

Generation means analysis of seed yield and its components in canola

Mohamed Ali Abdelsatar*^{ORCID} Tamer Hassan Ali Hassan, Asmaa Abd-EL-Halime Ahmed and Khaled M. Aboelkassem

Address:

Oil Crops Research Department, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt

*Corresponding author: **Mohamed Ali Abdelsatar**, mohamedtemraz1@yahoo.com

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ABSTRACT

To detect types of gene action especially epistasis for studied traits, six populations; P₁, P₂, F₁, F₂, BC₁ and BC₂ in two intra-specific crosses of canola (N.A.37 × Serw 4 and N.A.14 × Serw 6) were evaluated in a field trial during 2019/2020 season at Kafr-El-Hamam/Sharkia and Al-Arish/North Sinai Agricultural Research Stations, Agricultural Research Center, Egypt. Scaling and joint scaling tests revealed inadequacy of simple additive-dominance model in the inheritance of all studied traits in corresponding crosses at both locations. Significant negative heterosis and heterobeltiosis were found for days to first flower, plant height and first siliqua height, whereas significant positive were found for seed weight per plant and its components in the corresponding crosses at both locations. High to moderate values of narrow sense-heritability coupled with high (more than (20%) values of expected response from selection (as % of mean) were detected for days to the first flower in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, first siliqua height in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish and seeds weight per plant in the 1st cross at both locations. The major role of dominance gene effects as the ratio ((H/D)^{0.5}>1) along with the duplicate epistasis was detected in the inheritance of most studied traits in the corresponding crosses at both locations. Therefore, it is advisable to delay selection to advanced generation for improving most studied traits in most cases.

Keywords: *Brassica napus* L., Degree of dominance, Epistasis, Expected response from selection, Six populations

INTRODUCTION

Canola genotypes are characterized by having low erucic acid in oil and glucosinolate in meal is of great interest to the plant breeder in Egypt. Moreover, it has comparative advantages over the other oilseed crops such as its tolerance to a wide range of edaphic and climatic conditions in Egypt, hence it is an economically important oil crop for narrowing the gap between oil production and consumption requirements. Consequently, canola breeders should be focused on estimating the genetic architecture of additive, dominance and epistasis gene action involved in the expression of *quantitative* traits to develop high-yielding genotypes better than existing ones through generation mean analysis. Therefore, generation means analysis has been considered a powerful tool to reveal precise information on the relative magnitude of main effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genetic interactions controlling seed yield and its related traits compared with those based on one generation for the employed genotypes (Mather and Jinks, 1982).

In this respect, Marjanovic-Jeromela *et al.* (2014) found that the additive-dominant model was inappropriate for plant height in all crosses of rapeseed. Whereas, Singh *et al.* (2014) found that additive genetic variance formed the major part of genetic variance for the important yield component *i.e.* dry matter per plant. Habiba *et al.* (2016) indicated that non-additive gene action involved in most of the traits for different crosses under the two locations. Where, non-allelic interactions of additive × dominance and dominance × dominance governed in the inheritance of seeds oil content. In the study of Elnenny and Shafei Wafaa (2017), the inheritance of all studied traits was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Through generation mean analysis, Manjunath *et al.* (2017) revealed that model of additive gene effects was significant for days to maturity, number of primary and secondary racemes per plant, number of seeds per siliqua and oil content, whereas both additive and non-additive gene effects were found to be significant for main raceme length, number of siliquae on main raceme, seeds weight per plant and 1000-seed weight. Non-significant variation due to additive × additive type of epistasis for siliqua per main raceme, primary racemes, plant height, seeds per siliqua, 1000-seed weight and seeds yield per plant were found in Indian mustard by Devi *et al.* (2018), whereas additive and dominance genetic components were predominant in controlling these traits. Results of Bocianowski *et al.* (2019) indicated the importance of additive and epistatic effects for a number of racemes per plant and number of siliquae per plant, whereas 1000-seed weight was mainly controlled by epistatic effects. Additionally, Philanim *et al.* (2019) showed the predominance of both additive, dominance and their interaction effect for most of yield and its component traits, except for number of primary racemes per plant and number of secondary racemes per plant where the role of main gene effect (additive and dominance) was distinct. Precise information on inheritance of yield and yield-related traits is required for effective breeding and/or selection strategies to improve these traits in canola.

Therefore, the present work was carried out to obtain precise information on nature of gene action such as additive and dominant gene effects, non-allelic gene interaction (epistasis) controlling the studied traits, to determine heterosis and inbreeding depression and genetic parameters through generation mean analysis for all studied traits at contrasting locations.

MATERIALS AND METHODS

Plant material:

Four diverse canola (*Brassica napus* L.) genotypes were chosen to create two crosses, viz., N.A.37 × Serw 4 (Cross I) and N.A.14 × Serw 6 (Cross II). Names, pedigree and origin of the parental canola genotypes and their contents of erucic acid and glucosinolate were presented in [Table 1](#). Seeds of F₁ and their respective segregating generations i.e. F₂, BC₁ and BC₂ were created in the 2017/2018 and 2018/2019 winter seasons at Kafr-El-Hamam/Sharkia Agricultural Research Stations, ARC, Egypt as follow:

In the first season of 2017/2018, the four parental canola genotypes were sown and pair crosses were performed to obtain F₁ cross seeds. In the subsequent season of 2018/2019, two F₁ cross seeds were sown to produce F₁ plants. Each of the F₁ plants were crossed back to their respective parent to obtain first (F₁ × P₁) and second (F₁ × P₂) backcrosses. In the meantime, pair crosses were made to produce more F₁ seeds, also the F₁ plants were selfed to produce F₂ seeds.

Table 1. Names, pedigree and origin of parental genotypes and their contents of erucic acid and glucosinolate

Cross	Item	Parent	Pedigree	Origin	Erucic acid content	Glucosinolate content
I	P ₁	N.A.37	Import from U.S.A.	FAO U.S.A.	Low<2%	Low < 30 µmol/g
	P ₂	Serw 4	Anther culture	Egypt	Low<2%	Low < 30 µmol/g
II	P ₁	N.A.14	Import from U.S.A.	FAO U.S.A.	Low<2%	Low < 30 µmol/g
	P ₂	Serw 6	Anther culture	Egypt	Low<2%	Low < 30 µmol/g

Field evaluation trials:

In the third season of 2019/2020, the obtained seeds of six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) for each of the two crosses were evaluated in a field trial using a randomized complete block design with three replications at Kafr-El-Hamam/Sharkia and Al-Arish/North Sinai Agricultural Research Stations, ARC, Egypt. The soil texture of the experimental site at Kafr-El-Hamam is clay, including 8.72% sand, 35.46% silt and 55.82% clay, with pH of 7.6 and EC of 0.57 mmh/cm. However, the soil texture at Al-Arish is also clay, including 7.49% sand, 39.46% silt and 53.05% clay, with pH of 7.3 and EC of 6.49 mmh/cm. Each replicate for each the two crosses consisted of 160 plants in two ridges for each of non-segregating generations (the parents and F₁ population); 320 plants in four ridges for each of segregating generations (backcrosses and F₂ populations). Ridge length was 4 m, ridge to ridge and plant to plant spaces were 60 and 10 cm, respectively. For each cross combination, seeds of P₁, P₂, F₁, F₂, BC₁ and BC₂ were hand-planted on adjacent plots. The seedlings were thinned to two plants per hill on one side of the ridge. The other cultural practices were followed as recommended by the Oil Crops Research Department, Field Crops Research Institute, ARC, Egypt.

Evaluated traits:

Data were recorded on 30 individual plants for non-segregated populations (P₁, P₂ and F₁) and 100 plants for segregating populations i.e. BC₁, BC₂ and F₂ populations, which were randomly chosen for each replicate. The studied traits were days to first flower (day), plant height (cm), first silique height (cm), number of racemes per plant, 1000-seed weight (g), seeds weight per plant (g) and seeds oil content (%). Seeds oil content was determined, after drying seed at 70°C for 48 h, by the Soxhlet extraction technique, using diethyl ether (AOAC, 1990).

