

## GENETIC STUDIES ON YIELD AND YIELD COMPONENTS OF *BRASSICA CAMPESTRIS* L.

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### Abstract

*Inheritance of yield and its associated characters were studied in two varietal crosses involving three varieties of *Brassica campestris* L. Heritability estimates ranged from 81 per cent for seed yield per plant in cross-1 to 19 per cent for 10-fruit weight in cross-2. Transgressive segregation in both directions was observed in seed yield per plant and fruit length in cross-2 and in seed weight per 10-fruit and number of fruits per plant in cross-1. Over-dominance was observed in 10-fruit weight and 100-seed weight in both the crosses and number of seeds per fruit and number of fruits per plant respectively in cross-1 and cross-2. The estimates of dominance ( $\hat{h}$ ) gene effects were mostly larger than the additive ( $\hat{d}$ ) gene effects and were significant in almost all the characters. Epistasis was detected by chi-square test in all but in number of fruits per plant and fruit length in cross-2. Epistasis was found to be duplicate type in all cases except in number of fruits per plant and fruit length in cross-1 where it was complementary type. Absolute magnitude of the epistatic effects was more than the additive ( $\hat{d}$ ) and dominance ( $\hat{h}$ ) gene effects. Seed yield per plant was found to be correlated with other characters both phenotypically and genotypically. Phenotypic correlations appeared significant in all cases except that of number of fruits per plant with other associated characters.*

High yield is an important objective in any breeding programme but success in such breeding study depends greatly on the availability of genetic information about yield and its associated characters, because high yield results from suitable combination of its associated characters.

Yield was assumed to be a complex heritable character and dependent on the following components:

- (a) Number of fruits per plant
- (b) Number of seeds per fruit
- (c) Fruit length
- (d) 10-fruit weight

- (e) Seed weight per 10-fruit
- (f) 100-seed weight and
- (g) Seed yield per plant

Expression of each component is presumed to be controlled by polygenes. Knowledge concerning the inheritance of polygenically controlled characters increases the effectiveness of selection for the character. Individual gene effects are not measurable in quantitative characters, but statistical procedures have been developed and used to obtain basic information in such gene effects as a whole. For example, heritability is used to indicate the relative degree to which a character is transmitted from parents to offsprings. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Estimation of various types of gene effects including epistasis is of value because it provides information useful in choosing the most appropriate breeding procedure of further improvement. The magnitude to which a character is genotypically correlated is also of great value to the breeder in designing their breeding programme.

The present study, therefore, was undertaken in an attempt to determine (a) the magnitude of heritability estimates, (b) number of effective factors involved in conditioning the characters, (c) relative importance of additive, dominance variation and digenic epistasis and (d) magnitude of genotypic and phenotypic correlation of a number of quantitative characters which constitute the yield and yield components of *Brassica campestris* L.

### Materials and Methods

Three mustard varieties were chosen as parental materials from the breeding stock of East Pakistan Agricultural Research Laboratories, Dacca. Two crosses were made among the three varieties and each cross formed a genetic group which included six populations as described below:

Cross-1 .. .. .	P <sub>1</sub> , P <sub>2</sub> , their F <sub>1</sub> , F <sub>2</sub> ,
[Torja-7 (P <sub>1</sub> ) x Torja-BP (P <sub>2</sub> )]	B <sub>1</sub> (P <sub>1</sub> x F <sub>1</sub> ) and B <sub>2</sub>
	(P <sub>2</sub> x F <sub>1</sub> ) derivatives.
	(Group I)
Cross-2 .. .. .	P <sub>1</sub> , P <sub>2</sub> , their F <sub>1</sub> , F <sub>2</sub> ,
[Torja-7 (P <sub>1</sub> ) x Torja-TP (P <sub>2</sub> )]	B <sub>1</sub> (P <sub>1</sub> x F <sub>1</sub> ) and B <sub>2</sub>
	(P <sub>2</sub> x F <sub>1</sub> ) derivatives.
	(Group II)

