

Evaluation of Gene Action for Several Important Traits in Some Crosses of Canola (*Brassica napus* L.) Using Generation Mean Analysis

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Abstract

Generation mean analysis was performed using three crosses (DH4xDH5), (DH4xSerw5) and (DH5xSerw5) to study the nature and magnitude of gene effects on vegetative characters, seed yield and oil percentage in canola (*Brassica napus* L.) under two locations (Mansoura and Assiut). Type of gene action varied with the plant traits, crosses and locations. Genotype x locations interaction was statistically significant in the expression of all the plant traits. Number of components of generation means varied with crosses and locations. Non-additive gene action was involved in most of the traits in different crosses under the two locations. Also, the results showed that oil percentage (Oil %) trait influenced by types of epistatic gene effect, which included additive x dominance (ad) and dominance x dominance (dd), indicating the role of non-allelic interaction in the genetic expression of this trait. Therefore, it could be concluded that the production of hybrids is the best breeding program for the improvement the studied traits.

Keywords: *Brassica napus*; Generation Mean Analysis; Gene Action; Oil contents; Yield components

Introduction

The Brassicaceae family consists of many main field crops and vegetables such as rapeseed. Rapeseed was the third important vegetable oil source in the world with an annual growth rate beyond that of palm. Canola (*Brassica napus* L.) is the oilseed crop of cold season countries. In Egypt, new varieties have been introduced and tested for adaptation to Egyptian environment; especially it is successfully grown during winter season in newly reclaimed sandy soil (Sharaan and Ghallab, 2002).

The optimal selection and breeding procedures for genetic improvement of any crop is mainly dependent on the knowledge of type

and relative amount of genetic component and the presence of non-allelic interaction for different traits in the plant materials under investigations. Selection program leads to maximum progress in improving a trait when the additive gene action is the main component. Heterosis in F1 hybrids may be exploited by choosing parental cultivars in which the non-additive effects predominated in the inheritance of the more important trait. On the other hand, to form a population with genetic variability for the traits studied, hybridization between genetically diverse parents must be done. Plant breeders and geneticists frequently use generation mean analysis to obtain information of gene action controlling the economic traits in ra-

peseed. Marjanovic-Jeromela *et al.* (2014) found that the additive dominant model did not suitable evidence for plant height in all crosses of rapeseed. Singh *et al.* (2014) found that Additive genetic variance formed the major part of genetic variance for the important yield component dry matter per plant. Cheema and Sadaqat (2004) reported about the role of changes in environment-gene effects for different traits contributing to yield components. Khuble *et. al.* (1998) revealed that both additive and non-additive gene effects were controlling the expression of various traits and predominant presence of non-additive gene action was found to control the yield in *B. juncea*. Sheikh and Singh, (1998), found that non-additive gene action was contributed for most traits including oil content and additive genetic variance was more important for plant height in Indian mustard (*B. juncea*) whereas non-additive gene action appeared to be predominant for all traits except days to maturity, which was governed by additive gene action (Patel *et al.*, 1996). While, Singh and Singh (1994) reported that dominance and epistasis effects were more important for days to first flower, plant height, siliquae/plant and yield/plant in different generations in *B. juncea*.

Therefore, the present study was carried out to obtain information about gene action controlling the morphological characters, yield and its components in the three canola crosses in order to introgression of desirable genes into canola.

Materials and Methods

Experimental design:

Six basic sets of generations namely P₁, P₂, F₁, F₂, BC₁ and BC₂ were derived from three crosses involving three contrasting genotypes of canola. Three homozygous double haploid line of canola (*Brassica napus* L.) i.e. DH4, DH5 and Serw5 were used as parents in this study. The crosses were referred as: Cross1 (DH4xDH5), Cross2 (DH4xSerw5) and Cross3 (DH5xSerw5). These crosses among the accessions were sown in winter 2011, at experimental farm, Faculty of Agriculture Mansoura Univ. In winter 2012, F₁ seeds were planted in the field to produce F₂ seeds; subsequent flower buds were back crossed to produce the first backcross (BC₁) and second backcross (BC₂) generations. Parents, F₁, F₂, BC₁ and BC₂ from each of the three crosses were sown in 2013 in a randomized complete block design (RCBD) with three replications, at two locations i.e. experimental farm, Faculty of Agriculture Mansoura Univ. and experimental farm, Faculty of Agriculture Assiut Univ. Data from these six generations were recorded on 5 plants for P₁, P₂, F₁ and 15 plants for F₂ and 10 plants for BC₁, BC₂ chosen at random from each plot. The data were recorded for the following Agronomical traits: Number of days to 50 % flowering (NDF); Number of Branches/plant (NB/p); Plant height (PH cm); Number of pod/ branches (NP/b); Weight of 100 seeds (W100s gm), Seed yield per plant in grams (S.Y/P) and Oil percentage (Oil %) in seeds.

Statistical and Genetic Analysis: Using SAS software (SAS 9.1), analyses of variances were done for six populations (The two parents ,F₁,

F₂, BC₁ and BC₂) within each cross with respect to all the studied traits. In addition, analysis of variance according to (RCBD) analysis of variance for the studied traits was made to detect the significance of the observed differences among and within crosses (Singh and Narayanan, 2000).

Estimation of Heterosis (H_L):

Estimates of Heterosis (%) were calculated as the percent deviation of F₁ mean performance over that either mid or better parent as follows according to (Abd-El-Haleem *et al.*, 2010):

Heterosis from the mid-parents:

$$H_{MP}\% = \frac{F_1 - MP}{MP} \times 100 = \frac{F_1 - \frac{P_1 + P_2}{2}}{\frac{P_1 + P_2}{2}} \times 100$$

Where, Heterosis deviation = $F_1 - MP$ & Variance of heterosis deviation = $V_{F_1} + \frac{1}{4}(V_{P_1} + V_{P_2})$

Heterosis from the better-parent:

$$H_{BP}\% = \frac{F_1 - BP}{BP} \times 100$$

Where, Heterosis deviation = $F_1 - MP$ & Variance of heterosis deviation = $V_{F_1} + V_{BP}$

The t values of T-test were calculated as follows:

$$\pm t_H = \frac{\text{Heterosis deviation}}{\sqrt{\text{Variance of heterosis deviation}}}$$

Estimation of Inbreeding depression (I.D.): Its value was computed as the percent deviation of F₂ mean than their corresponding F₁ mean from the following equation according to (Abd-El-Haleem *et al.*, 2010):

$$I.D.\% = \frac{F_1 - F_2}{F_1} \times 100$$

The t values of T-test of I.D. were calculated as follows: $\pm t_{I.D.} = \frac{F_1 - F_2}{\sqrt{V_{F_1} + V_{F_2}}}$

The scaling test (A, B and C) and their variances were calculated for each trait to test the deviations of segregation from the additive and

dominance model of gene effects (were computed according to (Mather and Jinks, 1982) and the formulae outlined by Soher and Abd El-Aziz (2013) as follows:

$$A = 2\overline{BC_1} - \overline{F_1} - \overline{F_2} \quad \& \quad VA = 4V_{BC_1} + V_{P_1} + V_{F_2}$$

$$B = 2\overline{BC_2} - \overline{F_2} - \overline{F_1} \quad \& \quad VB = 4V_{BC_2} + V_{P_2} + V_{F_1}$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{F_1} - \overline{F_2} \quad \& \quad VC = 16V_{F_2} + 4V_{F_1} + V_{P_1} + V_{P_2}$$

Where

V_{P_1} , V_{P_2} , V_{F_1} , V_{F_2} , V_{BC_1} and V_{BC_2}

were estimated according to (Scheffe, 1959).

