MANIFESTATION OF GENETIC BEHAVIOR IN INTRASPECIFIC CROSSES OF TOMATO II-NATURE OF GENETIC VARIATION FOR YIELD AND QUALITY CHARACTERISTICS

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ABSTRACT

Inheritance of seven quantitative traits related to fruit yield and quality characteristics was studied in six intraspecific crosses of tomato (*Lycopersicon esculentum Mill*) namely $Campbell_{1327}$ x Floradad, $Campbell_{1327}$ x Line 37, $Campbell_{1327}$ x $Homestead_{24F}$, $Campbell_{1327}$ x Strain B, Line 37 x Strain B and $Homestead_{24F}$ x Line 37, in addition to their F_2 and backcrosses generations. The significant test of mean squares indicated the presence of significant differences among crosses and populations within crosses for all studied traits except total fruit weight/plant, which showed insignificant differences among crosses. The Strain-B was the best parent for yield as number and weight of fruits as well as flesh thickness. In addition, the results revealed that the three types of gene action (additive, dominance and epistasis) were contributed to the genetic variability with different magnitudes for all studied traits. The predominated gene action for total yield as number and weight of fruits and quality characters was dominance in most of studied crosses. Therefore, most of crosses exhibited desirable heterosis over their high parent, especially in the case of total yield as number and weight of fruits per plant. These results suggested the improvment of these characters could be achieved through the production of hybrids to make use of heterosis.

INTRODUCTION

Increasing productivity together with better quality are the major objectives of tomato breeders. To improve any quantitative character, gather informations about gene action of the character must be known with respect to the relative magnitudes of additive and non-additive genetic variances. A breeding program is usually making use of the informations concerning the relative importance of these two components. When the additive gene action makes up the main component in the genetic variation, a maximum progress could be expected through a selection program. On the other hand, the presence of a relatively high non-additive gene action indicates that a hybrid approach would perform a good prospect for the considered character, as a result of the direct relationship between the dominance gene effects and heterosis. In this respect, Khalil *et al.* (1983) studied the inheritance of total yield as number and weight of fruits in the six populations of the cross (Kecskemeti Jublleum x Kecskemeti Exprt) and they indicated that the additive effect was predominating for high fruit number and low fruit weight. Similarly, Metwally *et al.* (1990) and Zanata (1994) studied combining ability among some tomato varieties and concluded that additive gene effect is more important in the inheritance of total fruit weight per plant. On the other hand, Dhaliwal *et al.* (2000) indicated that over dominance is predominating in the inheritance of total yield as number and weight of fruits per plant.

Concerning fruit quality characters, average fruit weight was found to be a quantitatively inherited character (Khalil *et al.*, 1983) with partial dominance of smaller size fruit (Khalil *et al.*, 1983; Salib, 1999 and Abdel-Ati *et al.*, 2000) while no dominance was observed in 4 out of 21 studied hybrids (Hatem, 1994). Fruit firmness was governed by additive gene action (Dobhol *et al.*, 1999), or partial dominance (Khalil *et al.*, 1988 and Salib, 1999). Similar trend was observed in most of other quality characters, such as TSS% (Conti *et al.*, 1988); flesh thickness (Dobhol *et al.*, 1999) and number of locules per fruit (Amaral Junior *et al.*, 1996).

MATERIAL AND METHODS

Genetic materials: The genetic materials used in the present investigation included eight genetically diverse inbrid lines. These inbred lines were: Campbell $_{1327}$, Strain-B, Line-73, Homestead $_{24F}$, Floradata, Scotia, Siberia and Bush $_{506}$. On October 15th, 1997 seeds were sown in seedling trays under fiberglass green house at Kaha Experimental Station, Kaliobia Governorate. Transplanting took place 45 days after sowing. These inbreds were crossed in all possible combinations excluding reciprocals to obtain 28 single crosses. During the 1998 summer planting, preliminary evaluation for the parents and their hybrids was made to choose the best hybrids with respect to earliness and good fruit quality. These chosen crosses were as follow:

Cross (1)- Campbell $_{1327}$ X Floradad
Cross (2)- Campbell $_{1327}$ X Line-73
Cross (3)- Campbell $_{1327}$ X Homestead $_{24F}$
Cross (4)- Campbell $_{1327}$ X Strain-B
Cross (5)- Line-73 X Strain-B
Cross (6)- Homestead $_{24F}$ X Line-73.

