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Generation Mean Analysis for Fruit Yield and Component Traits in Tomato (*Solanum lycopersicum* L.)

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ABSTRACT: Information of gene action governing the yield and its components is very crucial for formulating sound breeding programmes. In order to generate this information for tomato lines, the present investigation was carried out at Main Vegetable Research Station, Anand Agricultural University (AAU), Anand during *kharif-rabi* 2022-23. The experimental material comprised of six families developed from ten diverse lines. Each family is composed of six generations *viz.*, P_1, P_2, F_1, F_2, B_1& B_2 evaluated with three replications in compact family block p;design (CFBD) to perform generation mean analysis. Results of simple scaling tests and joint scaling tests revealed adequacy of three parameter model in one out of eighty-four possible cases and adequacy of six parameter model in eighty two out of eighty-four possible cases.

Keywords: Tomato, Generation mean analysis, Scaling test, Gene action, Gene interaction.

INTRODUCTION

Tomato is the world's second-most widely cultivated vegetable crop trailing potato. Total area under tomato cultivation in the world was 5.05 million hectares, with production of 186 million tonnes and the average productivity of 37.0 tonnes/ha in 2020. China stands first in the major tomato growing countries followed by India, Turkey, Egypt, Iran, USA, Mexico, Italy, Brazil and Spain (Anonymous, 2020). Tomato [(*Solanum lycopersicum* L.), (2n = 20x = 24)] is self-pollinated, day-neutral, extensively cultivated and globally consumed vegetable crop in world (Sikder *et al*., 2013). As yield is not simply an inherited trait, many genes' action and interaction determine inheritance and potential yield. Many yield attributing characters have positive and/or negative association, it is very hard to isolate line possessing all desirable traits. Hence, estimation of components of gene action and genetic variance is very essential to formulate robust breeding programmes. Knowledge of the nature and magnitude of gene effects controlling inheritance of yield and its attributing traits would aid in the choice of efficient breeding methods, ultimately aid in accelerating the pace of its genetic improvement and breaking the yield barriers. Most of the yield attributing traits generally show continuous variation and they are influenced by environment (Lecomte *et al.*, 2004).

Amount of genetic variability present in the breeding material and knowledge of genetic control of commercial traits is very crucial for breeding programmes in order to isolate improved cultivars and hybrids through proper breeding methodology. Even though tomato is self-pollinated crop, easy emasculation, better pollen dispersal, profuse flowering and higher seed multiplication ratio lead to better adoption and commercialization of hybrids (Damor *et al*., 2021). Considerable important work has been done in this crop, but better information in the genetics of fruit yield, yield attributing traits and quality parameters of this crop, grown in middle Gujarat agro-climatic condition is still needed.

Generation mean analysis (Mather and Jinks 1982) is a useful tool for determining the nature of gene effects (additive, dominance and their digenic interaction) involved in the expression of traits such as yield and its associated traits. The scaling test examines generation means to determine presence or absence of epistatis as well as complementary (additive × additive) or duplicate (additive × dominance) and (dominance × dominance) interaction at digenic level. The present study was carried out to study the nature of gene action involved for the inheritance of yield and associated traits in six tomato crosses.

MATERIAL AND METHODS

The six generations of six crosses (2012/TODVAR-1 × AVTOV 1007, GAT-5 × 2015/TOLCV RES-1, 2014/TODVAR-5 × AVTOV 1002, 2016/TODVAR-12 × AVTOV 1005, 2017/TODVAR-8 × 2015/TOLCV RES-1, 2017/TODVAR-8 × 2015/TOLCV RES-4) comprising of P_1, P_2, F_1, F_2, B_1 and B_2 were developed from ten diverse parents *viz*., 2012/TODVAR-1, AVTOV 1007, GAT-5, 2015/TOLCV RES-1, 2014/TODVAR-5, AVTOV 1002, 2016/TODVAR-12, AVTOV 1005, 2017/TODVAR-8 and 2015/TOLCV RES-4. The crosses were made in *kharif-rabi* 2020-21 and 2021-22 and evaluation of the experimental material was done during *kharif-rabi* 2022-23.

