

**DIALLEL CROSS ANALYSIS OF CANOLA (*Brassica napus* L.)
UNDER DIFFERENT ENVIRONMENTS**

By

El-Hosary, A.A.*; Afiah, S.A.N.**; El-Badawy, M.*
and Hassan, A.I.**

* Agron. Dept. Fac. Agric. Sci. Moshtohor, Zagazig Univ. (Benha Branch)

** Plant Breeding Unit, Plant Genetic Resources Dept. Desert Research Center

ABSTRACT

Six diverse [Lirasol (P_1), Duplo (P_2), Canola-103 (P_3), Silvo (P_4), Sido (P_5) and Cresor (P_6)] canola varieties and their 15 F_1 half diallel crosses were evaluated for seed yield and its attributes under two salinity levels at Ras Sudr, South Sinai and normal conditions at Moshtohor, Kalubia. Mean squares due to general and specific combining ability were significant for all traits studied at the three environments, suggesting the importance of both additive and non-additive components of genetic variations. The largest part of the total genetic variability was a result of additive and additive x additive gene action types for all traits studied as detected by GCA/SCA ratio. Sedo (P_5) and Canola-103 (P_3) seem to be a good combiners for seed yield and most of its attributes while, Duplo (P_2) was the best one for seed yield and number of siliques/plant under all environments studied.

Five, ten and six crosses showed significant positive SCA effects for seed yield/plant in low salinity, high salinity and normal experiments, respectively. The three crosses $P_2 \times P_5$, $P_3 \times P_4$ and $P_5 \times P_6$ exhibited significant positive S_{ij} effects in the three experiments.

From the twenty one diallel set, ten genotypes gave (s) value <1 , out of them, canola-103 (P_3), $P_2 \times P_3$ and $P_2 \times P_5$; the later two crosses exhibited high yielding ability under high salinity level. Moreover, P_3 considered to be a good combiner for seed yield/plant and one or more of its components under different environments studied. Hence, selection for both low (S) value and high yielding capacity at the stress environment would be a useful criterion to exploit more tolerant genotypes.

High heritability values were detected for all traits studied except number of racemes/plant in low salinity and number of seeds/siliques and seed index in high salinity experiments, revealing that the most of phenotypic

variability in each trait was due to additive genetic type. Therefore, a pedigree selection program for these traits might be quite promising.

Key words: Canola breeding, Salinity stress, Susceptibility index, Diallel crosses, Genetic parameters, Gene action, Heritability.

INTRODUCTION

Canola (*Brassica napus* L.) is one of major oil crops in the world. In Egypt, canola recently hopefully to contribute in reducing oil deficiency gap. The degree of self sufficiency in plant oil decreased from about 55.31% in 1975 to about 27.6% in 1992 and will to be about 16.4% in 2000 (Saleh, 1995). For increasing total production to bridge this gap between our production and consumption from edible oil, breeding programs under normal and saline environments have gained much attention in order to release high productivity genotypes and meet the increasing demand for oil needs.

The oil production can be increased horizontally by using the salt affected soils at new desert lands and vertically by increasing productivity per feddan. Hybridization between widely diverse parental genotypes is one of the most important procedures for the plant breeder that enables him to isolate new genetic variabilities and consequently select or synthesize a new variety (Mani and Rao, 1975).

Information on the relative importance of general and specific combining ability is important in the development of efficient Canola breeding programs particularly under the stress conditions. Genetically GCA is associated with additive genes, while SCA is attributed primarily to non-additive (dominance and epistasis). It is very essential that the breeder should evaluate the potentialities and eventually combining ability have proved to be of considerable use in crop plants. It will enable to restrict the choice of fewer but efficient and productive genotypes based on their combining ability for creating a highly productive basic core material which will serve as a source material for fashioning productive varieties required for specific needs.

The diallel analysis as outlined by Hayman (1954) attempts to partition phenotypic variation into genotypic and environmental components and to further subdivide genotypic variation into its additive and dominance components. Those values can be used to draw inferences about the genetic system. The concept of general and specific combining ability has become increasingly important to plant breeders because of the widespread use of hybrid varieties in many crops. The data in these experiments were analyzed using both Hayman (1954) and Griffing (1956) procedures. Each method provides unique information about the nature of the genetic system, and together they more clearly resolve the mechanisms of inheritance than do each alone. The study was undertaken to determine the genetic systems affecting seed yield and its

attributes to gain an insight into the relationships among these traits in order to facilitate Canola improvement under different environments.

MATERIAL AND METHODS

The genetic material used in this investigation as a parental varieties of canola were; Lirasol (P₁), Duplo (P₂), Canola-103 (P₃), Silvo (P₄), Sido (P₅) and Cresor (P₆). These divergent varieties have been screened for salt tolerance throughout the breeding program of Desert Research Center (DRC). The oil of such varieties is low in erucic acid (< 2% of total fatty acids moreover, canola-103 (P₃) and Silvo (P₄) are free from erucic acid under Ras Sudr saline conditions (Afiah *et al.*, 1999). In 1996/1997 season, all possible cross combinations excluding reciprocals were made between these parents giving a total of fifteen crosses at the Experimental Station of Moshtohor Fac. Agric. Sci., Kalubia Governorate. In 1997/1998 season, the half diallel set (15 F₁ crosses and their 6 parents) were evaluated under three environments; normal conditions of Moshtohor and two levels of saline conditions at Ras-Sudr Agricultural Experiment Station of DRC, South Sinai. Soil and irrigation water analysis at all environments are shown in Table (1). The three experiments were conducted in randomized complete block design with three replicates. Each replicate consisted of two and one ridge for each parent and F₁ cross, respectively, each ridge was of four meter length and 50 cm width. Seeds were sown in hills of 25 cm apart on 18th and 23rd October at Moshtohor and Ras Sudr, respectively. After 28 days from sowing, seedlings were thinned at one plant/hill. The other cultural practices were applied as usually recommended for the ordinary canola fields in each location. Twelve guarded plants were randomly sampled at harvest for recording the data of each genotype in all traits studied, i.e. plant height, number of racemes/plant, number of siliques/plant, number of seeds/siliques, 1000-seed weight and seed yield/plant.