The t vales of T-test are calculated as follows:

$$\pm t = \frac{\text{Deviation}}{\text{Standard error}} = \frac{\text{Deviation (value of A or B or C)}}{\sqrt{\text{Variance of deviation}}}$$

$$t_{(A)} = \frac{A}{\sqrt{VA}} \quad \& \quad t_{(B)} = \frac{B}{\sqrt{VB}} \quad \& \quad t_{(C)} = \frac{C}{\sqrt{VC}}$$

In each test, the degrees of freedom are sum of the degrees of freedom of various generations involved. Also, the significance of any one of these scales is taken to indicate the existence of non- allelic interaction (Singh and Chaudhary, 1977).

Therefore, the six parameter model is used for estimating various genetic components i.e.: m, a, d, aa, ad and dd, which stand for mean effects, additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effect, respectively. These genetic components and their variances were calculated according to (Jinks and Jones, 1958; khodambashi *et al.*, 2012) as follows:

$$[m] = \overline{F_2} \quad \& \quad V_m = V_{F_2}$$

$$[a] = \overline{BC_1} - \overline{BC_2} \quad \& \quad V_a = V_{BC_1} + V_{BC_2}$$

$$[d] = F_1 - 4F_2 - \frac{1}{2}F_1 - \frac{1}{2}F_2 + 2\overline{BC_1} + 2\overline{BC_2} \quad \&$$

$$V_d = V_{F_1} + 16V_{F_2} + \frac{1}{4}V_{P_1} + \frac{1}{4}V_{P_2} + 4V_{BC_1} + 4V_{BC_2}$$

$$\begin{aligned}
 [aa] &= 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2} \\
 &\& V_{aa} = 4V_{BC_1} + 4V_{BC_2} + 16V_{F_2} \\
 [ad] &= \overline{BC_1} - \frac{1}{2}\overline{P_1} - \overline{BC_2} + \frac{1}{2}\overline{P_2} \\
 &\& V_{ad} = V_{BC_1} + \frac{1}{4}V_{P_1} + V_{BC_2} + \frac{1}{4}V_{P_2} \\
 [dd] &= \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2} \quad \& \\
 V_{dd} &= V_{P_1} + V_{P_2} + 4V_{F_1} + 16V_{F_2} + 16V_{BC_1} + 16V_{BC_2}
 \end{aligned}$$

Standard error of these parameters and calculated “t” values were estimated according to (Gamble, 1962; Singh and Chaudhary, 1977) in a similar manner as done in case of scaling test.

In the absence of non-allelic interaction, the additive-dominance model is adequate. Thus, m, a and d their variances were estimated according to (Jinks and Jones, 1958) as follows:

$$\begin{aligned}
 [m] &= \frac{1}{2}\overline{P_1} + \frac{1}{2}\overline{P_2} + 4\overline{F_2} - 2\overline{BC_1} - 2\overline{BC_2} \\
 &\& V_a = \frac{1}{4}V_{P_1} + \frac{1}{4}V_{P_2} \\
 [d] &= 6\overline{BC_1} + 6\overline{BC_2} - 8\overline{F_2} - \overline{F_1} - \frac{3}{2}\overline{P_1} - \frac{3}{2}\overline{P_2} \\
 &\& V_d = 36V_{BC_1} + 36V_{BC_2} + 64V_{F_2} + V_{F_1} + \frac{9}{4}V_{P_1} + \frac{9}{4}V_{P_2}
 \end{aligned}$$

Significance of the genetic effects is tested in a similar manner as done in case of scaling test.

Analysis of variance:

Analyses of variances were done for populations (P1, P2, F1, F2, BC1 and BC2) within each cross with respect to all the studied traits. In addition, analysis of variance according to Split Block Design for the studied traits was made to detect the significance of the observed difference among and within crosses.

Results and Discussion

Analysis of variance: in this investigation, six agronomical traits

and oil % in seeds were studied in DH4, DH5, Serw5 and there F₁'s, F₂'s, Bc1 and Bc2 of Canola. Therefore, several analyses of variance were made in order to test the significance of difference among crosses as well as among populations within crosses from the combined data over all the two locations and the obtained results are presented in Table 1. The results indicated the presence of significant differences among crosses for all studied traits. Also, the results revealed that the populations within each cross exhibited significant differences for the studied three crosses except for Pop. within Cross 1 and 2 in the case of weight of 100 seeds (W100s gm) and for Pop. within Cross 3 for Number of pod/ branches (NP/b) and seed yield per plant in grams (S.Y./P) which showed insignificant difference. This significant variation suggested the existence of some sort of genetic variability between the used parental lines which might reflect their difference in their genetic background. Therefore, the comparisons between genotypic means are valid and the partition of this genotypic variance to its components could be made. On the other hand, the population within crosses interacted significantly with locations for all studied traits. Also, populations within each cross interacted significantly with locations in all cases except for Pop. within Cross 1 x L for weight of 100 seeds and Pop. within Cross 2 x L for number of pod/ branches (NP/b) and weight of 100 seeds. These results referred that these crosses and their populations behaved differently in different environmental conditions.