Field Experiment. The six generations of these six crosses were raised in Compact Family Block Design (CFBD) at Main Vegetable Research Station (MVRS), Anand Agricultural University (AAU), Anand during *kharif-rabi* 2022-23 with three replications. An individual replication had six families as blocks and each block consisted of one row of each P_1, P_2 and F_1 generation, four rows of each F_2 generation and two rows of each B_1 and B_2. 25 days old seedling then transplanted to well-prepared field keeping inter and intra-row spacing of 90 × 45 cm. The observations for different characters were recorded on randomly selected plants from each experimental unit from each replication. Observations were recorded on five plants each for P_1, P_2 and F_1, on twenty plants for F_2 and on ten plants for B_1 and B_2, respectively.

RESULTS AND DISCUSSION

Analysis of variance between the family comparison depicted significant differences among the families for all the traits. For estimation of components of gene effect, Simple Scaling Tests (Hayman and Mather, 1955) were applied. The non-significance test of all the Simple Scaling Tests suggest adequacy of additive dominance model; hence, principle gene effects *i.e.* additive and dominance were estimated as suggested by Jinks and Jones (1958) three parameters model (m, d and h). For the families and characters, wherein any of the Simple Scaling Test was significant, six parameters model (m, d, h, i, j and l) as suggested by Hayman (1958) was applied to partition the gene effect into epistatic components including principle gene effects. However, for confirmation of adequacy of additive dominance model, and to realize presence of higher order interallelic interactions, Joint Scaling Test as suggested by Cavalli (1952) was also applied. Further, the results were confirmed by significance of $\chi 2$ test. The opposite sign of [h] and [l] indicated duplicate gene interaction. While, equal sign of [h] and [l] indicated complimentary gene interaction.

Days to Flowering. Additive dominance model was found to be inadequate since estimates of individual simple scaling tests, A, B, C and D found significant for the all six families except, family II and VI. In family II and VI scales A and D found significant. Further, presence of higher order epistasis was indicated and confirmed by significance of χ^2 test value of joint scaling test, which indicated inadequacy of the additive-dominance model in all the six families for days to first flowering. Significant additive and dominance components of gene action were reported for the families I, II, III and IV indicating importance of both components. While, in family IV, additive component was found significant. All the families except, family I possessed significant estimates of additive × additive [i] and additive × dominance [j] type of epistatic gene interaction. Dominance × dominance [l] epistatic interaction found significant for all the families. The results were in accordance with the findings of Damor *et al*. (2021).

Branches per Plant. Additive dominance model found inadequate since simple scaling tests, A and D found significant in family I, B in family II, A and B in family III, A in family IV, C and in family V and B and C in family VI. Further the results were confirmed by significance of χ^2 test for all families. Additive component of gene action was recorded significant for family III and IV; whereas dominance component was significant for family I and V. Additive × additive [i] type of epistatis found significant in family I, V and VI. While, additive × dominance [j] interaction reported significant in family II and IV. Dominance × dominance [l] type of epistatic interaction found significant in family I, II, III and VI. From the signs of [h] and [l], complimentary epistatis reported for branches per plant except, in family I. Duplicate epistatis reported in family I was in accordance with findings of Das *et al.* (2020) who reported both duplicate and complementary type of epistatis. Analysis contradicted the findings of Parida *et al.* (2021); Kumar and Srivastava (2021) who reported adequacy additive dominance for the inheritance of branches per plant.

Plant Height. For plant height, simple additive dominance was found inadequate as scaling testes were found significant in all families. Significance of χ^2 test value from the joint scaling for all families confirmed the results. Significance of additive component of gene action was reported for family I, II and III; whereas only family I exhibited significant estimate of dominance component. Predominant role principal component of gene action (*i.e.* additive and dominant) recorded in family I. Additive × additive [i] type of epistatic interaction found significant in family I and III. Additive × dominance [j] interaction was found significant only in family II; whereas higher estimates of dominance × dominance [l] epistatis gene interaction reported in in family IV and V which indicates role of non additive gene effects. Complementary epistatis was reported to govern the traits in all families except family I. The results were in accordance with the study of Negi *et al*. (2013).