Crosses between parents were first made during the winter of 1965-66. Back-crosses of F<sub>1</sub> hybrids to their parents, selfing of F<sub>1</sub> hybrids and the fresh crosses for F<sub>1</sub> seeds were made during the winter of 1966-67. Thus six generations (P<sub>1</sub>,

P<sub>2</sub>, B<sub>1</sub>, B<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub>) formed a genetic group, which was treated as an unit in the sowing scheme. Six populations of each group were randomly grown in each of the three replications. One replication was put in a block of 19' x 25' size. Passage between blocks was three feet wide as was the boarder all round the blocks. Each block consisted of twenty rows with twenty-six plants in each row. Space between rows as well as between plants was one foot. The boarder rows on two sides of a block were sown with parental seeds and were treated as non-experimental, while of the remaining eighteen rows, seeds of each of P<sub>1</sub>, P<sub>2</sub>, B<sub>1</sub>, B<sub>2</sub> and F<sub>1</sub> were sown in two rows each and F<sub>2</sub> seeds were sown in eight rows. Two plants on two ends of each of these rows were treated as non-experimental. Thus there were 48 plants for each of P<sub>1</sub>, P<sub>2</sub>, B<sub>1</sub>, B<sub>2</sub> and F<sub>1</sub> progenies and 192 plants for F<sub>2</sub> generation in each block. Data were collected on an individual plant basis for the following characters:

#### Number of fruits

per plant: .. .. The number of fruits in each plant was counted.

Number of seeds per fruit: Number of seeds from the first fruit of each plant was counted.

Fruit length: .. .. The first fruit of each plant was measured in cm from the base to apex for the fruit length.

10-fruit weight: .. First 10 fruits, of each plant were taken and their weight was taken in gm after uniform drying.

Seed weight per 10-fruit: Seed weight of first 10 fruits of each plant were weighed in gm after proper drying.

100-seed weight: .. 100 seeds from each plant were weighed after proper drying.

Seed yield per plant: .. Seeds of each individual plant were weighed in gm after proper drying.

The collected data were analysed by following the biometrical techniques of Mather (1949) and of Allard (1960). Warner's (1952) method was followed to determine the heritability. The expected genetic advance was calculated by following the formula of Lush (1949). The number of effective factors was calculated according to Goodwing (1944). The techniques of Hayman (1958) were followed for the detection and separation of epistatic variation. Genotypic and phenotypic correlations were determined by following the formula used by Petr and Frey (1966).

### Experimental Results

Mean, standard deviation and variances of each of the six progenies ( $P_1$ ,  $P_2$ ,  $B_1$ ,  $B_2$ ,  $F_1$  and  $F_2$ ) for all characters were calculated separately for the two crosses. Mean variances of  $P_1$ ,  $P_2$  and  $F_1$  provided the value for the environmental ( $\hat{E}$ ) variation, whereas the values for additive ( $\hat{D}$ ) and dominance ( $\hat{H}$ ) components of variation were derived from the variances of  $B_1$ ,  $B_2$  and  $F_2$ . They are shown in Table I. From the estimated values of environmental ( $\hat{E}$ ), additive ( $\hat{D}$ ) and dominance ( $\hat{H}$ ) variations, heritability, average degree of dominance, expected genetic advances in  $F_3$  means over  $F_2$  means at 5 per cent level of selection and percentage of genetic advance in terms of  $F_2$  mean were calculated for all the characters studied under the two crosses. Number of effective factors were also determined on the assumption that the genes are isodirectionally distributed among the parents. The results obtained are shown in Table I.