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

S.O.V.	D.F.	NDF	NB/p	PH	NP/b	W100	S.Y/P	Oil%
Location (L)	L-1=1	29241.0**	103.4**	1346.9*	905225**	2.079**	656007**	897.80**
R / L	L(r-1)=4	344.2**	42.1**	7216.8**	22773**	0.096**	29687**	3.06**
Crosses (C)	c-1=2	158.6**	18.0**	9691.8**	4409**	0.022*	10624*	22.09**
C x L	(c-1)(L-1)=2	51.6	8.3	2967.6**	2093*	0.004	4022	10.66**
Rep. within C x L (error a)	L(r-1)(c-1)=8	71.1*	5.4	797.8**	1211*	0.003	7991*	0.96
Pop. within Crosses	c(p-1)=15	173.3**	24.4**	2013.6**	5038**	0.012**	10791**	35.42**
Pop. within Cross 1	p-1=5	118.8**	40.8**	2194.5**	5965**	0.006	15943**	38.13**
Pop. within Cross 2	p-1=5	272.6**	22.8**	1076.8**	8206**	0.006	13154**	33.67**
Pop. within Cross 3	p-1=5	128.4**	9.6*	2769.3**	944	0.024**	3276	34.47**
Pop. within Crosses x L	c(p-1)(L-1)=15	77.8**	12.3**	1312.0**	2423**	0.010*	15195**	11.80**
Pop. within Cross 1x L	(p-1)(L-1)=5	100.4*	20.7**	1478.6**	1792*	0.006	21825**	7.38**
Pop. within Cross 2x L	(p-1)(L-1)=5	26.2	11.5**	988.3**	2956**	0.005	15659**	12.38**
Pop. within Cross 3x L	(p-1)(L-1)=5	106.7**	4.6	1469.1**	2521**	0.019**	8102*	15.66**
Rep W Pop.xCrosses (error b)	cL(p-1)(r-1)=60	55.0**	5.7**	882.0**	1980**	0.007	5611**	1.77**
Rep. within Pop. x cross 1	L(p-1)(r-1)=20	59.8*	6.2**	899.9**	1776**	0.008	6110**	0.71*
Rep. within Pop. x cross 2	L(p-1)(r-1)=20	31.2	7.0**	889.3**	2315**	0.004	6093*	3.53**
Rep. within Pop. x cross 3	L(p-1)(r-1)=20	74.2**	3.9	856.8**	1848**	0.008*	4631	1.09*

*, ** Significant at 0.05 and 0.01 levels probability, respectively

Where: L = Locations=2, r = replications=3, p = no. of populations=6, c = no. of crosses=3

Mean performance:

The six population means and their stander error of studied crosses for all traits were calculated and the obtained results are shown in Tables 2, 3 and 4. The mean values showed that the inbred line DH4 was the highest parent for number of branches/plant (NB/p) (9.20), number of pod/ branches NP/b (104.7), weight of 100 seeds (W100s gm) (0.35) and Seed yield per plant in grams (S.Y./P) (114.1), while this inbred was the lowest parent for number of days to 50 % flowering (NDF) (65.7) and Oil% (33%). The inbred line DH5 was the earliest parent for number of days to 50 % flowering (NDF) (60.2) and the highest for Oil% (36.75%), while it appeared to be the shorter parent for plant height (PH cm) (183.5) and the lowest parent for weight of 100 seeds (W100s gm) (0.34). The parental line Serw5 was the highest parent for plant height (PH cm) (192.7), while it was

the lowest parent for number of pod/ branches (NP/b) (88.7) and Seed yield per plant in grams (S.Y./P) (93.2). On the other hand, the results showed that the crosses which involved at least one of the highest parents with respect to any one of studied traits had the highest mean values for these traits. For instance, the 1st cross (DH4xDH5) was the earliest for number of days to 50 % flowering (NDF) and the highest hybrid for weight of 100 seeds (W100s gm) with means values 61.1 and 0.33 gm, respectively. In addition, the 2nd cross (DH4xSerw5) was highest hybrid for number of pod/ branches NP/b, seed yield per plant in grams (S.Y./P) and Oil% with means values 100.3, 93.2 and 37.25%, respectively. While, the 3rd cross (DH5xSerw5) was highest hybrid for number of branches/plant (NB/p) and plant height (PH cm) with means values 7.73 and 203.0, respectively. The results showed that the F2 generations

of the (1st and 3rd) and (1st, 2nd and 3rd) appeared to be superior over their F₁ hybrids for number of days to 50 % flowering (NDF) and Oil% in the two locations and their combined. These findings reflected the presence of transgressive segregation and/or epistasis which indicated to the role of additive and epistasis gene effects in the inheritance of these traits with respect to the previous crosses. Furthermore, the F₂ generations of the three crosses in the two locations and their combined were less than corresponding values of F₁ hybrids for the number of branches/plant (NB/p), plant height (PH), number of pod/branches (NP/b), weight of 100 seeds (W100) and Seed yield per plant in grams (S.Y./P). These results reflect the presence of heterotic effect and non-additive genetic variance plays the major role in the inheritance of these traits.

The results also revealed that the backcrosses means of most of studied crosses tended toward the respective recurrent parents in most of studied traits preferred the role of ad-

ditive and dominance gene action effects. Also, these results showed desirable negative values of heterosis over mid-parents and better-parent for number of days to 50% flowering trait of all studied crosses except for 3rd cross with values -2.94, -6.95, -4.90 and -5.43, respectively. While the 3rd cross (DH5xSerw5) showed positive values of heterosis over mid-parents and better-parent for the number of branches/plant (NB/p), plant height (PH) and number of pod/branches (NP/b). Also, the 1st (DH4xDH5) and 2^{sd} (DH4xSerw5) crosses showed positive values of heterosis over mid-parents and better-parent for the Oil %. Positive inbreeding depression was observed for plant height trait for all crosses with values 6.45, 1.80 and 4.68, respectively. In addition, the 1st (DH4xDH5) and 2^{sd} (DH4xSerw5) crosses showed positive inbreeding depression for number of pod/branches (NP/b). This indicates the role of dominant gene action in the inheritance of this trait.

Table 2. Mean performance of six generations in three canola crosses for two locations and their combined data as well as heterosis and inbreeding depression for vegetative traits.

