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VARIABILITY, GENE EFFECTS AND GENETIC PARAMETERS IN SIX-POPULATIONS OF FOUR CANOLA CROSSES AS AFFECTED BY DIFFERENT LEVELS OF SOIL SALINITY

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ABSTRACT

Six-population analysis of four canola Crosses evaluated under low (LSL) and high (HSL) salinity levels in newly reclaimed soil revealed that parental differences in each Cross were significant for all seven studied traits. Variability was different from location to another due to varied ratios of genetic and non-genetic variance components as well as to different salinity levels in favour of low one. Increasing salinity greatly affected trait means and genetic parameter values. Except for number of pods of Cr.4 under LSL, all traits of all Crosses showed significant A, B and C scaling tests under both LSL and HSL, indicating non-allelic interactions. In all Crosses, additive effect (d) was more important than dominance (h) one for flowering time (fl.t.), while the reverse was true for the other traits. dxd interaction effect was significantly positive (in most Crosses) for fruiting zone length (fr.z.l.), numbers of branches (brs), and pods (pods) and seed yield/plant (s.y/pl), under both levels of salinity, and seed oil content (s.oil) (%) under LSL, whereas it was significantly negative for fl.t of Crosses 1&4 and seed index (SI) of Crosses 1&2 under the two levels. The other interactions effects were different from one trait to another as influenced by Crosses and locations. Most traits (relative to MP) and some of them (relative to BP) of all Crosses except Cr.3 showed positive heterosis, under LSL & HSL. Whereas F_1 of Cr.3 showed negative MP and BP heterosis for fl.t. under HSL indicating its importance for breeding for earliness. Desirable inbreeding depression was recorded for fl.t (Cr.1, 2&4) fr.z.l.(Cr.2, 3&4) and SI (all Crosses) under LSL and for fr.z.l.(Cr.1), brs (Cr.4) , SI (Cr.1, 3&4) and seed oil % (Cr.1, 2&4) under HSL. Broad (h^2_b) and narrow (h^2_n) sense heritability and expected genetic advance (G_s) showed varied values depending upon the traits, parents, and salinity levels. The F_1 of Cr.3 recorded the highest s.y/pl. (due to it superiority in brs, pods and/or SI) and seed oil content under both HSL and LSL, in addition to its earliness under LSL, and it had the second (after Cr.2) F_2 high yielding plants. It had also the highest yielding BC_1 under the two levels of salinity, whereas Cr.2 had the highest yielding BC_2. Thus, Cr.3, followed by Cr.2, could be considered as promising genetic materials and could be used in further breeding programs (depending on their gene effects) to improve canola crop.

Key words: ***Canola Crosses, Six-population analysis, Gene action, Potance ratio, Heterosis, Inbreeding depression, Genetic advance and Heritability.***

IINRTODUCTION

Narrowing the wide gap between local production and consumption of vegetable oil, need a wide expansion of oil crops in new and marginal land outside the Nile valley and Delta far from the competition of the main crops occupied most of the old land. But the new areas frequently suffer from harsh environmental conditions such as salinity and drought. So, it is

important to incorporate a new oil crop able to grow well under these conditions such as canola (*Brassica napus* L) in the crop rotation to be as a source of edible oil (erucic acid free) and animal feed meal (glucosinolate free). Canola is a good choice for planting in these areas, where it successfully grows well during winter season (Sharaan 1986) and under wide soil variations of drought and salinity (Sharaan and Hassan 1988, Afiah *et al* 2000 and Ghallab and Sharaan 2002).

To achieve this goal, it is needed to breed canola genotypes adapted to these harsh abiotic conditions, especially salinity. Six-population breeding method is frequently used for genetical analysis to collect information about the variability within and among segregating and non-segregating generations, inheritance of different traits, the nature of gene effects controlling the traits behaviour, and thus determine the suitable subsequent breeding procedure to develop superior genotypes.

The present work was designed to study variability, gene actions and interactions and some-other genetic parameters affecting seven yield and quality traits in six-populations of four canola Crosses and their effect by two salinity levels in newly reclaimed land.

MATERIALS AND METHODS

Four F_1 canola Crosses, selected from a previous study (Sharaan and Ghallab 2002) were used in the present study, which executed during the period from 2003 to 2005 at the Experimental Farm of the Fayoum Fac. of Agriculture. These four F_1–Crosses were; Cr.1 (35/9 × 26/18), Cr.2 (35/9 × Drakkar), Cr.3 (35/9 × Hanna) and Cr.4 (26/18 × Drakkar). The 35/9 and 26/18 parents are salt tolerant local selections (Afiah *et al* 2000) where Drakkar and Hanna are German varieties. Each two parents of any Cross were different in some yield and quality traits.

In 2003/4 season, the parents of each Cross were re-Crossed to get enough F_1 seeds as well as Crossed with their corresponding F_1 to get BC_1 and BC_2 seeds, and some of F_1 plants were kept to produce F_2 seeds. In 2004/5 season, under each salinity level all populations (P_1, P_2 , F_1 , F_2 , BC_1 & BC_2) of the four Crosses were planted in RCBD with four replications in newly reclaimed sandy soil of two levels of salinity, i.e., high (HSL) with 17.4 and low (LSL) with 8.45 m mohs/cm of total soluble salt. Each plot contained 13 ridges of 3.5 long and 60cm apart. The six populations were represented by 2, 1, 2, 3, 2 & 3 ridges, respectively. During sampling, the outer two ridges/plot were excluded. The obtained data of the last season were subjected to analysis of variance and the means were compared by LSD test (Gomez and Gomez 1984).

The scaling test A, B & C for additive-dominance model were applied following Mather and Jinks (1982) to test the appropriate genetic model formulae (A , B & C) and their variances and to test the presence of

non-allelic interaction. Gene effects, additive (d), dominance (h), add. x add. (i), add. x dom. (j) and dom. x dom. (l), were determined according the methods mentioned by Jinks & Jones (1958). In the case where non-allelic interaction were absent, additive (D), dominance (H) and environmental (E) variances were calculated using the formulae of Mather and Jinks (1982). Heterosis relative to MP and BP and inbreeding depression, ID (Bhatt 1971), broad (h^2_b) and narrow (h^2_n) sense heritability and potance ratio (P) (Mather and Jinks 1982) and expected genetic advance, G_s (Allard 1960) were also estimated.

RESULTS AND DISCUSSION

The data revealed, generally that the differences between each parental pair in all Crosses were significantly different for all of the seven studied traits, as indicated by "t" test, under both LSL and HSL (Table 1&2). Thus, employment of these canola genotypes displayed fair amount of genetic variability, valid to ascertain types of gene actions and interactions controlling the inheritance of the traits under study. Also, in general, variability expressed as standard error, which was oftenly higher in segregating generations than non-segregating ones, differed from location to another due to the different generation responses to environmental influences. Similar results were early reported by many canola investigators (Sharaan 1986, Sharama and Gill 1994, Noureldin *et al* 1994, El-Hosary *et al* 1999, Afiah *et al* 2000 and Ghallab and Sharaan 2002). The data indicated also that increasing salinity greatly affected all trait means and genetic parameters. Afiah *et al* (2000) and Sharaan and Ghallab (2005) reported similar results. All the studied traits of all analyzed Crosses showed significant A, B and/or C scaling tests under both LSL and HSL (Table 2), indicating the presence of epistemic effects, which consequently estimated. While, insignificant scaling tests showed by number of pods (in Cross4) under LSL, indicated that non-allelic interactions were absent and the additive-dominance model was adequate.

