

GENETICAL ANALYSIS OF YIELD AND ITS ATTRIBUTES FOR F₁ CROSSES IN SESAME

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ABSTRACT

A half diallel set involving six diverse parental sesame genotypes and their F₁ were evaluated at Ismailia Agricultural Research Station, ARC, Ismailia Governorate, Egypt using a randomized complete block design with three replications. Highly significant genotypes and its components (parents, hybrids and parents vs. hybrids) mean squares were detected for all studied traits. Highly significant mean squares were associated with general (GCA) and specific (SCA) combining ability for all studied traits. Also, additive gene action in genetic control of most studied traits was observed. The parent P5 seemed to be the best combiners for seed yield/fad and one or more of its components. The most desirable inter- and intra-allelic interactions (SCA) were detected in F₁ hybrids, P5 x P6 and P1 x P3 for seed weight plant⁻¹ and P1 x P3 and P2 x P4 for seed yield fad⁻¹ which also revealed the highest heterotic effects over mid and better parents. Significant or highly significant values and high values of the dominance component (HI) were also observed for the most studied traits indicating the presence of over-dominance and its confirmed by (HI/D)^{0.5} (more than 1). The parents of P2 and P4 for seed weight plant⁻¹ and P1 and P4 for seed yield fad⁻¹ carried the most dominant genes responsible for the expression of these traits, In the contrary P5, P3 and P6, for seed weight plant⁻¹, and P5, for seed yield fad⁻¹, possessed high concentration of recessive genes.

Key words: *Sesame, Sesamum indicum, Heterosis, Combining ability, Gene action, graphical analysis*

INTRODUCTION

Sesame is one of the most important oilseed crops not only in the Egypt but also in the world. Increasing sesame production is one of the major targets of ARC in Egypt that could be achieved by increasing both the cultivated area and productivity. Consequently, evaluation of a large number of exotic and local lentil germplasm for detecting early maturing genotypes of high yield potential and good seed quality is an important goal of the sesame breeding program. Many investigators have conducted variety evaluation experiments to yield and yield components and found wide significant variability of sesame genotypes for studied traits (Hassan and Sedeck 2015 and Abhijatha *et al* 2017)

Improving yield of sesame is the major challenge for sesame breeder, therefore to achieve high yield of sesame, great attention should be given to have information on nature of gene action and selection based on heterotic effects and *per se* performance as well as general and specific combining ability effects for yield and its related traits. The heterotic effects helps the breeders to determinate the preferable crosses for yield and yield attributing traits. Combining ability analysis of Griffing (1956) is most widely used as biometrical tool of diallel analysis to identify the best combiners which may be hybridized either to exploit heterosis or to build up the favorable fixable genes. Moreover, the half diallel analysis developed by

Hayman (1954 & 1960) and Jinks (1954) also give the breeders with detailed information about the type of gene action, which helps the breeder in the selection of desirable parents for crossing programs and in deciding a suitable breeding procedure for genetic improvement of agronomic traits.

The present study was conducted to estimate types gene action, mid and better parent hetrosis, the magnitude of both general (GCA) and specific (SCA) effect along with information on the nature of gene action responsible for controlling genetic expression of the studied traits.

MATERIALS AND METHODS

To genetically improve yield of sesame, 6 genetically diverse parental sesame genotypes *i.e.* N.A.554 (P1), Shandwell 3 (P2), Zahar12 (P3), Zahar14 (P4), Zahar18 (P5) and M2A24 (P6), the pedigree of twenty genotypes is shown in Table (1). were received from Oil Crops Research Dept., FCRI, ARC, Giza, Egypt for crossing by hand emasculation and pollination using half diallel mating design excluding reciprocals during 2017 summer season to produce sufficient seeds for 15 F1 crosses at Ismailia Agricultural Research Station, ARC, Ismailia Governorate, Egypt.

Table 1. Origin and pedigree of the sesame genotypes studied.

Genotypes	Origin	Pedigree
1. N.A.554 (P1)	Egypt	F.A.O
2. Shandwell 3 (P2)	Local variety	A line selected from Giza32 X N.A.130
3. Zahar12 (P3)	Egypt	A line selected from N.A.777X N.A.413
4. Zahar14 (P4)	Egypt	A line selected from N.A777 X N.A413
5. Zahar18 (P5)	Egypt	A line selected from N.A777 X N.A413
6. M2A24 (P6)	Egypt	A line selected from LineB21X Laine574

In 2018 summer growing season, seeds of the six parents along with their 15 F1 crosses were evaluated at Ismailia Agricultural Research Station behaved as sandy soil, ARC, Ismailia Governorate, Egypt. The experimental design was arranged as randomized complete block design with three replications, where each entry either parents or their 15 F1 hybrids were contiguous sown without leaving separators in two ridges with 4 m long, 0.60 cm broad and plants spaced 10 cm within ridge. All other agricultural practices for growing sesame either soil preparation, soil fertilization or cultivation were followed as recommended packages.