Fruit Length. Significant values of individual scaling tests were reported for fruit length in all families. Further, it is supported by significance of χ^2 test values. Significant values for additive genetic component were observed for all families under study for fruit length. While, significant estimates of dominance component were reported in family III and IV. Significant estimates of additive × additive [i] and dominance × dominance [l] were reported in family I with higher

magnitude of dominance × dominance [l] inter allelic gene interaction. On the other hand, additive [l] gene action with additive × dominance [j] epistatis interaction was reported in family II. In family III and IV, both principle gene action components with all three epistatis interaction *viz.* additive × additive [i], additive × dominance [j], dominance × dominance [l] with higher magnitude of dominance × dominance [l] type of gene interaction found to govern the fruit length. Four out of six families (*viz.* I, II, III and IV) showed duplicate type of gene interaction indicating complex inheritance of fruit length. Magnitude of all type epistatis was higher in all families, which governs the character fruit length. Importance of additive gene effect and duplicate epistatis were in accordance with the findings of Chauhan *et al.* (2019).

Fruit Girth. Additive dominance model was found to be inadequate since individual scaling tests had significant estimates for the fruit girth. It was further supported by χ^2 test value of joint scaling test at three degree of freedom for all families under study. Significant estimates of additive gene effect were reported for family II, III and V; whereas family I, III and IV exhibited significant estimates of dominance gene effect for the trait under study. Family I possessed significant estimate of additive × additive [i] type of gene interaction along with significant dominance gene effect. Additive gene effect along with additive × dominance [j] epistatis interaction found to govern the character in family II. All three types of epistatis gene interactions (*viz*. additive × additive [i], additive × dominance [j], dominance × dominance [l]) were found significant along with significant in families III and IV; however, family III also exhibited significant estimate of dominance component of principle gene effect. In family IV, dominance gene effect with additive × dominance [j] found significant. Only additive × dominance [j] gene interaction reported significant in family VI. All families except, family II had opposite signs of [h] and [l] stating presence of duplicate type of gene interaction. The findings were partially in accordance with Patel *et al.* (2010).

Average Fruit Weight. Significant estimates of the individual simple scaling test as well as significance of χ^2 test value from joint scaling test revealed presence of digenic interaction in the all six families under study. Significant estimates of principle gene effect components *i.e.* additive and dominance components were reported only in family I and VI but in negative direction. Family I and VI exhibited significant estimates of additive × additive [i] and dominance × dominance [l] epistatic interaction with estimates of dominance × dominance [l] in positive direction revealing preponderance of non-additive gene action in the inheritance of average fruit weight in these families. Additive × dominance [j] gene interaction was found significant in family II and III along with significant dominance × dominance [l] interaction in family III. Family IV and V epistatis interaction additive × additive [i] and dominance × dominance [l] with higher estimates of dominance × dominance [l] interaction. Here, both duplicate (4 families) and complimentary (2 families) gene interaction reported in the analysis of this trait. Similar findings with more prominent dominance gene effects were reported by Patel *et al.* (2010); Chauhan *et al.* (2019). Duplicate epistatis for this trait was also reported by Mawasid *et al.* (2019); Kumar and Srivastava (2021); Parida *et al.* (2021).

Pericarp Thickness. The failure of additive-dominance model was observed due to significance of scaling tests in all the families. The χ^2 test value of joint scaling tests were significant for the all families under study. Significant additive gene effect was recorded for family V only; whereas significant estimates of dominant gene effect were recorded in family IV, V and VI. Only additive × dominance [j] and dominance × dominance [l] gene interaction was found significant in family I and III, respectively. While, heterozygous [additive × dominance] inter allelic interaction along with dominance × dominance [l] found significant in family II. All three types of intergenic interactions *viz.* additive × additive [i], additive × dominance [j] and dominance × dominance [l] were found significant in families IV and V. Significant additive × additive [i] and additive × dominance [j] epistatic interactions were reported for the family VI. Duplicate type of epistatis was observed in all the families except, family I, as [h] and [l] had opposites sign which reveals complex inheritance for the character under study.

Fruit Yield per Plant. Inadequacy of additive dominance to explain the inheritance of fruit yield per plant was revealed by significance of individual scaling test for all the families. The outcomes were supported by significance of χ^2 test values from the joint scaling test for all families. This revealed presence of digenic interaction for the character under study. Significant estimates of both additive and dominance gene action components were found for the families IV, V and VI. Although, significant value of dominance gene action was reported for family III. Only additive × dominance [j] and dominance × dominance [l] epistatis interaction found significant in family II and III, respectively. Additive × dominance [j] and dominance × dominance [l] type of epistatis interactions were found significant in family VI and V, along with significant dominance × dominance [l] interaction in family V. Significant estimate of dominance × dominance [l] interaction component with higher magnitude was reported in family VI. Duplicate type of epistatis was reported in all families. Similar findings with presence of non-allelic interaction along with were reported by Patel *et al.* (2010) reported higher non additive gene action comparable to additive gene actions responsible for fruit yield per plant. Duplicate epistatis for this trait was reported by Chauhan *et al.* (2019); Parida *et al.* (2021).