Flowering time (fl.t)

The parental genotypes were earlier under LSL with 1-3 days than under HSL, but the reverse was observed for all F_1's of all Crosses except Cross 4 under HSL (Table 1). Early flowering of these three F_1's may be attributed to their heterozygous combinations. The different behaviour of Cross4 may be due to that its combination between two different parents (26/18 × Drakkar) while the other three Crosses had common parent (P_1 35/9). The earliest F_1's were of Cross 3 (92.31) under LSL and Cross1 (88.94 days) under HSL. It is worth to note that, F_1 of Cross3 deviated to the earlier parent in both locations having an advantage over the other Crosses, while the reverse was true for F_1 of the Cross 4. All F_2's were earlier than their respective F_1's in the two locations except F_2 of Cross 3 under LSL.

Table 1. Mean performance and standard error for different traits of the six population of the four studied canola Crosses

Traits	Cross / Population	Low salinity				High salinity			
		Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4
Flowering (days)	P_1	95.00+0.08	95.00+0.08	95.00+0.08	91.00+0.14	96.04+0.13	96.04+0.13	96.04+0.13	92.94+0.21
	P_2	91.00+0.14	94.36+0.05	90.56+0.21	94.36+0.05	92.94+0.21	95.94+0.21	93.99+0.04	95.94+0.21
	F_1	94.98+0.24	97.53+0.09	92.31+0.64	96.55+0.17	88.94+0.21	90.11+0.38	89.01+0.15	96.56+0.21
	F_2	94.38+1.28	91.76+0.20	96.38+1.28	94.63+0.43	88.88+0.43	88.83+0.60	88.38+0.43	90.33+0.60
	BC_1	88.68+0.26	94.63+0.20	94.81+1.07	89.13+0.43	86.88+0.43	87.71+0.53	87.13+0.43	87.88+0.42
	BC_2	91.56+1.49	88.47+0.11	94.25+0.85	89.56+0.21	87.93+0.26	88.13+0.43	88.56+0.21	88.86+0.48
	Parental diff .(t)	**	**	**	**	**	*	**	**
Fruiting zone length Cm	P_1	48.46±0.42	48.46±0.42	48.46±0.42	58.48±0.66	48.6±0.54	48.6±0.54	48.6±0.54	58.91±0.90
	P_2	58.48±0.66	66.25±0.38	79.19±0.37	66.25±0.38	58.91±0.90	51.1±0.86	57.05±0.88	51.1±0.86
	F_1	61.87±1.27	94.03±1.35	73.07± 1.35	75.59±1.36	36.34±1.02	64.13±0.91	58.48±1.10	66.59±1.03
	F_2	59.67±1.65	64.72±1.57	64.41±2.00	64.69±1.73	40.76±1.30	50.25±1.39	54.19±1.49	53.22±1.17
	BC_1	59.68±3.43	87.33±2.10	69.66±2.01	72.79±2.13	53.38±1.65	51.98±2.08	65.37±2 84	76.63±1.83
	BC_2	72.63±1.43	73.08±2.69	84.97±3.26	73.82±3.19	51.88±2.35	60.9±2.53	60.73±3.19	73.43±2.13
	Parental diff .(t)	**	**	**	**	**	**	*	**
Number of branches / plant	P_1	5.71±0.07	5.71±0.07	5.71±0.07	6.36±0.07	4.95±0.06	4.95±0.06	4.95±0.06	5.5±0.09
	P_2	6.36±0.07	6.22±0.11	6.69±0.04	6.22±0.11	5.5±0.09	4.88±0.10	5.68±0.11	4.86±0.10
	F_1	6.45±0.08	7.45±0.11	7.3±0.14	8.16±0.12	4.45±0.08	6.29±0.07	6.55±0.12	5.4±0.12
	F_2	5.53±0.15	5.72±0.14	5.4±0.19	5.64±0.13	3.97±0.11	5.29±0.13	4.98±0.14	5.53±0.16
	BC_1	5.87±0.24	7.3±0.20	6.34±0.22	7.69±0.21	5.33±0.18	6.26±0.19	5.85±0.20	6.44±0.26
	BC_2	7.24±0.23	6.09±0.21	6.53±0.29	7.13±0.22	5.78±0.16	5.6±0.23	5.51±0.31	6.57±0.26
	Parental diff .(t)	**	**	*	**	**	**	*	**
Number of pods / plant	P_1	212.6±0.96	212.6±0.96	212.6±0.96	273.9±0.56	109.94±3.42	109.9±3.42	109.9±3.37	177.7±6.50
	P_2	273.9±0.56	253.6±0.65	182.0±1.68	253.6±0.65	177.72±6.40	185.0±6.65	120.7±3.31	185.0±6.75
	F_1	246.3±7.15	276.3±8.63	335.6±17.35	206.0±15.79	158.45±6.02	215.5±7.26	178.6±5.29	152.4±10.32
	F_2	168.7±9.42	195.9±12.20	224.5±18.28	224.2±20.79	100.19±9.07	127.7±12.97	159.8±12.41	147.8±11.65
	BC_1	188.8±16.62	301.2±14.42	244.3±23.63	305.1±41.96	173.84±14.48	197.3±22.61	206.6±23.73	213.6±18.70
	BC_2	206.3±14.40	255.1±23.48	236.9±27.36	205.3±17.93	128.68±15.69	250.5±17.12	173.3±19.17	226.8±22.29
	Parental diff .(t)	**	**	**	**	**	**	*	**
Seed index (g)	P_1	3.51±0.05	3.51±0.05	3.51±0.04	3.68±0.004	3.16±0.03	3.16±0.03	3.16±0.03	2.47±0.03
	P_2	3.68±0.004	2.65±0.02	2.87±0.01	2.65±0.02	2.47±0.03	2.32±0.02	2.53±0.03	2.32±0.02
	F_1	3.34±0.01	3.46±0.02	3.34±0.01	3.33±0.08	3.01±0.17	3.02±0.01	3.08±0.01	2.63±0.04
	F_2	4.56±0.08	3.64±0.08	3.76±0.07	3.39±0.12	4.4±0.43	2.84±0.08	3.56±0.08	3.00±0.07
	BC_1	3.06±0.06	2.84±0.06	3.8±0.05	3.69±0.09	2.86±0.34	2.68±0.06	3.3±0.07	3.18±0.06
	BC_2	3.72±0.08	3.72±0.08	3.88±0.06	3.75±0.09	3.25±0.37	3.32±0.06	3.5±0.07	3.42±0.07
	Parental diff .(t)	*	**	**	**	**	**	**	*
Seed yield/plant (g)	P_1	13.18±0.07	13.18±0.07	13.18±0.07	12.48±0.04	5.05±0.25	5.05±0.25	5.05±0.25	11.65±0.32
	P_2	12.48±0.04	11.77±0.09	12.70±0.08	11.77±0.09	11.65±0.32	8.11±0.25	4.49±0.33	8.11±0.26
	F_1	16.45±0.30	17.41±0.93	19.79±0.69	7.77±0.65	7.75±0.34	10.75±0.33	14.71±0.50	7.97±0.37
	F_2	10.31±0.54	11.37±1.05	10.53±0.78	9.56±0.70	4.40±0.36	5.67±0.42	6.77±0.54	6.64±0.43
	BC_1	13.78±1.01	16.36±1.58	17.97±1.21	13.03±1.47	7.93±0.52	8.46±0.54	14.18±1.10	12.65±0.68
	BC_2	17.73±0.71	18.19±1.62	15.18±0.95	13.32±1.03	7.78±0.53	10.76±0.84	10.15±0.95	12.7±0.83
	Parental diff .(t)	**	**	**	**	**	**	*	**
Oil content %	P_1	40.53±0.04	40.53±0.04	40.53±0.04	41.58±0.04	40.01±0.01	40.01±0.01	40.01±0.01	40.09±0.04
	P_2	41.58±0.04	40.64±0.02	40.3±0.05	40.64±0.02	40.09±0.04	40.53±0.09	39.68±0.06	40.53±0.09
	F_1	41.85±0.01	42.83±0.06	43.83±0.06	41.94±0.02	39.71±0.04	39.78±0.06	40.91±0.04	39.78±0.09
	F_2	41.92±0.23	41.53±0.15	41.66±0.32	41.44±0.21	40.16±0.21	41.15±0.17	40.72±0.11	40.54±0.13
	BC_1	41.88±0.23	41.66±0.13	42.06±0.32	43.01±0.19	40.61±0.15	40.34±0.13	39.67±0.11	40.98±0.11
	BC_2	42.96±0.13	43.34±0.13	41.55±0.17	41.86±0.13	42.17±0.23	40.79±0.15	39.63±0.09	40.12±0.11
	Parental diff .(t)	**	*	**	**	*	**	**	**