Statistical and biometrical analyses:

Regular analysis of variance was firstly performed for testing the significance of six populations within each cross for all the studied traits (Gomez and Gomez, 1984).

Mode of gene action:

The A, B, C and D scaling tests as outlined by Mather (1949) and Hayman and Mather (1955) were applied to test the presence of non-allelic interactions. Joint scaling test proposed by Cavalli (1952) as indicated by "χ²" was applied for testing the goodness of fit of the adequate genetic model controlling the studied traits. Due to unknown biased effect of non-allelic interaction, the simple genetic model {m, d and h} was applied when epistasis was absent. Whereas, in the presence of non-allelic interaction, the analysis was proceeded to compute the interaction types involved using the six parameters genetic model according to Jinks and Jones (1958).

Heterosis and its related parameters:

The amount of heterosis was expressed as the percentage increase of F₁ above mid-parents and better parents. Inbreeding depression was calculated as the difference between the F₁ and F₂ means expressed as a percentage of the F₁ mean. The T-test was used to determine the significance of these deviations, where the standard error (S.E.) was calculated as follows: S. E. for mid-parent heterosis = $(VP_1 + VP_2 + VF_1)^{0.5}$, S. E. for better parent heterosis = $(VF_1 + VBP)^{0.5}$ and S. E. for inbreeding depression = $(VF_1 + VF_2)^{0.5}$. The Potency Ratio (PR) was computed from generation means as per Peter and Frey (1966) to determine the degree of dominance as follows: In F₁ generation, $\hat{h}_1 = PR_1 = (\bar{F}_1 - \bar{P}) / (\bar{P}_1 - \bar{P})$ and In F₂ generation, $\hat{h}_2 = PR_2 = 2(\bar{F}_2 - \bar{P}) / (\bar{P}_1 - \bar{P})$. Where, PR = relative potency of the gene set, F₁ = first-generation mean, P₁ = the mean of an inferior parent, P₂ = the mean of a superior parent, \bar{P} = mid-parents value $(P_1 + P_2) / 2$. Complete dominance was indicated when Potence ratio = +1, Partial dominance is indicated when Potence ratio is between -1 and +1, Over-dominances indicated when potency ratio exceeds ±1. Absence of dominance is indicated when Potence ratio = 0. The positive and negative signs indicate the direction of dominance of either parent. Based on the potency ratio, the degree of dominance in respect of different traits

were classified as follows, Complete dominance was indicated when Potence ratio = +1, Partial dominance is indicated when Potence ratio is between -1 and +1, Over-dominances indicated when potency ratio exceeds ± 1 . Absence of dominance is indicated when Potence ratio = 0. The positive and negative signs indicate the direction of dominance of either parent. Also, two types of epistasis *i.e.* F_2 deviation (E_1) and back-crosses deviation (E_2) were measured as suggested by Mather and Jinks (1982). Potence ratio (P) was also calculated according to Peter and Frey (1966).

Variance components and their related parameters

Variance components such as additive, dominance and environment were estimated as described by Mather and Jinks (1982). Broad and narrow-sense heritability were estimated using a method proposed by Warner (1952). The degree of dominance ratio was measured using $[H/D]^{0.5}$, where H is the dominance variance and D is additive variance. The expected response from selection (R) was also estimated using Falconer (1989) formula as follows: $(R) = I.hns.\sigma A$. Where: I: The selection differential at 5% selection intensity, h^2ns : Square root of narrow-sense heritability and σA : Square root of additive genetic variance.

RESULTS

Mean performance:

Mean performance of six populations *i.e.* P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 for all studied traits are presented in Table (2). There are highly significant differences between parental canola in the two crosses for all studied traits at both locations. The shortest time to first flower, the short-statured plants and first siliqua height were desirable to avoid pathological injury and sowing more than one crop per year and for helping in mechanical harvesting and developing lodging resistance. In general, F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were earlier in flowering by (12.94 % and 29.08 %), (16.33 % and 20.41 %), (15.09 % and 8.28 %) and (19.41% and 18.70 %) in the 1st cross and (12.62 % and 20.58 %), (3.05 % and 10.18 %), (7.26 % and 5.02 %) and (1.38 % and 10.76 %) in the 2nd cross than their respective inferior parent at Kafr-El-Hamam and Al-Arish, respectively. The same direction, moreover, was detected in plant height and first siliqua height which can be showed through F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were shorter statured plants by (6.64 % and 8.80 %), (5.41 % and 7.90 %), (5.04 % and 10.45%) and (3.17 % and 13.38 %) in the 1st cross and (11.55 % and 6.90 %), (8.19 % and 6.69 %), (7.77 % and 3.93%) and (6.14 % and 6.52 %) in the 2nd cross than their respective inferior parent at Kafr-El-Hamam and Al-Arish, respectively. In case of first siliqua height, similarly, F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were shorter by (21.28 % and 8.03 %), (13.36 % and 11.60 %), (8.28 % and 5.19 %) and (18.13 % and 17.05 %) in the 1st cross and (19.26 % and 11.19 %), (12.38 % and 8.40 %), (5.24 % and 1.68%) and (11.05 % and 10.76 %) in the 2nd cross than their respective inferior parent at Kafr-El-Hamam and Al-Arish, respectively.

However, in contrast to earliness in flowering and short-statured plants and first siliqua height, the increase in seeds weight per plant and its attributing traits are preferred. A progressive increase was observed in F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 for number of racemes per plant by (43.15 % and 35.70 %), (32.80 % and 30.20 %), (37.46 % and 34.66%) and (39.95 % and 35.71 %) in the 1st cross and (42.23 % and 54.00 %), (31.85 % and 43.64 %), (36.27 % and 47.64 %) and (38.56 % and 47.53 %) in the 2nd cross than their respective superior parent at Kafr-El-Hamam and Al-Arish, respectively. In case of 1000-seed weight (g), F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were the heavier weight of 1000-seed by (14.01 % and 2.26 %), (7.48 % and 10.87 %), (7.01 % and 6.91%) and (4.43 % and 7.33 %) in the 1st cross and (16.62 % and 15.75 %), (8.43 % and 8.87 %), (9.14 % and 6.65 %) and (6.39 % and 2.88 %) in the 2nd cross than their respective superior parent at Kafr-El-Hamam and Al-Arish, respectively. Consequently, seeds weight per plant of F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were heavier by (17.98 % and 28.15 %), (17.36 % and 25.72 %), (14.47 % and 23.83 %) and (19.46 % and 27.36 %) in the 1st cross and (24.22 % and 33.81 %), (21.02 % and 29.59 %), (20.68 % and 29.38 %) and (24.43 % and 31.70 %) in the 2nd cross than their respective superior parent at Kafr-El-Hamam and Al-Arish, respectively.

Concerning seeds oil content, F_1 and their respective segregating generations *i.e.* F_2 , BC_1 and BC_2 were a higher proportion of seeds oil by (7.48 % and 8.16 %), (3.74 % and 3.72 %), (1.99 % and 4.05 %) and (4.06 % and 4.87 %) in the 1st cross and (5.19 % and 10.50 %), (1.18 % and 5.42 %), (7.58 % and 2.75 %) and (5.13 % and 8.93 %) in the 2nd cross than their respective superior parent at Kafr-El-Hamam and Al-Arish, respectively.

Scaling test:

To determine gene action controlling inheritance of all studied traits in the corresponding crosses at each location, the scaling test (A, B, C and D) and joint scaling test (χ^2) was used as shown in Table (3). The results of scaling test showed that one or more of the four scales were significant or highly significant for all study traits, which was also confirmed by highly significant joint scaling test (χ^2). As a result, the adequacy of the six parameters model to explain the type of gene action controlling the traits in the two crosses at both locations. In this connection, the complex genetic model was found to be controlling the inheritance of these traits (Table 3).