Traits	Number of days to 50 % flowering (NDF)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
Crosses	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	60.6 ± 0.9	70.7 ± 5.4	65.7 ± 6.6	60.6 ± 0.9	70.7 ± 5.4	65.67 ± 6.56	51.9 ± 1.3	68.5 ± 8.0	60.2 ± 10.44
P ₂	51.9 ± 1.3	68.5 ± 8.0	60.2 ± 10.4	59.9 ± 0.4	69.9 ± 2.2	64.93 ± 5.66	59.9 ± 0.4	69.9 ± 2.2	64.9 ± 5.66
F ₁	54.1 ± 1.0	68.1 ± 4.2	61.1 ± 8.2	56.7 ± 1.7	67.5 ± 3.2	62.10 ± 6.39	56.9 ± 1.0	70.6 ± 0.9	63.8 ± 7.53
F ₂	58.9 ± 2.8	68.2 ± 3.4	63.5 ± 5.8	56.4 ± 1.5	67.1 ± 0.9	61.78 ± 5.97	59.5 ± 1.8	69.2 ± 4.7	64.3 ± 6.22
BC ₁	58.4 ± 1.1	66.5 ± 4.1	62.5 ± 5.1	58.8 ± 0.9	72.3 ± 1.0	65.57 ± 7.43	57.4 ± 1.2	67.8 ± 5.6	62.6 ± 6.79
BC ₂	58.2 ± 0.6	68.3 ± 2.6	63.3 ± 5.8	60.7 ± 1.3	73.5 ± 0.4	67.13 ± 7.06	57.4 ± 0.5	72.9 ± 3.4	65.1 ± 8.73
LSD _{0.05}	2.6	8.8	4.33	2.1	5.0	2.56	2.0	8.4	4.11
LSD _{0.01}	3.6	12.3	5.87	3.0	7.0	3.47	2.8	11.8	5.57
H _{Mp} %	-3.91	-2.15	-2.94	-5.97	-3.98	-4.90	1.79	1.97	1.89
H _{Bp} %	4.11	-0.58	-6.95	-5.45	-3.43	-5.43	9.63	3.02	5.87
I. D.%	-8.88	-0.03	-3.95	0.43	0.59	0.52	-4.45	1.95	-0.91
Traits	Number of Branches/plant (NB/p)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
Crosses	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	10.9 ± 1.3	7.5 ± 1.4	9.20 ± 2.20	10.9 ± 1.3	7.5 ± 1.4	9.20 ± 2.20	8.4 ± 0.7	6.9 ± 1.5	7.63 ± 1.35
P ₂	8.4 ± 0.7	6.9 ± 1.5	7.63 ± 1.35	7.5 ± 1.3	7.1 ± 1.0	7.27 ± 1.09	7.5 ± 1.3	7.1 ± 1.0	7.27 ± 1.09
F ₁	6.8 ± 0.3	6.3 ± 1.4	6.53 ± 0.96	8.3 ± 0.8	6.6 ± 0.6	7.43 ± 1.11	8.0 ± 1.2	7.5 ± 1.4	7.73 ± 1.23
F ₂	6.1 ± 0.6	6.6 ± 0.4	6.34 ± 0.53	7.2 ± 1.5	6.8 ± 1.2	6.99 ± 1.26	7.4 ± 0.6	6.2 ± 1.0	6.78 ± 0.99
BC ₁	6.7 ± 0.9	7.0 ± 0.6	6.83 ± 0.67	7.9 ± 1.0	6.8 ± 1.0	7.35 ± 1.05	7.0 ± 0.6	6.2 ± 0.7	6.60 ± 0.75
BC ₂	7.0 ± 0.9	7.0 ± 0.9	7.00 ± 0.78	7.5 ± 0.9	7.0 ± 0.3	7.27 ± 0.62	6.7 ± 0.1	6.8 ± 0.6	6.75 ± 0.37
LSD _{0.05}	1.5	2.0	1.18	2.1	1.8	1.29	1.6	1.9	1.18
LSD _{0.01}	2.1	2.8	1.59	2.9	2.5	1.76	2.2	2.7	1.60
H _{Mp} %	-29.41	-12.96	-22.38	-9.82	-9.59	-9.72	0.84	7.18	3.80
H _{Bp} %	-37.42	-16.81	-28.99	-23.93	-12.39	-19.20	-4.76	5.66	1.31
I. D.%	10.78	-5.67	2.89	12.63	-2.36	5.98	7.78	17.26	12.36
Traits	Plant height (PH cm)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
Crosses	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	195.5 ± 12.2	174.3 ± 12.9	184.9 ± 16.2	195.5 ± 12.2	174.3 ± 12.9	184.9 ± 16.2	185.3 ± 15.1	181.7 ± 5.5	183.5 ± 10.4
P ₂	185.3 ± 15.1	181.7 ± 5.5	183.5 ± 10.4	199.3 ± 7.0	186.0 ± 10.8	192.7 ± 10.9	199.3 ± 7.0	186.0 ± 10.8	192.7 ± 10.9
F ₁	181.7 ± 2.5	182.0 ± 10.4	181.8 ± 6.8	190.0 ± 12.5	180.3 ± 11.6	185.2 ± 12.0	213.3 ± 9.5	192.7 ± 17.2	203.0 ± 16.8
F ₂	165.9 ± 12.1	174.3 ± 12.2	170.1 ± 11.8	187.6 ± 10.2	176.1 ± 12.2	181.8 ± 11.9	199.0 ± 6.8	188.0 ± 6.2	193.5 ± 8.4
BC ₁	171.0 ± 17.1	181.5 ± 8.8	176.3 ± 13.4	194.0 ± 19.1	190.8 ± 8.3	192.4 ± 13.3	180.5 ± 11.8	182.5 ± 14.4	181.5 ± 11.8
BC ₂	178.2 ± 18.3	190.5 ± 9.8	184.3 ± 14.8	182.7 ± 15.5	188.4 ± 8.8	185.5 ± 11.7	179.0 ± 10.5	189.1 ± 17.7	184.1 ± 14.2
LSD _{0.05}	24.7	18.2	14.5	23.7	19.4	14.5	18.7	23.0	14.1
LSD _{0.01}	34.7	25.5	19.7	33.1	27.2	19.6	26.2	32.3	19.0
H _{Mp} %	-4.60	2.25	-1.29	-3.76	0.09	-1.92	10.92	4.81	7.93
H _{Bp} %	-7.09	0.18	-1.68	-4.68	-3.05	-3.89	7.02	3.58	5.36
I. D.%	8.69	4.21	6.45	1.29	2.34	1.80	6.72	2.42	4.68

*, ** Significant at 0.05 and 0.01 levels probability, respectively

Table 3. Mean performance of six generations in three canola crosses for two locations and their combined data as well as heterosis and inbreeding depression for Yield traits.