The stress susceptibility index was computed for yielding ability according to Fischer and Maurer (1978). Useful heterosis for each trait of individual cross were expressed as percent increase of F₁ performance above the better parent value using, Mather and Jinks (1982). Estimates of both general and specific combining ability were computed by method 2, model 1 of Griffing (1956). Diallel cross analysis proposed by Hayman (1954) was employed to estimate the relative magnitudes of genetic components of the total variability to provide sufficient information of the genetic nature of each trait under investigation.

RESULTS AND DISCUSSION

Table (2) presents the analysis of variance for plant height, number of racemes/plant, siliques/plant, seeds/siliques, 1000-seed weight and seed yield per plant at high and low salinity levels as well as normal conditions. Significant

Table (1): Soil and irrigation water analysis of the three experimental sites during 1997/98 growing season.

a). Soil mechanical analysis (0-40 cm depth).

Location	Coarse sand (%)	Fine sand (%)	Silt (%)	Clay (%)	Texture
Moshtohor	6.36	11.87	17.22	64.55	Clay
Ras Sudr (low)	22.61	45.48	16.58	15.33	Sandy loam
Ras Sudr (high)	48.30	28.40	6.20	17.10	Sandy clay

b). Soil chemical analysis (over composited samples before sowing and at harvest).

Location	CaCO ₃	pH	ECe		Soluble cations (meq/100 g)				Soluble anions (meq/100 g)		
			dSm ⁻¹	ppm	Na ⁺	K ⁺	Ca ⁺⁺	Mg ⁺⁺	Cl ⁻	SO ₄ ⁻	HCO ₃ ⁻
Moshthor	3.04	8.10	2.82	1805	15.20	0.49	8.18	4.30	16.40	11.59	0.18
Ras Sudr (low)	42.8	7.35	7.78	4979	47.30	3.90	16.8	9.80	45.8	20.1	11.9
Ras Sudr (high)	48.3	7.37	8.14	5210	48.04	6.02	21.21	10.86	49.0	25.2	11.8

c). Irrigation water chemical analysis (average over five irrigations during the growing season).

Cation water enrichment analysis (averaged over the first 30 days of the growing season)										
Salinity level	pH	EC		Cations (meq/L.)				Anions (meq/L.)		
		dSm ⁻¹	ppm	Na ⁺	K ⁺	Ca ⁺⁺	Mg ⁺⁺	Cl ⁻	SO ₄ ⁻	HCO ₃ ⁻
Moshtohor	7.43	1.41	902	11.50	0.45	1.10	1.05	4.85	3.90	5.35
Ras Sudr (low)	7.58	6.08	3890	38.92	0.40	18.40	4.29	43.55	15.60	2.86
Ras Sudr (high)	7.65	10.95	7008	69.17	0.41	24.73	15.45	67.83	39.55	2.38

Table (2): Mean squares for all traits studied under the two salinity levels (low and high) and normal environments and the susceptibility index (S) of yielding ability.

S.O.V.	d.f.	Plant height			No. of racemes/plant			No. of siliques/plant		
		Low	High	Normal	Low	High	Normal	Low	High	Normal
Reps.	2	1.16	3.19	8.56	0.001	0.032	1.40**	4.33	15.73	59.06
Genotypes	20	529.20**	283.51**	524.28**	0.404**	1.24**	6.91**	2424.3**	2571.7**	4648.34**
GCA	5	1617.0**	758.33**	1072.86**	0.784**	3.55**	20.36**	6641.2**	7304.1**	9984.06**
SCA	15	166.60**	125.23**	341.42**	0.277**	0.47**	2.43**	1018.7**	994.18**	2917.77**
Error	40	13.21	9.21	31.52	0.025	0.022	0.154	12.68	7.45	133.21
GCA/SCA		9.71	6.06	3.14	2.83	7.55	8.38	6.52	7.35	3.42
S. of V.	d.f.	No. of seeds/siliques			1000-seed weight			Seed yield/plant		
		Low	High	Normal	Low	High	Normal	Low	High	Normal
Reps.	2	0.14	0.70	3.02	0.002	0.005	0.039	0.005	0.002	1.98
Genotypes	20	14.53**	19.09**	15.82**	0.221**	0.350**	0.169**	8.261**	7.377**	27.98**
GCA	5	32.20**	33.49**	47.34**	0.471**	0.420**	0.446**	19.52**	20.21**	70.59**
SCA	15	8.64**	14.29**	5.31**	0.138**	0.326**	0.077**	4.51**	3.10**	13.78**
Error	40	0.291	0.338	1.003	0.015	0.011	0.017	0.020	0.017	0.485
GCA/SCA		3.73	2.34	8.92	3.41	1.29	5.79	4.33	6.52	5.12
										0.00013
										0.0025**
										0.023**

*, ** Denote significance at $P \leq 0.05$ and 0.01 , respectively.

differences among genotypes were obtained in all traits and accounted for a major portion of the phenotypic variation in the three separate experiments.