Mode of gene action:

Mean effects of a parameter (m) that reflects the contribution due to the overall mean (additive) plus the locus effects and interaction of the fixed loci (dominance) found to be highly significant for all studied traits in the corresponding crosses at both locations. Negative (desirable) and significant direction of the additive gene action (a) was detected for days to first flower in the 2nd cross at Kafr-El-Hamem, plant height in the corresponding crosses at Kafr-El-Hamam, while positive

(desirable) and significant for a number of racemes per plant in the 2nd cross at Al-Arish, 1000-seed weight in the 1st cross at Kafr El-Hamam and in the 2nd cross at both locations and seeds oil content in the 2nd cross at Kafr-El-Hamam.

Table 2. Mean performance of six populations in the two canola crosses for all studied traits at Kafr-El-Hamam (K) and Al-Arish (A) during 2019/2020 season

Cross	†L	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	LSD 5%	LSD 1%
Days to first flower (day)									
CI	K	94.58 ± 0.09	96.98 ± 0.09	83.74 ± 0.08	81.30 ± 0.66	82.18 ± 0.47	79.20 ± 0.64	7.34	10.43
	A	88.61 ± 0.19	89.52 ± 0.34	68.64 ± 0.33	73.59 ± 0.55	81.83 ± 0.39	74.65 ± 0.55	7.45	10.59
CII	K	89.19 ± 0.25	92.09 ± 0.17	79.20 ± 0.27	86.55 ± 0.55	83.16 ± 0.43	87.98 ± 0.41	5.80	8.26
	A	83.91 ± 0.25	86.18 ± 0.14	69.59 ± 0.21	76.16 ± 0.51	79.90 ± 0.40	75.76 ± 0.45	6.32	8.99
Plant height (cm)									
CI	K	176.59 ± 0.32	182.69 ± 0.37	165.60 ± 0.35	167.52 ± 0.86	168.11 ± 0.80	171.17 ± 0.61	5.31	7.55
	A	146.74 ± 0.27	156.04 ± 0.34	134.88 ± 0.31	136.00 ± 0.55	132.86 ± 0.52	129.42 ± 0.49	3.05	4.34
CII	K	167.93 ± 0.29	176.05 ± 0.28	150.54 ± 0.34	155.21 ± 0.69	155.82 ± 0.60	158.21 ± 0.44	3.64	5.17
	A	148.81 ± 0.28	158.21 ± 0.26	139.20 ± 0.31	139.48 ± 0.48	143.19 ± 0.47	139.70 ± 0.37	5.58	7.94
First siliqua height (cm)									
CI	K	49.80 ± 0.23	51.61 ± 0.25	41.06 ± 0.19	43.93 ± 0.38	45.99 ± 0.34	42.16 ± 0.29	3.32	4.72
	A	40.50 ± 0.19	42.26 ± 0.22	37.49 ± 0.15	36.29 ± 0.31	38.50 ± 0.28	34.60 ± 0.24	2.93	4.16
CII	K	45.47 ± 0.18	47.14 ± 0.19	38.13 ± 0.15	40.46 ± 0.33	43.21 ± 0.30	40.95 ± 0.23	2.66	3.79
	A	37.27 ± 0.15	39.28 ± 0.19	33.52 ± 0.15	34.38 ± 0.27	36.66 ± 0.27	33.65 ± 0.21	2.53	3.60
Number of racemes per plant									
CI	K	5.57 ± 0.10	6.13 ± 0.14	10.79 ± 0.24	9.13 ± 0.17	9.81 ± 0.15	10.21 ± 0.17	1.83	2.60
	A	4.38 ± 0.12	5.34 ± 0.09	8.31 ± 0.19	7.66 ± 0.14	8.18 ± 0.13	8.31 ± 0.15	1.29	1.83
CII	K	5.40 ± 0.11	6.03 ± 0.07	10.44 ± 0.20	8.85 ± 0.14	9.47 ± 0.13	9.82 ± 0.14	1.41	2.01
	A	3.80 ± 0.10	4.16 ± 0.05	9.03 ± 0.21	7.37 ± 0.12	7.94 ± 0.12	7.92 ± 0.12	1.54	2.19
1000-seed weight (g)									
CI	K	3.81 ± 0.06	4.14 ± 0.04	4.81 ± 0.04	4.47 ± 0.04	4.45 ± 0.04	4.33 ± 0.03	0.42	0.60
	A	3.39 ± 0.02	3.05 ± 0.02	3.47 ± 0.03	3.81 ± 0.03	3.64 ± 0.03	3.66 ± 0.02	0.28	0.40
CII	K	3.78 ± 0.04	3.94 ± 0.03	4.73 ± 0.03	4.31 ± 0.03	4.34 ± 0.03	4.21 ± 0.02	0.27	0.39
	A	3.40 ± 0.03	2.94 ± 0.02	4.03 ± 0.02	3.73 ± 0.03	3.64 ± 0.03	3.50 ± 0.02	0.26	0.36
Seed weights per plant (g)									
CI	K	31.56 ± 0.30	36.49 ± 0.38	44.49 ± 0.31	44.16 ± 0.38	42.67 ± 0.31	45.31 ± 0.33	4.01	5.70
	A	23.75 ± 0.16	27.23 ± 0.18	37.90 ± 0.27	36.66 ± 0.32	35.75 ± 0.27	37.49 ± 0.27	2.84	4.05
CII	K	31.17 ± 0.25	33.97 ± 0.24	44.83 ± 0.30	43.01 ± 0.34	42.83 ± 0.30	44.95 ± 0.30	2.85	4.05
	A	23.80 ± 0.14	25.38 ± 0.12	38.35 ± 0.19	36.05 ± 0.28	35.94 ± 0.26	37.16 ± 0.24	2.55	3.62
Seeds oil content (%)									
CI	K	42.76 ± 0.07	42.45 ± 0.14	46.22 ± 0.14	44.42 ± 0.15	43.63 ± 0.13	44.57 ± 0.14	1.47	2.09
	A	43.61 ± 0.14	42.58 ± 0.16	47.48 ± 0.14	45.29 ± 0.18	45.45 ± 0.15	45.84 ± 0.16	1.89	2.69
CII	K	42.55 ± 0.14	41.17 ± 0.10	44.88 ± 0.11	43.06 ± 0.11	46.04 ± 0.10	44.85 ± 0.09	0.91	1.30
	A	42.13 ± 0.11	41.98 ± 0.05	47.07 ± 0.07	44.54 ± 0.12	43.32 ± 0.10	46.26 ± 0.09	0.82	1.17

†L = Location.

The dominance gene effects found to be negative (desirable) and highly significant for days to first flower, plant height and first siliqua height in the corresponding cross at both locations, while positive (desirable) and highly significant for a number of racemes per plant, seeds weight per plant and seeds oil content in the corresponding crosses at both locations and 1000-seed weight in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations. The magnitude of dominance gene effects (d) was larger than the corresponding values of additive effects (a) in the two crosses at both locations for most studied traits. The digenic type of additive gene action (additive × additive) was negative (desirable) and significant for days to first flower in the corresponding crosses at Kafr-El-Hamam, plant height in the 1st cross at Al-Arish, while positive (desirable) and significant for number of racemes per plant in corresponding crosses at both locations, seeds weight/plant in the 2nd cross at both locations and seeds oil content in the 1st cross at Al-Arish and in 2nd the cross at both locations. The digenic type of dominance gene action (dominance × dominance) was negative (desirable) and significant for days to first flower in the 2nd cross at Kafr-El-Hamam and plant height in the 1st cross at Kafr-El-Hamam, while positive (desirable) and significant for a number of racemes per plant in the two crosses at Al-Arish, 1000-seed weight in the two crosses at Kafr-El-Hamam, seeds weight per plant in the 1st cross at Al-Arish and seeds oil content in the 2nd cross at Kafr-El-Hamam. The epistasis type of additive × dominance was negative (desirable) and significant for days to first flower in the corresponding crosses at Al-Arish, first siliqua height in the 2nd cross at both locations, while positive (desirable) and significant for 1000-seed weight in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations and seeds oil content in the 1st cross at Kafr-El-Hamam.

