominance and dominance \times dominance epistasis interaction exhibited by family III. However, significant values for additive gene action and dominance \times dominance epistasis interaction reported in family IV (Table 4).Similar

results were also obtained by Patel *et al.* (2010), Triveni *et al.* (2017) and Kumar and Srivastava (2017) for titrable acidity for tomato.

CONCLUSION

The present investigation revealed that the additive and additive \times additive type fixable gene effects were found responsible in the expression of fruit yield per plant and its contributing traits in different cross combinations. This suggests simple selection or a pedigree method could help for improvement of these traits. The result of non-additive gene action and epistatic gene effects for fruit yield and its related traits in different cross combinations revealed that recurrent selection, bi-parental mating, inter se mating between desirable segregants followed by selection or multiple crosses.

REFERENCES

- Amin, A., Kouser, P. W. and Kumar, P.** (2017). Gene action studies for yield and its attributing traits in tomato (*Solanum lycopersicum*L.) under Kashmir conditions. *Journal of Pharmacognosy and Phytochemistry*, 6 (6),1859-1861.
- Anderson, L. K., Covey, P. A., Larsen, L. R., Bedinger, P. A. and Stack, S. M.** (2010). Structural difference in chromosomes distinguish species in the tomato clade. *Journal of Cytogen Genome Resources*, 2, 1-14.
- Anonymous** (2019). State Directorates of Horticulture for 2018-19.
- Bhalala, K.** (2018). Exploitation of heterosis and assessment of combining ability using Line \times tester analysis over environment in tomato. (*Solanum lycopersicum* L.), (Doctoral thesis, Department of genetics and plant breeding, Anand agricultural University, Anand).
- Cavalli, L. L.** (1952). An analysis of Linkage in Quantitative inheritance. ED. E. C. Reeve& C. H.Waddington MNSO, London.pp.135-144.
- Chi, N. N.** (2017). *Genetic analysis and heritability estimates for heat tolerance traits in tomato (Solanum lycopersicum (L.))* (Master's, Texas A & M University).
- Dagade, S. B. and Dhaduk, L. K.** (2016). Diallel cross analysis of nutritional characters of tomato. *International Journal of Farm Sciences*,6 (2), 65-72.
- Devi, E., Singh, N.B., Bijyadevi, A., Singh, N.G. and Laishram, J. M.** (2005). Gene action for fruit yield and its components in tomato (*Lycopersicon*

esculentum Mill.), *Indian Journal of Genetics*, 65 (3), 221-222.

***Falconer, D. S.** (1989). *Introduction to Quantitative genetics*. Longman, Edinburgh.

Gester, H. (1997). The potential role of lycopene for human health. *J. Am. Coll. Nutr.* 16(2), 26-109.

Hamada, M. S., Hamaiel, A. F., Faried S. M. and Sara, A. A. Elkomey (2016). Nature of gene action for some economic characters of tomato (*Lycopersicon esculentum* L.) varieties. *J. Agric. Res. Kafir El.* 42(2), 24-33.

Hayman, B. I. and Mather, K. (1955). The description of genetic interaction in continuous variation, *Biometrics*, 11, 69-82.

Hayman, B. I. (1958). The separation of epistatic from additive and dominance variation in generation heridity, 12, 371-390.

Kaushik, P. and Dhaliwal, M.S. (2018). Diallel analysis for morphological and biochemical traits in tomato cultivated under the influence of tomato leaf curl virus. *Agronomy*, 8 (153), 01-15.

Kumar, R. and Srivastava, K. (2017), Gene effects and heritability for yield and quality traits in tomato (*Solanum lycopersicum* L.), *Agriways*, 5 (2), 104-112.

Mather, K. (1949). *Biometrical Genetics* (IIIrd Ed.). Chapman and Hall Ltd., London.

***Panse, V. G. and Sukhatme, P. V.** (1969). *Statistical methods for agricultural workers*. Indian Council of Agricultural Research, New Delhi.

Patel, U. J., Kathiria, K.B., Patel, J. S. and Saiyad, I. M. (2010). Heterobeltiosis and inbreeding depression in tomato (*Lycopersicon esculentum* Mill.), *International Journal of Plant Sciences*, 5 (2), 636-638.

Rajan, B., R. E., Kumar, C. P. S. and Joshi, J. L. (2018). Generation mean analysis for some quality traits in tomato (*Lycopersicon esculentum* Mill.), *Plant Archives*, 18 (2), 2083-2086.

Rajan, B., R. E., Kumar, C. P. S., Joshi, J. L. and Muraleedharan, A. (2019). Generation mean analysis for fruit yield and component traits in tomato (*Lycopersicon esculentum* Mill.), *Plant Archives*, 19 (1), 448-451.

Rattan P. and Chadha, S. (2009). Gene action studies for yield & its contributing characters, *Biological Forum - An International Journal*, 1(2), 8-10.

Shalaby, T. A. (2013). Mode of gene action, heterosis and inbreeding depression for yield and its components in tomato (*Solanum lycopersicum* L.), *Scientia Horticulturae* 164, 540-543. Shankar, A., Reddy, R.V.S.K., Sujatha, M. & Pratap, M. (2013). Genetic Variability Studies in F₁ Generation of tomato (*Solanum lycopersicon*L.), *Journal of Agriculture and Veterinary Science (IOSR-JAVS)*, 4 (5), 31-34.

***Snedecor, G. W.** (1938). *Statistical Methods*. Collegiate Press, Ins.

Somraj, B., Reddy, R. V. S. K., Reddy, K. R., Saidaiah, P. and Reddy, M. T. (2017), Generation mean analysis for quality and physiological traits of tomato (*Solanum lycopersicum* L.) under high temperature condition, *Journal of Pharmacognosy and Phytochemistry*, 6 (4), 198-200.

Thainukul, N., SasinanSakdarueakrot, S. and Liang, Y. (2017). The evaluation of genetic inheritance, heritability and correlations coefficient of mutant tomato. *Sch. J. Agric. Vet. Sci.*, 4(5), 209-213.

Triveni, D., Saidaiah, P. K., Ravinder, R. K. and Pandravada, S. R. (2017). Studies on combining ability and gene action for growth and quality characters in tomato (*Solanum lycopersicum*(L.)), *Int. J. Pure App. Biosci.* 5 (4), 1835-1840.

Zdravkovic, J., Pavlovic, N., Girek, Z., Jokanovic, M., Savic, D., Zdravkovic, M. and Cvikic, D. (2011). *Pak. J. Bot.*, 43(3), 1575-1580.