The measurements were recorded for: plant height, branches number plant⁻¹, fruiting zone length, capsules number plant⁻¹, 1000-seed weight and seed yield plant⁻¹ based on five competitive plants/plot. Seed yield/fad (kg) was estimated from the plants in the central area being 1.8 m² in each experimental plot, then converted to faddan.

Statistical analysis

The analysis of variance was made for all studied traits as described by Gomez and Gomez (1984). Heterosis was determined for individual hybrids as the percentage deviation of F1 means performance from either mid parents or better parents values. The analysis of general and specific combining ability was done according to method 2 model 1 of Griffing (1956). The combining ability ratio was calculated according to Baker (1978) as follow: $2MS_{gca}/(2MS_{gca} + MS_{sca})$. Hayman analysis of variance (ANOVA) was computed according to Hayman (1954a) following Jones (1965) modification. A graphical analysis (Hayman 1954 a, and Jinks 1954) was performed to determine the frequency of dominant and recessive alleles in the parental sesame genotypes evaluated. Genetic components along with related genetic parameters were estimated according to Hayman (1954b).

RESULTS AND DISCUSSION

Genotypic effects

It is apparent from the ANOVA of the 6 x 6 half diallel mating in Table (1 & 2) that genotypic effects and their components (parents and their F1 crosses) were significant or highly significant for all studied traits the existence of sufficient magnitude of genetic variability among genotypes, parents and crosses which allows to improve these characters.

Table 2. Mean squares of genotypes and their components for all studied traits at 2018 summer season.

SOV	df	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
Genotypes	20	684.28**	1.82**	762.23**	618.58**	0.97**	27.49**	32437.66**
Parents (P)	5	662.67**	3.11**	1132.83**	277.45**	0.82**	22.16**	37224.54**
Crosses (C)	14	650.82**	1.47**	667.52**	776.32**	1.07**	29.49**	32574.40**
P vs C	1	1260.69**	0.36*	235.28*	115.89**	0.31*	26.21*	6588.89**
Error	40	83.29	0.08	53.96	14.86	0.06	3.63	341.48

Similar results were reported by Ramesh *et al* (2014) and Fahmy *et al* (2015). The mean squares parents vs. crosses or non allelic interaction were significant or highly significant for all studied traits, indicating presence of sufficient amount of heterosis among hybrids. This was

confirmed by the values of mean deviation of F1's from the mid-parents (b1) (Jones, 1965) in Table (3) which were highly significant for all studied traits. The significant or highly significant of b2 values were obtained for all traits, indicating asymmetry of gene distribution for these traits. Finally, item b3 was highly significant for most studied traits indicating the existence of inconsistent allelic and non-allelic interaction or dominance effects specific to individual crosses for all traits (Kersey 1965 and Mather and Jinks 1971).

Table 3. Jones analysis for all studied traits at summer season 2018.

SOV	df	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
A	5	289.93**	0.89**	588.50**	212.61**	0.15**	10.01**	11925.35**
b1	1	420.23**	0.12*	78.43*	38.63**	0.10*	8.74*	2196.30**
b2	5	35.62	0.40**	61.38*	80.53**	0.55**	6.62**	12468.75**
b3	9	279.32**	0.62**	194.86**	291.06**	0.32**	10.15**	10231.58**
B	15	207.48**	0.51**	142.60**	204.06**	0.38**	8.88**	10441.62**
TOTAL	20	228.09**	0.61**	254.08**	206.19**	0.32**	9.16**	10812.55**
a*b	10	31.03	0.04	14.05	6.57	0.01	1.98	89.93
b1*B	2	10.10	0.04	12.81	8.10	0.01	0.956	100.10
b2*B	10	19.65	0.02	21.55	6.59	0.01	1.10	169.37
b3*B	18	32.42	0.02	18.77	2.80	0.03	0.869	97.77
b*B	30	26.67	0.02	19.30	4.42	0.02	0.95	121.79
TOTAL *B	40	27.76	0.03	17.99	4.95	0.02	1.21	113.83

Where; *P<0.05, **P<0.01, a=additive effects, b=total non-additive (dominance) effects, b1=mean deviation of F1's from their mid-parents, b2=test if there is equal or unequal distribution among parents and b3=detect existence of unique dominance of each F1, i.e., presence of considerable amount of heterotic effect specific to some crosses, B=block