The mean performance of the six parental varieties and their crosses for the studied traits under the three environments are presented in Table (3). For number of racemes/plant and number of seeds/siliquae in the low salinity, number of seeds/siliquae in normal experiment and 1000-seed weight in high salinity and normal experiments, all the hybrids were within the range of parental varieties. The parental varieties P_1 , P_6 and P_4 gave the highest values for plant height in the low, high and normal experiments, respectively. However, the parents P_3 in the low and high salinity and P_6 in normal experiment had the lowest values for this trait.

For number of racemes/plant, the two hybrids $P_2 \times P_3$ and $P_2 \times P_5$ in high salinity experiment and $P_3 \times P_5$ in normal experiment had significantly increased mean values relation to best parent.

For number of siliquas/plant, the three crosses $P_2 \times P_3$, $P_2 \times P_5$ and $P_2 \times P_6$ in the low and high salinity experiments at six crosses $P_2 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_5$, $P_3 \times P_6$ and $P_3 \times P_5$ in the normal experiment had significant number of siliquas more than the best parent.

Both crosses $P_2 \times P_3$ and $P_3 \times P_4$ gave the highest number of seeds/siliquae in the high salinity experiment. Also, P_5 and the three crosses $P_1 \times P_6$, $P_2 \times P_4$ and $P_5 \times P_6$ gave the heavier seeds than all other genotypes studied under high salinity level. It is worthy to note that $P_2 \times P_3$ F_1 cross exhibited higher mean performance for seeds/siliquae under high salinity level than the low one meantime, its seeds were heavier at low than high salinity level experiments.

For seed yield per plant, the two hybrids $P_2 \times P_3$ and $P_2 \times P_5$ in the low and high salinity experiments, three hybrids $P_2 \times P_3$, $P_2 \times P_5$ and $P_3 \times P_5$ in the normal experiment gave significantly increased mean values relative to their respective best parent. The high seed yield per plant of the previous hybrids could be attributed to high one or more of 1000-seed weight, number of seeds/siliquae, number of siliquas/plant and number of racemes/plant. Differential responses in seed yield and some of its attributes previously reported for F_1 canola crosses under two planting dates (early and late plantings) by Afiah (1991) and at two locations (Moscow and Genesee) by Starmer *et al.*, (1998).

The susceptibility index (S) to high level of salinity stress relative to adequate conditions (normal) computed for seed yield/plant (Table 3). Ten genotypes had (S) value <1 , out of them, canola-103 (P_3), $P_2 \times P_3$ and $P_2 \times P_5$. The later two crosses exhibited high yielding ability under high salinity level as mentioned before moreover, P_3 considered to be a good combiner for seed yield/plant and one or more of its components under different environments

Table (3): Mean performance for all traits studied under the two salinity levels (low and high) and normal environments as well as the susceptibility index of yielding ability (S).