Experimental Procedures: Seeds of the chosen F_1 hybrids and their parents were sown on 10th August 1999 and transplanted under fiberglass green house at Kaha Experimental Station. Some flowers from each parent and F_1 plants were self-pollinated in order to increase seeds from parental genotypes as well as to produce F_2 generation's seeds. Some F_1 plants were also backcrossed to their parents in order to obtain BC_1 and BC_2 seeds. In addition, the crosses between these parents were done again in the same manner to increase F_1 seeds. Parental lines, F_1, F_2, BC_1 and BC_2 generations of the six crosses were evaluated in 2000 summer planting at Baramon Experimental Farm of Horticultural Research Institute, Mansoura. The field experiment was arranged in a split plot design with three replications. Each block/replicate consisted of 6 main plots which included the six crosses. Each main plot is divided into 6 sub-plots, which included the six generations. Sub-plots size was two rows for each parent as well as each F_1 hybrids, three rows for each back cross and four rows for each F_2 generation. Each row was 5 meters long and 1 meter apart. The plants were spaced at 33 cm on side ridges. All cultural practices were applied as recommended for tomatoes production.

Data were recorded on individual plants for the following characters: total number of fruits per plant (TNF) and total weight of fruits per plant (TWF) as yield traits; average fruit weight (AFW), number of locules per fruit (NLF), flesh thickness (FT), fruit firmness (FF) and total soluble solids percentage (TSS%) as fruit characteristics.

Statistical Analysis: Analysis of variance according to split-plot design for the studied traits was made to detect the significance of the observed difference among and within crosses (Singh and Narayanan, 2000). The scaling tests (A,B and C) were determined according to the formulae outlined by (Mather and Jinks, 1982) for testing deviations of segregation from the additive and dominance model of gene effects. Then, Standard errors of A, B and C was worked out by taking the square root of corresponding variances and t values were calculated by dividing the effects of A, B and C by their respective standard error. The calculated t values of these three tests were compared against tabulated values of t at 5% and 1% levels of significance. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Therefore, the six parameter-model is used to estimate various types of gene effects.

While, If the (t) test is insignificant, the additive-dominance gene effects is adequate to interpret the nature of gene action.

Six-parameter models are m, a, d, aa, ad and dd, these stand for mean effects, additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects, respectively. These genetic components, variance, standard error and calculated "t" values were estimated according to Gamble (1962). In the absence of non-allelic interaction. The additive dominance model is adequate. Thus, m, a and d were estimated according to Jinks and Jones (1958). Significance of the genetic effects is tested in a similar manner as done in case of scaling test.

Heritability in broad sense was calculated using the formula outlined by Allard (1960) and Falconer (1981). Heritability in narrow sense was estimated by the application of the formula outlined by Mather and Jinks (1982). The minimum number of pairs genes responsible for the difference between parents were determined for each character using Wright' s formula (Burton, 1951). The expected genetic gain resulting from selection in a character (G.S) was computed by the Formula reported by Allard (1960).

RESULTS AND DISCUSSION

Analyses of variance: The results of the analysis of variance and the mean squares of crosses and populations within crosses for all studied traits are presented in Table 1. The results indicated the presence of highly significant differences among crosses as well as among populations within crosses for all studied traits except total fruit weight (TWF), which exhibited insignificant difference among crosses. The differences among populations within each cross were significant in most studied crosses with respect to the studied traits. These results confirmed the different genetic constitutions of the studied crosses. Therefore. the comparisons between genotypic means are valid and the partition of this genotypic variances to their components could be made.

Mean performances: The six population means and standard errors of the studied crosses were calculated for all studied traits and the obtained results are shown in Table 2. The data recorded on the different genotypes revealed that the highest parent for total yield as number (TNF) and weight of fruit /plant (TWF) as well as flesh thickness (FT) was the variety Strain-B with the mean values of 27.1, 2.24 kg and 4.15, respectively. However, the highest one for average fruit weight (AFW), number of

Table 1: Analysis of variance and the mean squares of crosses and their populations for all studied traits.

S.O.V	d.f	TNF	TWF	AFW	NLF	FT	FF	T.S.S. %
Reps (R)	2	1.75	0.13	7.07	0.01	0.39*	0.09*	0.06
Crosses (C)	5	114.99**	0.23	889.54**	3.05**	2.03**	6.23**	0.27**
Rep.W.C. (Ea)	10	3.90	0.06	59.89	0.04	0.09	0.01	0.01
Pop-W.C	30	39.24**	0.33**	254.36**	1.05**	1.16**	1.05**	0.17**
Pop-W.C1	5	11.83**	0.24*	134.13**	0.53**	2.80**	0.87**	0.18
Pop-W.C2	5	9.12	0.35*	189.26	0.52**	1.75**	0.25**	0.21*
Pop-W.C3	5	25.15	0.12**	407.47	0.89**	1.26**	1.14**	0.21**
Pop-W.C4	5	49.58**	0.22**	301.12*	2.35**	3.29**	0.16*	0.22**
Pop-W.C5	5	72.44*	0.73**	138.62	1.26**	4.19**	3.13**	0.11**
Pop-W.C6	5	67.34**	0.33	355.57	0.78**	1.67**	0.76**	0.07
R-W.pop x C(Eb)	60	4.38	0.04	103.27	0.03	0.03	0.02	0.03
R-W.pop x C1	10	0.75	0.03	5.83	0.02	0.01	0.01	0.05
R-W.pop x C2	10	2.00	0.04	162.79	0.05	0.06	0.01	0.03
R-W.pop x C3	10	10.51	0.01	87.97	0.04	0.07	0.02	0.01
R-W.pop x C4	10	0.19	0.02	41.59	0.02	0.01	0.02	0.02
R-W.pop x C5	10	8.29	0.03	213.22	0.01	0.02	0.06	0.01
R-W.pop x C6	10	4.54	0.12	108.23	0.04	0.03	0.02	0.03