The earliest F_2's were of Cross2 (91.76) under LSL and of Cross3 (88.38 days) under HSL. BackCross populations flowered earlier than their F_2's in both locations except BC_1 of Cross 2 under LSL and BC_2 of Cross 3 under HSL. All BC_1's were earlier than their P_1, and the earliest BC_1's were of Cross1 (88.68) under LSL and of Cross3 (87.13 days) under HSL. All BC_2's, except those of Cross1 and Cross 3 under LSL, came to flowered after shorter time than that of their P_2. The earliest BC_2's were of Cross2 (88.47) under LSL and of Cross1 (87.93 days) under HSL

Concerning gene effects (Table 2), it was noticed that additive (d) had greater magnitude (irrespective to significance) than dominance one (h) for all Crosses under both LSL and HSL. This result confirmed early reports by Sharama (1978) and Chaudhary *et al* (1997). Whereas, Dahanayake and Galwey (1999) reported that, dominance effects were the most important, but non-allelic interaction effects were common in cases where dominance effect was large. Cross2 showed positive and significant estimates of all gene effects under LSL, while it exhibited negative value for "h" and positive value for "l" under HSL, reflecting its great influence by location as well as its inconsistency, and consequently flowered early under LSL. Also under LSL, Cross1 and Cross 4 gave negative and significant estimates for "h", "i" and "j" epestatic effects which may have resulted in positive hybrid vigor towards lateness. It is of interest to note that, "l" effect was positive and significant in Crosses 1, 2 and 4 under LSL and in all Crosses under HSL, reflecting the importance of dominance x dominance effect in the inheritance of this trait. This result was in line with those detected by Sheikh and Singh (1998). As indicated by potance ratios, Cross2 and Cross4 showed over-dominance and Cross1 showed partial dominance towards lateness while Cross3 showed partial dominance towards the earlier parent under LSL. However, under HSL all crosses except Cross 4 showed over-dominance towards earliness.

As shown in Table (3) Cross 4 had positive and significant heterosis relative to MP (4.17& 2.25) and BP (6.10 & 3.90%) under LSL and HSL respectively, reflecting its invalidity for breeding for earliness. This result confirmed the previous mentioned one concerning the performance of this Cross. In connection to this result, Engqvist and Becker (1991) found positive heterosis, while Abou-Ghazala (2001) estimated negative heterosis. On the contrary, Cross 3 had negative and significant heterosis (-6.32 and -5.30%) under HSL relative to MP and BP, respectively, reflecting its importance in further breeding for earliness under soil salinity stress. Additional advantage of Cross 3 was observed from its negative inbreeding effect (-4.40%) where its F_2 was earlier than its F_1 that could be selected for earliness under salinity stress. Heritability (h^2) estimates varied in the two locations due to salinity effect on variance components. Heritability in broad sense ''h^2_b'' percentages were from 98.25 (Cross1) to 86.87 (Cross 2) and

Table2. Scaling tests, gene effects and components of genetic variance for different traits of the four studied canola Crosses

Traits	Estimate	Low salinity				High salinity			
		Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4
Flowering (days) cm	A	-12.63**±0.57	-3.27**±0.42	2.31±2.23	-9.3**±0.88	-11.23**±0.89	-10.74**±1.14	-10.79**±0.88	-13.75**±0.90
	B	-2.85±3.00	-14.95**±0.23	5.63*±1.84	-11.79**±0.46	-6.03**±0.59	-9.8**±0.96	-5.87**±0.45	-14.78**±1.01
	C	1.54±5.15	-17.36**±0.83	15.31*±5.29	0.04±1.75	-11.35**±1.78	-16.9**±2.52	-14.54**±1.74	-20.7**±2.45
	Additive (d)	-2.89±1.52	6.16**±0.23	0.56 ±1.37	-0.44 ±0.48	-1.05 ±0.50	-0.42 ±0.68	-1.44*±0.48	-0.98 ±0.64
	Dominance (h)	-15.05*±5.96	1.98* ±0.94	-7.84±5.84	-17.26**±1.97	-11.45**±1.99	-9.51**±2.78	-8.13**±1.96	-5.71 ±2.73
	Add. x Add. (i)	-17.03*±5.95	-0.86±0.93	-7.38±5.81	-21.13**±1.96	-5.9*±1.98	-3.64±2.75	-2.13 ±1.96	-7.83*±2.71
	Add.x Dom. (j)	-4.89**±1.52	5.84**±0.23	-1.66±1.37	1.24*±0.48	-2.6**±0.51	-0.47 ±0.69	-2.46**±0.48	0.52±0.66
	Dom. x Dom. (l)	32.51**±7.96	19.08**±1.23	-0.56±7.61	42.21**±2.59	23.15**±2.67	24.18**±3.72	18.79**±2.58	36.36**±3.55
	Potance Ratio	0.99	8.92	-0.21	2.31	-3.58	-117.50	-5.86	1.42
Fruiting zone length	A	9.03±6.98	32.16**±4.43	17.79**±4.26	11.51*±4.51	21.82**±3.49	-8.77*±4.29	23.66**±5.81	27.77**±3.92
	B	24.91**±3.19	-14.13*±5.56	17.68**±6.67	5.81±6.53	8.50±4.89	6.57±5.22	5.92±6.54	29.17**±4.46
	C	7.99±7.12	-43.88**±6.86	-16.14±8.45	-17.14*±7.49	-17.15**±5.68	-26.97**±5.95	-5.84±6.45	-30.30**±5.27
	Additive (d)	-12.95**±3.71	14.25**±3.41	15.31**±3.83	-1.04±3.83	1.51±2.87	-8.92**±3.28	4.65±4.28	3.20±2.81
	Dominance (h)	34.34**±10.02	98.59**±9.37	60.86**±11.15	47.69**±10.43	30.05**±7.82	39.05**±8.67	41.08**±10.5	98.82**±7.42
	Add. X Add. (i)	25.94**±9.93	61.92**±9.27	51.61**±11.07	34.46**±10.33	47.46**±7.74	24.77**±8.61	35.42**±10.43	87.24**±7.32
	Add.x Dom. (j)	-7.94*±3.93	23.14**±3.42	0.06±3.84	2.85±3.85	6.66*±2.92	-7.67*±3.32	8.87*±4.31	-0.70±2.88
	Dom.xDom. (l)	-59.87**±16.46	-79.96**±15.27	-87.08**±17.5	-51.78**±17.06	-77.78**±12.8	-22.56±14.4	-65.0**±18.28	-144.17**±12.2
	Potance Ratio	1.68	4.12	0.60	3.40	-3.38	11.43	1.34	2.97
Number of branches/ plant	A	-0.42±0.48	1.45**±0.42	-0.32±0.46	0.85±0.44	1.27**±0.38	1.29**±0.39	0.2±0.43	1.98**±0.53
	B	1.67**±0.48	-1.49**±0.44	-0.92±0.60	-0.13±0.47	1.61**±0.34	0.03±0.47	-1.22±0.63	2.88**±0.55
	C	-2.86**±0.64	-3.93**±0.62	-5.37**±0.80	-6.34**±0.59	-3.45**±0.48	-1.25*±0.55	-3.81**±0.63	0.97±0.68
	Additive (d)	-1.37**±0.33	1.21**±0.29	-0.19 ±0.36	0.56±0.30	-0.45 ±0.24	0.66* ±0.30	0.34 ±0.37	-0.13 ±0.37
	Dominance (h)	4.52**±0.91	5.38**±0.82	5.24**±1.05	8.93**±0.81	5.55**±0.66	3.95**±0.79	4.02**±0.94	4.1**±0.98
	Add. X Add. (i)	4.1**±0.90	3.9**±0.81	4.14**±1.04	7.06**±0.80	6.33**±0.65	2.57**±0.79	2.78**±0.93	3.88**±0.97
	Add.x Dom. (j)	-1.04**±0.34	1.47**±0.29	0.3±0.36	0.49±0.31	-0.17±0.25	0.63*±0.30	0.71±0.37	-0.45±0.37
	Dom. X Dom. (l)	-5.35**±1.47	-3.86**±1.30	-2.9±1.65	-7.77**±1.34	-9.2**±1.08	-3.89**±1.31	-1.76±1.60	-8.7**±1.62
	Potance Ratio	1.29	5.79	2.24	26.67	-2.80	39.22	3.37	0.68
Number of pods / plant	A	-81.33*±34.01	113.5**±28.20	-59.48±50.36	130.21±85.40	79.3**±29.8	69.14±45.93	124.7*±47.87	97.1*±39.33
	B	-107.6**±29.68	-25.59±47.75	-43.87±57.44	-48.94±38.82	-78.8*±32.6	100.52**±35.6	47.31±38.84	116.* ±46.25
	C	-304.5**±40.32	-235.26**±51.77	-167.72*±80.97	-42.58±88.97	-203.8**±38.9	215.07**±54.3	51.36±50.98	-76.5 ±51.8
	Additive (d)	-17.5 ±21.99	49.06 ±27.04	7.47 ±36.15		45.15* ±21.35	-53.22 ±28.4	33.33 ±30.50	-13.2±29.09
	Dominance (h)	118.6*±58.36	366.35**±73.35	202.61*±104.30		218.9**±56.5	452.8**±77.29	183.89*±78.87	260.7**±75.4
	Add. X Add. (i)	115.5*±57.92	323.16**±72.84	64.37±102.84	----------	204.3**±56.1	384.7**±76.9	120.64±78.66	289.67**±74.5
	Add.x Dom. (j)	13.1±22.00	69.54* ±27.05	-7.81±36.17	----------	79.05**±21.7	-15.69±28.61	38.69±30.60	-9,5±29.47
	Dom. X Dom. (l)	73.4±96.76	-411.0**±119.92	38.97±165.74	----------	-204.8*±93.8	-554.4**±125.8	-292.64*±132.24	-502.6**±127.4
	Additive (D)				101729.50				
	Dominance (H).				86844.65				
	Environment (E).				2666.07				
	Potance ratio	0.10	2.11	9.05	.....	0.43	1.81	11.80	-7.96
	$\sqrt{H/D}$				0.92				