### Separation of Epistatic Variation

In absence of epistasis the data fits better with three-parameter model of Hayman (1958) and  $\hat{m}^*$ ,  $\hat{d}^*$ , and  $\hat{h}^*$  measures a constant, additive and dominance. When epistasis is present,  $\hat{m}$ ,  $\hat{d}$ ,  $\hat{h}$ ,  $\hat{i}$ ,  $\hat{j}$ , and  $\hat{l}$  respectively measures a constant, additivity, dominance and the three kinds of digenic epistasis [dominance x dominance ( $\hat{l}$ ), dominance x additive ( $\hat{j}$ ) and additive x additive ( $\hat{i}$ )]. The first step in the examination of means was to find out the values of  $\hat{m}^*$ ,  $\hat{d}^*$ , and  $\hat{h}^*$  in terms of non-epistatic model and to test for goodness of fit. The values calculated for  $\hat{m}^*$ ,  $\hat{d}^*$  and  $\hat{h}^*$  in terms of three-parameter model for both the crosses are shown in Table II and Table III. The  $\chi^2$  values were found to be significant for all the characters in both the crosses except in number of fruits per plant and fruit length. Significant  $\chi^2$  values indicated presence of epistasis. In presence of epistasis the values for  $\hat{m}$ ,  $\hat{d}$ ,  $\hat{h}$ ,  $\hat{i}$ ,  $\hat{j}$  and  $\hat{l}$  were calculated in terms of six-parameter model for all characters including the characters, number of fruits per plant and fruit length, where  $\chi^2$  values were not significant at 5 per cent level. The results obtained are shown in Table II and Table III.

The estimates of mean effects ( $\hat{m}$ ) were positive and were highly significant for all the characters in both the crosses. The additive ( $\hat{d}$ ) and dominance ( $\hat{h}$ ) gene effects were low in magnitude compared to mean effects. The additive gene effects ( $\hat{d}$ ) were observed to be significant in 10-fruit weight, 100-seed weight and

number of fruits per plant in cross-2 whereas in cross-1 it was non-significant in fruit length, 100-seed weight and seed yield per plant. On the other hand dominance gene effects ( $\hat{h}$ ) were significant in all the characters except fruit length and 100-seed weight in both the crosses. Dominance gene effect was also non-significant in seed weight per 10-fruit under cross-2.

Additive x dominance ( $\hat{j}$ ) type of epistasis was found to be significant in all the characters under both the crosses except in number of fruits per plant under cross-2. Additive x additive ( $\hat{i}$ ) interaction was non-significant only in seed weight per 10-fruit under the two crosses and in 10-fruit weight and 100-seed weight respectively in cross-2 and cross-1, whereas dominance x dominance ( $\hat{l}$ ) type of epistasis was found to be non-significant for 10-fruit weight in cross-1 and for fruit length and number of fruits per plant under cross-2.

The absolute magnitude of all the three components of genic interaction ( $\hat{i}$ ,  $\hat{j}$  and  $\hat{l}$ ) were less than the mean effects in most of the characters. The estimates of all the three types of epistasis were significant in four characters under cross-1 and in three characters under cross-2.

Comparing the sign of  $\hat{h}$  and  $\hat{l}$  it is observed that epistasis was duplicate type in all the characters under both the crosses except in number of fruits per plant and number of seeds per fruit under cross-1 where epistasis was found to be complementary type.

Columns to the right side of the observation in the upper half of Table II and Table III show that the difference between the observed mean values and their expectations based on the three-parameter model is due to different types of epistasis which appear to have suppressed the dominance in most of the characters studied under two crosses.

#### *Genotypic and Phenotypic Correlation*

The genotypic and phenotypic correlations between different characters under study are shown in Table IV and Table V. For the most part, the phenotypic and genotypic correlation for any pair of characters appeared to be of comparable magnitude, the latter having mostly larger values than the former. All the characters were found to be highly correlated with the seed yield per plant. The close phenotypic and genotypic correlation between different associated characters and seed yield per plant indicates that plant breeders may use any one of these characters as a selection criterion in  $F_2$  generation to achieve genetic advance in seed yield per plant. Number of fruits per plant was found to have a very little or

no correlation with other characters. High correlation was indicated between 10-fruit weight and seed weight per 10-fruit, whereas moderately high correlations were noted between other characters. Phenotypic correlations were found to be significant in all the characters except in number of fruits per plant which exhibited insignificant correlation with other associated characters but it had a significant phenotypic correlation with the seed yield per plant.

### Discussion

The collected data exhibited wide range of distribution and no distinguishable groups in them suggesting that yield and yield components are controlled by polygenes. The number of effective factors differentiating the two parents in both the crosses were, however, estimated to be one to three for all the characters except in case of 10-fruit weight where the number of effective factors were detected to be six and seven in cross-1 and cross-2 respectively.