Traits	Number of pod/ branches (NP/b)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
Crosses	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	136.7 ± 20.8	72.7 ± 4.8	104.7 ± 37.6	136.7 ± 20.8	72.7 ± 4.8	104.7 ± 37.6	122.6 ± 38.6	70.1 ± 6.4	96.3 ± 38.0
P ₂	122.6 ± 38.6	70.1 ± 6.4	96.3 ± 38.0	108.5 ± 42.3	68.9 ± 15.3	88.7 ± 35.8	108.5 ± 42.3	68.9 ± 15.3	88.7 ± 35.8
F ₁	122.0 ± 30.5	70.0 ± 8.8	96.0 ± 34.8	132.9 ± 36.8	67.8 ± 1.3	100.3 ± 42.6	119.5 ± 25.6	78.7 ± 4.8	99.1 ± 27.7
F ₂	117.1 ± 16.1	60.6 ± 5.7	88.9 ± 32.8	128.3 ± 10.4	67.7 ± 6.9	98.0 ± 34.2	129.0 ± 17.1	74.7 ± 8.4	101.9 ± 32.1
BC ₁	156.0 ± 4.6	72.8 ± 8.8	114.4 ± 46.0	158.5 ± 28.3	73.8 ± 3.1	116.1 ± 49.8	141.3 ± 10.2	61.7 ± 3.8	101.5 ± 44.2
BC ₂	142.4 ± 22.5	75.8 ± 4.4	109.1 ± 39.3	165.2 ± 34.6	82.6 ± 4.2	123.9 ± 50.3	132.2 ± 37.8	70.0 ± 5.9	101.1 ± 41.8
LSD _{0.05}	43.8	11.9	21.5	54.7	13.3	26.7	55.1	14.8	27.0
LSD _{0.01}	61.4	16.7	29.1	76.7	18.6	36.1	77.3	20.8	36.6
H _{Mp} %	-5.89	-1.87	-4.46	8.40	-4.19	3.79	3.40	13.34	7.14
H _{Bp} %	-10.73	-3.62	-8.26	-2.78	-6.70	-4.14	-2.56	12.37	2.87
I. D.%	3.99	13.50	7.46	3.41	0.21	2.33	-8.00	5.15	-2.77
Traits	Weight of 100 seeds (W100s gm)								
Crosses	DH4xDH5			DH4xSerw5			DH5xSerw5		
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	0.38 ± 0.04	0.31 ± 0.07	0.35 ± 0.06	0.38 ± 0.04	0.31 ± 0.07	0.35 ± 0.06	0.42 ± 0.02	0.27 ± 0.06	0.34 ± 0.09
P ₂	0.42 ± 0.02	0.27 ± 0.06	0.34 ± 0.09	0.41 ± 0.01	0.29 ± 0.03	0.35 ± 0.07	0.41 ± 0.01	0.29 ± 0.03	0.35 ± 0.07
F ₁	0.38 ± 0.03	0.28 ± 0.06	0.33 ± 0.07	0.38 ± 0.02	0.27 ± 0.04	0.32 ± 0.07	0.41 ± 0.04	0.22 ± 0.06	0.32 ± 0.11
F ₂	0.41 ± 0.02	0.32 ± 0.03	0.36 ± 0.05	0.38 ± 0.04	0.31 ± 0.04	0.35 ± 0.05	0.41 ± 0.05	0.34 ± 0.04	0.38 ± 0.05
BC ₁	0.39 ± 0.03	0.32 ± 0.04	0.36 ± 0.05	0.39 ± 0.02	0.29 ± 0.04	0.34 ± 0.06	0.42 ± 0.05	0.30 ± 0.03	0.36 ± 0.07
BC ₂	0.40 ± 0.03	0.30 ± 0.01	0.35 ± 0.06	0.41 ± 0.02	0.31 ± 0.03	0.36 ± 0.06	0.42 ± 0.01	0.34 ± 0.06	0.38 ± 0.06
LSD _{0.05}	0.04	0.09	0.047	0.05	0.08	0.043	0.05	0.09	0.049
LSD _{0.01}	0.06	0.12	0.063	0.07	0.11	0.058	0.08	0.12	0.067
H _{Mp} %	-4.84	-4.34	-4.63	-5.69	-10.02	-7.55	-1.77	-19.71	-9.02
H _{Bp} %	-8.36	-10.09	-5.09	-9.03	-13.30	-7.10	-1.93	-21.76	-9.89
I. D.%	-6.90	-14.56	-10.14	-2.13	-15.84	-7.85	-1.97	-52.76	-20.08
Traits	Seed yield per plant in grams (S.Y/P)								
Crosses	DH4xDH5			DH4xSerw5			DH5xSerw5		
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P ₁	180.9 ± 36.6	47.3 ± 11.5	114.1 ± 77.1	180.9 ± 36.6	47.3 ± 11.5	114.1 ± 77.1	148.9 ± 63.4	48.0 ± 4.0	98.5 ± 68.4
P ₂	148.9 ± 63.4	48.0 ± 4.0	98.5 ± 68.3	132.3 ± 82.2	54.1 ± 21.1	93.2 ± 68.7	132.3 ± 82.2	54.1 ± 21.1	93.2 ± 68.7
F ₁	76.2 ± 29.9	53.3 ± 21.8	64.8 ± 26.6	115.7 ± 25.0	70.7 ± 18.1	93.2 ± 31.5	135.3 ± 16.7	49.4 ± 3.9	92.4 ± 48.3
F ₂	74.6 ± 15.2	61.2 ± 19.9	67.9 ± 17.4	89.1 ± 28.5	65.3 ± 5.0	77.2 ± 22.4	97.3 ± 32.5	57.3 ± 6.3	77.3 ± 30.3
BC ₁	115.7 ± 31.3	74.3 ± 22.5	95.0 ± 33.3	141.7 ± 33.6	65.6 ± 5.6	103.6 ± 46.9	113.9 ± 21.0	59.0 ± 12.7	86.5 ± 33.8
BC ₂	113.4 ± 14.6	73.8 ± 15.4	93.6 ± 25.5	145.1 ± 43.6	83.8 ± 9.6	114.5 ± 43.9	108.4 ± 42.2	77.1 ± 25.4	92.7 ± 35.5
LSD _{0.05}	63.6	30.5	33.4	81.4	23.6	40.1	86.9	26.4	43.0
LSD _{0.01}	89.1	42.8	45.3	114.1	33.1	54.4	121.9	37.0	58.3
H _{Mp} %	-53.77	11.86	-39.06	-26.10	39.54	-10.05	-3.76	-3.23	-3.62
H _{Bp} %	-57.86	11.00	-43.24	-36.02	30.72	-18.28	-9.13	-8.69	-6.19
I. D.%	2.19	-14.89	-4.84	23.02	7.60	17.17	28.10	-15.97	16.32

*, ** Significant at 0.05 and 0.01 levels probability, respectively

Table 4. Mean performance of six generations in three canola crosses for two locations and their combined data as well as heterosis and inbreeding depression for Oil % trait.