Continued Table2

Seed index g	A	-0.73**±0.12	-1.3**±0.12	0.74**±0.11	0.38±0.21	-0.44 ±0.70	-0.82**±0.13	0.36*±0.14	1.26**±0.12
	B	0.41*±0.16	1.34**±0.16	1.55**±0.13	1.53**±0.21	1.01±0.75	1.31**±0.12	1.39**±0.14	1.89**±0.14
	C	4.35**±0.31	1.49**±0.31	1.95**±0.27	0.56±0.51	5.93**±1.74	-0.16 ±0.33	2.38**±0.31	1.94**±0.30
	Additive (d)	-0.65**±0.10	-0.89**±0.09	-0.08 ±0.08	-0.06±0.13	-0.39 ±0.50	-0.64**±0.09	-0.2 ±0.10	-0.24 *±0.09
	Dominance (h)	-4.92**±0.37	-1.07**±0.36	0.49 ±0.31	1.52*±0.55	-5.17*±1.99	0.93*±0.38	-0.39±0.36	1.45**±0.34
	Add. x Add. (i)	-4.67**±0.36	-1.45**±0.36	0.34±0.31	1.35*±0.55	-5.36*±1.98	0.65±0.38	-0.63±0.36	1.21**±0.34
	Add.x Dom. (j)	-0.57**±0.10	-1.32**±0.10	-0.4**±0.08	-0.58**±0.13	-1.46±1.00	-2.12**±0.18	-1.03**±0.10	-0.63**±0.18
	Dom. x Dom. (l)	4.99**±0.50	1.41*±0.49	-2.63**±0.42	-3.26**±0.73	4.79±2.65	-1.13*±0.48	-1.12*±0.50	-4.37**±0.46
	Potance Ratio	-3.07	0.88	0.47	0.32	0.57	0.68	0.76	3.03
Seed yield/plant	A	-2.08±2.05	2.13±3.30	2.97 ±2.52	3.81±3.00	3.06**±1.13	1.12±1.16	8.6**±2.27	5.69**±1.45
	B	6.53**±1.45	7.2*±3.37	-2.14±2.02	5.1*±2.16	-3.84**±1.15	2.66±1.73	1.1±2.00	9.33**±1.72
	C	17.32**±2.23	-14.3**±4.58	23.34**±3.42	-5.57 ±3.09	14.58**±1.63	-11.99**±1.84	11.86**±2.43	-9.13**±1.92
	Additive (d)	-3.95**±1.23	-1.83 ±2.26	2.79 ±1.54	-0.28 ±1.79	0.16 ±0.74	-2.3*±1.00	4.03**±1.45	-0.05±1.08
	Dominance (h)	25.4**±3.29	28.57**±6.24	31.02**±4.44	12.12**±4.60	13.21**±2.10	19.93**±2.64	31.49**±3.67	22.25**±2.79
	Add. x Add. (i)	21.78**±3.27	23.63**±6.17	24.17**±4.39	14.48**±4.55	13.81**±2.06	15.76**±2.62	21.56**±3.63	24.16**±2.76
	Add.x Dom. (j)	-4.31**±1.24	-2.54±2.26	2.55±1.54	-0.64±1.79	3.45**±0.77	-0.77±1.02	3.75*±1.47	-1.82±1.10
	Dom.xDom. (l)	26.24**±5.42	32.9**±10.15	-24.9**±7.03	-23.39**±7.8	13.03**±3.39	-19.54**±4.41	31.25**±6.3	-39.18**±4.71
	Potance Ratio	10.32	6.99	28.47	-6.61	-0.18	2.72	35.36	-1.08
Oil content %	A	1.38*±0.47	-0.04±0.27	-0.24±0.64	2.49**±0.39	1.5**±0.31	0.88**±0.26	-1.59**±0.22	2.10**±0.23
	B	2.5**±0.26	3.21**±0.27	-1.02*±0.35	1.14**±0.26	4.54**±0.47	1.28**±0.32	-1.34**±0.19	-0.06±0.25
	C	1.86±0.94	-0.73 ±0.61	-1.85±1.29	-0.35 ±0.86	1.12±0.86	4.49**±0.68	1.36**±0.44	1.99**±0.55
	Additive (d)	-1.08**±0.27	-1.68**±0.18	0.51 ±0.36	1.14**±0.23	-1.56**±0.28	-0.46 ±0.20	0.04 ±0.14	0.86**±0.15
	Dominance (h)	2.81 *±1.08	6.15**±0.70	4.00*±1.47	4.83**±0.97	4.57 **±1.02	-2.82**±0.78	-3.22**±0.51	-0.48±0.60
	Add. x Add. (i)	2.01±1.08	3.9**±0.70	0.59±1.47	3.99**±0.97	4.91**±1.02	-2.33*±0.77	-4.29**±0.51	0.05±0.59
	Add.x Dom. (j)	-0.56 ±0.27	-1.62**±0.18	0.39±0.36	0.68*±0.23	-1.52**±0.28	-0.2±0.20	-0.12±0.14	1.08**±0.16
	Dom. x Dom. (l)	-5.89**±1.43	-7.07**±0.95	0.68±1.94	-7.62**±1.26	-10.94**±1.41	0.17±1.04	7.22**±0.70	-2.09*±0.82
	Potance Ratio	1.53	41.81	29.06	1.79	-9.08	-1.91	6.42	-2.43

Table3. Heterosis, inbreeding effect, heritability and expected genetic advance percentages for different traits of the four studied canola Crosses.