Genotypes	Plant height (cm)			Number of racemes/plant			Number of siliques/plant			Number of seeds/silique			1000-seed weight (g)			Seed yield/plant (g)		
	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal
P ₁	134.33	106.33	148.17	5.70	4.97	6.17	121.3	106.0	277.3	20.33	21.77	23.07	2.82	2.51	2.78	6.81	5.65	17.40
P ₁ x P ₂	124.33	101.33	144.30	5.97	5.43	4.93	161.7	139.7	317.3	19.93	19.13	22.83	3.01	3.19	2.78	8.61	7.24	19.67
P ₁ x P ₃	103.33	94.67	153.60	5.97	4.27	7.10	168.0	144.0	262.3	20.80	22.57	21.97	2.96	2.65	3.11	10.34	8.53	18.13
P ₁ x P ₄	131.33	112.67	158.13	5.37	5.13	5.50	132.3	100.3	285.0	14.90	17.97	20.13	3.08	2.65	2.98	6.16	4.63	16.63
P ₁ x P ₅	141.00	99.67	162.33	5.37	4.67	8.97	142.3	131.0	303.7	20.87	18.80	23.90	3.07	3.17	2.81	8.19	7.32	20.63
P ₁ x P ₆	137.33	118.67	151.60	5.33	5.03	6.67	135.0	119.7	263.3	16.13	16.40	23.20	3.36	3.30	3.03	7.04	6.36	17.67
P ₂	109.00	91.00	143.07	6.43	6.13	4.80	180.7	173.7	306.3	18.70	18.00	23.17	2.93	2.78	2.76	9.85	8.65	21.40
P ₂ x P ₁	116.00	99.67	140.70	5.27	6.47	5.80	203.7	180.3	372.0	18.27	22.97	24.63	3.03	2.46	2.71	10.20	9.56	23.87
P ₂ x P ₄	123.33	111.33	151.07	6.47	6.13	5.97	151.3	133.3	310.3	15.97	17.97	21.17	3.26	3.24	2.69	7.80	7.62	18.07
P ₂ x P ₅	113.67	93.00	170.80	6.17	6.43	8.97	214.7	204.0	388.3	15.73	19.93	22.10	3.56	2.65	2.80	12.36	10.41	26.50
P ₂ x P ₆	131.33	93.67	153.77	5.93	6.30	5.90	201.0	188.0	283.0	16.00	20.67	24.57	3.06	2.79	2.75	9.90	7.81	20.17
P ₃	99.67	86.33	148.40	5.13	4.47	5.87	149.7	132.7	264.7	21.87	19.80	20.90	2.96	2.18	3.13	9.19	7.31	17.57
P ₃ x P ₄	120.67	105.33	160.33	5.73	5.23	7.00	157.3	150.7	303.3	20.73	19.27	23.70	3.06	2.18	3.30	9.65	8.07	18.67
P ₃ x P ₅	115.00	97.00	180.43	5.53	5.47	9.70	155.3	144.0	364.7	19.80	20.57	19.70	3.12	3.01	3.28	9.84	8.34	24.17
P ₃ x P ₆	130.67	115.00	158.33	5.33	4.73	5.80	133.0	120.7	320.0	17.90	15.97	22.73	3.00	2.88	2.99	6.97	6.80	21.87
P ₄	132.33	110.33	166.07	5.83	5.13	4.40	100.3	88.7	283.3	17.90	16.33	16.40	3.17	2.81	2.86	5.65	3.86	14.33
P ₄ x P ₅	121.67	97.67	169.37	5.57	5.27	8.00	127.3	110.3	329.7	16.10	15.03	16.87	3.69	3.05	3.36	7.13	5.26	19.20
P ₄ x P ₆	150.33	108.33	132.50	5.83	5.13	6.73	145.3	130.0	237.0	17.60	17.93	20.70	3.28	2.85	3.27	8.65	6.69	15.80
P ₅	110.33	95.67	160.17	5.93	5.37	8.80	166.7	140.3	302.7	15.77	14.93	18.83	3.33	3.34	3.19	8.65	6.86	18.80
P ₅ x P ₆	130.00	101.00	170.57	6.13	5.73	7.90	158.0	138.3	291.7	14.80	17.93	21.73	3.92	3.25	3.35	9.12	7.46	21.97
P ₆	141.67	123.33	126.53	5.43	4.77	5.37	132.0	114.7	245.7	17.87	17.60	19.67	3.00	2.96	3.28	6.95	6.05	15.70
New LSD																		
0.05	5.223	4.361	8.572	0.241	0.213	0.564	5.117	3.922	2.658	0.775	0.835	1.529	0.187	0.151	0.199	0.203	0.187	1.001
0.01	6.885	5.749	11.277	0.318	0.281	0.743	6.745	5.170	3.503	1.022	1.101	2.012	0.246	0.199	0.262	0.268	0.247	1.319

studied (Table 4). Hence, selection for both low (S) value and high yielding capacity at the stress environment would be a useful criterion to exploit more tolerant genotypes. Similar findings earlier reported by Kelman and Qualset (1991); El-Saied and Afiah (1998) and Afiah *et al.*, (1999 b).

Significant mean square values for GCA and SCA were detected in separate experiments for all studied traits (Table 2), indicating the presence of both additive and non additive gene effects among the parents. To reveal the nature of genetic variance which had the greater role, GCA/SCA ratio was computed and the high values which largely exceeded the unity were detected for all traits at the three experiments, revealing that the largest part of the total genetic variability associated with these traits was a result of additive and additive by additive gene action types. Grosse *et al.*, (1992) tested 21 F_1 crosses and their parents at four environments under North German conditions and found that, the GCA effects were more important than the SCA effects for all traits studied except biomass.

Estimates of GCA effects " \hat{g}_i " for individual parent in the three experiments for each trait are presented in Table (4). High positive values would be interest under all traits in question. The parental variety P_1 gave significant positive \hat{g}_i effects for seeds/siliquae in the three experiments and plant height at low and high salinity. The variety P_2 showed significant positive \hat{g}_i effects for siliquas/plant and seed yield/plant in the three experiments, racemes/plant at low and high levels of salinity and seeds/siliquae at high salinity level and normal conditions. The parental variety P_3 gave significant positive \hat{g}_i effects for siliquas/plant and seed yield per plant in the three experiments, seeds/siliquae at low and high salinity and 1000-seed weight at normal experiment. The parental variety P_4 showed significant positive \hat{g}_i effects for plant height at the three experiments and 1000-seed weight at low salinity. The parental variety P_5 gave significant positive \hat{g}_i effects for racemes, siliquas, seed yield/plant, 1000-seed weight at the three experiments, and plant height at normal experiment (Moshtohor location). The parental variety P_6 showed significant positive \hat{g}_i effects for 1000-seed weight at the three experiments, plant height at low and high levels of salinity and seeds/siliquae at normal experiment. It could be concluded that the variety P_5 seems to be good combiner for yield and its components. Brandle and Mc.Vetty (1989) reported that GCA effects of six parental canola genotypes differed across three environments for the majority of traits studied. While, Prakash *et al.*, (1987) detected two out of eight parents of Indian mustard as good combiners for most of the studied traits.

Specific combining ability effects were computed whenever, significant SCA variance were obtained (Table 5). For plant height, the two crosses $P_3 \times P_5$ and $P_5 \times P_6$ in the three experiments, the crosses $P_2 \times P_3$ and $P_4 \times P_5$ at low salinity, $P_1 \times P_6$, $P_1 \times P_3$ and $P_2 \times P_4$ at high salinity and $P_1 \times P_6$, $P_2 \times P_5$, $P_2 \times P_6$ and $P_5 \times P_6$ showed significant positive SCA effects.