Cross (1) = Campbell $_{1327}$ x Floradad
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Cross (3) = Campbell $_{1327}$ x Homestead $_{24F}$
Cross (4) = Campbell $_{1327}$ x Strain–B
Cross (5) = Line-73 x Strain -B
Cross (6) = Homestead $_{24F}$ x Line-73
***,** Significant at 0.05 and 0.01 levels of probability, respectively.**

Table 2: Mean performance and standard errors of populations within each cross for all studied traits.

Trait	Crosses	P1	P2	F_1	F_2	BC1	BC2
TNF	1	20.6±0.55	19.5±0.44	22.6±0.32	19.6±1.08	22.7±0.64	24.5±1.03
	2	20.6±0.55	19.7±0.48	24.0±0.55	19.5±1.47	22.4±1.25	20.9±1.04
	3	20.6±0.55	19.6±3.49	21.5±0.43	27.5±1.64	19.0±1.12	22.3±1.34
	4	20.6±0.55	27.1±0.28	30.7±0.20	32.1±0.41	25.7±0.23	26.1±0.38
	5	19.7±0.48	27.1±0.28	32.2±1.09	31.5±2.46	23.8±1.25	23.4±2.32
	6	19.6±3.49	19.7±0.48	24.3±0.92	26.5±1.48	30.3±1.43	29.8±1.62
TWF (Kg)	1	2.13±0.06	1.81±0.02	2.47±0.03	1.99±0.07	2.49±0.07	2.40±0.05
	2	2.13±0.06	1.89±0.06	2.74±0.08	1.84±0.18	2.41±0.16	2.09±0.11
	3	2.13±0.06	1.66±0.04	2.18±0.02	2.17±0.10	2.03±0.92	2.10±0.07
	4	2.13±0.06	2.24±0.03	2.66±0.06	2.56±0.10	2.36±0.07	1.93±0.09
	5	1.89±0.06	2.24±0.03	3.23±0.08	2.60±0.13	2.26±0.25	1.96±0.11
	6	1.66±0.04	1.89±0.06	2.55±0.08	2.13±0.32	2.29±0.28	2.41±0.24
AFW (gm)	(1)	103±0.90	92±1.70	110±0.30	101±2.00	109±0.30	98±2.60
	(2)	103±0.90	96±6.20	115±5.60	94±9.50	108±9.50	100±7.00
	(3)	103±0.90	85±5.40	102±2.70	80±7.50	107±7.80	94±5.00
	(4)	103±0.90	83±0.70	87±2.00	80±5.80	92±3.50	74±5.80
	(5)	96±6.20	83±0.70	100±0.90	90±11.80	94±9.10	85±9.80
	(6)	85±5.40	96±6.20	105±1.70	84±7.80	75±6.70	80±6.70
NLF	(1)	5.88±0.06	4.68±0.04	4.43±0.04	5.15±0.12	5.46±0.10	5.11±0.09
	(2)	5.88±0.06	5.35±0.06	5.16±0.05	4.62±0.20	5.45±0.17	5.47±0.13
	(3)	5.88±0.06	4.71±0.06	4.39±0.05	4.61±0.16	5.12±0.15	4.60±0.09
	(4)	5.88±0.06	4.63±0.05	4.01±0.05	3.87±0.12	3.57±0.11	3.57±0.03
	(5)	5.35±0.06	4.63±0.05	4.47±0.04	3.43±0.11	4.15±0.10	4.80±0.06
	(6)	4.71±0.06	5.35±0.06	5.31±0.04	4.13±0.18	4.28±0.14	4.61±0.14
FT	(1)	3.71±0.05	2.89±0.04	5.32±0.05	4.64±0.12	5.31±0.07	4.82±0.11
	(2)	3.71±0.05	3.37±0.03	4.05±0.07	4.69±0.30	5.31±0.18	4.99±0.18
	(3)	3.71±0.05	3.57±0.11	4.22±0.11	4.47±0.32	5.15±0.30	4.98±0.15
	(4)	3.71±0.05	4.15±0.01	4.95±0.04	5.46±0.11	5.17±0.08	6.68±0.09
	(5)	3.37±0.03	4.15±0.01	6.56±0.03	6.07±0.14	4.84±0.12	5.10±0.08
	(6)	3.57±0.11	3.37±0.03	5.37±0.04	4.52±0.23	4.50±0.17	4.67±0.17
FF	(1)	9.30±0.03	10.14±0.04	9.73±0.04	8.88±0.10	8.69±0.08	9.43±0.09
	(2)	9.30±0.03	9.10±0.05	9.35±0.04	8.69±0.11	9.52±0.09	9.03±0.07
	(3)	9.30±0.03	7.81±0.04	8.85±0.04	8.74±0.11	9.62±0.07	8.95±0.09
	(4)	9.30±0.03	9.71±0.04	9.40±0.04	9.61±.013	9.50±0.14	9.95±0.06
	(5)	9.10±0.05	9.71±0.04	10.2±0.10	11.5±0.21	10.0±0.15	11.7±0.17
	(6)	7.81±0.04	9.10±0.05	8.64±0.05	8.78±0.11	8.71±0.83	9.26±0.08
T.S.S.%	(1)	6.02±0.06	5.54±0.04	5.62±0.03	5.56±0.20	5.82±0.12	5.29±0.18
	(2)	6.02±0.06	5.80±0.06	6.24±0.08	5.81±0.13	5.99±0.14	5.45±0.06
	(3)	6.02±0.06	5.70±0.06	6.09±0.03	5.36±0.10	5.91±0.07	5.86±0.09
	(4)	6.02±0.06	5.57±0.03	6.00±0.05	5.62±0.12	6.21±0.10	4.62±0.08
	(5)	5.80±0.03	5.57±0.03	5.69±0.05	5.34±0.08	5.35±0.08	5.67±0.07
	(6)	5.70±0.06	5.80±0.06	5.87±0.04	5.81±0.18	5.51±0.17	5.94±0.08