Combining ability

It is of great interest to note that general (GCA) and (SCA) specific combining abilities were highly significant for all traits as shown in Table (4). Again the (a) component as primary tests of the significance of additive and (b) component as indicator to the presence of non-additive effects (Jones 1965) in Table (2) were highly significant for all traits, revealing that both additive and non-additive gene action played a major role in the gene expression of these traits, but the preponderance was in favor of additive gene action in genetic control of all studied traits except 1000-seed weight. The estimates of backer ratio and (a/b) ratio of Jones method, revealed the

genetic gain is achievable through selection in early segregating generations for all traits except 1000-seed weight. The genetic variance was previously reported on sesame to be mostly due to non-additive gene action for No. of capsules/plant (Thiyagu *et al* 2007 and Preveenkumar *et al* 2012), plant height (Mothilal and Manoharan 2004, and Thiyagu *et al* 2007), No. of primary branches/plant (Thiyagu *et al* 2007), seed yield/plant (Preveenkumar *et al* 2012) and all studied traits (Azeez and Morakinyo 2014), while additive gene action was reported for Plant height (Preveenkumar *et al* 2012), thus and seed weight (Azeez and Morakinyo 2014).

Table 4. Combining ability mean squares for all studied traits at summer season 2018.

SOV	df	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
GCA	5	289.93**	0.89**	588.50**	212.61**	0.15**	10.01**	11925.35**
SCA	15	207.48**	0.51**	142.60**	204.06**	0.38**	8.88**	10441.62**
Error	40	27.76	0.03	17.99	4.95	0.02	1.21	113.83
baker ratio		0.74	0.78	0.89	0.68	0.44	0.69	0.70

Degree of Heterosis

To provide accurate information about presence of dominance and over dominance types of gene action in the expression of various traits, mid-parent (Heterosis, M.P) and better parent (Heterobeltiosis, B.P) were estimated for all studied traits as shown in Table (5).

Heterosis

Concerning heterosis relative to mid parent, the shortest crosses were detected in P3 x P5 (-9.35) followed by P1 x P5 (-6.57), due to these crosses have highly significant negative heterosis relative to mid parents. The more branches were detected in P3 x P5 (59.78) followed by P4 x P5 (20.17), the tallest fruiting length were detected in P3 x P5 (26.05) followed by P5 x P6 (16.77), more capsules number were found in the crosses P2 x P6 (49.66) followed by P2 x P4 (36.11), the heaviest seed weight were detected in P4 x P6 (61.29) followed by P2 x P4 (26.61), the heaviest seed weight plant⁻¹ were detected in P1x P3 (42.83) followed by P3 x P4 (34.28) and the highest seed yield fad⁻¹ were detected in P1 x P3 (67.73) followed by P1 x P4 (35.98), These crosses have highly significant positive heterosis relative to mid parents.

Table 5. Heterosis and heterobeltiosis of fifteen sesame F1 crosses for all studied traits at summer season 2018.