Number of fruits per plant, seed weight per 10-fruit and seed yield per plant in both the crosses and number of seeds per fruit and fruit length respectively in cross-1 and cross-2 were found to have high heritability compared to other characters. These characters with high heritability and high genetic gain, may likely respond better during selection breeding compared to other characters with low heritability and low genetic advance (Johnson *et al.* 1955 and Lerner 1958).

Transgressive segregation was observed in either direction in seed weight per 10-fruit and number of fruits per plant in cross-1 and in fruit length and seed yield per plant in cross-2. Transgressive segregation towards higher performance was indicated in seed weight per 10-fruit under cross-2 whereas it was suggested towards lower performance in some other characters under the same cross.

Dominance relationship as measured by  $(\hat{H}/\hat{D})^{\frac{1}{2}}$ , shows overdominance in 10-fruit weight, seed weight per 10-fruit and 100-seed weight in both the crosses and in number of fruits per plant and number of seeds per fruit respectively in cross-2 and cross-1, though it was not expressed in the  $F_1$  and  $F_2$  plants. This was probably due to the fact that  $\hat{H}$  values were derived from sums of squares of all the plus and minus  $\hat{h}$  values, while under direct observation of  $F_1$  and  $F_2$  plants, only average effects were expressed after some of the plus and minus values had cancelled each other.

The magnitude of the estimates of additive ( $\hat{d}$ ) effects was smaller compared to those of other gene effects. This suggests that additive gene effects have a minor contribution to the inheritance of the most of the characters under study. However, in some of the characters such as number of fruits per plant, 10-fruit weight

etc. where additive ( $\hat{d}$ ) gene effects have relatively large values suggesting that they contribute significantly in the inheritance of these traits. This coupled with relatively high heritability values in these characters suggests that some progress may be achieved through selection.

Dominance ( $\hat{h}$ ) gene effects appeared to have major contribution in the inheritance of some of the characters studied under both the crosses. The negative dominant gene effect suggests its diminishing effect on the expression of different characters. In comparison to the additive ( $\hat{d}$ ) gene effects it appeared to be more significant in the inheritance of most of the characters. This suggests that as the inheritance of a quantitative character becomes more complex, the contribution of dominance ( $\hat{h}$ ) gene effects to the inheritance becomes greater.

The relative magnitude of additive x additive ( $\hat{i}$ ) gene effects was comparable to that of dominance ( $\hat{h}$ ) gene effects and was greater than additive ( $\hat{d}$ ) gene effects in most of the characters. This suggests that additive x additive ( $\hat{i}$ ) gene effects had considerable contribution in the inheritance of most of the characters. Additive x dominance ( $\hat{j}$ ) gene effects was found to be the most widespread of the three kinds of epistasis in the inheritance of the characters studied. Dominance x dominance ( $\hat{l}$ ) gene effects being associated with positive sign indicates that this type of gene action may have an enhancing effect in the expression of the characters. The magnitude of epistasis may, however, be biased by the presence of linkage (Kempthorne 1957).

The six genetic parameter estimates provided a test for different types of gene action, and supply useful information for the improvement of the traits under study. However, these genetic effects cannot be interpreted in terms of genetic variance. The variation observed in the detection of epistasis was mostly due to dominance ( $\hat{h}$ ) and epistatic gene effects which suggests the adoption of such breeding procedures that would make the best use of them. Procedures worth adopting may be the use of synthetic varieties and recurrent selection of reciprocal recurrent selection as suggested by Comstock *et al.* (1949) and Dickerson (1952).

The degree of association of plant characters has always been a helpful basis of selection. The high correlation observed between seed yield per plant and its associated characters suggested that all the traits contribute to seed yield and that selection for seed yield would be worthwhile using any one of the associated characters as a criterion for selection but the presence of duplicate epistasis in most of the characters studied may likely hinder the progress.