Table (4): Estimates of general combining ability effects of the parental genotypes for all traits studied under the two salinity levels (low and high) and normal environments.

Parental varieties	Plant height (cm)			No. of racemes/plant			No. of siliques/plant		
	Low	High	Normal	Low	High	Normal	Low	High	Normal
P ₁	4.194**	2.375**	-2.139*	-0.079*	-0.369**	-0.160*	-12.125**	-14.597**	-14.694**
P ₂	-5.722**	-4.958**	-4.581**	0.258**	0.701**	-0.701**	26.833**	28.653**	22.472**
P ₃	-10.931**	-4.542**	0.849	-0.263**	-0.290**	0.044	4.708**	5.194**	5.972**
P ₄	4.944**	4.417**	2.515*	0.050	-0.032	-0.597**	-20.583**	-20.181**	-8.986**
P ₅	-3.806**	-5.125**	11.303**	0.113*	0.110**	1.794**	6.500**	5.611**	22.431**
P ₆	11.319**	7.833**	-7.947**	-0.079*	-0.119**	-0.381**	-5.333**	-4.681**	-27.194**
LSD ($\hat{g}_i - \hat{g}_j$):									
0.05	2.120	1.770	3.275	0.093	0.086	0.229	2.078	1.592	6.734
0.01	2.837	2.369	4.382	0.124	0.115	0.306	2.780	2.130	9.009
Parental varieties	No. of seeds/siliques			1000-seed weight			Seed yield/plant		
	Low	High	Normal	Low	High	Normal	Low	High	Normal
P ₁	0.914**	0.801**	1.124**	-0.139**	0.003	-0.101**	-0.709**	-0.606**	-1.067**
P ₂	-0.336**	0.585**	1.557**	-0.054*	-0.086**	-0.227**	1.096**	1.238**	1.875**
P ₃	1.906**	1.672**	0.115	-0.140**	-0.151**	0.072**	0.719**	0.713**	0.721**
P ₄	-0.611**	-0.840**	-2.281**	0.059*	-0.048*	0.033	-1.139**	-1.256**	-2.379**
P ₅	-0.894**	-1.232**	-0.901**	0.224**	0.229**	0.114**	0.540**	0.286**	1.750**
P ₆	-0.978**	-0.986**	0.386*	0.050*	0.052*	0.110**	-0.507**	-0.375**	-0.900**
LSD ($\hat{g}_i - \hat{g}_j$):									
0.05	0.315	0.339	0.584	0.073	0.061	0.075	0.081	0.076	0.406
0.01	0.422	0.453	0.782	0.097	0.081	0.099	0.108	0.101	0.543

*, ** Denote significance at $P \leq 0.05$ and 0.01 , respectively.

Table (5): Estimates of specific combining ability effects for all traits studied under the two salinity levels (low and high) and normal environments.

Crosses	Plant height			No. of racemes/plant			No. of siliques/plant			No. of seeds/silique			1000-seed weight			Seed yield/plant		
	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal	Low	High	Normal
P ₁ x P ₂	1.326	0.964	-3.754	-0.355	-0.245	0.025	0.419	0.025	0.419	0.025	0.419	0.101	0.025	0.419	0.101	-0.296	-0.571	-0.580
P ₁ x P ₃	-14.565	-6.119	0.117	0.565	-0.420	0.067	-0.052	-0.052	-0.052	0.067	-0.052	0.126	0.067	-0.052	0.126	1.810	1.251	-0.959
P ₁ x P ₄	-2.440	2.923	2.984	-0.380	0.189	0.038	-0.155	-0.155	-0.155	-0.340	-0.850	-0.021	-0.016	-0.155	0.038	-0.511	-0.683	0.641
P ₁ x P ₅	15.976	-8.536	-1.604	0.057	-0.420	0.088	-0.210	-0.210	-0.210	0.375	2.367	0.379	-0.190	0.088	-0.210	-0.164	0.462	0.512
P ₁ x P ₆	-2.815	5.506	6.913	-0.118	0.176	0.270	0.391	0.391	0.391	-1.881	-2.271	1.650	0.270	0.391	0.008	-0.363	0.162	0.195
P ₂ x P ₃	8.018	6.214	-10.341	-0.472	0.710	-0.145	43.00	-0.145	-0.145	-1.301	1.854	0.579	0.050	-0.154	-0.145	-0.137	0.437	1.833
P ₂ x P ₄	-8.524	8.923	-1.641	0.415	0.118	0.080	0.517	0.517	0.517	-1.005	-0.633	0.133	0.080	0.517	-0.126	-0.852	0.647	-0.867
P ₂ x P ₅	-1.440	0.131	9.305	0.053	0.276	0.219	-0.358	-0.358	-0.358	-1.035	1.725	0.133	0.219	-0.358	-0.100	2.209	1.715	3.437
P ₂ x P ₆	1.101	-12.161	11.521	0.011	0.372	0.210	-0.634	-0.634	-0.634	-0.685	2.213	1.312	-0.107	-0.634	-0.146	0.790	-0.225	-0.246
P ₃ x P ₄	2.018	2.506	2.196	0.203	0.210	-0.037	-0.475	-0.475	-0.475	0.790	1.440	0.121	-0.037	-0.475	0.189	1.551	1.442	0.887
P ₃ x P ₅	5.101	3.714	13.509	-0.060	0.301	-0.135	0.075	0.075	0.075	-1.026	-3.575	0.921	-0.135	0.075	0.081	0.065	0.170	2.158
P ₃ x P ₆	5.643	8.756	10.659	-0.068	-0.203	-0.082	0.125	0.125	0.125	-0.393	-1.750	-1.263	-0.082	0.125	-0.190	-1.761	-0.716	2.608
P ₄ x P ₅	-4.107	-4.577	0.776	-0.339	-0.157	0.228	0.012	0.012	0.012	1.190	0.904	1.283	0.228	0.012	0.207	-0.790	-0.948	0.391
P ₄ x P ₆	9.435	-6.869	-16.841	0.120	-0.061	-0.001	-0.011	-0.011	-0.011	1.190	0.904	1.283	-0.001	-0.011	0.118	1.778	1.147	-0.359
P ₅ x P ₆	-2.149	-4.661	12.438	0.357	0.397	0.471	0.118	0.118	0.118	-1.326	1.296	0.937	0.471	0.118	0.117	0.572	0.375	1.679
LSD S ₀ -S ₆	5.610	4.684	8.666	0.246	0.228	0.606	5.497	5.497	5.497	0.831	0.897	1.546	0.190	0.162	0.200	0.216	0.290	1.075
0.05	7.586	6.267	11.594	0.329	0.305	0.810	7.355	7.355	7.355	1.111	1.200	2.048	0.254	0.216	0.268	0.289	0.268	1.438
LSD S ₀ -S ₆	5.194	4.336	8.023	0.228	0.211	0.560	5.889	5.889	5.889	0.771	0.830	1.431	0.176	0.150	0.185	0.200	0.185	0.995
0.01	6.949	5.802	10.734	0.305	0.282	0.750	6.809	6.809	6.809	1.031	1.111	1.915	0.236	0.201	0.248	0.268	0.248	1.312