Locules per Fruit. The estimates of the individual simple scaling tests as well as χ^2 test value of joint scaling test were significant for all the families under the study. Both additive and dominance components of gene action were found significant for the family I, III and IV. While, additive gene action found significant in family V and dominance gene action in family VI. All three types of gene interaction *viz.* additive × additive [i], additive × dominance [j] and dominance ×

dominance [l] were found significant I, III, IV and VI. Significance of additive × additive [i] gene interaction was found significant in family II and additive × additive [i] and additive × dominance [j] in family V. Duplicate type of epistatis reported in families I, II, IV and VI; while complimentary epistatis recorded for families III and IV. Higher magnitude of dominance × dominance [l] gene interaction recorded for families I, III and IV indicating role of non-additive effects for inheritance of this trait. Due to presence of non-allelic interaction selection should be postponed to later generations.

Lycopene Content. The individual estimates of simple scaling tests as well as χ^2 test value of the joint scaling test indicated the non-adequacy of additive-dominance model due to significance of individual scaling tests for all six families. Significant estimates of additive gene effect were reported in family I and III; while significant dominance gene effect was reported in family III only. Significant additive × dominance [j] and dominance × dominance [l] type of epistatis interaction were reported in family I, II, V and VI. Whereas, significant dominance × dominance [l] and additive × dominance [j] epistatic interactions were found in family III and IV, respectively. Duplicate epistatis reported in the family I, III, IV and VI; whereas complimentary epistatis reported in the family II and V. Higher magnitude of dominance gene effect with additive × additive [i] type of gene interaction reveals the role of both fixable and non-fixable gene effects. Higher magnitude of dominance × dominance [l] gene interaction was profound in family II and V. Similar findings were reported by Kumar and Srivastava (2017).

Total Soluble Solids. Additive and dominance model was inadequate for all the six families, as significant values of individual scaling tests were reported for seeds per fruit. In addition of this, significant estimates of χ^2 test of joint scaling test indicated presence of non-allelic interactions. Significant values of dominance gene effect as well as dominance × dominance [l], additive × additive [i] and additive × dominance [j] gene interaction effect was reported in family I. All six parameters in family II found significant, revealing the predominant role of dominance, additive genetic effects and additive × dominance [j], dominance × dominance [l] and additive × additive [i] type of epistasis gene interaction in the expression of the trait under study. Significant additive and dominant gene effects along with significant additive × additive [i] and dominance × dominance [l] interactions was reported in family III and V with higher magnitude of dominance × dominance [l] interaction. However, additive gene effect coupled with additive × dominance [j] and dominance × dominance [l] interaction found to govern the character in family IV. Duplicate type of gene interaction in five out of six families. The similar findings were reported by Kumar and Srivastava (2017).

Moisture Content. Additive dominance was found inadequate to explain since the values of individual scaling tests were found significant for all families along with significant estimates of χ^2 test value. Significant estimates of additive gene effect were reported for family I and II; whereas significant dominance effect was reported in family III. Significant additive effect along with significant additive × dominance [j] interaction epistatis reported in family I. In family II, significant additive gene effect along with all three types of gene interaction *viz.* additive × additive [i], additive × dominance [j] and dominance × dominance [l] found significant with higher magnitude of additive × additive [i] type of interaction revealing. Significant dominance effect coupled with significant additive × additive [i] and dominance × dominance [l] type of gene interaction reported in family III. Whereas, only significant dominance × dominance [l] and additive × additive [i] gene interactions were reported in family IV and V, respectively. Only mean value was found significant in family VI and other parameters were found non-significant due to difference in comparable environmental or difference in fertility and viability. Abundance of inter genic interactions suggests postponement of the selection for the character under study.