Cross	Plant height		Branches number plant ⁻¹		Fruiting zone length		Capsule number plant ⁻¹	
	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.
P1 X P2	14.47*	18.77*	-14.41**	1.06**	3.97	13.66*	-35.89**	-40.10**
P1 X P3	10.16	18.76*	4.08**	8.51**	13.76*	20.91**	-3.95	-9.69**
P1 X P4	2.90	4.75	5.60**	40.43**	10.73*	39.41**	27.74**	12.86**
P1 X P5	-6.57	-2.16	-20.47**	-11.69**	8.08	27.88**	6.81*	2.93
P1 X P6	11.85	17.63*	-1.27**	24.47**	12.09*	21.19**	-34.42**	-36.51**
P2 X P3	1.80	14.16	2.61**	15.69**	-0.90	15.74*	-14.87**	-15.45**
P2 X P4	6.08	12.12	-22.54**	-14.06**	12.29*	27.97**	36.11**	13.39**
P2 X P5	8.04	9.00	19.02**	58.44**	-9.71	-2.87	13.72**	10.12**
P2 X P6	-6.33	2.41	-5.54**	0.00	-3.76	-2.76	49.66**	35.69**
P3 X P4	25.06**	32.30**	-16.28**	5.88**	15.27**	56.13**	4.33	-12.61**
P3 X P5	-9.35	2.66	59.78**	85.71**	26.05**	59.96**	12.84**	10.00**
P3 X P6	12.98	15.67*	-12.65**	4.90**	-5.68	8.87	3.56	-5.53
P4 X P5	7.15	14.32	20.17**	81.82**	-6.77	-1.59	-2.99	-17.00**
P4 X P6	3.59	6.97	-27.76**	-24.48**	-21.99**	-10.05	-4.51	-13.14**
P5 X P6	12.66	24.36**	-30.00**	0.00	16.77**	27.02**	12.14**	4.75
LSD 5%	13.04	15.06	0.41	0.48	10.50	12.12	5.51	6.36
LSD 1%	17.45	20.15	0.55	0.64	14.05	16.22	7.37	8.51
Cross	1000-seed weight		Seed weight plant ⁻¹		Seed yield fad ⁻¹			
	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.		
P1 X P2	-6.91**	-9.22**	-5.54**	-10.15**	-1.53	-17.05		
P1 X P3	-12.06**	-12.06**	42.83**	22.99**	67.73**	52.41**		
P1 X P4	-7.45**	-16.31**	16.70**	11.11**	35.98**	34.93*		
P1 X P5	3.27**	0.71**	-16.93**	-23.04**	15.17	-6.38		
P1 X P6	-10.66**	-22.70**	23.77**	19.68**	-20.85	-31.46*		
P2 X P3	-4.00**	-6.38**	27.83**	15.07**	-5.76	-26.50		
P2 X P4	26.61**	17.16**	-3.71**	-3.81*	27.04*	6.35		
P2 X P5	-8.21**	-8.21**	3.05*	-8.82**	-42.52**	-45.00**		
P2 X P6	15.61**	2.24**	-15.34**	-22.00**	-37.28**	-39.30*		
P3 X P4	6.67**	-3.55**	34.28**	20.76**	-1.24	-9.63		
P3 X P5	-13.45**	-15.60**	-21.74**	-36.76**	-34.58*	-50.56**		
P3 X P6	9.84**	-4.96**	32.69**	11.09**	-34.42*	-47.59**		
P4 X P5	17.74**	8.96**	-6.27**	-16.99**	2.28	-17.35		
P4 X P6	61.29**	53.51**	4.75**	-3.40*	-13.22	-25.34		
P5 X P6	-9.70**	-20.15**	24.34**	18.95**	-0.85	-8.05		
LSD 5%	0.35	0.41	2.72	3.14	26.41	30.49		
LSD 1%	0.47	0.55	3.64	4.21	35.34	40.81		

Heterobeltiosis

Negative and desirable heterosis relative to better parent was detected in P1 x P5 (-2.16) for shorting height of plant on one hand. On the other hand, the positive and desirable heterosis of better parents were detected in P3 x P5 (85.71) followed by P4 x P5 (81.82) for more branches plant⁻¹, P3 x P5 (59.96) followed by P3 x P4 (56.13) for the tallest fruiting zone length, P2 x P6 (35.69) followed by P2 x P4 (13.39) for more capsules number, P4 x P6 (53.51) followed by P2 x P4 (17.16) for the heaviest seed weight, P1 x P3 (22.99) followed by P3 x P4 (20.76) for the highest seed weight plant⁻¹ and P1 x P3 (52.41) followed by P1 x P4 (34.39) for the highest seed yield fad⁻¹. These hybrids considered as the best one to carry the genes responsible for improving seed yield of sesame.

Performance associated with combining ability

Performance and general combining ability effects (GCA)

It is clear from the results in Tables 6 and 7, that the shortest parents were detected in P3 (141.47) followed by P6 (148.20) and this confirmed by negative and highly significant GCA effects of these parents, indicating that these parents possessed more decreasing alleles towards shortness.

The highest values of mean performance coupled with highly significant GCA effects were detected in P4 for more branches plant⁻¹ and the tallest fruiting zone length. The parents P2 behaved as the highest capsules number, P1 was the heaviest seed weight, P5 was the highest seed weight plant⁻¹ and seed yield fad⁻¹, These promising parents were coupled with highly significant GCA effects for these previous mentioned traits. Significant variation for yield and yield related traits were reported by Anjay *et al* (2013), Narendra *et al* (2013) and Fahmy R.M., M.A. Abd EL-Satar and T.H.A.Hassan (2015).

Performance and specific combining ability effects (SCA)

Concerning the performance of all genotypes (Table 6), the data show that the shortest cross combinations were P3 x P5 (145.23) followed by P2 x P6 (151.77).

The best cross combinations were P3 x P5 and P4 x P5 for No. of branches plant⁻¹, P2 x P4 and P5 x P6 for fruiting zone length, P2 x P6 and P4x P6 for capsules number plant⁻¹, P2 x P6 and P2 x P4 for 1000-seed weight, P5 xP6 and P1 x P6 for seed weight plant⁻¹fad and P2 x P4 and P1 x P3 for seed yield fad⁻¹.

The specific combining ability values (SCA) of hybrids are presented in Table (8). The shortest crosses due to SCA effects were detected in P3 x P5 for the shortest height of plant.

Table 6. Mean performance of sesame parents and their F1 crosses for all studied traits at summer season 2018.