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Cross (5) = Line-73 x Strain -B
Cross (6) = Homestead $_{24F}$ x Line-73

locules per fruit (NLF) and T.S.S.% was the variety $Campbell_{1327}$. Although, the variety Floradata was inferior parent for flesh thickness (FT) and T.S.S. percentage, it was the highest parent for fruit firmness (FF). Most F_1 hybrids showed superiority over their high parent for total number of fruit per plant, total fruit weight per plant, average fruit weight (AFW) and flesh thickness (FT) with means ranged from 21.5 (3^{rd} cross) to 32.2 (5^{th} cross), 2.18 kg (3^{rd} cross) to 3.23 kg (5^{th} cross), 87 g (4^{th} cross) to 115 g (2^{nd} cross) and 4.05 (2^{nd} cross) to 6.56 (5^{th} cross), respectively. Also, most F_1 hybrids fall between means of the parents with respect to number of locules/fruit (NLF), fruit firmness (FF) and total soluble solids (T.S.S%). These findings reflected that, dominance genes controlled these traits were more frequent in these crosses and may explain the reduction that exist in the most of F_2 generations than their corresponding F_1 hybrids. The means also showed that the highest backcrosses for total fruit number/plant and total fruit weight /plant were BC_1 of the 6^{th} cross (30.3) and BC_1 of the 1^{st} cross (2.49 kg), respectively. In addition, the highest backcrosses for average fruit weight (AFW), flesh thickness (FT), fruit firminess and T.S.S.% were BC_1 of the 1^{st} cross (109 g) BC_2 of the 4^{th} cross (6.68), BC_2 of the 5^{th} cross (11.7) and BC_1 of the 4^{th} cross (6.21), respectively. Generally, the means of most backcrosses strongly tended to be toward the respective recurrent parents, reflecting the role of additive and epistasis gene effects.

Gene action: The results of scaling tests (A, B and C) for all studied traits are presented in Table 3. These tests were insignificantly different in the cases of 2^{nd}, 6^{th}, (2^{nd}, 4^{th} and 5^{th}), 3^{rd}, 6^{th} and (1^{st} and 6^{th}) crosses for total number of fruits, total weight of fruits, average fruit weight, number of locules per fruit, fruit thickness and total soluble solids percentage (TSS%), respectively. These findings indicated the absence of epistasis and the additive-dominance model is adequate to interpret gene effects in these crosses. While, the six parameter model is valid to explain the nature of gene action for other crosses. Therefore, the estimates of the various types of effects contributing to the genetic variability of the six crosses for all studied traits were determined and the obtained results are shown in Table 4. The results showed that the mean effect parameter (m), which reflect the contribution due to overall mean (additive) plus the local effects (dominance) found to be significant for all studied traits with respect to the studied crosses except the second cross in the cases of total number of fruits per plant and average fruit weight. Although, the additive gene effects (a) were significant in the 4^{th} cross for total fruit weight/plant, the

Table 3: Scaling tests (A, B and C) and their standard error for all studied traits