Traits	Estimates	Low salinity				High salinity			
		Cross1	Cross2	Cross3	Cross4	Cross1	Cross2	Cross3	Cross4
Flowering (days)	Heterosis%(MP)	2.13*	3.00*	-0.51	4.17*	-5.87	-6.12	-6.32**	2.25**
	Heterosis%(BP)	4.37**	3.35**	1.93	6.10**	-4.30**	-6.07**	-5.30**	3.90**
	Inbreeding effect (%	0.64	5.91**	-4.40**	1.99**	0.07	1.43*	0.71	6.46**
	Heritability (b.s)	98.25	86.87	90.61	90.60	80.33	80.44	92.58	87.24
	Heritability (n.s)	59.89	74.39	86.11	75.00	64.00	69.26	75.00	84.85
	Gs%	3.35	0.68	4.72	1.39	1.27	1.92	1.49	2.31
Fruiting zone Length ,cm	Heterosis%(MP)	15.71**	63.94**	14.49**	21.2**	-32.39**	28.65**	10.71**	21.06**
	Heterosis%(BP)	5.80	41.93**	-7.72	14.09	-38.3**	25.50**	2.52	13.04*
	Inbreeding effect (%	3.56	31.17**	11.85**	14.42**	-12.16**	21.65**	7.34**	20.08**
	Heritability (b.s)	95.64	94.66	96.57	95.69	93.24	94.93	94.60	89.87
	Heritability (n.s)	78.63	68.87	92.98	82.69	86.25	74.06	38.22	62.31
	Gs%	63.35	45.25	76.29	64.54	80.05	59.88	30.71	40.02
Number of branches/plant	Heterosis%(MP)	6.98**	24.86**	17.74**	29.81**	-14.88**	28.08**	23.31**	4.22**
	Heterosis%(BP)	1.49**	19.72**	9.11**	28.38**	-19.18**	27.17**	15.34**	-1.85**
	Inbreeding effect (%	14.34**	23.16**	25.95**	30.89**	10.68**	15.93**	23.98**	-2.48**
	Heritability (b.s)	96.35	91.71	94.97	90.22	91.31	93.79	92.33	92.99
	Heritability (n.s)	85.87	87.30	84.54	70.14	83.88	73.42	68.63	69.25
	Gs%	68.87	58.72	75.12	47.09	66.90	52.40	57.51	57.35
Number of pods / plant	Heterosis%(MP)	1.26	18.53	70.06	-21.88	10.17**	46.16**	54.86**	-15.98
	Heterosis%(BP)	-10.07	8.95	57.84	-24.78	-10.84	16.50	47.98	-17.63
	Inbreeding effect (%	31.52**	29.10	33.09	-8.84	36.77**	40.74**	10.52	3.04
	Heritability (b.s)	96.86	97.28	93.24	96.46	93.21	96.51	98.23	92.36
	Heritability (n.s)	69.28	82.05	69.66	67.60	47.11	85.15	81.04	50.39
	Gs%	112.73	148.86	140.24	170.35	114.60	251.77	183.42	115.77
Seed index (g)	Heterosis%(MP)	-7.04**	12.36**	4.77**	5.22**	6.94**	-10.45**	8.47**	-2.41**
	Heterosis%(BP)	-9.12**	-1.53**	-4.84**	-9.57**	-4.65**	-4.25**	-2.35**	-4.23**
	Inbreeding effect (%	-36.32**	-5.27**	-12.32**	-1.75**	-46.01**	6.02**	-15.41**	-13.97**
	Heritability (b.s)	87.22	84.40	80.26	82.74	94.43	95.06	92.68	84.66
	Heritability (n.s)	36.42	47.84	51.30	76.53	63.63	89.28	41.98	52.94
	Gs%	2.53	4.16	3.72	11.14	25.47	10.78	3.74	5.28
Seed yield /plant (g)	Heterosis%(MP)	28.20**	39.59**	52.96**	-19.41**	-7.17**	63.31**	208.23**	-19.32**
	Heterosis%(BP)	24.79**	32.11**	50.17**	-21.70**	-33.45**	32.52**	191.09**	-31.58**
	Inbreeding effect (%	37.33**	34.71**	46.79**	2.20*	43.18**	47.27**	53.94**	16.69**
	Heritability (b.s)	98.24	95.09	94.64	94.92	84.31	92.94	92.25	91.30
	Heritability (n.s)	73.17	70.44	82.99	29.48	64.18	64.64	58.44	51.59
	Gs%	111.06	175.90	159.70	60.34	131.23	140.04	136.48	97.91
Oil content %	Heterosis%(MP)	1.95**	5.54**	8.45**	2.04**	-0.84**	-1.21**	2.67**	-1.32**
	Heterosis%(BP)	0.67**	5.40**	8.13**	0.89**	-0.94**	-1.84**	2.25**	-1.85**
	Inbreeding effect (%	-0.16	3.05**	4.95**	1.21**	-1.13**	-3.44**	0.47**	-1.92**
	Heritability (b.s)	97.88	91.04	97.53	97.77	97.30	86.25	82.55	66.67
	Heritability (n.s)	70.25	52.80	71.56	83.00	28.59	60.29	36.00	61.11
	Gs%	1.62	0.78	2.27	1.76	0.63	1.01	0.39	0.80

from 92.58 (Cross3) to 80.33% (Cross1) under LSL and HSL, respectively. The h^2_n percentages were from 86.11 (Cross 3 which gave the highest expected genetic advance ''Gs'' of 4.72) to 59.89 (Cross1) and 84.85 (Cross4 which gave the highest "Gs" of 2.31) to 46.00% (Cross1) under LSL and HSL respectively.

Fruiting zone length (fr.z.l)

As shown in Table (1), P_2 possessed the tallest fruiting zone of most genotypes under LSL than those of HSL, while P_1 seemed to be less affected by salinity levels. But, all F_1's had taller fruiting zone under LSL than under HSL. The tallest fruiting zone (94.03cm) was recorded by F_1 of Cross 2. While, Cross4 had the tallest fruiting zone (66.59cm) under HSL. F_1 of Cross1, on the other hand, had the shortest fruiting zone in both environments. All F_2's, except that of Cross1 under HSL, possessed shorter fruiting zones than their respective F_1's due to increasing segregants in negative direction. fr.z.l. of all BC's exceeded their corresponding ones of F_2's and parents (except BC_2 of Cross1 under HSL) which encouraged their use in further breeding for improving this trait. BC_1 (87.33) of Cross2 and BC_2 (84.97cm) of Cross3 under LSL as well as BC_1 (76.63) and BC_2 (73.4 cm) of Cross4 under HSL showed the tallest fruiting zone.