Traits	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
P1	163.53	3.13	84.17	66.37	4.70	17.40	357.00
P2	175.83	4.27	99.87	76.40	4.47	15.70	521.30
P3	141.47	3.40	74.77	75.37	4.70	12.57	291.80
P4	157.87	5.20	127.77	50.90	3.80	15.73	351.50
P5	178.97	2.57	115.00	71.57	4.47	20.40	570.63
P6	148.20	4.77	97.83	62.13	3.43	18.63	487.77
LSD 5%	4.76	0.15	3.83	2.01	0.13	0.99	9.64
LSD 1%	6.37	0.20	5.13	2.69	0.17	1.33	12.90
P1 X P2	194.23	3.17	95.67	45.77	4.27	15.63	432.43
P1 X P3	168.00	3.40	90.40	68.07	4.13	21.40	544.10
P1 X P4	165.37	4.40	117.33	74.90	3.93	19.33	481.70
P1 X P5	160.00	2.27	107.63	73.67	4.73	15.70	534.20
P1 X P6	174.33	3.90	102.00	42.13	3.63	22.30	334.33
P2 X P3	161.50	3.93	86.53	64.60	4.40	18.07	383.13
P2 X P4	177.00	3.67	127.80	86.63	5.23	15.13	554.40
P2 X P5	191.67	4.07	97.00	84.13	4.10	18.60	313.83
P2 X P6	151.77	4.27	95.13	103.67	4.57	14.53	316.43
P3 X P4	187.17	3.60	116.73	65.87	4.53	19.00	317.67
P3 X P5	145.23	4.77	119.60	82.90	3.97	12.90	282.10
P3 X P6	163.63	3.57	81.40	71.20	4.47	20.70	255.63
P4 X P5	180.47	4.67	113.17	59.40	4.87	16.93	471.60
P4 X P6	158.53	3.60	88.00	53.97	5.83	18.00	364.17
P5 X P6	184.30	2.57	124.27	74.97	3.57	24.27	524.70
LSD 5%	6.74	0.21	5.42	2.84	0.18	1.41	13.64
LSD 1%	9.01	0.28	7.25	3.81	0.24	1.88	18.25

Table 7. General combining ability effects of six sesame parents for all studied traits at summer season 2018.

Traits	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
P1	1.58	-0.37**	-4.92**	-5.95**	-0.06	0.61	17.99**
P2	6.43**	0.16**	-2.35	6.59**	0.11*	-1.37**	18.25**
P3	-8.49**	-0.04	-9.56**	2.31**	0.04	-0.89*	-66.32**
P4	0.99	0.49**	12.23**	-5.29**	0.18**	-0.56	-0.53
P5	5.41**	-0.37**	8.87**	4.17**	-0.05	0.61	46.36**
P6	-5.92**	0.13*	-4.28**	-1.83*	-0.21**	1.59**	-15.75**
LSD gi 5%	3.44	0.11	2.77	1.45	0.09	0.72	6.96
LSD gi 1%	4.60	0.15	3.70	1.94	0.12	0.96	9.31
LSD gi-gj 5%	9.44	0.30	7.60	3.99	0.26	1.97	19.11
LSD gi-gj 1%	12.63	0.40	10.17	5.34	0.34	2.64	25.58

The valuable positive SCA effects were detected in P3 x P5 and P4 x P5 for more branches plant⁻¹, P3 x P5 and P5 x P6 for capsule zone length, P2 x P6 and P1 x P4 for capsule number plant⁻¹, P4 x P6 and P2 x P4 for 1000-seed weight, P5 x P6 and P1 x P3 for seed weight plant⁻¹ and P1 x P3 and P2 x P4 for seed yield fad⁻¹. The SCA represents the non-additive which can be associated with heterobeltiosis (Parameshwarappa and Salimath 2010). It is therefore suggested that SCA performance might be considered as a criterion for selecting the best crosses. A perusal of F1 hybrids revealed that P5 x P6 for seed yield and most of the yield contributing traits, SCA effects along with mid and better parent heterosis.

Table 8. Specific combining ability effects of six sesame parents for all studied traits at summer season 2018.