Cross		TNF	TWF	AFW	NLF	FT	FF	T.S.S. %
1	A	2.25±1.2	0.36±0.1**	5.70±1.2**	0.12±0.2	1.60±0.2**	-1.75±0.2**	-0.03±0.3
	B	6.91±2.1**	0.52±0.1**	-6.00±5.6	0.60±0.2**	1.45±0.2**	-0.92±0.2**	-0.58±0.4
	C	-6.70±4.4	-0.92±0.3	-9.70±8.4	0.16±0.5	1.32±0.2**	-3.59±0.4**	-0.54±0.8
2	A	0.17±2.6	-0.05±0.3	-3.33±19.8	-0.13±0.4	2.86±0.4**	0.38±0.2	-0.37±0.3
	B	-1.96±2.2	-0.44±0.3	-10.30±16.2	0.42±0.3	2.57±0.4**	-0.39±0.2	-1.13±0.2**
	C	-10.32±6.0	-2.15±0.7**	-53.6±39.9	-3.06±0.8**	3.58±1.0**	2.34±0.4**	-1.06±0.6
3	A	-4.07±2.4	-0.25±0.2	9.70±15.9	-0.02±0.3	2.38±0.6**	1.10±0.1**	-0.23±0.2
	B	3.48±3.7	0.35±0.1**	1.70±11.7	0.09±0.2	2.18±0.3**	1.24±0.2**	-0.05±0.2
	C	26.88±7.1**	0.53±0.4	-71.42±31.0*	-0.93±0.7	2.17±1.3	0.14±0.5	-1.42±0.4**
4	A	0.14±0.5	-0.07±0.2	-6.00±7.4	-2.74±0.2**	1.68±0.2**	-1.70±2.3	0.40±0.2
	B	-5.53±0.7**	-1.05±0.2**	-22.1±11.9	-1.50±0.1**	4.26±0.2**	0.79±0.1**	-0.33±0.2
	C	19.27±1.7**	0.57±0.4	-39.4±23.5	-3.06±0.5**	4.08±0.5**	0.62±0.6	-1.10±0.5*
5	A	-4.28±2.8	-0.60±0.5	-7.33±19.2	-1.52±0.2**	-0.25±0.2	0.74±0.3*	-0.78±0.2**
	B	-12.45±4.8**	-1.56±0.2**	-13.7±19.7	0.50±0.1**	-0.50±0.2*	3.46±0.4**	0.09±0.2
	C	14.98±10.1	-0.20±0.6	-20.3±47.8	-5.22±0.4**	3.63±0.6**	6.90±0.9**	-1.37±0.4**
6	A	16.77±3.1**	0.38±0.6	-39.0±14.5**	-1.45±0.4**	0.05±0.4	0.96±0.2**	-0.54±0.3
	B	15.74±2.8**	0.38±0.5	-40.0±14.9**	-1.44±0.3**	0.60±0.4	0.78±0.2**	0.20±0.2
	C	18.33±7.6*	-0.14±1.3	-54.0±32.3	-4.17±0.7**	0.41±0.9	0.92±0.4*	0.02±0.7

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Cross (5) = Line-73 x Strain -B
Cross (6) = Homestead $_{24F}$ x Line-73
*, ** Significant at 0.05 and 0.01 levels of probability, respectively.

Table 4: Types of gene action for all studied traits in the six crosses.