Duplicate [(Additive × Dominance) and (Dominance × Dominance)] epistasis of non-allelic gene interaction as revealed by different signs of (d) and (dd) in canola crosses (Table 4) was observed for days to first flower in the 1st cross at both locations and in the 2nd cross at Al-Arish, plant height in the 1st cross at Al-Arish and in the 2nd cross at both locations, first siliqua height in the corresponding crosses at both locations, number of racemes per plant in the corresponding crosses at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish, seeds weight per plant in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, and seeds oil content in the 1st cross at both locations and in the 2nd cross at Al-Arish.

Complimentary (additive × additive) epistasis of non-allelic gene interaction as revealed by same signs of (d) and (dd) in canola crosses was showed for days to first flower in the 2nd cross at Kafr-El-Hamam, plant height in the 1st cross at Kafr-El-Hamam, number of racemes per plant in the corresponding crosses at Al-Arish, 1000-seed weight in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, seeds weight per plant in the 1st cross at Al-Arish, and seeds oil content in the 2nd cross at Kafr-El-Hamam.

Table 3. Scaling test (A, B, C and D) and joint scaling test (χ^2) in the two canola crosses for all studied traits at Kafr-El-Hamam (K) and Al-Arish (A) during 2019/2020 season

Cross	†L	A	B	C	D	χ^2
Days to first flower						
CI	K	-13.97** ± 0.95	-22.32** ± 1.28	-33.84** ± 2.64	1.22 ± 1.53	682.82**
	A	6.42** ± 0.87	-8.87** ± 1.19	-21.07** ± 2.31	-9.31** ± 1.28	50837.75**
CII	K	-2.08* ± 0.94	4.68** ± 0.87	6.52** ± 2.27	1.96 ± 1.24	13026.27**
	A	6.30** ± 0.86	-4.25** ± 0.93	-4.64* ± 2.09	-3.35** ± 1.18	73114.92**
Plant height						
CI	K	-5.97** ± 1.67	-5.95** ± 1.32	-20.40** ± 3.53	-4.24* ± 1.99	188.34**
	A	-15.90** ± 1.12	-32.07** ± 1.09	-28.54** ± 2.32	9.72** ± 1.31	3989.11**
CII	K	-6.83** ± 1.28	-10.17** ± 0.99	-24.22** ± 2.88	-3.61* ± 1.57	296.42**
	A	-1.64 ± 1.03	-18.01** ± 0.85	-27.52** ± 2.06	-3.93** ± 1.13	851.28**
First siliqua height						
CI	K	1.12 ± 0.74	-8.36** ± 0.65	-7.80** ± 1.59	-0.29 ± 0.88	182.79**
	A	-0.99 ± 0.61	-10.55** ± 0.54	-12.57** ± 1.31	-0.52 ± 0.72	446.96**
CII	K	2.82** ± 0.65	-3.37** ± 0.52	-7.01** ± 1.37	-3.23** ± 0.75	89.10**
	A	2.52** ± 0.58	-5.50** ± 0.48	-6.05** ± 1.16	-1.54* ± 0.65	302.59**
Number of racemes per plant						
CI	K	3.26** ± 0.40	3.50** ± 0.44	3.23** ± 0.84	-1.77** ± 0.40	860.17**
	A	3.67** ± 0.34	2.97** ± 0.36	4.28** ± 0.71	-1.18** ± 0.35	319.46**
CII	K	3.09** ± 0.35	3.16** ± 0.35	3.09** ± 0.71	-1.58** ± 0.34	1384.46**
	A	3.04** ± 0.33	2.65** ± 0.32	3.47** ± 0.66	-1.11** ± 0.30	14307.13**
1000-seed weight						
CI	K	0.28** ± 0.11	-0.29** ± 0.08	0.32 ± 0.18	0.17 ± 0.08	12856.20**
	A	0.42** ± 0.07	0.80** ± 0.06	1.84** ± 0.14	0.31** ± 0.07	299.91**
CII	K	0.17* ± 0.08	-0.25** ± 0.06	0.04 ± 0.14	0.06 ± 0.07	4952.89**
	A	-0.15* ± 0.06	0.02 ± 0.04	0.51** ± 0.12	0.32** ± 0.06	19131.71**
Seeds weight per plant						
CI	K	9.29** ± 0.76	9.64** ± 0.82	19.61** ± 1.71	0.34 ± 0.89	934.71**
	A	9.85** ± 0.63	9.84** ± 0.62	19.87** ± 1.39	0.09 ± 0.74	511.04**
CII	K	9.66** ± 0.71	11.10** ± 0.71	17.24** ± 1.53	-1.76* ± 0.80	398.28**
	A	9.74** ± 0.57	10.59** ± 0.53	18.31** ± 1.20	-1.01 ± 0.66	807.17**
Seeds oil content						
CI	K	-1.72** ± 0.30	0.48 ± 0.34	0.04 ± 0.68	0.64 ± 0.36	353229.29**
	A	-0.20 ± 0.36	1.62** ± 0.37	0.01 ± 0.81	-0.71 ± 0.43	412.97**
CII	K	4.65** ± 0.26	3.65** ± 0.24	-1.25* ± 0.52	-4.77** ± 0.26	16693.98**
	A	-2.56** ± 0.24	3.47** ± 0.21	-0.07 ± 0.52	-0.49 ± 0.28	728078.63**

†L = Location.

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

Heterosis and its related parameters:

To draw the valid conclusion respecting the magnitude of heterosis relative to the mid parents (average heterosis) and better parents (heterobeltiosis), inbreeding depression percentage, potency ratio (\hat{h}_1) for F_1 and (\hat{h}_2) for F_2 , F_2 deviation (E_1) and back-crosses deviation (E_2) for all studied traits in the corresponding cross at both locations were estimated as shown in [Table \(5\)](#).

Significant negative (desirable) heterosis and heterobeltiosis were found for days to first flower to produce a high yield in a short period, especially intensive cropping systems. Similarly, short-statured plants and first siliqua height in the corresponding crosses at both locations ([Table 5](#)) are suitable for mechanical harvesting and lodging resistance.

However, in contrast to earliness in flowering and short-statured plants and first siliqua height, significant positive (desirable) heterosis and heterobeltiosis were found for number of racemes per plant, 1000-seed weight, seeds weight per plant and seeds oil content in the corresponding crosses at both locations.

Significant and negative (desirable) inbreeding depression was found for days to first flower, plant height and first siliqua height in the corresponding crosses at both locations, except for days to first flower in the 1st cross at Kafr-El-Hamam and first siliqua height in the 1st cross at Al-Arish. However, significant positive (desirable) inbreeding depression (inbreeding gain) was detected for number of racemes per plant, 1000-seed weight, seeds weight per plant and seeds oil content in the corresponding crosses at both locations, except for 1000-seed weight in the 1st cross at Al-Arish.

Table 4. Estimation of gene effects of the six-parameter genetic model in the two canola crosses for all studied traits at Kafr-El-Hamam (K) and Al-Arish (A) during 2019/2020 season