Traits	Plant height	Branches number	Fruiting zone length	Capsules number	1000 seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
P1 X P2	18.17**	-0.39**	-0.02	-24.14**	-0.15	-1.36	-17.64*
P1 X P3	6.85	0.04	1.92	2.44	-0.21*	3.92**	178.60**
P1 X P4	-5.25	0.51**	7.06*	16.87**	-0.55**	1.52	50.41**
P1 X P5	-15.04**	-0.76**	0.72	6.18**	0.48**	-3.28**	56.01**
P1 X P6	10.63**	0.37**	8.24*	-19.35**	-0.47**	2.34**	-81.74**
P2 X P3	-4.50	0.05	-4.51	-13.57**	-0.12	2.56**	17.37*
P2 X P4	1.53	-0.75**	14.96**	16.06**	0.57**	-0.70	122.85**
P2 X P5	11.78**	0.51**	-12.48**	4.11*	-0.33**	1.60	-164.61**
P2 X P6	-16.80**	0.21	-1.19	29.64**	0.29**	-3.45**	-99.90**
P3 X P4	26.61**	-0.62**	11.10**	-0.42	-0.05	2.69**	-29.31**
P3 X P5	-19.74**	1.40**	17.33**	7.15**	-0.39**	-4.58**	-111.77**
P3 X P6	9.99*	-0.29*	-7.72*	1.45	0.27*	2.24**	-76.12**
P4 X P5	6.02	0.77**	-10.90**	-8.75**	0.37**	-0.88	11.94
P4 X P6	-4.58	-0.79**	-22.91**	-8.18**	1.50**	-0.80	-33.38**
P5 X P6	16.77**	-0.97**	16.72**	3.37*	-0.54**	4.30**	80.26**
LSD Sij 5%	7.79	0.25	6.27	3.29	0.21	1.63	15.78
LSD Sij 1%	10.43	0.33	8.40	4.41	0.28	2.18	21.12
LSD sij-sik 5%	14.09	0.45	11.34	5.95	0.38	2.94	28.52
LSD sij-sik 1%	18.85	0.60	15.17	7.96	0.51	3.94	38.17
LSD sij-skl 5%	13.04	0.41	10.50	5.51	0.35	2.72	26.41
LSD sij-skl 1%	17.45	0.55	14.05	7.37	0.47	3.64	35.34

Graphical analysis

Graphical analysis of the parent-off spring covariance (W_r) and array variance (V_r) and their related statistics were made to get a clear

picture about the inheritance for all studied traits (Table 8 and Figures 1 -7). Additive-dominance model of inheritance was observed as regression coefficient (b) of (Wr/Vr) insignificantly departed from unity for all studied traits, except capsules number plant⁻¹ and 1000-seed weight, indicating the presence of an inter-allelic interaction in the inheritance of these traits. The regression line intercepted the positive side of Wr axis for capsule number plant⁻¹, indicating the presence of partial dominance, while it passed below the point of origin for the rest of traits indicating presence of over-dominance in the inheritance of these ones.

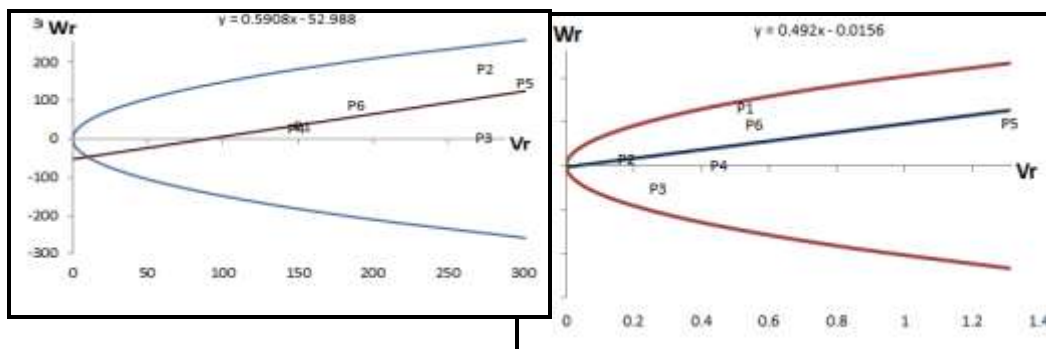


Fig. 1. Wr/Vr graphs for plant height at Summer season 2018.

Fig. 2. Wr/Vr graphs for branches number plant-1 at Summer season 2018.

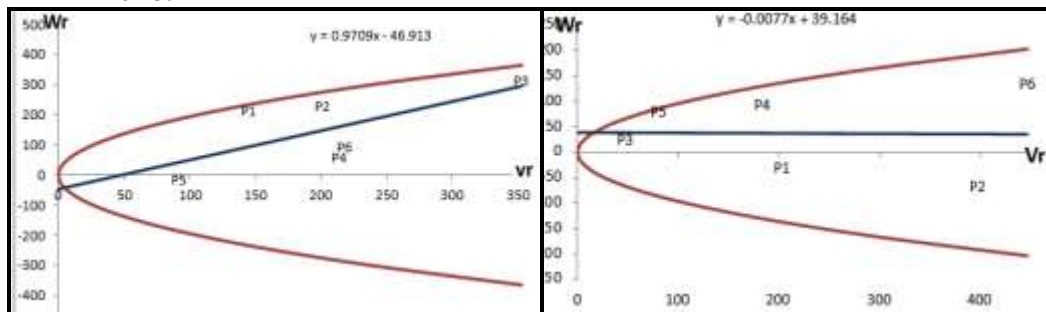


Fig. 3. Wr/Vr graphs for fruiting zone length at Summer season 2018.