Cross	Traits	M	A	d	aa	ad	dd
1	TNF	19.63±1.1**	-1.78±1.2	18.35±4.9	15.85±4.9**	-2.33±1.3	-25.01±6.6**
2		11.60±6.7	0.47±0.4	19.18±15.4	-	-	-
3		27.53±1.6**	-3.27±1.8	-26.03±7.6**	-27.47±7.4**	-3.77±2.2	28.06±9.9**
4		32.1±0.4**	-0.40±0.4	-17.83±1.9**	-24.66±1.9**	2.83±0.5	30.05±2.5**
5		31.5±2.5**	0.42±2.6	-22.85±11.2*	-31.63±11.2*	4.12±2.7	48.29±14.6**
6		26.5±1.5**	0.48±1.9	18.82±8.4*	14.18±8.3	0.51±1.9	-46.69±10.8*
1	TWF	1.99±0.07**	0.08±0.1	2.30±0.3**	1.80±0.3*	-0.08±0.1	-2.68±0.4**
2		1.84±0.2**	0.32±0.2	2.40±0.8**	1.67±0.8*	0.19±0.2	-1.19±1.1
3		2.17±0.1**	-0.06±0.1	-0.15±0.5	-0.43±0.5	-0.30±0.1**	0.33±0.6
4		2.56±0.1**	0.43±0.1**	-0.12±0.5	-1.68±0.5*	0.49±0.1**	2.78±0.6**
5		2.60±0.1**	0.30±0.3	-0.79±0.8	-1.96±0.8*	0.55±0.3	4.11±1.2**
6		0.87±1.5	-0.11±0.1	3.34±3.4	-	-	-
1	AFW	101.3±2.0**	11.30±2.7**	21.20±9.8*	9.30±9.7	5.80±2.3*	-8.89±13.5
2		59.5±4.5	3.80±3.1	82.20±104.1	-	-	-
3		79.9±7.5**	13.30±9.3	90.30±35.5*	82.70±35.3*	4.00±9.7	94.10±84.5
4		81.7±27.8**	10.30±0.6**	-11.70±61.7	-	-	-
5		89.8±44.5*	6.50±3.1*	-11.20±12.4	-	-	-
6		84.0±7.8**	-5.00±9.5	10.00±36.7	-25.00±36.4	0.50±10.3	103.70±49.8
1	NLF	5.15±0.1**	0.36±0.1**	0.20±0.6	0.55±0.6	-0.24±0.1	-1.27±0.7
2		4.6±0.2**	-0.013±0.2	2.90±0.9**	3.35±0.9**	-0.28±0.2	-3.64±1.2*
3		4.3±0.8**	0.58±0.04**	1.16±1.7	-	-	-
4		3.87±0.1**	-0.02±0.1	-2.43±0.5**	-1.19±0.5*	-0.63±0.1**	5.43±0.7**
5		3.43±0.1**	-0.65±0.1**	3.68±0.5**	4.19±0.5**	-1.01±0.1**	-3.17±0.7**
6		4.13±0.2**	-0.32±0.2	1.55±0.8	1.27±0.8	-0.01±0.2	1.62±1.1
1	FT	4.64±0.1**	0.49±0.1**	3.74±0.6**	1.72±0.6**	0.08±0.1	-4.77±0.7**
2		4.69±0.3**	0.31±0.3	2.35±1.1*	1.84±1.1	0.15±0.3	-7.26±1.4**
3		4.47±0.3**	0.17±0.3	2.97±1.4*	2.39±1.4	0.10±0.3	-6.95±1.9**
4		5.46±0.1**	-1.51±0.1**	2.88±0.5**	1.86±0.5**	-1.29±0.1**	-7.80±0.7**
5		6.07±0.1**	-0.27±0.15	-1.59±0.6**	-4.39±0.6**	0.12±0.2	5.14±0.8**
6		3.22±1.1**	0.10±0.05	3.06±2.4	-	-	-
1	FF	8.88±0.1**	-0.84±0.2**	1.82±0.5**	0.92±0.5	-0.42±0.2*	1.75±0.6**
2		8.69±0.1**	0.48±0.1**	2.48±0.5**	2.34±0.5**	0.38±0.1**	-2.34±0.6**
3		8.74±0.1**	0.67±0.1**	2.49±0.5**	2.20±0.5**	-0.72±0.1	-4.54±0.6**
4		9.61±0.1**	-0.45±0.2*	0.36±0.6	0.47±0.6	-0.25±0.2	-1.56±0.8
5		11.51±0.2**	-1.66±0.2**	-1.93±0.9*	-2.70±0.9**	-1.36±0.2**	-1.50±1.2
6		8.78±0.1**	-0.56±0.1**	1.00±0.5*	0.82±0.5	0.09±0.1	-2.56±0.7**
1	T.S.S. %	5.82±0.9**	0.24±0.04**	-0.82±2.1	-	-	-
2		5.81±0.1**	0.5±0.2*	-0.01±0.6	-0.33±0.6	0.43±0.2*	1.73±0.8*
3		5.36±0.1**	0.05±0.1	2.33±0.5**	2.09±0.5**	-0.11±0.1	-1.77±0.6**
4		5.62±0.1**	0.59±0.1**	1.38±0.5**	1.17±0.5*	0.37±0.1**	-1.24±0.7
5		5.34±0.1**	-0.32±0.1**	0.68±0.4	0.67±0.4	-0.45±0.1**	0.02±0.6
6		6.10±0.8**	-0.06±0.03	-0.91±1.8	-	-	-

Cross (1) = Campbell $_{1327}$ x Floradad
Cross (2) = Campbell $_{1327}$ x Line-73
Cross (3) = Campbell $_{1327}$ x Homestead $_{24F}$
Cross (4) = Campbell $_{1327}$ x Strain -B
Cross (5) = Line-73 x Strain -B
Cross (6) = Homestead $_{24F}$ x Line-73
***, ** Significant at 0.05 and 0.01 levels of probability, respectively.**

dominance gene effect (d) were positive or negatively significant in the 3^{rd}, 4^{th}, 5^{th} and 6^{th} crosses for total fruit number/plant and the 1^{st}, 2^{nd} and 4^{th} crosses for total fruit weight /plant. While, the values of dominance effects (d) were larger than the corresponding values of additive effects (a) in most of crosses for the yield as number and weight of fruits. These results suggested that the dominance effects predominated in the inheritance of these traits. In addition, most of crosses showed significant additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) gene effect.