1000 Seed Weight. Significance estimates of individual simple scaling tests revealed inadequacy of additive dominance model to explain inheritance of 1000 seed weight. The results of simple scaling test were confirmed by significance of χ^2 test value of joint scaling test except, family VI. Even though, scale C found significant in family VI, non-significant χ^2 test was reported. 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. Significant estimates of additive gene effect were reported in all six families under study. Whereas, significant estimates of dominance gene effects were reported for the family IV and VI. In family I, only additive × dominance [j] gene interaction found significant. All three epistatic interactions *viz.* additive × additive [i], additive × dominance [j] and dominance × dominance [l] along with significant additive gene effect reported in family II and V. In family III, additive × dominance [j] and dominance × dominance [l] epistatis interaction were found significant. In family IV, significant additive × additive [i] and additive × dominance [j] were reported along with significant principle gene effects. From the sign of [h] and [l], duplicate epistatis depicted to govern the character in all the families except, family III. The findings were partially in accordance with Damor *et al.* (2021) as they also recorded importance inter allelic interactions.

Seed to Pulp Ratio. Additive-dominance model found inadequate to explain the inheritance of this novel character since, estimates of simple scaling test were found significant for all the families except, family II and also confirmed by significance of χ^2 test for these families. Adequacy of additive-dominance model of family II confirmed by non-significant value of χ^2 test of joint scaling test for this family. Family I exhibited significant value of additive × dominance [j] type of inter allelic interaction. Significant and higher value of

dominance component of gene action along with significant additive × additive [i] and additive × dominance [j] gene interaction was reported in family III. While, all six parameters of generation mean were found significant for family IV. Significant principle gene effect components *viz.* additive and dominance along with significant additive × dominance [j] and dominance × dominance [l] epistatis gene interaction and additive × additive [i], additive × dominance [j] and dominance × dominance [l] reported for families V and VI, respectively. Four out of six families possessed opposite signs of [h] and [l] components indicating prevalence of duplicate gene interaction; whereas complimentary gene interaction reported for the remaining two families.

Table 1: Analysis of variance of generation means in six families of tomato for characters under study.

Source	Degree of freedom	Mean sum of square							
		Days to flowering	Branches per plant	Plant height	Fruit Length	Fruit girth	Average fruit weight	Pericarp thickness	Fruit yield per plant
Analysis of variance between families									
Replication	2	2.12	0.01	45.04	0.10	0.01	1.019	0.003	0.37
Families	5	17.77**	1.04**	2288.62**	0.21*	1.072**	32.29**	0.681*	3.33**
Error	10	0.65	0.13	16.05	0.03	0.15	3.65	0.009	0.59

Source	Degree of freedom	Mean sum of square					
		Locules per fruit	Lycopene content	Total soluble solids (TSS)	Moisture content	1000 seed weight	Seed to pulp ratio
Analysis of variance between families							
Replication	2	0.069	0.000*	0.032*	1.95**	0.123**	0.001*
Families	5	1.21**	0.015**	0.958**	5.13**	0.275**	0.027**
Error	10	0.018	0.000	0.003	0.32	0.005	0.000

Table 2: Estimates of simple scaling test and gene effects for characters under study.