Cross	† L	Mean	Additive	Dominance	Additive x Additive	Dominance x Dominance	Additive x Dominance	Types of epistasis
Days to first flower								
CI	K	81.30** ± 0.66	2.97** ± 0.79	-14.47** ± 3.07	-2.44 ± 3.07	4.17 ± 4.12	38.72** ± 0.79	Duplicate
	A	73.59** ± 0.55	7.19** ± 0.67	-1.81 ± 2.59	18.61** ± 2.57	7.65* ± 3.55	-16.16** ± 0.70	Duplicate
CII	K	86.55** ± 0.55	-4.83** ± 0.59	-15.36** ± 2.50	-3.92 ± 2.48	-3.38 ± 3.28	1.32* ± 0.61	Complementary
	A	76.16** ± 0.51	4.14** ± 0.60	-8.76** ± 2.37	6.69** ± 2.35	5.27 ± 3.18	-8.75** ± 0.62	Duplicate
Plant height								
CI	K	167.52** ± 0.86	-3.06** ± 1.01	-5.56 ± 4.00	8.48* ± 3.98	-0.01 ± 5.36	3.44** ± 1.04	Complementary
	A	136.00** ± 0.55	3.44** ± 0.72	-35.95** ± 2.65	-19.43** ± 2.62	8.09* ± 3.69	67.40** ± 0.75	Duplicate
CII	K	155.21** ± 0.69	-2.39** ± 0.74	-14.23** ± 3.17	7.22* ± 3.14	1.67 ± 4.14	9.78** ± 0.77	Duplicate
	A	139.48** ± 0.48	3.49** ± 0.60	-6.44** ± 2.29	7.87** ± 2.26	8.19** ± 3.16	11.78** ± 0.63	Duplicate
First siliqua height								
CI	K	43.93** ± 0.38	3.84** ± 0.44	-9.07** ± 1.77	0.57 ± 1.75	4.74* ± 2.39	6.66** ± 0.48	Duplicate
	A	36.29** ± 0.31	3.90** ± 0.37	-2.85 ± 1.46	1.04 ± 1.45	4.78* ± 1.97	10.49** ± 0.39	Duplicate
CII	K	40.46** ± 0.33	2.26** ± 0.38	-1.72 ± 1.52	6.45** ± 1.51	3.09 ± 2.04	-5.90** ± 0.40	Duplicate
	A	34.38** ± 0.27	3.01** ± 0.34	-1.68 ± 1.30	3.08* ± 1.29	4.01* ± 1.79	-0.11 ± 0.36	Duplicate
Number of racemes per plant								
CI	K	9.13** ± 0.17	-0.41 ± 0.23	8.47** ± 0.84	3.53** ± 0.80	-0.12 ± 1.23	-10.30** ± 0.24	Duplicate
	A	7.66** ± 0.14	-0.13 ± 0.19	5.81** ± 0.73	2.36** ± 0.70	0.35 ± 1.05	-9.00** ± 0.21	Complementary
CII	K	8.85** ± 0.14	-0.35 ± 0.19	7.89** ± 0.72	3.16** ± 0.69	-0.04 ± 1.05	-9.41** ± 0.20	Duplicate
	A	7.37** ± 0.12	0.02 ± 0.16	7.28** ± 0.64	2.22** ± 0.60	0.19 ± 0.93	-7.91** ± 0.17	Complementary
1000-seed weight								
CI	K	4.47** ± 0.04	0.12* ± 0.05	0.51** ± 0.18	-0.33 ± 0.17	0.29 ± 0.26	0.34** ± 0.06	Complementary
	A	3.81** ± 0.03	-0.02 ± 0.04	-0.37* ± 0.15	-0.62** ± 0.15	-0.19 ± 0.21	-0.61** ± 0.04	Complementary
CII	K	4.31** ± 0.03	0.13** ± 0.04	0.75** ± 0.14	-0.12 ± 0.14	0.21 ± 0.20	0.20** ± 0.04	Complementary
	A	3.73** ± 0.03	0.14** ± 0.03	0.23 ± 0.13	-0.64** ± 0.12	-0.09 ± 0.17	0.77** ± 0.04	Duplicate
Seeds weight per plant								
CI	K	44.16** ± 0.38	-2.64** ± 0.45	9.78** ± 1.81	-0.69 ± 1.77	-0.17 ± 2.49	-18.24** ± 0.51	Duplicate
	A	36.66** ± 0.32	-1.74** ± 0.38	12.24** ± 1.50	-0.17 ± 1.48	0.00 ± 2.06	-19.53** ± 0.40	Complementary
CII	K	43.01** ± 0.34	-2.12** ± 0.42	15.78** ± 1.63	3.52* ± 1.60	-0.72 ± 2.27	-24.29** ± 0.45	Duplicate
	A	36.05** ± 0.28	-1.22** ± 0.35	15.78** ± 1.35	2.02 ± 1.33	-0.43 ± 1.85	-22.34** ± 0.36	Duplicate
Seeds oil content								
CI	K	44.42** ± 0.15	-0.94** ± 0.19	2.33** ± 0.73	-1.28 ± 0.71	-1.10 ± 1.02	2.52** ± 0.21	Duplicate
	A	45.29** ± 0.18	-0.40 ± 0.22	5.80** ± 0.87	1.41 ± 0.86	-0.91 ± 1.19	-2.84** ± 0.24	Duplicate
CII	K	43.06** ± 0.11	1.19** ± 0.13	12.57** ± 0.53	9.55** ± 0.51	0.50 ± 0.75	-17.85** ± 0.16	Complementary
	A	44.54** ± 0.12	-2.94** ± 0.14	5.99** ± 0.56	0.98 ± 0.55	-3.01** ± 0.76	-1.89** ± 0.15	Duplicate

†L = Location.

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

Potence ratio:

Potence ratio of the corresponding crosses in the F₁ and F₂ generations at both locations as shown in [Table \(5\)](#), indicated over-dominance towards the better parent for all studied traits. Significant negative (desirable) F₂ deviations (E₁) toward the inferior (better) parent were observed for days to first flower, plant height and first siliqua height in the corresponding crosses at both locations, except for days to first flower in the 2nd cross at Kafr-El-Hamam which was positive, for which positive E₁ toward the superior (undesirable) parent in flowering. On the other hand, significant positive (desirable) F₂ deviations (E₁) toward the superior (better) parent were detected for number of racemes per plant, 1000-seed weight, seeds weight per plant and seeds oil content, except for seeds oil content in the 2nd cross at both negative locations, for which negative E₁ toward the inferior (undesirable) parent. Insignificant F₂ deviations either positive or negative sign were detected for days to first flower in the 2nd cross at Al-Arish, 1000-seed weight in the two crosses at Kafr El-Hamam and seeds oil content in the corresponding crosses at both locations.

Backcross deviation (E₂) was significant negative (desirable) for days to first flower in the 1st cross at both locations, plant height in the corresponding crosses at both locations and first siliqua height in the two crosses at both locations. Conversely, significant positive (desirable) backcross deviations (E₂) was observed for number of racemes per plant in the two crosses at both locations, 1000-seed weight in the 1st cross at both locations, seeds weight per plant in the corresponding crosses at both locations and seeds oil content in the 1st cross at Al-Arish and in the 2nd cross at both locations.

Variance components and their related parameters:

Results given in [Table \(6\)](#) indicate that both additive (D) and dominance (H) genetic variances were significant for days to first flower, plant height, first siliqua height and seeds weight per plant in the corresponding crosses at both locations. Moreover, number of racemes per plant possessed significant dominance gene action in the corresponding crosses at both

locations and seeds oil content had significant additive gene action in the 1st cross at Al-Arish and significant dominance gene action in the 1st cross at Kafr-El-Hamam.

Table 5. Heterosis and its related parameters in the two canola crosses for all studied traits at Kafr-El-Hamam (K) and Al-Arish (A) during 2019/2020 season