Number of fruits per plant has a very low or no correlation with other characters but it has a significant correlation with seed yield per plant. Since transgressive segregation has been detected for higher performance in number of fruits per plant with high heritability and complementary type of epistasis, it may be proved to be of value in selection breeding for higher seed yield in mustard.

The investigation has limitation in that it is based on one year's data and derived values may be associated with environmental interaction. This point may be taken into consideration in future references.

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TABLE I

Values of  $\hat{D}$ ,  $\hat{H}$ ,  $\hat{E}$ ,  $(\hat{H}/\hat{D})^{\frac{1}{2}}$ , heritability, genetic advance, genetic advance in % on  $F_2$  mean and number of effective factors for the two crosses

Name of cross	Character studied	$\hat{H}$	$\hat{D}$	$\hat{E}$	$(\hat{H}/\hat{D})^{\frac{1}{2}}$	Heritability in per cent $[\frac{1}{2}\hat{D} \times 100] /$ $VF_2]$	Genetic advance $[K\delta A(\delta a^2 /$ $\delta^2 A)]$	Genetic advance in % on $F_2$ mean	Number of effective factor $[\frac{1}{2}(P_1-P_2)^2 /$ $\hat{D}]$
Cross-1  (Torla-7 x Torla- BP)	Number of fruits per plant	1416.3200	2038.3400	340.6800	0.8335	59.46	50.30	47.18	0.3659
	Number of seeds per fruit	41.2940	13.0268	11.4356	1.7810	23.03	2.52	11.65	0.0978
	Fruit length	0.1160	0.0880	0.0500	0.3613	35.77	0.25	8.80	0.1928
	10-fruit weight	0.1280	0.0996	0.0127	1.1313	32.95	0.24	2.20	6.2222
	Seed weight per 10-fruit	0.0040	0.0148	0.0010	1.1418	79.56	0.14	25.92	1.1418
Cross-2  (Torla-7 x Torla- TP)	100-seed weight	0.0112	0.0026	0.0009	2.7054	26.00	0.03	0.09	0.5384
	Seed yield per plant	0.2624	11.9794	1.2967	0.1515	81.47	4.51	72.30	0.6405
	Number of fruits per plant	3043.6800	1336.5000	261.0000	1.5090	41.44	34.58	41.44	0.5574
	Number of seeds per fruit	17.8028	48.7363	3.2733	0.3651	75.91	8.85	43.59	1.2843
	Fruit length	0.0800	0.3600	0.0400	0.4711	75.00	0.73	23.93	0.6669
Cross-2  (Torla-7 x Torla- TP)	10-fruit weight	0.5196	0.0902	0.0158	0.7202	19.40	0.17	14.07	5.5714
	Seed weight per 10-fruit	0.0284	0.0214	0.0012	1.1489	56.31	0.4156	26.00	2.0607
	100-seed weight	0.0124	0.0044	0.0006	1.6781	37.28	0.05	16.92	0.2045
	Seed yield per plant	—3.0532	9.1022	2.7855	..	69.24	3.63	57.52	0.7648

TABLE II

Observed mean and its difference from the expected mean, constant additivity, dominance and the

	Number of fruits per plant		Number of seeds per fruit		Fruit length		10-fruit weight	
	Mean	Difference	Mean	Difference	Mean	Difference	Mean	Difference
P <sub>1</sub>	90.89 ± 1.33	1.91	17.75 ± 0.30	0.65	2.66 ± 0.02	0.02	0.83 ± 0.01	0.00
P <sub>2</sub>	145.52 ± 2.10	0.50	35.17 ± 0.04	0.73	3.49 ± 0.03	0.25	1.95 ± 0.01	0.02
F <sub>1</sub>	102.72 ± 2.20	3.86	27.90 ± 0.03	2.32	2.88 ± 0.01	0.01	1.22 ± 0.01	0.04
F <sub>2</sub>	106.61 ± 2.20	-1.32	21.64 ± 0.25	-4.04	2.92 ± 0.17	-0.01	1.17 ± 0.02	-0.11
B <sub>1</sub>	71.94 ± 3.13	-21.92	20.69 ± 0.04	-0.66	2.73 ± 0.05	-0.03	1.08 ± 0.04	0.07
B <sub>2</sub>	118.46 ± 5.11	3.48	26.96 ± 0.08	-3.05	2.69 ± 0.03	-0.43	1.40 ± 0.04	-0.15