*, ** Denote significance at P<0.05 and 0.01, respectively.

For number of racemes/plant, four, eight and eight crosses showed significant positive SCA effects at low, high and normal experiments, respectively. Also, the cross $P_3 \times P_4$ gave significant positive SCA effect at the three experiments. Moreover, the crosses $P_1 \times P_3$, $P_2 \times P_3$ and $P_2 \times P_5$ had the highest values of SCA effects in the same order.

For number of siliques/plant, both crosses ($P_2 \times P_3$) and ($P_2 \times P_5$) in the three experiments, $P_1 \times P_3$, $P_2 \times P_6$, $P_3 \times P_4$ and $P_4 \times P_6$ in low and high salinity, and $P_3 \times P_5$, $P_3 \times P_6$ and $P_4 \times P_5$ in the normal experiment showed significant positive SCA effects.

The cross $P_4 \times P_6$ in the three experiments, $P_1 \times P_2$, $P_1 \times P_5$, $P_3 \times P_4$ and $P_3 \times P_5$ at low salinity experiment, $P_1 \times P_3$, $P_2 \times P_3$, $P_2 \times P_5$, $P_2 \times P_6$, $P_3 \times P_4$ and $P_3 \times P_5$ at high salinity experiment and $P_1 \times P_5$, $P_2 \times P_3$ and $P_2 \times P_6$ in normal experiment showed significant positive S_{ij} values for number of seeds/siliques.

For 1000-seed weight, four, five and two crosses showed significant positive SCA effects at low, high and normal experiments, respectively. The crosses $P_5 \times P_6$, $P_2 \times P_4$ and $P_4 \times P_5$ gave the highest best SCA effects in the same order.

For seed yield per plant, five, ten and six crosses showed significant positive SCA effects in low, high and normal experiments, respectively. While, the three crosses $P_2 \times P_5$, $P_3 \times P_4$ and $P_5 \times P_6$ had significant positive SCA effects in the three experiments.

In crosses showing high specific combining ability involving only one good combiner, such combinations would show with desirable transgressive segregate. Providing that the additive genetic system present in the good combiner as well as the complementary and epistatic effects in the crosses, act in the same direction to reduce undesirable plant characteristics and maximize the character view. Therefore, most of the previous crosses might be of prime importance in breeding program for traditional breeding procedures.

Data were further subjected to the diallel analysis proposed by Hayman (1954) to obtain more information about the genetic behavior for the traits under test. The computed parameters for all traits at the three experiments are presented in Table (6). With the exception of number of siliques/plant in normal experiment and 1000-seed weight at low salinity experiment, the additive component (\hat{D}) reached the significance level of probability for all traits. This finding is in harmony with that reached above in Table (2). For both exceptional cases, insignificant (\hat{D}) values in spite of significant GCA mean squares were obtained. Dominance may have a role in GCA estimate as emphasized by Jinks (1954). Moreover, the computed t^2 was significant (Table 6), revealing the presence of complementary type of epistasis. Therefore, the contradiction in magnitude detected herein between \hat{D} and GCA estimates for both cases, could

Table (6): Analysis of genetic parameters in F_1 half diallel set of canola for all traits studied under the two salinity levels (low and high) and normal environments.