Fig. 4. Wr/Vr graphs for capsule number plant-1at Summer season 2018.

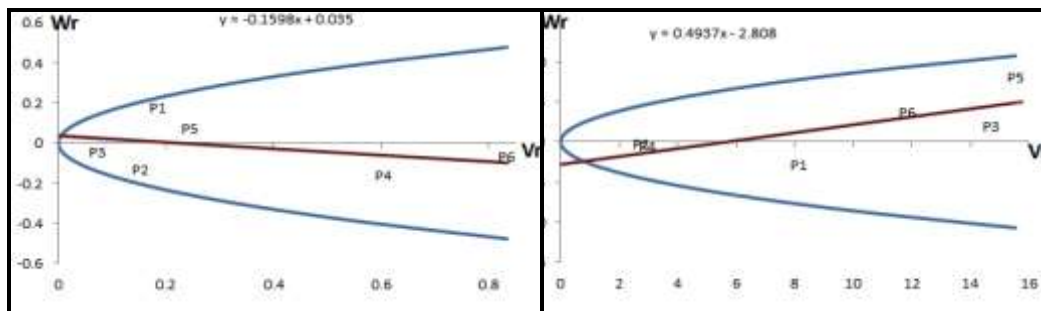


Fig. 5. Wv/Vr graphs for 1000-seed weight at Summer season 2018.

Fig. 6. Wv/Vr graphs for seed weight plant-1 at Summer season 2018.

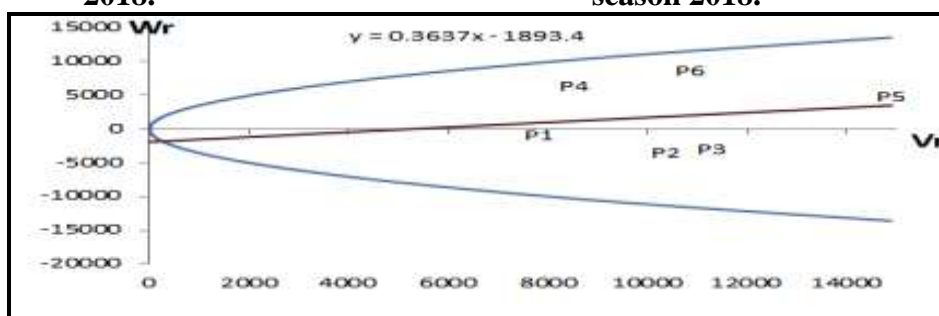


Fig. 7. Wv/Vr graphs for seed yield fad⁻¹ at Summer season 2018

The contradiction between both types of analysis might be a logical result of the presence of complementary type of non-allelic interaction which inflated the ratios of $(H1/D)^{1/2}$ and distorted the (Vr, Wv) graphs (Hayman 1954b and Mather and Jinks 1971). The array points of parental genotypes were widely scattered for all traits, indicating presence of genetic diversity among the tested parents.

The parental following genotypes, P1 and P4 for plant height, P2 and P3 for branches number plant⁻¹, P5 for fruiting zone length, P3 and P5 for capsule number plant⁻¹, P3, P1 and P5 for 1000 seed weight, P2 and P4 for seed weight plant⁻¹ and P1 and P4 for seed yield fad⁻¹, seemed to possess the most dominant genes responsible for the expression of these traits which being closer to the origin of regression graph. In the contrary, the parental following genotypes, P2, P3 and P5 for plant height, P5 for branches number plant⁻¹, P3 for fruiting zone length, P6 and P2 for capsules number plant⁻¹, P6 and P4 for 1000-seed weight, P5, P3 and P6 for seed weight plant⁻¹ and P5 for seed yield fad⁻¹, contained the recessive genes for these traits which might be due to be farthest ones from the origin of regression graph.

Genetic components and related genetic parameters

With respect to genetic components which estimated by the Hayman's diallel analysis as shown in Table (9). The data revealed that the components of additive (D) and dominance (H1 & H2) effects were positive and significant or highly significant for most traits, indicating the important of both additive and non-additive components in the inheritance of above traits. The magnitude of dominance (H1 & H2) was significant or highly significantly higher than additive components (D) for all traits, indicating the presence of over-dominance for the previous traits. Value of H1 was greater than H2 indicating that frequency of gene distribution in the parents was unequal, and that was also supported by the ratio of H2/4H1 (<0.25) which showing asymmetrical gene distribution at the loci in the parents showing dominance for all the traits.