	3-parameter model		6-parameter model		3-parameter model		6-parameter model		3-parameter model		6-parameter model	
	Mean	Difference	Mean	Difference	Mean	Difference	Mean	Difference	Mean	Difference	Mean	Difference
m	107.93 ± 6.15	106.61 ± 3.46	25.68 ± 1.44	21.64 ± 0.25	2.94 ± 0.006	2.93 ± 0.17	1.28 ± 0.004	1.17 ± 0.02				
d	-28.02 ± 0.66	-46.42 ± 3.46	-8.66 ± 0.03	-6.27 ± 0.50	-0.37 ± 0.010	0.04 ± 0.03	-0.55 ± 0.004	-0.32 ± 0.03				
h	-18.14 ± 1.33	-61.12 ± 8.70	-0.20 ± 0.03	10.18 ± 0.36	-0.15 ± 0.011	-1.07 ± 0.09	-0.20 ± 0.006	0.11 ± 0.08				
i		-45.64 ± 8.58		8.74 ± 0.21		-0.88 ± 0.08		0.28 ± 0.08				
j		-19.20 ± 3.52		2.44 ± 0.06		0.37 ± 0.04		0.24 ± 0.04				
l		-106.93 ± 15.01		4.68 ± 0.29		1.95 ± 0.08		-0.02 ± 0.15				
Chi square	111.2496		57.2158		47.4218		12.8317					
P	<0.01		<0.01		<0.01		<0.01					

\*Differences were found out by subtracting expected values of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> (as obtained under 3-parameter model) from their re-  
 F<sub>1</sub> = m +  $\frac{1}{2}$ h, F<sub>2</sub> = m, B<sub>1</sub> = m +  $\frac{1}{2}$ d and B<sub>2</sub> = m -  $\frac{1}{2}$ d.

Types of epistasis in cross- (Torla-7 x Torla-BP)

Seed weight per 10-fruit		100-seed weight		Seed yield per plant	
Mean	Difference	Mean	Difference	Mean	Difference
1.45 ± 0.003	0.02	0.33 ± 0.002	—0.02	3.98 ± 0.14	0.06
1.72 ± 0.003	+0.03	0.40 ± 0.003	—0.03	9.52 ± 0.13	0.44
1.55 ± 0.002	+0.01	0.40 ± 0.003	—0.03	6.75 ± 0.12	1.61
1.54 ± 0.005	—0.01	0.37 ± 0.003	—0.01	6.25 ± 0.20	0.25
1.47 ± 0.009	—0.02	0.36 ± 0.008	—0.00	4.35 ± 0.26	—0.79
1.60 ± 0.009	—0.01	0.36 ± 0.010	—0.04	5.03 ± 0.32	—2.83

3-parameter model	6-parameter model	3-parameter model	6-parameter model	3-parameter model	6-parameter model
0.55 ± 0.0002	0.54 ± 0.005	0.38 ± 0.0010	0.37 ± 0.003	6.50 ± 0.03	6.25 ± 0.20
0.13 ± 0.0011	—0.13 ± 0.002	—0.04 ± 0.0011	—0.002 ± 0.01	—2.71 ± 0.04	—0.68 ± 0.24
0.03 ± 0.0019	—0.05 ± 0.001	—0.03 ± 0.0002	—0.02 ± 0.017	0.27 ± 0.08	—6.24 ± 0.68
	—0.02 ± 0.012		—0.05 ± 0.017		—6.24 ± 0.67
	0.01 ± 0.002		0.03 ± 0.007		2.08 ± 0.24
	0.15 ± 0.015		0.15 ± 0.032		14.48 ± 1.09
22.9677		75.7911		33.3659	
P < 0.01		P < 0.01		P < 0.01	

we observed values. Expected values were estimated as follows:  $P_1 = m + d - \frac{1}{2}h$ ,  $P_2 = m - d - \frac{1}{2}h$ ,