Data listed in Table (2) clearly show that dominance was higher than additive effect for all Crosses under LSL and HSL. Cross2 exhibited positive and significant additive gene action under LSL while, it had negative additive effect under HSL, and may be superiority of its F_1 under HSL is a result of this effect. All Crosses in both locations were similar concerning their positive and significant "h" and "i" and negative and significant "l" (except Cross2 under HSL) components, reflecting the important role of dominance and epestatic effects in the inheritance of this trait. Thus, all Crosses (except Cross3, which showed partial dominance) showed over–dominance towards tallness in both locations. The results obtained herein are in general agreement with those reported by Abo El–Wafa *et al* (2004) and Sharaan and Ghallab (2005).

F1 heterosis values estimated under LSL were positive and significant for all Crosses (Table 3) and exceeded their MP's in a range from 63.94 (Cross2) to 14.49 (Cross3) for fruiting zone length, while only F1 of Cross2 surpassed its BP. These results reflected the importance of Cross2 for improving this trait. Also under HSL, the Crosses 2, 3 and 4 showed positive heterosis in ranges from 28.65 (Cross 2) to 10.7 (Cross 3) relative to their MP's and from 25.50 (Cross 2) to 13.04% (Cross4) relative to their BP's, confirming again the importance of Cross2 for this trait. While Cross1 under LSL recorded negative heterosis relative to its MP (-32.39) and BP (-38.30 %). The Crosses 2, 4 and 3 showed positive inbreeding effects of (31.17 & 21.65), (14.24 & 20.08) and (11.85 & 7.34 %) under LSL and

HSL, respectively. h2b values were ranged from 96.27 (Cross 3) to 94.66 (Cross 2) under LSL and from 94.93 (Cross 2) to 89.87 (Cross 4). The h2n estimates were between 92.98 (Cross 3 which gave the highest "Gs", 67.29) and 68.78 (Cross 2) under LSL and between 86.25 (Cross 1 which showed the highest "Gs", 80.05 %) and 38.22 (Cross 3) under HSL.

Number of branches/plant (brs)

Parental genotypes and their F_1's possessed higher number of branches under LSL than those under HSL (Table 1). The greatest branching F_1's were showed by Cross4 (8.16) under LSL and Cross3 (6.55) under HSL, while $F_1$of Cross1 was the lowest one (6.45& 4.45) in the two locations in the same order. All F_1 hybrids in the two locations (except Cross1 under HSL) deviated towards the greater branching parent, reflecting the feasibility of improving this trait depending upon the hybrids. All F_2's in both locations (except Cross4 under HSL) produced smaller number of branches than those of respective F_1's, due to segregation in negative direction. However, all BC's exceeded their F_2's,. All BC_1's and all BC_2's (except of Cross2 under LSL and Cross3 in the two locations) exceeded their corresponding parents.

Under both locations, dominance gene effects were higher than additive ones (Table 2). In this respect, Singh and Chauhan (1987) and Abo El-Wafa *et al* (2004) reported that dominance had greater effect than additive on branches number. It is worth to mention that, Cross2 had positive and significant additive effect under the two levels of salinity, indicating its consistency and reflected superiority of its F_2 (Table 1). Cross2 had also positive and significant "h, i and j" interaction effects at both locations, which may be positively affected its F_1 over its two parents. The trait showed similar genetic variance components at both locations, where positive "i" and "h" were exhibited by all crosses, and negative "l" interactions was showed by Crosses 1, 3 and 4, indicating the relative consistency of this trait under the two levels of salinity. These results support those previously reported by Badwal *et al* (1987), Yadav *et al* (1987) and Chaudhary *et al* (1997). It is seemed that negative "l" interaction was of smaller effect than other positive ones especially for Cross4 under LSL and Cross3 under HSL and these F_1's were superior in the two locations, as early observed in Table (1). Potance ratios indicated that under LSL, all crosses exhibited over–dominance towards greatest number of branches. While under HSL, Cross2 and Cross3 showed over–dominance and Cross4 showed partial dominance towards high number of branches, but Cross1 exhibited over-dominance towards the fewest number of branches.

Under LSL, all crosses showed positive heterosis estimates (Table 3) in the ranges 29.81 and 28.38 (Cross 4) to 6.98 and 1.49 (Cross1) relative to their MP's and BP's, respectively, and consequently the two crosses

recorded positive F_2 inbreeding effects ranged from 30.39 (Cross 4) to 14.34 % (Cross1). Positive heterosis detected by Khulbe *et al* (1998), Ali *et al* (2000) and Sharaan and Ghallab (2005) support the present results. Under HSL, three out of the four crosses namely Cross 2 (28.08), Cross 3 (23.31) and Cross 4 (4.22) surpassed their respective MP's while only two crosses namely Cross 2 (27.17) and Cross3 (15.34%) surpassed their BP's. Crosses 3, 2 and 1 recorded positive inbreeding effects of 23.98, 15.93 and 10.68%, respectively. The h^2_b and h^2_n estimated under LSL were of ranges from 96.35 for Cross1 to 90.22 for Cross 4 as well as from 87.00 for Cross 2 to 70.14% for Cross 4. The ranges of h^2_n under HSL were from 93.79 (Cross 2) to 91.31(Cross1) for h^2_b and from 83.88 (Cross1 which gave the highest "Gs", 66.90 %) to 68.63 (Cross3) for h^2_n.

Number of pods/ plant (pods)

Parental genotypes and their F_1 and F_2 plants carried more number of pods under LSL compared with those under HSL (Table 1). Except for Cross4 in both locations and Cross1 under HSL, all F_2 hybrids surpassed their respective parents. The highest podding F_1's were of Cross3 (335.56) under LSL and of Cross2 (215.54) under HSL, while Cross4 recorded the lowest number of pods (206.04 and 152.39) in the two locations, respectively. Except for F_2 of Cross4 under LSL all F_2 plants had a fewer number of pods than their corresponding F_1's, due to increasing segregation towards negative direction. The highest number of pods was produced by F_2 of Cross 3 (224.51 and 156.76) under low and high salinity level, respectively, reflecting its consistency for this trait compared to the other crosses. All BC's (except BC_2 of Cross4 and BC_1 of Cross3 under LSL) exceeded their respective F_2 means. BC_1 of Cross4 (305.08 and 213.59) and BC_2 of Cross2 (252.12 and 250.53) produced the highest number of pods under LSL and HSL respectively.

A, B and or C scaling tests were significant for all crosses at both locations, except Cross 4 under LSL (Table 2). These results revealed absence of non-allelic interaction effects of Cross4 under low salinity; while it was presented in the other cross-cases. This result is in full agreement with that reported by Abo El-Wafa *et al* (2004), who detected insignificant scaling tests for number of pods/plant in one out of five crosses studied. The gene effect of Cross4 under LSL was mainly additive, where "D" was higher than "H' and greatly higher than "E" variance components, as indicated by $\sqrt{H/D} < 1$ (0.92) and confirming the importance of the additive and/or additive x additive gene effects. Cross1 under HSL also showed positive additive effect. At both locations, Cross3 showed significant positive dominance effects, which may be caused by superiority of its F_1 under LSL or F_2 under both low and HSL (Table 1). Crosses 1&2 had positive "h" and "i" effects in the two locations. Positive "j" and

negative "l" interactions were exhibited also by Cross 2 at both locations. Significant epistatic effects were early detected by Sachan and Singh (1987), Gupta *et al* (1987), and Varsha *et al* (1999). The four crosses under HSL showed negative "l" interaction effects. These gene action and interaction effects resulted, as indicated by potance ratios, in over-dominance for Cross2 and Cross3 at the two locations and partial dominance for Cross1 at both locations and Cross4 in LSL towards positive direction, and over-dominance in Cross4 towards lowest number of pods under high salinity levels.