Genetic parameters	Plant height	No. of branches /plant	No. of siliques /plant	No. of seeds/sili- quae	1000- seed weight	Seed yield/ plant
\hat{A} Low	248.97**	0.18**	880.96**	4.430**	0.03	2.63**
\hat{D} High	186.79**	0.32*	886.23**	5.84**	0.07*	2.64**
Normal	181.17**	2.37**	484.64	6.43*	0.045**	5.85**
\hat{A} Low	31.31	0.09	-200.56	-0.28	-0.04	-0.76
\hat{F} High	105.37*	-0.22*	-384.42	3.34*	0.05	-0.78
Normal	95.42*	-1.07**	-731.62*	-1.15	-0.01	-4.31*
\hat{A} Low	207.15**	0.38**	1271.68**	11.40**	0.17**	5.63**
\hat{H}_1 High	174.87**	0.66*	1230.31**	20.18**	0.46**	3.68**
Normal	455.65**	2.67**	3941.31**	5.75**	0.104**	16.88**
\hat{A} Low	195.72**	0.35**	114.22**	10.17**	0.14	5.53**
\hat{H}_2 High	144.06*	0.48	1155.95**	16.26**	0.39**	3.43**
Normal	339.38*	2.34**	2848.96**	4.93**	0.07**	12.24**
\hat{A} Low	61.07*	-0.005	830.15**	2.93*	0.10**	2.42**
\hat{h}^2 High	1.71	0.23	735.57**	3.28*	-0.0009	3.29**
Normal	192.97*	3.29**	2276.43**	4.94**	-0.003	19.65**
\hat{A} Low	4.21	0.016	4.09	0.095	0.004	0.006
\hat{E} High	2.97	0.007	2.61	0.113	0.004	0.005
Normal	10.14	0.071	43.23	0.37**	0.006	0.19
\hat{A} Low	0.85	1.45	1.20	1.60	2.45	1.46
$[\hat{H}_1/\hat{D}]^{1/2}$ High	0.97	1.42	1.18	1.86	2.54	1.18
Normal	1.59	1.06	2.85	0.95	1.52	1.70
$\hat{H}_2/4\hat{H}_1$ Low	0.24	0.23	0.22	0.22	0.21	0.25
High	0.21	0.182	0.23	0.20	0.21	0.23
Normal	0.186	0.22	0.18	0.21	0.18	0.18
\hat{K}_D/\hat{K}_R Low	1.14	1.42	0.83	0.96	0.53	0.82
High	1.82	0.62	0.69	1.36	1.34	0.78
Normal	1.4	0.65	0.58	0.83	0.82	0.64
r Low	0.08	0.64	0.60	-0.43	0.44	0.083
High	0.24	-0.83	0.39	-0.11	-0.65	-0.47
Normal	-0.28	-0.63	0.19	-0.73	0.48	0.48
r^2 Low	0.01	0.41	0.36	0.18	0.19	0.01
High	0.06	0.68	0.16	0.013	0.421	0.22
Normal	0.08	0.40	0.04	0.54	0.23	0.23
$h^2(ns)$ Low	0.71	0.36	0.68	0.53	0.56	0.56
High	0.59	0.74	0.70	0.43	0.29	0.68
Normal	0.52	0.74	0.60	0.72	0.64	0.70
\hat{t}^2 Low	2.98	2.26	0.70	3.45	12.83**	2.24
High	0.08	1.14	1.47	0.04	0.006	2.28
Normal	0.634	1.42	13.03*	0.86	3.60	66.62**

*, ** Denote significance at $P \leq 0.05$ and 0.01 , respectively.

be attributed to the great role of both allelic and non-allelic genetic types of the expression of both cases.

Significant values for the dominance component \hat{H}_1 were obtained for all the studied traits in the three experiments. This results indicate that both additive and dominance types of gene action were involved in determining the performance of single cross progeny in most the studied traits. With the exception of plant height at low and high salinity experiments and number of seeds/siliquae at normal experiment, the H_1 was greater than \hat{D} suggesting that non-additive genetic type is more important than the additive genetic one. These results are in line with those reported by Afiah and Abdel-Sattar (1998). Also, Thukral and Singh (1987) stated that seed yield/plant was governed by non-additive gene effects in 9 x 9 rapeseed diallel cross.

The relative of \hat{D} and \hat{H}_1 estimated as weight measure of the average degree of dominance at each locus. With the exception of plant height at low and high salinity experiments and number of seeds/siliquae at normal experiment, the degree of dominance estimated by $(\hat{H}_1/\hat{D})^{0.5}$ was over dominance which suggested that the over dominance are important in the inheritance of these traits. For the exceptional cases partial dominance were detected. Similar results were obtained by Afiah *et al.*, (1999 a) in wheat under saline conditions.

The average frequency of negative vs. positive alleles in parental population from one quarter were obtained by computing the ratio $H_2/4H_1$. Values which largely deviate from one quarter were obtained for plant height and number of racemes/plant at high salinity and normal experiments, number of siliquas/plant, 1000-seed weight and seed yield per plant at normal experiment, and number of seeds/siliquae at high salinity experiment, revealing that negative and positive alleles were unequally distributed among the parents. The symmetry vs. asymmetry in gene frequency was also examined by estimating the F component. Significant positive F values were detected for plant height at high salinity and normal experiments, and number of seeds/siliquae at high salinity experiment, revealing asymmetry with dominance alleles being more frequent. However, significant negative F values were obtained for number of racemes/plant at high salinity and normal experiment, number of siliquas/plant and seed yield/plant at normal experiment, revealing that asymmetry with recessive alleles being more frequent. The same conclusion could again be drawn from the corresponding proportion $[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F} / (4\hat{D}\hat{H}_1)^{0.5} - \hat{F}]$ gene distribution was previously recorded for some traits by Thukral and Singh (1987) in canola and by Afiah *et al.*, (1999 a) in wheat under two salinity levels.