Observed mean and its difference from the expected

Number of fruits per plant		Number of seeds per fruit		Fruit length		
Mean	Difference	Mean	Difference	Mean	Differ	
P <sub>1</sub>	82.17 ± 1.26	1.75	13.63 ± 0.16	-1.23	2.70 ± 0.02	-0
P <sub>2</sub>	136.74 ± 1.24	1.80	29.46 ± 0.18	-0.90	3.52 ± 0.02	0.
F <sub>1</sub>	126.14 ± 1.25	3.55	14.29 ± 0.16	-8.32	2.93 ± 0.02	-0
F <sub>2</sub>	97.07 ± 2.26	-18.05	20.32 ± 0.30	2.34	3.05 ± 0.03	0.
B <sub>1</sub>	91.58 ± 3.71	-9.91	17.67 ± 0.45	3.55	2.93 ± 0.04	-0.
B <sub>2</sub>	117.59 ± 5.23	-11.16	18.21 ± 0.69	-3.36	2.96 ± 0.07	0.

	3-parameter model	6-parameter model	3-parameter model	6-parameter model	3-parameter model	6-parameter model
m	115.12±0.40	97.07±2.26	17.98±0.05	20.32±0.30	3.01±0.005	3.05
d	-27.26±0.50	-26.01±3.70	-7.75±0.07	-0.54±0.47	0.39±0.007	-0.02
h	14.89±1.17	46.75±9.10	-9.26±0.11	-16.77±1.18	0.11±0.013	-0.60
i		30.06±9.83		-9.52±1.18		-0.42
j		-1.28±4.19		7.38±0.48		0.38
l		22.79±15.80		9.43±2.04		0.72
Chi square	5.1201		81.3921		7.4743	
	P<0.20>0.10		P<0.01		P<0.10>0.05	

TABLE III

constant, additivity, dominance and the three types of epistasis in cross- (*Toria-7* x *Toria-TP*)

10-fruit length		Seed weight per 10-fruit		100-seed weight		Seed yield per plant	
Mean	Difference	Mean	Difference	Mean	Difference	Mean	Difference
0.87 $\pm$ 0.02	0.27	0.44 $\pm$ 0.004	0.05	0.34 $\pm$ 0.002	-0.04	3.81 $\pm$ 0.16	0.45
2.13 $\pm$ 0.01	0.23	0.86 $\pm$ 0.003	0.07	0.27 $\pm$ 0.002	-0.03	9.10 $\pm$ 0.17	-0.07
1.28 $\pm$ 0.02	0.00	0.55 $\pm$ 0.003	-0.04	0.38 $\pm$ 0.002	-0.03	6.00 $\pm$ 0.23	0.22
1.30 $\pm$ 0.02	0.90	0.56 $\pm$ 0.078	-0.03	0.35 $\pm$ 0.003	-0.01	6.31 $\pm$ 0.17	0.21
1.12 $\pm$ 0.03	0.04	0.54 $\pm$ 0.012	0.05	0.03 $\pm$ 0.009	-0.05	5.02 $\pm$ 0.33	0.13
1.41 $\pm$ 0.07	-0.29	0.26 $\pm$ 0.060	-0.07	0.35 $\pm$ 0.012	-0.02	4.89 $\pm$ 0.26	-2.42