Traits	Oil percentage (Oil %)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
Crosses	DH4xDH5			DH4xSerw5			DH5xSerw5		
Generations	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
P₁	36.5 ± 0.5	29.5 ± 0.5	33.00 ± 3.86	36.5 ± 0.5	29.5 ± 0.5	33.00 ± 3.86	40.2 ± 0.3	33.3 ± 0.6	34.83 ± 3.76
P₂	40.2 ± 0.3	33.3 ± 0.6	36.75 ± 3.76	37.2 ± 0.3	32.7 ± 0.3	34.92 ± 2.48	37.2 ± 0.3	32.7 ± 0.3	34.92 ± 2.48
F₁	38.3 ± 0.3	36.0 ± 0.5	37.17 ± 1.33	40.0 ± 0.5	34.5 ± 0.5	37.25 ± 3.05	36.8 ± 0.3	32.5 ± 0.5	34.67 ± 2.40
F₂	41.0 ± 0.2	37.3 ± 1.2	39.14 ± 2.17	40.3 ± 0.3	35.9 ± 1.4	38.08 ± 2.57	37.9 ± 1.3	34.6 ± 1.3	36.25 ± 2.18
BC₁	40.7 ± 0.7	36.4 ± 0.4	38.54 ± 2.38	38.8 ± 0.9	34.7 ± 2.3	36.75 ± 2.75	40.8 ± 0.1	33.3 ± 0.9	37.04 ± 4.19
BC₂	39.7 ± 0.5	37.2 ± 1.0	38.42 ± 1.55	38.5 ± 2.7	38.3 ± 1.9	38.42 ± 2.08	42.0 ± 0.4	37.3 ± 0.4	39.63 ± 2.63
LSD_{0.05}	0.81	1.3	0.74	2.1	2.4	1.56	1.1	1.3	0.80
LSD_{0.01}	1.13	1.9	1.00	3.0	3.4	2.08	1.5	1.8	1.08
H_{Mp}%	-0.00	14.59**	6.57	8.60**	10.99**	9.69	-4.74**	4.56*	-0.60
H_{Bp}%	-4.56**	8.00**	1.13	7.62**	5.61**	6.68	-8.30**	-0.51	-0.72
I. D.%	-6.96**	-3.55	-5.31	-0.69	-4.03	-2.24	-3.02	-6.32	-4.57

*, ** Significant at 0.05 and 0.01 levels probability, respectively

Gene action:

The results of scaling tests (A, B and C) for vegetative and yield traits in each location in addition to their combined data are shown in Tables 5 and 6, respectively. The values of scaling tests were non-significant in all crosses for all traits except for 1st cross (DH4xDH5) for number of days to 50 % flowering (NDF) in Mansoura location. This finding indicating 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. The results showed that the estimates of mean effects parameter (m), which reflects the contribution due to the overall mean (additive) plus the locus effects (dominance) found to be highly significant for number of days to 50 % flowering (NDF) in Mansoura location. In gen-

eral, the crosses exhibited different magnitude and sign of gene action types with different locations. Therefore, it could be more accurate, concentrating on the results obtained from the combined data over both locations. The results showed that the estimates of additive gene effects (a) values were positively for most of the studied crosses. While, the dominance gene effects (d) were larger in magnitude than the corresponding values of additive effects (a) in the three crosses except for number of branches/plant (NB/p) in all crosses and for number of days to 50 % flowering (NDF) in the 1st cross (DH4xDH5). This fact suggests that the major role of dominance gene action in the inheritance of these traits and the higher frequency of dominant genes in the parental lines, which involved in these crosses for these traits.

Table 5. The scaling test and estimates of the genetic components: additive, dominance and interaction parameters as well as standard errors of three canola crosses in two locations and their combined data for vegetative traits.

Traits	Number of days to 50 % flowering (NDF)																	
Crosses	DH4xDH5				DH4xSerw5				DH5xSerw5									
Scaling test and parameters	Mans.		Asu.		Comb.		Mans.		Asu.		Comb.							
A	2.20	± 4.32	-5.93	± 19.92	-1.87	± 18.60	0.40	± 4.82	6.33	± 18.49	3.37	± 20.48	5.87	± 6.74	-3.47	± 21.56	1.20	± 21.93
B	10.40*	± 4.79	0.00	± 18.50	5.20	± 20.12	4.87	± 11.07	9.60	± 16.62	7.23	± 20.44	-2.00	± 2.68	5.20	± 19.26	1.60	± 22.40
C	14.80	± 19.56	-2.91	± 39.49	5.94	± 40.08	-8.18	± 11.65	-7.20	± 33.46	-7.69	± 35.41	12.13	± 12.35	-2.78	± 28.22	4.68	± 33.80
m	58.87*	± 4.68	72.66	± 40.59	65.56	± 39.25	46.82*	± 14.91	47.20	± 32.87	47.01	± 38.35	64.20*	± 13.60	64.72	± 36.36	64.46	± 38.80
a	0.23	± 2.32	1.10	± 6.95	2.72	± 6.98	0.33	± 1.14	0.40	± 6.34	0.37	± 5.75	-4.00*	± 1.16	-0.70	± 6.07	-2.35	± 6.54
d	-4.40	± 19.49	13.48	± 95.33	-3.74	± 92.05	28.56	± 39.03	59.40	± 79.04	43.98	± 94.81	-11.67	± 31.10	12.12	± 94.00	0.23	± 99.06
aa	-2.20	± 19.28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-4.10	± 2.71	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-10.40	± 21.65	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Traits	Number of Branches/plant (NB/p)																	
Crosses	DH4xDH5				DH4xSerw5				DH5xSerw5									
Scaling test and parameters	Mans.		Asu.		Comb.		Mans.		Asu.		Comb.							
A	-4.27	± 5.03	0.13	± 3.90	-2.07	± 4.77	-3.40	± 5.51	-0.47	± 4.30	-1.93	± 5.33	-2.40	± 4.75	-1.93	± 4.43	-2.17	± 4.68
B	-1.20	± 4.71	0.87	± 4.60	-0.17	± 4.67	-0.73	± 4.82	0.40	± 3.88	-0.17	± 4.43	-2.13	± 5.80	-0.87	± 4.65	-1.50	± 5.21
C	-8.60	± 7.26	-0.44	± 8.60	-4.52	± 8.19	-5.98	± 11.07	-0.78	± 8.81	-3.38	± 10.24	-2.36	± 8.53	-4.16	± 9.71	-3.26	± 9.41
m	6.50	± 7.30	5.76	± 8.61	6.13	± 8.06	7.32	± 10.58	6.59	± 8.45	6.96	± 9.66	10.11	± 9.21	5.61	± 8.68	7.86	± 9.25
a	1.23	± 2.05	0.33	± 1.39	0.78	± 1.96	1.70	± 1.87	0.23	± 1.47	0.97	± 1.86	0.47	± 1.73	-0.10	± 1.42	0.18	± 1.61
d	-2.03	± 19.02	2.96	± 20.38	0.46	± 19.90	-1.34	± 24.57	0.66	± 19.59	-0.34	± 22.56	-8.82	± 23.25	0.41	± 20.19	-4.21	± 22.31
aa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Traits	Plant height (PH cm)																	
Crosses	DH4xDH5				DH4xSerw5				DH5xSerw5									
Scaling test and parameters	Mans.		Asu.		Comb.		Mans.		Asu.		Comb.							
A	-35.20	± 53.51	6.7	± 38.5	-14.3	± 48.5	2.5	± 49.1	27.0	± 40.3	14.7	± 46.0	-37.7	± 45.4	-9.3	± 52.7	-23.50	± 49.87
B	-10.67	± 56.76	17.3	± 44.0	3.3	± 51.8	-24.0	± 52.5	10.4	± 46.2	-6.8	± 49.9	-54.7	± 45.3	-0.4	± 55.2	-27.53	± 52.48
C	-80.64	± 77.10	-22.7	± 103.8	-51.7	± 92.9	-24.6	± 79.8	-16.6	± 92.5	-20.6	± 90.0	-15.3	± 69.2	-1.0	± 86.2	-8.17	± 83.49
m	155.66	± 93.98	131.3	± 108.9	143.5	± 103.9	194.3*	± 85.1	126.2	± 94.3	160.3	± 92.6	269.3	± 81.9	192.6*	± 94.1	230.95*	± 91.02
a	5.10	± 14.38	-3.7	± 13.6	0.7	± 14.8	-1.9	± 9.9	-5.8	± 14.2	-3.9	± 13.6	-7.0	± 12.4	-2.2	± 14.8	-4.58	± 13.86
d	14.92	± 245.01	121.3	± 245.4	68.1	± 251.1	-22.7	± 219.0	145.5	± 219.8	61.4	± 224.3	-225.3	± 208.5	-18.4	± 238.7	-121.85	± 229.31
aa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