Table 9. Estimation of genetic components for all studied traits at summer season 2018.

Traits	Plant height	Branches number	Fruiting zone length	Capsules number	100-seed weight	Seed weight plant ⁻¹	Seed yield fad ⁻¹
E	26.53	0.03	17.51	4.77	0.02	1.15	115.004
D	194.36**	1.01**	360.10**	87.71	0.25	6.23*	12293.18**
F	89.60	1.02	128.72	28.89	0.60	6.05	16753.17
H ₁	728.31**	2.14**	542.29**	834.99*	1.70	34.43**	46757.43**
H ₂	714.34**	1.80**	499.40**	766.59*	1.22	29.31**	35750.77**
h ²	257.63**	0.06	41.11	22.39	0.06	5.02	1359.63
(H ₁ /D) ^{0.5}	1.94	1.46	1.23	3.09	2.59	2.35	1.95
H ₂ /4H ₁	0.25	0.21	0.23	0.23	0.18	0.21	0.19
K _D /K _R	1.27	2.06	1.34	1.11	2.70	1.52	2.07
h ² /H ₂	0.36	0.03	0.08	0.03	0.05	0.17	0.04
h ² _(n.s)	0.22	0.26	0.49	0.24	0.16	0.24	0.27
H ² _(b.s)	0.90	0.96	0.94	0.98	0.95	0.90	0.99

The F value was positive for all traits, indicated that the presence of higher number of dominant than recessives genes and it was confirmed by the high value of KD/KR for all traits. The overall dominance effects of heterozygous loci (h₂) were found to be positive for all studied traits, indicating that most of the dominant genes had positive effects. All estimates of environmental variance (E) were insignificant for all studied traits, indicating that all traits have not been greatly affected by environmental factors. The average degree of dominance overall loci (Table 9), as estimated by (H₁/D) ¹/₂ ratio was found to be more than unity for all

traits, indicating the role of over dominance gene effects in the inheritance of this traits. The h^2/H^2 values (Table 9) were less than unity for all studied traits implied to be overfed by one gene. Estimates of broad sense heritability, for all traits in Table (9) were very high, and varied from 0.90 to 0.99 on one hand. On the other hand, narrow sense heritability was found to be low for all studied traits except days to fruiting zone length, indicating that selection should be delayed to late segregating generations. However, fruiting zone length had relatively high narrow sense heritability (0.49) suggesting that selection would be effective for improving this trait.

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التحليل الوراثي للمحصول و مساهماته لهجن الجيل الأول في السمسم

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تم تقييم مجموعة من هجن أل F_1 نصف تبادلية متضمنة لستة تراكيب وراثية أبوية مختلفة من السمسم بمحطة البحوث الزراعية بالإسماعيلية، مركز البحوث الزراعية، محافظة الإسماعيلية، مصر. باستخدام تصميم القطاعات الكاملة العشوائية في ثلاث مكررات. وكان التباين الراجع للتراكيب الوراثية ، ومكوناتها (الآباء، الهجن وقوة الهجين) عالي المعنوية لجميع الصفات المدروسة. وكان التباين الراجع إلى القدرة العامة والخاصة على الانتلاف عالي المعنوية في كل الصفات تحت الدراسة. ولوحظ أن الفعل الجيني المضيف يتحكم في معظم الصفات تحت الدراسة مشيراً إلى أهمية الانتخاب في الأجيال الناعزالية المبكرة لتحسين معظم الصفات. كما أظهر الأب زهر ١٨ (P5) قدرة جيدة عامة على التآلف لمحصول البذور/فدان وواحد أو أكثر من مكوناته. في حين أعطت الهجن $P_1 \times P_3$ و $P_5 \times P_6$ لمحصول البذور/نبات و $P_1 \times P_3$ و $P_2 \times P_4$ قدرة خاصة على التآلف عالية المعنوية ، وأعطت أيضاً قوة هجين عالية المعنوية لمتوسط الآباء والأب الأفضل لمحصول البذور/فدان وواحد أو أكثر من مساهماته، وكان التأثير السياتي معنوياً وعالي المعنوية وأكبر من الجزء المضيف لمعظم الصفات المدروسة. وأشار أيضاً متوسط درجة السيادة لمعظم الصفات المدروسة إلى وجود سيادة فائقة . وأشار التحليل البياني أن الآباء P_2 و P_4 لمحصول البذور /نبات، P_1 و P_4 لمحصول البذور/فدان يحمل معظم الاليلات السائدة ، في حين أن الآباء P_5 ، P_3 و P_6 لمحصول البذور/نبات و P_5 لمحصول البذور /فدان يحمل معظم الاليلات المتنحية.

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