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 flowering															
I	-9.20**	-6.73**	-23.46**	-3.76**	163.38**	-	-	-	45.01**	-4.00**	14.00**	7.53	-1.23	8.39**	**C**
II	-10.53**	-2.00	-3.20	4.67*	45.63**	-	-	-	43.00**	-9.00**	-17.20**	-9.33*	-4.26*	21.86**	D
III	-17.40**	-8.86**	15.40**	3.43*	127.37**	-	-	-	43.36**	11.83**	-15.63**	-6.86*	13.13**	-1.66	C
IV	19.60**	10.93**	20.40**	-5.07**	181.56**	-	-	-	46.11**	-1.63	-1.10	10.13**	4.33**	-40.67**	C
V	9.33**	-23.33**	14.53**	14.27**	319.17**	-	-	-	45.46**	10.67**	-34.73**	-28.53**	16.33**	42.53**	D
VI	-17.00**	-0.07	-5.00	6.03**	105.06**	-	-	-	46.00**	-6.96**	-2.96	-12.06**	-8.46**	29.13**	**D**
Branches per plant															
I	-4.13**	-3.66**	-0.86	3.46**	187..09**	-	-	-	13.18**	0.83	-4.26**	-6.93**	-0.23	14.73**	D
II	-5.00**	-0.60	-6.46**	-0.43	36.56**	-	-	-	12.55**	0.53	2.66	0.86	-2.20**	4.73**	C
III	-4.20*	-5.33**	-7.13**	1.20	22.97**	-	-	-	12.85**	1.76*	0.59	-2.40	0.56	11.93**	C
IV	0.53	-3.33**	-2.66	0.06	13.82**	-	-	-	12.66**	1.53**	1.73	-0.13	1.93**	2.93	C
V	-0.53	-0.46	-4.46**	-1.73**	13.42**	-	-	-	11.68**	0.30	5.19**	3.46*	-0.03	2.46	C
VI	-1.40	-5.26**	-7.26**	-0.30	61.53**				13.05	0.39	2.33	0.59**	1.93	6.06**	**C**
Plant height															
I	-6.14	23.46**	-59.55	-38.43*	8.54*	-	-	-	172.38**	-27.79**	153.71**	76.87**	-14.80	-94.19	D
III	-28.99*	-41.44**	-79.97**	-4.76	16.94**	-	-	-	147.74**	1.91*	33.06	9.53**	6.22	60.91	C
IV	-57.13**	-40.10*	-80.25**	8.49	16.55**	-	-	-	151.67**	-1.23	7.57	-16.98	-8.51	114.22*	C
V	-50.34**	-20.37	-77.48**	-3.41	10.53*	-	-	-	100.28**	-8.03	35.23	6.83	-15.01	63.81	C
VI	-42.91**	-45.27**	-79.16**	4.51	31.72**	-	-	-	111.88**	4.76	14.77	-9.02	1.18	97.21**	**C**
Fruit length															
I	-1.38	-0.18	3.22*	2.39**	11.22*	-	-	-	9.60**	-1.27*	-2.10	-4.78**	-6.03	6.35*	D
II	3.64**	-0.98	-0.34	-1.50	12.18*	-	-	-	8.50**	2.02**	3.78	3.00	2.31**	-5.67	**D**
III	-6.14**	-4.26**	1.36	5.88**	159.52**	-	-	-	9.37**	-1.52**	-10.08**	-11.76**	-0.93**	22.16**	**D**
IV	3.29**	-4.13**	8.48**	4.6**	334.75**	-	-	-	10.54**	2.07**	-5.76**	-9.31**	3.71**	10.15**	**D**
V	6.50**	-0.56	9.20**	1.63**	244.92**	-	-	-	9.77**	2.68**	-1.84	-3.26**	3.53**	-2.68	**C**
VI	8.06**	3.50**	12.25**	0.34	280.80**	-	-	-	9.86**	1.05*	0.78	-0.69	2.27**	-10.86**	**C**
Fruit girth															
I	0.23	-0.85	8.40**	4.51**	49.07**	-	-	-	17.71**	-0.90	-6.31**	-9.02**	0.54	9.65**	**D**
II	-0.72	-5.28**	-7.18**	-0.59	20.69**	-	-	-	14.09**	2.13*	1.97	1.17	2.28*	4.82	**C**
III	-10.42**	-1.52	1.91	6.93**	245.24**	-	-	-	16.42**	-4.70**	-14.33**	-13.86**	-4.44**	25.81**	**D**
IV	2.76*	-4.04**	-5.83**	-2.27	21.71**	-	-	-	13.06**	1.11	7.65**	4.54	3.40**	-3.25	**D**