The scaling tests (A, B and C), M = Mean, [a] = Additive effects, [d] = Dominance effects, [aa] = Additive X additive effects, [ad] = Additive X dominance effects, [dd] = Dominance X dominance effects *, **: Significant at 5% and 1% level of probability, respectively.

Table 6. The scaling test and estimates of the genetic components: additive, dominance and interaction parameters as well as standard errors of three canola crosses in two locations and their combined data for yield traits.

Traits	Number of pod/ branches (NP/b)																										
Crosses	DH4xDH5					DH4xSerw5					DH5xSerw5																
Scaling test and parameters	Mans.			Asu.		Comb.		Mans.			Asu.		Comb.		Mans.			Asu.		Comb.							
A	53.4	±	79.6	2.9	±	43.5	28.2	±	113.2	47.4	±	99.0	7.1	±	29.8	27.3	±	121.1	40.6	±	87.3	-25.4	±	39.8	7.6	±	110.0
B	40.3	±	99.2	11.4	±	35.2	25.9	±	106.5	89.1	±	100.2	28.6	±	39.0	58.8	±	118.6	36.5	±	98.6	-7.7	±	39.4	14.4	±	101.4
C	-34.7	±	172.4	-40.5	±	62.5	-37.6	±	184.4	2.5	±	147.3	-6.5	±	70.8	-2.0	±	183.8	46.1	±	151.3	2.3	±	74.3	24.2	±	169.4
m	1.2	±	183.0	16.5	±	71.2	8.9	±	209.7	-11.4	±	149.1	28.6	±	72.4	8.6	±	207.4	84.5	±	159.0	104.9	±	82.4	94.7	±	196.0
a	7.0	±	29.7	1.3	±	9.1	4.2	±	30.1	14.1	±	29.6	1.9	±	11.1	8.0	±	29.2	7.1	±	33.2	0.6	±	11.5	3.8	±	29.6
d	342.8	±	438.5	122.7	±	180.6	232.8	±	520.8	414.8	±	394.1	117.2	±	170.8	266.0	±	531.7	143.2	±	400.6	-94.7	±	198.6	24.2	±	492.6
aa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Traits	Weight of 100 seeds (W100s gm)																										
Crosses	DH4xDH5					DH4xSerw5					DH5xSerw5																
Scaling test and parameters	Mans.			Asu.		Comb.		Mans.			Asu.		Comb.		Mans.			Asu.		Comb.							
A	0.02	±	0.13	0.05	±	0.22	0.03	±	0.21	0.02	±	0.17	-0.01	±	0.23	0.01	±	0.24	0.012	±	0.15	0.11	±	0.22	0.06	±	0.25
B	0.01	±	0.14	0.04	±	0.23	0.03	±	0.23	0.02	±	0.12	0.06	±	0.18	0.04	±	0.20	0.013	±	0.13	0.16	±	0.18	0.09	±	0.21
C	0.07	±	0.24	0.14	±	0.41	0.10	±	0.40	-0.01	±	0.26	0.11	±	0.45	0.05	±	0.42	0.017	±	0.30	0.36	±	0.41	0.19	±	0.44
m	0.44	±	0.25	0.34	±	0.44	0.39	±	0.42	0.35	±	0.30	0.35	±	0.47	0.35	±	0.45	0.406	±	0.32	0.37	±	0.42	0.39	±	0.42
a	-0.02	±	0.04	0.02	±	0.08	0.00	±	0.07	-0.01	±	0.04	0.01	±	0.07	0.00	±	0.07	0.001	±	0.03	0.01	±	0.07	0.00	±	0.07
d	-0.06	±	0.61	-0.02	±	1.07	-0.04	±	1.02	0.12	±	0.74	-0.08	±	1.10	0.02	±	1.07	0.034	±	0.74	0.03	±	1.00	0.03	±	1.02
aa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Traits	Seed yield per plant in grams (S.Y/P)																										
Crosses	DH4xDH5					DH4xSerw5					DH5xSerw5																
Scaling test and parameters	Mans.			Asu.		Comb.		Mans.			Asu.		Comb.		Mans.			Asu.		Comb.							
A	-25.6	±	164.9	48.1	±	118.7	11.2	±	163.3	-13.3	±	209.0	13.3	±	81.7	-0.0	±	188.7	-56.5	±	191.2	20.7	±	78.3	-17.9	±	168.6
B	1.5	±	190.2	46.4	±	89.2	24.0	±	161.0	42.2	±	215.6	42.8	±	97.7	42.5	±	182.4	-50.9	±	213.6	50.7	±	108.9	-0.1	±	180.4
C	-184.0	±	252.2	43.0	±	164.7	-70.5	±	230.2	-188.3	±	287.0	18.6	±	146.5	-84.9	±	247.5	-162.7	±	310.1	28.3	±	139.3	-67.2	±	273.6
m	5.0	±	278.2	-3.8	±	200.1	0.6	±	252.4	-60.6	±	303.8	13.2	±	157.9	-23.7	±	266.9	85.3	±	310.6	7.9	±	176.8	46.6	±	272.9
a	16.0	±	74.2	-0.4	±	15.2	7.8	±	67.7	24.3	±	80.9	-3.4	±	19.8	10.4	±	70.0	8.3	±	82.8	-3.1	±	21.4	2.6	±	67.7
d	207.1	±	726.2	203.1	±	505.6	205.1	±	659.0	422.4	±	818.7	151.1	±	399.8	286.8	±	720.3	-2.0	±	801.9	156.0	±	451.3	77.0	±	700.0
aa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

The scaling tests (A, B and C), M = Mean, [a] = Additive effects, [d] = Dominance effects, [aa] = Additive X additive effects, [ad] = Additive X dominance effects, [dd] = Dominance X dominance effects *, **: Significant at 5% and 1% level of probability, respectively.