Cross	†L	HMP%	HBP%	ID%	h ₁	h ₂	E1	E2
Days to first flower								
CI	K	-12.56**	-11.45**	2.92**	10.03	24.13	-8.46**	-18.14**
	A	-22.93**	-22.53**	-7.20**	44.55	67.54	-5.27**	-1.23
CII	K	-12.62**	-11.20**	-9.28**	7.90	5.65	1.63*	1.30
	A	-18.17**	-17.07**	-9.44**	13.64	15.68	-1.16	1.03
Plant height								
CI	K	-7.82**	-6.22**	-1.16**	4.60	7.95	-5.10**	-5.96**
	A	-10.91**	-8.09**	-0.83	3.55	6.62	-7.13**	-23.98**
CII	K	-12.47**	-10.35**	-3.10**	5.28	8.26	-6.05**	-8.50**
	A	-9.32**	-6.45**	-0.20	3.04	5.97	-6.88**	-9.82**
First siliqua height								
CI	K	-19.02**	-17.55**	-6.99**	10.67	14.98	-1.95**	-3.62**
	A	-9.40**	-7.43**	3.20**	4.43	11.58	-3.14**	-5.77**
CII	K	-17.66**	-16.15**	-6.12**	9.81	14.02	-1.75**	-0.28
	A	-12.43**	-10.07**	-2.58**	4.74	7.75	-1.51**	-1.49**
Number of racemes per plant								
CI	K	84.43**	75.91**	15.41**	17.43	23.13	0.81*	3.38**
	A	70.97**	55.51**	7.87**	7.14	11.57	1.07**	3.32**
CII	K	82.70**	73.11**	15.23**	14.93	19.81	0.77**	3.13**
	A	127.09**	117.38**	18.38**	28.44	38.20	0.87**	2.85**
1000-seed weight								
CI	K	21.16**	16.30**	7.06**	5.06	6.03	0.08	0.00
	A	7.70**	2.31*	-9.67**	1.46	6.88	0.46**	0.61**
CII	K	22.43**	19.93**	8.94**	10.72	10.99	0.01	-0.04
	A	27.19**	18.70**	7.55**	3.80	4.92	0.13**	-0.07
Seeds weight per plant								
CI	K	30.76**	21.92**	0.74	4.24	8.21	4.90**	9.46**
	A	48.68**	39.18**	3.26**	7.13	12.84	4.97**	9.85**
CII	K	37.64**	31.96**	4.06**	8.75	14.90	4.31**	10.38**
	A	55.96**	51.09**	6.00**	17.34	28.88	4.58**	10.16**
Seeds oil content								
CI	K	8.49**	8.08**	3.89**	22.63	22.77	0.01	-0.62*
	A	10.19**	8.89**	4.62**	8.53	8.54	0.00	0.71*
CII	K	7.22**	5.47**	4.06**	4.37	3.47	-0.31	4.15**
	A	11.92**	11.73**	5.36**	70.41	69.90	-0.02	0.45*

Where, †L = Location, HMP%: Heterosis relative to mid-parents and HBP%: Heterosis relative to better parents, ID%: inbreeding depression (\hat{h}_1): potency ratio in F₁ and \hat{h}_2 : potency ratio in F₂, and E₁: epistasis in F₂ deviations and E₂: Backcross deviation
*, ** Significant at 0.05 and 0.01 probability level, respectively

However, the preponderance was in favor of dominance gene action as indicated by (H/D)^{0.5} in the inheritance of days to first flower in the 1st cross at both locations and in the 2nd cross at Al-Arish, plant height in the 1st cross at both locations and in the 2nd cross at Al-Arish, first siliqua height in the 2nd cross at Al-Arish, number of racemes per plant in the corresponding crosses at both locations, 1000-seed weight in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, seeds weight per plant in the 1st cross at Al-Arish and in the 2nd cross at both locations and seeds oil content in the 1st cross at Kafr-El-Hamam. Environmental variance in the corresponding crosses at both locations was found to be insignificant for all studied traits.

Heritability estimates in both broad and narrow sense are presented in [Table \(6\)](#). High broad sense-heritability values (> 60 %) were detected for all studied traits in corresponding crosses at both locations, except for 1000-seed weight in the 1st cross at Kafr-El-Hamam which was moderate (40.81%).

High (> 60 %) to moderate (30 % - 60 %) estimates of narrow sense-heritability were found for all studied traits in the two crosses at both locations, except for plant height in the 1st cross at Al-Arish, number of racemes per plant in the corresponding crosses at both locations and 1000-seed weight in the 1st cross at Kafr-El-Hamam which was low (< 30 %). The differences in magnitude between broad and narrow sense-heritability were estimated for all studied traits.

High to moderate values of narrow sense-heritability coupled with high (more than 20%) values of expected response from selection (as % of mean) were detected for days to first flower in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, first siliqua height in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish and seeds weight per plant in the 1st cross at both locations. High heritability to moderate coupled with moderate (10-20 %) expected response from selection as percent mean were recorded for plant height in the corresponding crosses at Kafr-El-Hamam, first siliqua height in the 2nd cross at Al-Arish, number of racemes per plant in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 1st cross at Al-Arish and in the 2nd

cross at Kafr-El-Hamam, seeds weight per plant in the 2nd cross at both locations and seeds oil content in the 1st cross at Al-Arish. However, high heritability to moderate coupled with low (less than 10 %) expected response from selection as percent mean were recorded for plant height in the corresponding crosses at Al-Arish, 1000-seeds weight in the 1st cross at Kafr-El-Hamam and seeds oil content in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations.

Table 6. Variance components and their related parameters in the two canola crosses for all studied traits at Kafr-El-Hamam (K) and Al-Arish (A) during 2019/2020 season

Cross	†L	Additive variance	Dominance variance	Environmental variance	Average degree of dominance (H/D) ^{0.5}	Broad-sense heritability %	Narrow-sense heritability%	Expected response from selection (R% F ₂)
Days to first flower								
CI	K	144.58**	227.55**	0.68	1.25	99.48	55.67	22.73
	A	86.01**	153.16**	8.24	1.33	90.79	48.03	17.99
CII	K	144.68**	46.53**	5.14	0.57	94.24	81.18	25.80
	A	92.57**	107.25**	3.77	1.08	95.10	60.22	20.20
Plant height								
CI	K	273.07**	293.43**	10.66	1.04	95.16	61.90	15.99
	A	54.06**	218.24**	8.70	2.01	90.37	29.94	6.09
CII	K	241.61**	57.34**	8.38	0.49	94.16	84.17	18.93
	A	60.32**	126.05**	7.38	1.45	89.32	43.68	7.58
First siliqua height								
CI	K	52.09**	48.30**	4.56	0.96	89.31	61.02	26.44
	A	35.75**	32.52**	3.17	0.95	89.14	61.27	26.57
CII	K	42.17**	32.77**	2.71	0.88	91.53	65.92	26.84
	A	20.98**	38.90**	2.35	1.36	89.59	46.49	18.71
Number of racemes per plant								
CI	K	2.35	17.66**	2.66	2.74	67.75	14.25	13.07
	A	2.58	12.91**	1.75	2.23	72.11	20.62	19.64
CII	K	1.94	13.47**	1.71	2.64	71.76	16.02	12.96
	A	2.38	7.31*	1.66	1.75	64.52	25.44	21.72
1000-seed weight								
CI	K	0.14	0.32	0.22	1.50	40.81	19.20	7.61
	A	0.22	0.47	0.06	1.45	80.53	39.36	16.10
CII	K	0.19	0.28	0.09	1.22	63.75	36.58	12.47
	A	0.28	0.09	0.05	0.57	77.03	66.19	23.80
Seeds weight per plant								
CI	K	51.04**	32.34**	9.87	0.80	77.30	58.70	25.53
	A	32.57**	39.12**	3.86	1.10	87.10	54.42	23.66
CII	K	31.94**	48.91**	6.34	1.24	81.64	46.24	18.41
	A	20.65**	45.40**	2.12	1.48	91.09	43.39	17.11
Seeds oil content								
CI	K	5.55	10.93*	1.31	1.40	80.85	40.74	6.97
	A	12.39*	8.41	1.87	0.82	81.59	60.91	12.49
CII	K	3.31	2.61	1.24	0.89	65.06	46.70	5.95
	A	5.90	3.06	0.62	0.72	85.71	68.09	9.27

†L = Location

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

DISCUSSION

Mean performance:

Highly significant differences were detected between parental canola in response to their genetic background and their populations in the two crosses at both locations for all studied traits, suggesting the presence of considerable genetic variability valid for further biometrical analysis. Mean performance of F₁ and their respective segregating generations *i.e.* F₂, BC₁ and BC₂ had the lowest values of days to first flower, plant height and first siliqua height in both crosses at both locations than their respective inferior parent. This indicated that the dominance of gene action governed in the inheritance of these traits in the direction of inferior parent, has been reported by Abdelsatar *et al.* (2020). However, dominance gene action inherited the highest mean values of seeds weight per plant and its attributing traits in F₁ and their respective segregating generations *i.e.* F₂, BC₁ and BC₂. A result similar was reported by Elnenny and Shafei Wafaa (2017).

From above-mentioned differences within F₂, BC₁ and BC₂ generations, they can be used in effective selection in the future breeding programs for improving these traits under both locations.