V	5.67**	-7.83**	3.14	2.65*	92.40***	-	-	-	16.05**	5.53**	-2.73	-5.30**	6.75**	7.46**	**D**
VI	3.83**	-1.02	4.16	0.67	21.05**	-	-	-	16.36**	0.22	2.50	-1.35	2.43**	-1.45	**D**
Average fruit weight															
I	-4.41	-3.16	9.66*	8.62**	19.09**	-	-	-	38.37**	-2.94*	-1.38**	-1.72**	-6.22	24.82**	**D**
II	12.29**	-4.27	9.92	0.95	12.83*	-	-	-	44.61**	4.62	-1.09	-1.90	8.28**	-6.10	**C**
III	18.00**	3.84	24.68**	1.41	56.12**	-	-	-	45.55**	3.25	8.42	-2.83	7.07**	-19.00*	**D**
IV	-21.09**	-28.91**	-24.77**	12.61**	46.69**	-	-	-	43.33**	-2.85	-6.55	-25.23**	3.91	75.24**	**D**
V	-9.94*	-24.95**	-22.89**	6.00	41.55**	-	-	-	45.22**	-0.24	12.03	-12.00**	7.50	46.90**	**C**
VI	-14.78**	-11.48**	-2.19	12.04**	32.91**	-	-	-	43.41**	-3.53*	-19.30**	-24.08**	-1.65	50.35**	**D**
Pericarp thickness															
I	-1.04*	0.46	-0.45	0.06	9.72*	-	-	-	5.28**	0.20	0.30	-0.12	-0.75**	0.70	**C**
II	1.94**	0.23	1.65*	-0.26	27.40**	-	-	-	5.58**	0.37	0.11	0.53	0.85**	-2.71**	**D**
III	0.49	1.35**	1.19*	-0.32	18.36**	-	-	-	5.37**	-0.22	0.87	0.64	-0.42	-0.24*	**D**
IV	1.92**	0.46	-0.44	-1.41**	24.28**	-	-	-	3.86**	-0.44	3.07**	2.82**	0.73*	-5.21**	**D**
V	-1.03**	-3.12**	-2.50**	0.82**	51.00**	-	-	-	5.02**	0.74**	-1.73*	-1.64*	1.04**	5.79**	**D**
VI	1.79**	-1.60**	-1.68**	-0.94**	31.99**	-	-	-	5.11**	-0.60	3.27**	1.88*	1.70**	-2.07	**D**
Fruit yield per plant															
I	3.61	-0.09	9.00**	2.74	10.20*	-	-	-	9.78**	1.34	-3.03	-5.48	1.85	1.96	**D**
II	5.39**	-0.09	5.22	-0.03	9.12*	-	-	-	9.49**	1.63	1.67	0.07	2.74**	-5.37	**D**
III	4.45**	3.70**	5.52*	-1.31	14.32**	-	-	-	8.43**	0.93	6.46**	2.63	0.37	-10.79**	**D**
IV	-3.00	2.61	-7.52**	-3.57**	23.84**	-	-	-	6.77**	-2.72**	11.59**	7.14**	-2.81**	-6.75	**D**
V	-1.63	-8.53**	9.14**	9.67**	92.04**	-	-	-	13.89**	2.93**	-11.73**	-19.34**	3.44**	29.51**	**D**
VI	6.19**	3.56*	6.21*	-1.76	14.13**	-	-	-	8.81**	3.16**	6.22*	3.53	1.31	-13.29**	**D**
Locules per fruit															
I	-0.86*	-2.40**	2.33**	2.80	115.08**	-	-	-	4.13**	1.00**	-4.56**	-5.59**	0.76**	8.86**	D
II	0.60	-0.33	1.73**	0.73*	11.51*	-	-	-	4.20**	0.33	-0.06	-1.46*	0.46	1.19	D
III	-1.20**	2.66**	-1.46**	-1.46**	98.61**	-	-	-	3.71**	-0.76**	3.96**	2.93**	-1.93**	4.40**	C
IV	0.86*	-1.53**	4.80**	2.73**	86.74**	-	-	-	6.33**	0.53*	-3.20**	-5.46**	1.20**	6.13**	D
V	-0.46	1.26**	2.66**	0.93**	27.91**	-	-	-	4.90**	-1.40**	0.59	-1.86**	-0.86**	1.06	C
VI	1.13**	2.26**	1.00	-1.20**	31.41**	-	-	-	4.68**	-0.23	3.80**	2.40**	-0.56*	-5.80**	D
Lycopene content															
I	0.22**	0.55**	0.75**	-0.01	375.00**	-	-	-	0.45**	-0.22**	0.05	0.02	-0.16**	-0.80**	D
II	-0.30**	0.02	-0.13*	0.07	62.22**	-	-	-	0.53**	0.01	0.14	-0.14	-0.16**	0.43**	C
III	0.35**	0.34**	0.27**	-0.21**	88.19**	-	-	-	0.36**	-0.08**	0.54**	0.42**	-0.00	-1.11**	D
IV	0.17**	-0.12**	0.00	-0.02	37.70**	-	-	-	0.36**	0.02	0.13	0.05	0.14**	-0.11	D
V	-0.41**	-0.19**	-0.33**	0.13*	63.65**	-	-	-	0.47**	0.01	0.06	-0.27	-0.11*	0.88**	C
VI	-0.01	-0.21**	-0.20*	0.01	28.14**	-	-	-	0.43**	-0.02	-0.03	-0.02	0.09**	0.25*	**D**
Total soluble solids															
I	-1.51**	0.13	0.43	0.90**	52.83**	-	-	-	5.08**	0.10	-2.64**	-1.81**	-0.82**	3.19**	D
II	2.07**	0.76**	1.52**	-0.65**	111.80**	-	-	-	4.22**	1.04**	1.21**	1.31**	0.65**	-4.15**	D
III	-1.11**	-1.32**	0.50	1.47**	63.73**	-	-	-	4.43**	0.34*	-2.31**	-2.95**	0.10	5.39**	D
IV	0.43*	-2.46**	-1.29**	0.36	131.19**	-	-	-	3.43**	0.78**	-0.03	-0.73	1.45**	2.76**	D
V	-3.01**	-2.77**	-4.26**	0.76**	250.01**	-	-	-	4.06**	0.65**	0.12	-1.52**	-0.12	7.31**	C
VI	-2.10**	-2.23**	-1.13**	1.60**	98.82**	-	-	-	3.52**	-1.04**	-3.62**	-3.20**	0.06	7.54**	**D**
Moisture content															
I	-7.45**	0.17	-5.34	0.96	15.27**	-	-	-	90.52**	-3.28**	-4.52	-1.93	-3.81**	9.22	D
III	3.13	3.35	-2.45	-4.47**	16.99**	-	-	-	91.11**	-0.75	7.84**	8.94**	-0.10	-15.44**	D
IV	-5.95**	-6.45**	-7.33**	2.53	20.61**	-	-	-	91.57**	0.49	-4.55	-5.06	0.24	17.47**	D
V	-3.71*	-1.46	-4.57	0.30	5.87	-	-	-	91.26**	-0.14	-3.26	-0.61	-1.12	5.80	D
VI	-4.50**	-2.42	-7.23**	-0.15	15.27**	-	-	-	91.11**	-0.44	-0.58	0.30	-1.03	6.62	D