This fact may explain the presence of heterobilitosis in these crosses and reduction of F₂ generations than their F₁ hybrids mean in these crosses with respect to these traits. These results are agreed with Marjanovic-Jeromela *et al* (2014) for plant height in rapeseed (*Brassica napus* L.); Singh *et al.* (2014) for seed yield per plant in *Brassica juncea* L.; Cheema and Sadaqat (2004) for number of siliquae/plant which showed very high value of dominance compared to additive effects. Also, Ali *et al.* (2015) reported that plant height was controlled both by additive and non-additive gene actions; however, dominance was predominant due to greater SCA value.

The results of scaling tests (A, B and C) for Oil present in each location in addition to their combined data are shown in Tables 7. The values of scaling test were significantly in all crosses from the combined data. Also, the results showed that the estimates of mean effects parameter

(m), which reflects the contribution due to the overall mean (additive) plus the locus effects (dominance) found to be highly significant for all crosses. Dominance component was much higher than additive component. Additive x additive interaction term had negative sign in 1st cross (DH4xDH5) for two locations and in 2^{sd} cross (DH4xSerw5) in location one, while, it had positive sign in 3rd cross. On the other hand, Additive x dominance had positive sign in 1st cross (DH4xDH5) for two locations and in 2^{sd} cross (DH4xSerw5) in location one. Dominance x dominance interaction was positive in 2^{sd} cross (DH4xSerw5) in location one. These results are in agreement with Cheema and Sadaqat (2004) reported that additive and non-additive type of gene action controlling its expression for oil content. Also, Kant and Gulati (2001) reported different parameters across different crosses and environments.

Table 7. The scaling test and estimates of the genetic components: additive, dominance and interaction parameters as well as standard errors of three canola crosses in two locations and their combined data for Oil % trait.

Traits	Oil percentage (Oil %)								
	DH4xDH5			DH4xSerw5			DH5xSerw5		
	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.	Mans.	Asu.	Comb.
A	6.50** ± 1.61	7.33** ± 1.21	6.92 ± 6.15	1.17 ± 1.78	5.33 ± 4.94	3.25 ± 7.43	4.67** ± 1.11	4.50** ± 2.00	4.58 ± 10.24
B	0.83 ± 1.28	5.00* ± 2.20	2.92 ± 5.04	-0.17 ± 5.65	9.50** ± 3.82	4.67 ± 6.02	10.00** ± 1.47	9.33** ± 1.35	9.67 ± 6.17
C	10.67* ± 1.91	14.28* ± 4.66	12.47 ± 10.28	7.44** ± 2.11	12.39* ± 5.84	9.92 ± 12.51	0.78 ± 4.89	11.06** ± 5.27	5.92 ± 11.64
m	41.00* ± 0.43	37.28* ± 1.12	37.51* ± 10.36	40.28* ± 0.44	35.89* ± 1.43	35.96* ± 12.47	37.94** ± 1.21	34.56** ± 1.29	26.54* ± 13.16
a	1.00 ± 0.97	-0.75 ± 1.14	-1.88 ± 2.70	0.33 ± 2.93	-3.67 ± 3.09	-0.96 ± 2.29	-1.17 ± 0.88	-4.00** ± 1.12	-0.04 ± 3.18
d	-3.33 ± 2.63	2.64 ± 5.07	6.85 ± 24.92	-3.28 ± 6.14	5.86 ± 8.44	7.21 ± 30.29	12.06* ± 5.16	4.19 ± 5.64	30.71 ± 34.70
aa	-3.33 ± 2.59	-1.94 ± 5.03	- -	-6.44 ± 6.11	2.44 ± 8.42	- -	13.89* ± 5.15	2.78 ± 5.61	- -
ad	2.83 ± 1.01	1.17 ± 1.21	- -	0.67 ± 2.94	-2.08 ± 3.10	- -	-2.67 ± 0.90	-2.42* ± 1.15	- -
dd	-4.00 ± 4.31	-10.39 ± 6.53	- -	5.44 ± 11.90	-17.28 ± 13.66	- -	-28.56** ± 6.02	16.61* ± 6.91	- -

The scaling tests (A, B and C), M = Mean, [a] = Additive effects, [d] = Dominance effects, [aa] = Additive X additive effects, [ad] = Additive X dominance effects, [dd] = Dominance X dominance effects *, **: Significant at 5% and 1% level of probability, respectively.

Conclusion

According to the present study, it is concluded that environment-gene effects have dramatic changes for different traits contributing to yield or yield itself. So, for different environments one has to suggest different selection criteria for the improvement in the yield. For those traits that are controlled by additive gene action, simple selection in early segregated generations is suggested, whereas for those traits controlled by non-additive gene action selection in later generations would be more effective.

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تقييم الفعل الجيني لعدد من الصفات الهامة فى بعض هجن الكانولا بإستخدام تحليل متوسط الجيل
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الملخص

تمت دراسة طبيعة الفعل الجيني لبعض الصفات الخضرية و محصول البذرة ونسبة الزيت فى الكانولا من خلال تقييم ستة عشائر (ثلاثة من الهجن بالإضافة إلى الجيل الثانى والجيلين الرجعيين لكل هجين) تحت موقعين مختلفين (المنصورة وأسيوط) وهذه الهجن هى: (DH4xDH5) و (DH4xSerw5) و (DH5xSerw5). وقد أشارت النتائج إلى وجود اختلافات عالية المعنوية بين الهجن المدروسة وكذلك العشائر داخل الهجن فى كل الصفات المدروسة. علاوة على ذلك فإن تداخل كل من الهجن والعشائر داخل الهجن مع الموقعين كان عالى المعنوية فى كل صفات النبات مما يدل على أن الهجن والعشائر تختلف فيه طبيعة الفعل الجيني باختلاف الظروف البيئية. إضافة إلى ذلك أوضحت النتائج أن الفعل الجيني غير التجميى يلعب الدور الرئيسى لمعظم الصفات المدروسة، وأيضاً تأثرت صفة نسبة الزيت بطراز الفعل الجيني التفوقى والذى يشمل (تجميى X سيادى و سيادى X سيادى) مما يشير إلى دور التداخل بين العوامل غير الأليلية فى توريث هذه الصفة. ومن هذه النتائج يمكن أن نستنتج أن إنتاج الهجن هو الطريقة المثلى لتحسين هذه الصفات.