None of the F_1 hybrids, tested under LSL, showed heterosis relative either to MP's or BP's. (Table 3), and significant positive F_2 inbreeding effect was show only by Cross1 (31.52). While under HSL, Cross3 (54.86), Cross2 (46.16) and Cross1 (10.17%) showed significant positive heterosis relative to their corresponding MP's, but none of the crosses surpassed their better parents. Varsnney and Rao (1997), Ali *et al* (2000), Shrief *et al* (2002) and Sharaan and Ghallab (2005) obtained similar heterotic effects. Inbreeding effects detected under HSL were 40.74 (Cross2) and 36.77 (Cross1). The h^2_b estimates were from 97.28 (Cross2) to 93.24 (Cross3) under LSL, and from 98.23 (Cross3) to 92.36 (Cross4) under HSL. Values h^2_n were from 82.05 (Cross2 which had the highest "h^2_b" and "Gs", 170.35) to 67.60 (Cross4) under LSL, and from 85.15 (Cross2 which gave highest "Gs", 251.77) to 47.11% (Cross1) under HSL.

Seed index, g (SI)

Seeds of parental genotypes and their F_1 hybrids and segregating generations were heavier under LSL than those under HSL (Table 1). It was noticed that, the F_1's were of varied means under the two locations. Where under LSL, the F_1 means of Cross2 and Cross3 were intermediate but lighter for Crosses 1 and 4 than its parents. However, under HSL, the intermediate F_1 means were showed by Crosses 1, 2 and 3, while F_1 mean of Cross4 surpassed those of its parents. All F_2 means (except of Cross2 under HSL) exceeded their respective F_1's, due to inbreeding gain. It is interesting to note that Cross1 possessed the heaviest weights either under LSL (4.56) or HSL (4.40g), indicating its importance for improving this trait. Cross3 had the highest BC_1's (3.80 and 3.30) and BC_2's (3.88 and 3.50g) under LSL and HSL, respectively, reflecting their value in further breeding programs.

Gene effects data presented in Table (2) show that dominance was higher than additive effect at both locations. Negative additive effect was shown by Cross4 under HSL and by Cross1 under both salinity levels, indicating less important role of additive effect for improving this trait. Although Cross4 had positive "I&h" interaction effects in both locations, its F_1 & F_2 means were not superior. Crosses 1 and 2 showed negative "h","i" and "j" effects in Cross 1 under LSL and Cross 2 under HSL, but all seemed

to be of less effect compared to that of positive "i" interaction effect which caused superiority of F_1 of Cross2 and F_2 of Cross1 (Table 1). In this concern, the authors attributed the effect on this trait to different gene actions and interactions, i.e, to additive (Yadav *et al* 1987) to additive and dominance (Sachan and Singh 1987), to additive and non- additive (Yadav *et al* 1985, Singh and Chauhan 1987, and Rishipal and Kumar 1993) and to non-additive (Sheikh and Singh, 1998). All Crosses under LSL showed partial dominance towards positive direction (Crosses 2, 3 and 4) and negative direction (Cross 4). While under HSL, partial-dominance was detected for Crosses 1, 2 and 3 and over-dominance for Cross 4 towards positive direction.

Under LSL, negative heterosis was exhibited by Cross1 (-7.04) while positive heterotic effects were shown by Cross2 (12.36), Cross4 (5.22) and by Cross3 (4.77) relative to their respective MP's. Positive heterotic effect for seed index was previously found by Khulbe *et al* (1998), Tyagi *et al* (2000) and Abou-Ghazala (2001). However, all Crosses showed negative heterosis relative to their BP's, in a range from -9.57 (Cross4) to -1.53 (Cross 2), also all crosses showed negative inbreeding effects (Table 3). Under HSL heterosis relative to MP was negative for Cross4 (-2.41) and positive for Crosses 3 and 1 in a range from 8.47 (Cross 3) and 6.94 (Cross 1), and consequently inbreeding depression was negative for all Crosses except Cross2. Estimates of h^2_b were in ranges from 87.22 (Cross 1) to 80.26 (Cross 3) under LSL, and from 95.06 (Cross2) to 84.66% (Cross 4) under HSL. Values of h^2_n were in ranges from 76.53 (Cross4 which had the highest "Gs", 11.42%) to 36.42 (Cross 1) and from 89.28 (Cross 2) to 41.98% (Cross 3) under LSL and HSL, respectively. The highest "Gs" (25.47%) under HSL was produced by Cross1.

Seed yield (g)/ plant (s.y/pl.)

All parental genotypes and their F_1 and F_2 means were higher yielding under LSL than those under HSL (Table 1). All F_1 hybrids (except of Cross1 under HSL and of Cr.4 under both salinity levels) outyielded their respective parents. It is interesting to note that, the F_1 of Cross3 produced the highest plant yield either under LSL (19.79), due to its advantages concerning highest number of pods in addition to its earliness, or under HSL, (14.71g), due to its superiority in number of branches and seed index, in addition to that it was the second cross concerning number of pods. All F_2's yielded less than those of their F_1's, and the highest F_2 means were11.37 for Cross2 and 6.77g for Cross3 under LSL and HSL, respectively. But, all BC_1's were higher yielding than their F_2's. All BC_1's outyielded their P_1's, as well as all BC_2's (except Cross1 under HSL). Cross3 had the highest BC_1 either under LSL (17.97) or under HSL (14.18g), while the highest yielding BC_2 plants were of Cross 2 (18.19) under LSL and of Cross4 (12.70g) under

HSL. These above mentioned results, concerning seed yield/plant and its components, confirmed the importance of Cross3 as promising genetic material to be used further breeding for improving canola crop.

As shown in Table (2), dominance effect was higher than additive one in all Crosses tested under both locations. Positive additive effect was exhibited by Cross3 under HSL, which may have caused superiority of its F_2 (as a fixed effect) under HSL. While Cross1 under LSL and Cross 2 under HSL showed negative additive effects. The crosses showed similarity regarding significantly positive "h" and negative "i" and "l" interactions in both locations, but they differed concerning "j" interaction especially for Cross1. This may resulted in over-dominance for all crosses under LSL and for three of them under HSL, but with different direction. Canola investigators reported different gene actions and interactions affecting seed yield/plant, i.e. additive and dominance (Thakur and Sagwal 1997, and El-Hosary *et al* 1999); dominance (Engqvist and Becker 1991) non- additive (Yadav *et al* 1987 and Sheikh and Singh 1998); and additive and epitasis (Singh and Chauhan 1987, and Rishipal and Kumar 1993). As indicated by potance ratios, Crosses 1, 2 and 3 (towards positive) and Cross4 (toward negative direction) showed over-dominance under LSL. While under HSL, Cross1 showed negative partial dominance, Cross4 showed negative over dominance and Crosses 2 and 3 showed positive over-dominance.

The data listed in Table (3) reveale that Crosses 3, 2 and 1 under LSL surpassed their respective MP's in a range from 52.96 (Cross 3) to 28.02 (Cross 1), and outyielded their BP's in a range from 50.17 to 24.79 for the two crosses, respectively. Positive heterotic effects detected herein support those early reported by various canola authors (Labana *et al* 1978, Schuler *et al* 1992, Khulbe *et al* 1998, Tyagi *et al* 2000, Shrief *et al* 2002 and Sharaan and Ghallab 2005). While Cross 4 showed negative heterosis relative either to its MP (-19.41 & -19.32) or to its BP (-21.70 & 31.58%) under LSL and HSL, respectively. Under HSL, Cross3 (208.23 and 191.09) and Cross2 (63.31 and 32.52%) showed positive heterosis relative to their MP's and BP's, respectively. These results confirmed the mean performance results concerning the superiority of Cross 3. But unfortunately, all crosses showed positive inbreeding effects in the ranges from 46.79 (Cross3) to 2.20 (Cross 4) under LSL, and from 53.54 (Cross 3) to 16.69 (Cross 4) HSL. The h^2_b estimates were in the ranges from 98.24 (Cross1) to 94.64 (Cross 3) under LSL, and from 92.94 (Cross 2) to 84.31 (Cross1) under HSL. Estimates of h^2_n were in the ranges from 82.99 (Cross3) to 29.48% (Cross 4), and from 64.64 (Cross2 which had the highest "Gs", 140.04%) to 51.59% (Cross 4) under LSL and HSL, respectively. Cross4 showed the lowest "Gs", 60.34 and 97.91% under LSL and HSL, respectively.