The over all dominance effects of heterozygous loci symbolized as \hat{h}^2 were computed for all the studied traits in the three experiments. Significant \hat{h}^2 values were reached herein in number of siliquas/plant, number of seeds/siliquae and seed yield per plant in the three experiments, plant height at low salinity and

normal experiments, number of racemes/plant in the normal experiment and 1000-seed weight at low salinity experiment, indicating that dominance was unidirectional. Appreciable heterotic effects were previously reported by Thukral and Sagwal (1997).

Heritability in narrow sense was computed according to Mather and Jinks (1982). High heritability values were detected for all traits studied except number of racemes/plant in low salinity experiment, number of seeds/siliquae and 1000-seed weight in the high salinity experiment, revealing that the most of phenotypic variability in each trait was due to additive genetic type. Therefore, a pedigree selection program for these traits might be quite promising. For the exceptional cases, moderate or low heritability values were obtained. Campbell and Kondra (1978) obtained low heritability for seed yield and its components in parents, F_1 and F_2 of three oilseed rape crosses.

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* تحليل هجن الكانولا التبادلية تحت بيئات متباينة *

على عبدالمقصود الحصري* ، سامى عبدالعزيز نصر عافية** ،

محمود الزعبلوى البدوى* ، أحمد ابراهيم حسن**

* قسم المحاصيل-كلية الزراعة بمشتهر-جامعة الزقازيق (فرع بنها).

** وحدة تربية النباتات-قسم الأصول الوراثية-مركز بحوث الصحراء-المطرية-القاهرة.

فى هذه الدراسة تم اجراء كافة الهجن الدائرية (دون العكسية) بين ستة اصناف متباينة فى مستوى التحمل للظروف الملحية ، Lirasol (P_1)، Duplo (P_2)، Canola-103 (P_3)، Silvo (P_4)، Sido (P_5) and Cresor (P_6) والى يقل نسبة حامض الايروميك بكل منها عن ٢٪ (مختاره من خلال برنامج تربية النباتات بمركز بحوث الصحراء) - وفى الموسم التالى ١٩٩٧/١٩٩٨ أقيمت ثلاث تجارب لتقييم الهجن

- الناتجة وأبائها تحت مستويين من ملوحة التربة ومياه الري برأس سدر ، جنوب سيناء وتحت الظروف غير الملحية بمشتهر ، قليوبية.
- أوضح تحليل التباين معنوية الاختلافات الراجعة الى القدرة العامة والخاصة على التألف لكافة الصفات المدروسة تحت مختلف البيئات مما يبرز أهمية مكونات التباين الوراثي الاضافي والغير اضافي (السيادة والتفوق) وبحساب النسبة بينهما أتضح أن الجزء الأكبر من التباين الوراثي يرجع الى الفعل الجيني المضيف، مضيف \times مضيف في كل الصفات تحت الدراسة.
 - أبدى كلا من الاب الثالث (Canola-103) والخامس (Sedo) قدرة عالية على التألف بالنسبة للمحصول ومعظم الصفات المساهمة فيه. في حين كان الاب الثاني (Duplo) أحسن الإباء في القدرة العامة على التألف لصفتي المحصول وعند قرون النبات تحت كافة البيئات.
 - أوضحت قيم تأثيرات القدرة الخاصة على التألف معنوية في خمسة هجن تحت مستوى الملوحة المنخفضة، عشرة هجن تحت الملوحة المرتفعة ومئة هجن تحت الظروف غير الملحية منها ثلاثة هجن ($P_2 \times P_5$, $P_3 \times P_4$, $P_5 \times P_6$) تميزت بقدرة خاصة عالية على التألف في التجارب الثلاث بالنسبة لمحصول النبات من البذور. ومن الجدير بالذكر أن كلا منها انحدر عن أب أو أكثر عالي في قدرته العامة على التألف مما يزيد فرصة الانتخاب من أنساله لتحسين صفة المحصول تحت كل من البيئات المدروسة.
 - بتقدير معامل الحساسية للاجهاد الملحي (S) أعطى عشرة من التراكيب الوراثية تحت الدراسة (أباء وهجن) قيما أقل من الوحدة منها الاب الثالث (Canola-103) الذي يتمتع بقدرة عالية على التألف للمحصول وبعض مكوناته في البيئات الثلاث والهجنين ($p_2 \times p_3$, $p_2 \times p_5$) تميزا بكفاءة إنتاجية عالية تحت ظروف الملوحة المرتفعة وبالتالي يمكن الأخذ في الاعتبار نقص قيم (S) مع ارتفاع المحصول تحت ظروف الاجهاد البيئي كمعايير انتخابية لإنتاج تراكيب وراثية أكثر تحملا للظروف الملحية.
 - كانت قيم الكفاءة الوراثية بمعناها المحدود عالية بالنسبة لكافة الصفات تحت الدراسة فيما عدا عدد أفرع النبات في الملوحة المنخفضة وصفتى عدد بذور القرن ودليل البذرة في الملوحة المرتفعة مما يؤكد ان الاختلافات المظهرية في غالبية الصفات تحت الدراسة ترجع الى الفعل الجيني الاضافي وعليه يكون اتباع برنامج الانتخاب المنسب مجديا في تحسين مثل هذه الصفات.