Thus, the presence of significant non-allelic interaction may hinder the progress of selection leading to losses of favorable genotypes during the early generation of selection. Therefore, the improvment of these characters could be achieved through the production of hybrids to make use of heterosis. Similar results were obtained by many investigators among them, Natura-Jan (1992), Dhaliwal *et al.* (2000) and Amin *et al.* (2001). Regarding quality characteristics, the additive gene effects (a) were significant for number of locules/fruit in the 1^{st} and 3^{rd} crosses, thickness of flesh in the 1^{st} cross, T.S.S.% in the 1^{st}, 2^{nd} and 4^{th} crosses, fruit firmness in the 2^{nd} and 3^{rd} crosses and average fruit weight in the 1^{st}, 4^{th} and 5^{th} crosses, while the dominance gene effects (d) were significantly positive or negative for number of locules/fruit in the 2^{nd}, 4^{th} and 5^{th} crosses, thickness of flesh in the 1^{st}, 2^{nd}, 3^{rd}, 4^{th} and 5^{th} crosses, T.S.S. in the 3^{rd} and 4^{th} crosses, fruit firminess in the 1^{st}, 2^{nd}, 3^{rd}, 5^{th} and 6^{th} crosses and average fruit weight in the 1^{st} and 3^{rd} crosses. Generally, the results cleared that, the values of dominance gene effects (d) were larger in magnitude than the corresponding values of additive genetic effect (a) in most crosses for most of quality traits. This finding indicating the major role of dominance gene effects in the inheritance of these traits. In addition, most of these traits were significantly affected by one or more type of epsitatic effects (aa, ad and dd) as appeared in most of crosses, indicating the importance of epistatic effects in the inheritance of these fruit characteristics. These results are in accordance with the results obtained by Amaral Junior *et al.* (1996), Dobhol *et al.* (1999) and Amin *et al.* (2001).

Heritability and number of effective genes and genetic gain: The estimates of heritabilities in broad and narrow senses (h_b and h_n), number of effective genes and genetic gain for all studied traits in the six crosses are presented in Table 5. The results showed that the estimates of heritability in broad sense (h_b) and narrow sense (h_n) were large for total yield as number and weight of fruits for all studied crosses. The estimated

Table 5: Heritability, number of effective genes and genetic gain for all studied traits in the six crosses

Crosses	Traits	Heritability		No. effective genes	Genetic gain
		$h_{b\%}$	$h_{n\%}$		
(1)	TNF	83.09	75.91	0.05	2.93
(2)		87.17	77.67	0.70	4.08
(3)		87.93	86.09	0.22	5.03
(4)		80.95	80.19	45.66	1.16
(5)		91.69	84.83	1.78	7.44
(6)		82.34	61.74	0.64	4.05
(1)	TWF	84.72	74.64	5.81	0.19
(2)		86.09	84.44	1.84	0.54
(3)		84.59	71.75	1.51	0.27
(4)		81.95	81.65	2.68	0.30
(5)		79.57	66.25	10.44	0.32
(6)		80.94	65.38	0.56	0.74
(1)	AFW	70.27	27.03	5.17	0.00
(2)		73.51	44.90	0.33	0.02
(3)		78.30	46.95	0.32	0.01
(4)		94.67	60.66	0.08	0.01
(5)		90.48	72.32	0.13	0.03
(6)		61.02	51.57	0.37	0.02
(1)	NLF	84.15	78.57	5.41	0.34
(2)		93.97	86.52	0.77	0.62
(3)		87.71	87.65	5.09	0.52
(4)		78.74	69.60	16.9	0.42
(5)		76.09	73.02	4.76	0.27
(6)		91.11	81.90	0.73	0.53
(1)	FT	84.34	79.51	29.88	0.34
(2)		93.84	91.45	0.47	0.80
(3)		91.09	89.61	0.32	1.01
(4)		88.33	81.36	0.86	0.33
(5)		97.12	92.22	36.53	0.46
(6)		91.65	90.04	5.76	0.75
(1)	FF	86.96	53.86	3.60	0.19
(2)		86.95	83.48	0.34	0.32
(3)		87.71	85.77	10.02	0.33
(4)		92.72	81.66	0.47	0.40
(5)		90.08	84.98	1.87	0.63
(6)		80.65	75.77	8.28	0.29
(1)	T.S.S. %	94.64	81.41	0.29	0.59
(2)		75.14	61.82	0.97	0.29
(3)		72.78	68.66	1.03	0.24
(4)		[illegible]2.62	82.70	1.08	0.36
(5)		77.05	36.87	0.56	0.11
(6)		93.57	88.99	0.07	0.55