Seed oil content % (s. oil %)

Parental means had slightly higher S. oil (%) under LSL than those under HSL. This difference was more clear between F_1's (1-3%) and observed also in the segregating generations, reflecting the effective influence of salinity on this trait (Table 1). All F_1's under LSL surpassed their respective parents, while the reverse was true for all F_1's, except of Cross3, under HSL. It is worth to note that, Cross3 had seed oil percentage higher than that of its better parent in both locations, indicating its importance for this trait, in addition to its previously mentioned advantages. All F_2's (except Cross2 and Cross4 under HSL and of Cross1 in both locations) showed lower S. oil (%) than those of their F_1's, due to increased segregants with negative direction. The highest oil percentages were exhibited by F_2 of Cross1 (41.92) under LSL and F_2 Cross2 (41.15%) under HSL. Oil percentages were again increased in all BC's under LSL and in most of them under HSL. All BC_1's (except of Cross3 under HSL) and all BC_2's (except Cross4 under HSL) exceeded their P_1's and P_2's, respectively. Cross4 recorded the highest BC_1 (43.01 and 40.98%) under LSL and HSL, respectively. BC_2 of Cross2 (43.34) under LSL and of Cross1 (42.17%) under HSL showed the highest oil percentage.

Gene effect data listed in Table (2) clear that dominance effect was higher than the additive in all Crosses at the two locations, except Cross4 under HSL. These results are in line with those reported by Prakash *et al* (1987) and Chaudhary *et al* (1997) but contradict those of Engqvist and Becker (1991) who reported that only additive was the most important gene effect. Cross2 showed negative additive effect under LSL. Although the Cross 4 had positive additive effect at the two locations, its F_1 mean was not superior under HSL, but the effect of additive (as fixed residual) increased their F_2 mean. Positive and significant "h" and "i" under LSL and "l" interaction under HSL of Cross3, may be caused by superiority of its F_1 means in the two locations. As indicated by potance ratios, all Crosses under LSL showed over-dominance towards positive direction. Over-dominance, but towards negative direction for Crosses 1, 2 and 4 and positive for Cross3, was detected under HSL. However Hu-Zi (1988) reported partial dominance.

All Crosses under LSL showed positive heterotic effect relative either to their MP's, in a range from 8.45 to 1.95, or to BP's in a range from 8.13to 0.67% recorded by Cross3 and Cross1, respectively. Consequently, the highest inbreeding effect (4.95) was recorded by Cross3 (Table 3). Under HSL, Cross 3 also gave positive heterosis effect relative to MP (2.67) and BP (2.25%), reflecting its importance for improving this trait. The remainder Crosses under HSL had negative heterosis effects. Hari *et al* (1995), Pandey and Zehr (1999), Ali *et al* (2000) and Sharaan and Ghallab (2005) reported positive heterosis, whereas, Schuler *et al* (1992) and Falk *et*

al (1994) reported negative heterosis for seed oil content (%). Estimates of h^2_b were in the ranges from 97.88 (Cross1) to 91.04 (Cross 2) under LSL, and from 97.30 (Cross1) to 66.67% (Cross 4) under HSL. Values of h^2_n ranged from 83.00 (Cross4) to 52.80. (Cross 2) under LSL and from 61.11 (Cross 4) to 28.59% (Cross1) under HSL. The highest value of "Gs" estimated under LSL and HSL, 2.27 and 1.01% were recorded by Cross3 and Cross2, respectively.

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التباين والفعل الجيني والمعالم الوراثية في ستة عشائر لأربعة هجن من الكانولا وتأثرها بمستويات الملوحة المختلفة.

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تم تحليل متوسطات الاجيال الستة عشائر في أربعة هجن من الكانولا قيمت تحت مستوى منخفض وأخر مرتفع من الملوحة في أراضي حديثة الاستصلاح بمزرعة كلية الزراعة بالفيوم وأوضحت النتائج مايلي:-

اختلف أبوي كل هجين معنويا في السبعة صفات التي تم دراستها . كما اختلفت التباينات من موقع إلى آخر تبعا لاختلاف نسبة المكونات الوراثية إلى غير الوراثية وأيضا تبعا لمستوى الملوحة . زيادة مستوى الملوحة اثر بشدة على متوسطات الصفات وقيمة المعالم الوراثية. فيما عدا عدد القرون للهجين الرابع. تحت المستوى المنخفض للملوحة أظهرت جميع الصفات في كل الهجن معنوية في قيم المقاييس الثلاثة (A,B&C) دليل وجود تفاعل غير أليلي ضمن المؤثرات الوراثية الحاكمة لسلوكها ومظهرها. في كل الهجن كان الفعل الجيني الإضافي أكثر أهمية من الفعل السيادي لصفة التزهير فقط بينما كان العكس للصفات الأخرى. التفاعل الإضافي الإضافي كان

معنوي وموجب في معظم الهجن لصفات المنطقة الثمرية وعدد الأفرع وعدد القرون ومحصول النبات تحت كلا المستويين من الملوحة، صفة نسبة الزيت تحت مستوى الملوحة المنخفض، بينما كان معنوي وسالب لصفة التذهير للهجينين 4،1 وصفة البذرة للهجينين 2،1 تحت كلا المستويين من الملوحة . واختلفت التفاعلات الجينية الأخرى من صفة إلى أخرى تبعا لاختلاف الهجن والمواقع .

أظهرت معظم الصفات(نسبة لمتوسط الأبوين) وبعضها(نسبة للأب الأفضل) في كل الهجن (عدا الهجين الثالث) قوة هجين موجبة تحت كلا المستويين من الملوحة. بينما اظهر F_1 للهجين الثالث فقد اظهر قوة هجين سالبة لصفة التزهير – تحت المستوى العالي للملوحة– مما يدل على أهميته في التربية للتبكير . وقد ظهر تأثير مرغوب للتربية الداخلية لصفات التزهير (في هجن ا، 4،2) وطول المنطقة الثمرية (في الهجن 4،3،2) ودليل البذرة (في كل الهجن) تحت مستوى الملوحة المنخفض وكذلك طول المنطقة الثمرية (هجن 1) وعدد الأفرع (هجن4) ودليل البذرة (في الهجن 4،3،1) ونسبة الزيت في الهجن(4،2،1) تحت المستوى المرتفع للملوحة . وبالنسبة قيمة معامل التوريث بمعناه الواسع والضيق والتحسين الوراثي المتوقع فقد اختلفت باختلاف الصفات، والآباء ومستوى الملوحة. و مما يستحق الذكر أن الجيل الأول للهجين الثالث قد أعطى أعلى محصول نبات ونسبة زيت تحت كلا المستويين من الملوحة (لتميزه في عدد الأفرع أو عدد القرون أو دليل البذرة) علاوة على تميزه في التبكير فإن الجيل الثاني له كان أعلى محصول (بعد الهجين2) بالإضافة إلى ارتفاع محصول الهجين الرجعي الأول (BC_1) بينما الهجين 2 أعطى أعلىBC_2 محصولا .لذلك فإن الهجين 3 (يليه هجين2) تعتبر أساس واعد يمكن استخدامها في برامج تربيه لاحقة(باستغلال التأثير الجيني فيها) لإنتاج طرز محسنة من الكانولا.