Scaling test:

The results of scaling test and joint scaling test (χ^2) indicated the presence of non-allelic interaction (epistasis) as digenic model was adequate to explain the inheritance of all studied traits in corresponding crosses at both locations. In this connection, the complex genetic model was found to be controlling the inheritance of these traits (Table 3). These results

were reported by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020) they reported that genetic analysis showed that epistasis gene action governed in the inheritance of all studied traits.

Nature of gene action:

Dominance gene effects had major role in the inheritance of most studied traits. Moreover, the higher frequency of dominant genes was detected in the parental lines, which involved in the inheritance of most studied traits in both crosses at both locations. Since the negative value of (d) was detected in the corresponding canola crosses indicated that the alleles responsible for less value of these traits were dominant over the alleles controlling high value. However, phenotypic selection was more effective for improving days to first flower in the corresponding crosses at Kafr-El-Hamam, plant height in the 1st cross at Al-Arish, number of racemes per plant in corresponding crosses at both locations, seeds weight/plant in the 2nd cross at both locations and seeds oil content in the 1st cross at Al-Arish and in 2nd the cross at both locations, as verified by significant digenic type of additive gene action (additive × additive) for these cases. Significant digenic type of dominance gene action (dominance × dominance) for days to first flower in the 2nd cross at Kafr-El-Hamam and plant height in the 1st cross at Kafr-El-Hamam, a number of racemes per plant in the two crosses at Al-Arish, 1000-seed weight in the two crosses at Kafr-El-Hamam, seeds weight per plant in the 1st cross at Al-Arish and seeds oil content in the 2nd cross at Kafr-El-Hamam. This indicated that dominance × dominance gene interaction had major role in the genetic control of these traits. The significant interaction of additive × dominance for days to first flower in the corresponding crosses at Al-Arish, first siliqua height in the 2nd cross at both locations, 1000-seed weight in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations and seeds oil content in the 1st cross at Kafr-El-Hamam. This confirmed that the important role of additive × dominance gene interaction in the genetic system of these traits.

The opposite signs of (d) and (dd) in canola crosses (Table 4) was observed for days to first flower in the 1st cross at both locations and in the 2nd cross at Al-Arish, plant height in the 1st cross at Al-Arish and in the 2nd cross at both locations, first siliqua height in the corresponding crosses at both locations, number of racemes per plant in the corresponding crosses at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish, seeds weight per plant in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, and seeds oil content in the 1st cross at both locations and in the 2nd cross at Al-Arish. This suggested that duplicate [(Additive × Dominance) and (Dominance × Dominance)] epistasis of non-allelic gene interaction governed in the inheritance of these traits, which will pose hindrance to canola breeder. Thus, selection of these traits must be delayed to advanced generations to benefit from the reduction of digenic epistasis variation and exploit transgressive segregants due to significant one or more of types of epistasis and duplicate type epistasis.

The same signs of (d) and (dd) in canola crosses was observed for days to first flower in the 2nd cross at Kafr-El-Hamam, plant height in the 1st cross at Kafr-El-Hamam, number of racemes per plant in the corresponding crosses at Al-Arish, 1000-seed weight in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, seeds weight per plant in the 1st cross at Al-Arish, and seeds oil content in the 2nd cross at Kafr-El-Hamam. This indicated that complimentary (additive × additive) epistasis of non-allelic gene interaction controlled in the inheritance of these traits. Thus, selection of these traits must be delayed to advanced generations to benefit from the reduction of non-fixable genetic variation and exploit transgressive segregants. These results are in harmony with those obtained by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020) they indicated that importance of epistasis in controlling all traits under study. This indicated that the magnitudes of non-fixable gene action types (epistatic) were larger than the additive or dominance gene effects in the performance of corresponding crosses for most studied traits may suggest the improvement of most traits could be achieved through hybrid breeding method.

Heterosis and its related parameters:

Considerable heterosis and heterobeltiosis were observed for all studied traits as a result of duplicate type of epistasis. This confirmed that there is the large diversity between parental lines in their genetic background. Similar findings were reported by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020). Moreover, the strong of significance in heterosis and heterobeltiosis for all studied traits in the corresponding crosses at both locations could be due to the major magnitude of the non-additive gene action. These results are in agreement with Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020). The recommended heterosis effects estimated for the all studied traits indicated the importance of corresponding crosses in canola breeding programs for improving seeds weight per plant and its main components.

Inbreeding depression was significant for most studied traits. This is a logical result, since the amount of heterosis and heterobeltiosis (heterozygosity) in F₁ may be followed by a valuable reduction in F₂ performance in the corresponding crosses for all studied traits at both locations caused could be due to inbreeding. The obtained results were in harmony with those obtained by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019) and Philanim *et al.* (2019) and Abdelsatar *et al.* (2020). Contradiction between significant heterosis or heterobeltiosis and insignificant inbreeding depression estimates for plant height in the corresponding crosses at Al-Arish and seeds weight per plant in the 1st cross at Kafr-El-Hamam could be due to the presence of linkage between genes in these materials (Van der Veen, 1959).

Potence ratio:

Over-dominance towards the better (desirable) parent as revealed by potency ratio was detected for all studied traits. These results are in harmony with those obtained by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019),

Philanim *et al.* (2019) and Abdelsatar *et al.* (2020). Significant (desirable) F_2 deviations (E_1) toward the better parent were observed for most studied traits. These results may refer to the contribution of epistatic gene effects in the performance of most traits. Significant backcross deviation (E_2) for most studied traits indicated a large amount of epistasis inherited in the corresponding crosses at both locations, hence great attention will continue in it in the future breeding programs.

Variance components and their related parameters:

Both additive (D) and dominance (H) genetic variances (Table 6) were significant for most studied traits in the corresponding crosses at both locations, indicating that importance of both additive and non-additive components in the inheritance of these traits. Importance of over dominance was detected in the genetic mechanism controlling most studied traits, therefore hybrid breeding method could be used for improving these traits. Similar results were reported by Bocianowski *et al.* (2019) and Philanim *et al.* (2019). Insignificance of environmental effect on performance of all studied traits in the corresponding crosses at both locations was found, indicating a negligible influence of environment on the expression of all studied traits.

The differences in magnitude between broad and narrow sense-heritability estimates for all studied traits indicated that presence of both additive and non-additive gene effects in the inheritance of these traits. This conclusion was also confirmed by estimates of gene action parameters. Similar results were obtained by Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020).

Heritability in narrow sense along with an expected response from selection as percent mean (R%), as shown in Table (6), is normally more useful in predicting the genetic gain under selection than heritability estimates alone as confirmed by Johnson *et al.* (1955). Moreover, Dixit *et al.* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make effective selection, high heritability should be associated with high genetic gain. The importance of additive gene effects was observed in the inheritance of days to first flower in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, first siliqua height in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 2nd cross at Al-Arish and seeds weight per plant in the 1st cross at both locations. Thus, practicing selection for these traits would be effective in early segregating generation to enhance these traits and hence selecting high yielding genotypes. Both additive and non-additive gene action involved in the inheritance of plant height in the corresponding crosses at Kafr-El-Hamam, first siliqua height in the 2nd cross at Al-Arish, number of racemes per plant in the 1st cross at both locations and in the 2nd cross at Kafr-El-Hamam, 1000-seed weight in the 1st cross at Al-Arish and in the 2nd cross at Kafr-El-Hamam, seeds weight per plant in the 2nd cross at both locations and seeds oil content in the 1st cross at Al-Arish. Epistasis gene actions governed in the inheritance of plant height in the corresponding crosses at Al-Arish, 1000-seeds weight in the 1st cross at Kafr-El-Hamam and seeds oil content in the 1st cross at Kafr-El-Hamam and in the 2nd cross at both locations, thus practicing selection for these traits would not be effective in early segregating generation. Similar results were obtained by Elnenny *et al.* (2015), Elnenny and Shafei Wafaa (2017), Bocianowski *et al.* (2019), Philanim *et al.* (2019) and Abdelsatar *et al.* (2020).