3-parameter model	6-parameter model	3-parameter model	6-parameter model	3-parameter model	6-parameter model	3-parameter model	6-parameter model
3 1.39 $\pm$ 0.001	1.30 $\pm$ 0.02	0.59 $\pm$ 0.009	0.56 $\pm$ 0.078	0.34 $\pm$ 0.0006	0.35 $\pm$ 0.003	6.10 $\pm$ 0.05	6.31 $\pm$ 0.1
4 -0.62 $\pm$ 0.015	-0.30 $\pm$ 0.04	-0.20 $\pm$ 0.001	-0.08 $\pm$ 0.113	0.03 $\pm$ 0.0008	-0.04 $\pm$ 0.01	-2.42 $\pm$ 0.06	0.13 $\pm$ 0.24
6 0.23 $\pm$ 0.009	-0.37 $\pm$ 0.10	-0.02 $\pm$ 0.616	0.03 $\pm$ 0.0009	-0.08 $\pm$ 0.019	-0.65 $\pm$ 0.13	-5.87 $\pm$ 0.65	-5.42 $\pm$ 0.63
0 -0.16 $\pm$ 0.10	-0.16 $\pm$ 0.10	-0.08 $\pm$ 0.615	0.13 $\pm$ 0.011	0.08 $\pm$ 0.008	-0.78 $\pm$ 0.25	-0.78 $\pm$ 0.25	-0.78 $\pm$ 0.25
4 0.33 $\pm$ 0.04	0.33 $\pm$ 0.04	0.13 $\pm$ 0.011	0.13 $\pm$ 0.011	0.17 $\pm$ 0.036	10.51 $\pm$ 1.09	10.51 $\pm$ 1.09	10.51 $\pm$ 1.09
5 0.68 $\pm$ 0.18	0.68 $\pm$ 0.18	.....	.....	.....	.....	.....	.....
9.9585	17.5210	10.2460	147.8290				
P < 0.02	P < 0.01	P < 0.02	P < 0.01				

TABLE IV  
Genotypic and phenotypic correlations between different characters studied for cross-1  
(Torii-7 x Torii-BP)

	Correlation	Number of seeds per fruit	Fruit length	100-seed weight	10-fruit weight	Seed weight per 10-fruit	Seed yield per plant
Number of fruits per plant	Genotypic	0.0291	-0.0992	0.2310	0.3112	0.3215	1.0721
	Phenotypic	0.0026	-0.0164	0.0514	-0.1953	0.0447	0.9302*
Number of seeds per fruit	Genotypic		0.6512	0.3201	0.7210	0.6207	0.8219
	Phenotypic		0.4061*	-0.6966*	0.4608*	0.4500*	0.6635*
Fruit length	Genotypic**			-0.0999	0.5256	0.7291	0.9683
	Phenotypic***			0.4000*	0.7086*	0.2500	0.6544*
100-seed weight	Genotypic				0.7261	0.7001	0.9006
	Phenotypic				0.4385*	0.6786*	0.5213*
10-fruit weight	Genotypic					0.9207	0.7021
	Phenotypic					0.6000*	0.5567*
Seed weight per 10-fruit	Genotypic						0.9001
	Phenotypic						0.5621*

\*Significant values for phenotypic correlation

\*\*Genotypic correlation =  $\text{Cov}_{gAB} / \sqrt{(\delta^2_{gA})(\delta^2_{gB})}$

\*\*\*Phenotypic correlation =  $\text{Cov}_{pAB} / \sqrt{(\delta^2_{pA})(\delta^2_{pB})}$

TABLE V  
*Genotypic and phenotypic correlations between different characters studied for cross-2*  
*(Torla-7 x Torla-TP)*

	Correlation	Number of seeds per fruit	Fruit length	100-seed weight	10-fruit weight	Seed weight per 10-fruit	Seed yield per plant
Number of fruits per plant	Genotypic	-0.1215	-0.3210	0.0251	0.2512	0.5210	0.8052
	Phenotypic	0.0215	-0.3100	-0.0020	-0.2112	0.4210*	0.6772*
Number of seeds per fruit	Genotypic		0.7210	-0.5210	0.6521	0.7211	0.9215
	Phenotypic		0.6321*	-0.4210*	0.7252*	0.6200*	0.6251*
Fruit length	Genotypic			-0.2110	0.6521	0.7259	0.9000
	Phenotypic			0.3021	0.4221*	0.4232*	0.8729*
100-seed weight	Genotypic				0.7252	0.8250	0.8200
	Phenotypic				0.5210*	0.7291*	0.9221*
Seed weight per 10-fruit	Genotypic					0.8214	0.7001
	Phenotypic					0.6200*	0.9211*
10-fruit weight	Genotypic						0.8990
	Phenotypic						0.7200*

\*Significant values for phenotypic correlations