Contd.

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*	
1000 seed weight															
I	-0.58	2.14**	1.46**	-0.04	50.74**	-	-	-	3.72**	-0.61**	0.45	0.09	-1.36**	-1.64	D
II	-1.09**	0.31	1.35	1.06	54.58**	-	-	-	3.73**	-0.79**	-1.08	-2.13**	-0.70**	2.92**	D
III	0.33	-3.96**	-2.99**	0.31	143.11**	-	-	-	3.56**	1.20**	0.16	-0.63	2.14**	4.26**	C
IV	-0.54	0.92	3.30**	1.46**	20.39**	-	-	-	4.85**	-1.58**	-3.01*	-2.92*	-0.73*	2.54	D
V	-1.23**	0.75	1.86	1.17*	23.02**	-	-	-	4.05**	-0.59*	-1.83	-2.35*	-0.99**	2.83*	D
VI	-0.62	-0.07	-1.61*	-0.45	5.01	-	-	-	3.53**	-0.60*	0.22**	0.91	-0.27	-0.20	**D**
Pulp to seed ratio															
I	0.17**	0.03	0.12	-0.04	10.17	-	-	-	0.42**	0.03	0.17	0.08	0.06*	-0.03	C
II	-0.07	-0.01	-0.01	0.03	3.59	0.67**	0.13**	0.25	0.68**	0.11**	-0.05	-0.07	-0.03	0.16	D
III	0.21**	-0.15**	0.41**	0.17**	60.45**	-	-	-	0.62**	-0.00	-0.29**	-0.35**	0.18**	0.29	D
IV	-0.71**	0.21**	0.11	0.30**	274.90**	-	-	-	0.59**	-0.28**	-0.49**	-0.60**	-0.46**	1.10**	D
V	0.07	-0.44**	-0.28**	0.04	87.05**	-	-	-	0.60**	0.31**	0.11	-0.08	0.25**	0.45**	C
VI	0.08	-0.47**	-0.16	0.11*	94.37**	-	-	-	0.54**	0.24**	-0.03	-0.22*	0.27**	0.61**	**D**

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

CONCLUSIONS

The present investigation revealed that main effects *viz.*, additive and dominance along with additive × additive (i), additive × dominance (j) and dominance × dominance (l) were present at more or less extent indicating the importance of these interactions for the inheritance of the various traits. The result of epistatic gene effects for fruit yield and its related traits in different cross combinations revealed that recurrent selection and bi-parental mating between desirable segregants followed by selection would be profitable for development of desirable hybrids/lines/varieties.

FUTURE SCOPE

The segregating material can be advanced in order to produce advanced lines with superior traits. They can be employed further in breeding programmes.

Conflict of Interest. None.

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