CONCLUSION

The preponderance of the dominance gene effects with the presence of types of epistasis either duplicate or complementary was detected in most studied traits in the corresponding crosses at both locations. This indicated that selection would be effective in the latest generations to benefit from desirable transgressive segregations, hence useful for the effective utilization of all three types of gene effects simultaneously.

REFERENCES

- Abdelsatar, M.A., Mourad, Kh.A. & Ibrahim, Suzan A.K. (2020). The genetic system controlling agronomic traits in canola. *Egyptian Journal of Plant Breeding*, 24(2):349– 381.
- AOAC. (1990). Official Methods of Analysis. 15th ed., 770–771. Virginia, USA: Association of Official Analytical Chemists.
- Bocianowski, J., Nowosad, K., Dobrzycka, A., & Wolko, J. (2019). Estimation of additive and epistatic gene effects for phenotypic and biochemical traits in double haploid lines of winter rapeseed (*Brassica napus* L.). *Indian Journal of Genetics and Plant Breeding*, 79 (3), 563-570.
- Cavalli, L. L. (1952). An analysis of linkage in quantitative inheritance. *An analysis of linkage in quantitative inheritance*. In: E. C. R. Reeve & C.H. Waddington (Eds), Quantitative Inheritance. p . 135-144. HMSO, London.
- Devi, A., Kumar, K., Dwivedi, R., Dwivedi, S., Kumari, P., Tripathi, N., & Dwivedi, D. K. (2018). Triple Test Cross Analysis for Seed Yield, Oil Content and Its Component for Indian mustard (*Brassica juncea* L. Czern and Coss.). *International Journal of Current Microbiology and Applied Sciences*, 7: 4246-4253.
- Dixit, P. K., Bhargava, P. D., Saxena, D. K., & Bhatia, L. K. (1970). Estimates of genotypic variability of some quantitative characters in groundnut (*Arachis hypogaea* L.). *Indian Journal of Agriculture Science*, 40: 197-201.
- Dixit, P.K., Saxena, P.D. & Bhatia, L.K. (1970). Estimation of genotypic variability of some quantitative characters in groundnut. *Indian Journal of Agriculture Science*, 40: 197-201.
- Elnenny, E. M. M., & Shafei, Wafaa W. M. (2017). Genetical Analysis for Seed Yield and It's Components in Canola. *Egyptian Journal of Plant Breeding*, 21 (7):1239-1250.
- Elnenny, E. M. M., Abd EL-Satar, M. A., & Ahmed, Fadia. H. (2015). Genetic variability, selection criteria and genetic divergence in some canola genotypes. *Egyptian Journal of Plant Breeding*, 19(7):2081– 2097.
- Falconer, D.S. (1989). Introduction to Quantitative Genetics. 3rd ed. John Wiley and Sons. Inc., New York.

- Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research*. 2nd ed. New York: John Willey and Sons Inc.
- Habiba, Rehab. M., Abd El-Aziz, M. H., & Amein, K. A. (2016). Evaluation of gene action for several important traits in some crosses of canola (*Brassica napus* L.) using generation mean analysis. *Assiut Journal of Agriculture Science*, 47(3), 9-23.
- Hayman, B.I. & Mather K. (1955). The description of genetic interaction in continuous variation. *Biometrics*, 11 (1): 69-82.
- Jinks, J.L. & Jones R.M. (1958). Estimation of the components of heterosis. *Genet.*, 43 (2): 223- 224.
- Johnson H.W., Robinson H.F. & Comstock R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47: 314-318.
- Manjunath, H., Phogat, D. S., Kumari, P., & Singh, D. (2017). Genetic analysis of seed yield and yield attributes in Indian mustard (*Brassica juncea* L.) Czern and Coss.). *Electronic Journal of Plant Breeding*, 8 (1): 182-186.
- Marjanović-Jeromela, A., Marinković, R., Jocković, M., Mitrović, P., Milovac, Ž., Hristov, N., ... & Stamenković, B. (2014). Evaluation of genetic variance components for some quantitative traits in rapeseed (*Brassica napus* L.). *Genetika*, 46(1), 179-185.
- Mather, K. & Jinks J.L. (1982). *Biometrical Genetics*, 3rd ed. Chapman and Hall, London.
- Mather, K. (1949). *Biometrical Genetics*. Methuen Co. Ltd., London.
- Peter, F.C & Frey K.J. (1966). Genotypic correlation, dominance and heritability of quantitative characters in oats, *Crop. Sci* 6: 259-262.
- Philanim, W.S., Pant U., Bhajan R. & Tondonba S.P. (2019). Gene Action for Quantitative Traits through Generation Mean Analysis in Indian Mustard (*Brassica juncea* L.). *International Journal of Current Microbiology and Applied Sciences*, 8(8): 260-266.
- Singh, V. V., Ram, B., Singh, M., Meena, M. L., & Chauhan, J. S. (2014). Generation mean analysis of water stress tolerance parameters in Indian mustard [*Brassica juncea* (L.) Czern & Coss] crosses. *Sabrao Journal of Breeding and Genetics*, 46(1): 76-80.
- Van Der Veen, J. H. (1959). Tests of non-allelic interaction and linkage for quantitative characters in generations derived from two diploid pure lines. *Genetica*, 30(1), 201-232.
- Warner, J.N. (1952). A method of estimating heritability. *Agronomy Journal*, 44, pp. 427-430.



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تحليل متوسطات الاجيال لمحصول البذور و مكوناته في الكانولا

محمد علي عبد الستار علي*، تامر حسن علي حسن، أسماء عبدالحليم أحمد و خالد محمد السيد ابو القاسم

قسم بحوث المحاصيل الزيتية، معهد بحوث المحاصيل الحقلية، مركز البحوث الزراعية، 9 شارع الجامعة، الجيزة، مصر

* بريد المؤلف المراسل: mohamedtemraz1@yahoo.com - Orcid: [0000-0003-0780-1444](https://orcid.org/0000-0003-0780-1444)

الملخص العربي

للكشف عن انماط التفوق في كل الصفات تحت الدراسة، تم تقييم ست عشائر في هجينين من الكانولا (N.A.37 × Serw 6) في تجربة حقلية في الموسم الشتوي 2020/2019 في محطة بحوث كفر الحمام بالشرقية و العريش بشمال سيناء، مركز البحوث الزراعية، مصر. و كشف Scaling test و joint scaling test عن عدم كفاية نموذج المضيف- السيادة البسيط في وراثه كل الصفات تحت الدراسة في الهجينين تحت الدراسة في كلا الموقعين. أظهرت النتائج ان قوة الهجين لمتوسط الاباء، و أفضل الاباء كانت سالبة و معنوية لعدد الايام حتي ظهور اول زهرة، ارتفاع النبات و ارتفاع اول خردلة، في حين كانت موجبة و معنوية لمحصول البذور للنبات و مكوناته في الهجينين في كلا الموقعين. و كانت قيم كفاءة التوريث بالمعني الخاص مرتفعة لمتوسطة مقرونة مع الاستجابة المتوقعة من الانتخاب (أكبر من 20%) لصفة عدد الايام حتي ظهور أول زهرة في الهجين الاول في كفر الحمام و في الهجين الثاني في كلا الموقعين، ارتفاع اول خردلة في الهجين الاول في كلا الموقعين و في الهجين الثاني في كفر الحمام، وزن الالف بذرة في الهجين الثاني في العريش و وزن البذور/نبات في الهجين الاول في كلا الموقعين. و النتائج كشفت عن الدور الرئيسي لتأثيرات الجينات السائدة حيث كان متوسط درجة السيادة أكبر من الواحد جنباً إلى جنب مع التفوق المكرر في وراثه معظم الصفات تحت الدراسة في الهجينين في كلا الموقعين. لذلك من المستحسن التأخير في الانتخاب للأجيال المتأخرة لتحسين معظم الصفات في معظم الحالات.

الكلمات المفتاحية: براسيكا نابيس، درجة السيادة، التفوق، الاستجابة المتوقعة من الانتخاب و العشائر الستة.