Cross (1) = Campbell $_{1327}$ x Floradad
Cross (2) = Campbell $_{1327}$ x Line-73
Cross (3) = Campbell $_{1327}$ x Homestead $_{24F}$.
Cross (4) = Campbell $_{1327}$ x Strain –B
Cross (5) = Line-73 x Strain -B
Cross (6) = Homestead $_{24F}$ x Line-73

values of broad sense ranged from 80.95 (4^{th} cross) to 91.69 (5^{th} cross) and from 79.57 (4^{th} cross) to 86.09 (2^{nd} cross) for total fruit number per plant and total fruit weight per plant, respectively. While, the estimated values of heritability in narrow (h_n) sense were slightly lower than the corresponding values of h_b and ranged from 61.74 (6^{th} cross) to 86.09 (3^{rd} cross) and from 65.38 (6^{th} cross) to 84.44 (2^{nd} cross) for these traits, respectively. The estimated values of heritability in broad sense ranged from 76.09 (5^{th}cross) to 93.97 (2^{nd}cross) and from 84.34 (1^{st} cross) to 97.12 (5^{th}cross), from 72.78 (3^{rd}cross) to 94.64 (1^{st}cross); from 80.65 (6^{th}cross) to 92.72 (4^{th}cross) and from 61.02 (6^{th}cross) to 94.67 (4^{th}cross) for number of locules/fruit, thickness of flesh, T.S.S.%, fruit firmness and average fruit weight, respectively. While, the estimated values of heritability in narrow sense ranged from 73.02 (5^{th}cross) to 87.7 (3^{rd}cross); from 79.51 (1^{st}cross) to 92.22 (5^{th}cross); from 36.87 (5^{th}cross) to 88.99 (6^{th}cross); from 53.86 (1^{st}cross) to 85.77 (3^{rd}cross) and from 27.03 (1^{st}cross) to 72.32 (5^{th} cross) for the same traits, respectively. These findings confirmed that both additive and dominance genetic effects play an important role in the expression of these traits and the dominance effects were predominated. Similar results were obtained by Reddy and Reddy (1992), Salib (1999) Hassan *et al.* (2000) and Amin *et al.* (2001).

It is evident that minimum number of genes controlling total fruit number per plant and total fruit weight per plant were ranged from 1 to 46 and 1 to 11 pairs of genes, respectively. While, it ranged from 1 to 17, 1 to 37, 1 to 2 , 1 to 11 and 1 to 6 pairs of genes for number of locues/fruit, thickness of flesh, T.S.S%, fruit firmness and average fruit weight, respectively. These results indicated that these traits were inherited as a quantitative characters.

Furthermore, the values of genetic advance (genetic gain) under 5% selection of the F_2 plants for improving total fruit number and total fruit weight per plant ranged form 1.16 to 7.44 and from 0.19 to 0.74, respectively. The values for number of locules /fruit, thickness of flesh, T.S.S.%, fruit firmness and average fruit weight were low and ranged from 0.27 to 0.62 and from 0.33 to 1.01 and from 0.11 to 0.60 and from 0.19 to 0.63 and from 0.01 to 0.03, respectively. Similar results were obtained by Salib (1999) who indicated that these traits have low genetic gain values.

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الملخص العربى

مظاهر السلوك الوراثى في هجن الطماطم
٢ – طبيعة التباين الوراثى لصفات المحصول والجودة

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توريث سبعة من الصفات الكمية المتعلقة بالمحصول والجودة تم دراستها من خلال ستة هجن بالإضافة الى الجيل الثانى والجيلين الرجعيين لكل هجين بغرض تحديد الفعل الجينى السائد فى توريث هذه الصفات لإمكانية تحديد برنامج التربية المناسب لتحسين هذه الصفات.

ويمكن تلخيص أهم النتائج المتحصل عليها فى الآتى:

- أشارت إختبارات المعنوية لمتوسط المربعات أن هناك إختلافات معنوية بين الهجن وأيضا بين العشائر داخل كل هجين لكل الصفات المدروسة فيما عدا صفة الوزن الكلى لثمار النبات والتى أظهرت أن ليس هناك إختلاف معنوى بين الهجن المدروسة فى هذه الصفة.
- الصنف Strain-B كان أحسن الأباء فى صفات المحصول بالإضافة الى سمك اللحم.
- أشارت النتائج أيضا الى أنه بالرغم أن كل من طرز التفاعل الجينى (الإضافة – السيادة – التفوق) ساهمت فى التباين الوراثى بقيم مختلفة فى هذه الصفات، كان الفعل الجينى السيادى له الدور الأكبر فى توريث كل من صفات المحصول والجودة فى معظم الهجن المدروسة. وبناء على ذلك أظهرت معظم الهجن قوة هجين مرغوبة مقارنة بأحسن آبائها فى هذه الصفات.
- ولذلك يمكن أن نستخلص من هذه النتائج أن إنتاج الهجن هو الوسيلة المثلى للتوصل الى أعلى إنتاج وأحسن جودة.