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Genetic Analysis of Six Parental Sesame Genotypes for Yield and Its Attributes in F_1 Crosses

M. T. M. Abd El-Kader[1], R. M. Fahmy[2], H. F. A. El-Shaer[1] and M. A. Abd El-Rahman[1]

[1] Agric. Botany-Genetics Dept., Fac. of Agric., Al-Azhar Univ. Cairo Egypt.
[2] Genetic Resources Res. Sec., Field Crop Res. Inst., Agric. Res. Center, Egypt.

Corresponding author: M.T.M.Abd El-Kader, Agric. Botany-Genetics department, Faculty of Agriculture, Al Azhar University, Cairo, Egypt.

E-mail: tarek0360@gmail.com

ABSTRACT

To identify superior hybrids and create desirable combinations, a half diallel set involving six parental sesame genotypes was conducted in 2014 season. Six parental sesame genotypes and their 15 F1 crosses were evaluated at Bahteem Research Station in summer season 2015 using randomized complete block design with three replications. Genotypes and its components (parents, hybrids and parents vs. hybrids) mean squares were highly significant for all studied traits. General (GCA) and specific (SCA) combining ability mean squares were highly significant for all studied traits.

Also, additive gene action was governed in most studied traits. The best combiners for seed yield/plot and one or more of its components were detected NA.77 (P3) and NA.78 (P4). The highest heterotic effects over mid and better parents were detected in F_1 hybrids, NA.80 x NA.35 (P1 xP5) and NA.80 x NA.40 (P1 xP6) for seed yield/plant and seed yield/plot and one or more of its attributes. Significant or highly significant values and high values of the dominance component (H_1) were also observed for the most studied trait, indicating that the presence of over-dominance and its confirmed by $(H/D)^{0.5}$ (more than 1).

The effective selection and high narrow sense heritability were detected for days to 50% flowering (62%), days to physiological maturity (77%) ranging from 62 to77. The parents of NA.77 (P3), NA.59 (P2), NA.78 (P4) carried the most dominance genes responsible for the expression of seed yield/plant and plot in contrary NA.80 and NA.35 for seed yield/plot possessed high concentration of recessive genes.

Key words: Sesame, *Sesamum indicum*, Half diallel analysis, Heterosis, Combining ability, Gene action.
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1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the most important oil seed crops with high oil content, rich nutritive value but also for the quality and quantity (42-59%) of its oil which is rich in vitamin E and has a significant amount of Linoleic acid that can control blood cholesterol levels. The present sesame varieties under cultivation have limited yield potential as most of the varieties evolved and released for cultivation, are selection from local or closely related population [17].

Therefore, to establish a sound basis for achieving high yield of sesame, great attention must be given to detect information on heterotic effects, *Per se* performance, general and specific combining ability effects of parents along with genetic components of variance for yield and associated traits.

The heterotic effects helps the breeders to identify the desirable hybrids either had significantly positive for yield and yield attributing traits or significantly negative for earliness traits depending on the genetic potential 0of parents. Combining ability analysis of [3] is most widely used as biometrical tool by 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 [4]; [5] and

[6] also provide the breeders with detailed information about the type of gene action and genetic system, which helps the breeder in the selection of desirable parents for crossing programs and in deciding a suitable breeding procedure for genetic improvement of various quantitative traits. A suitable breeding methodology and the identification of superior parents are the most important pre-requisites for the development of early maturing and high yielding genotypes.

For genetic improvement of the crop, combining ability analysis has been utilized to know the nature and extent of gene action controlling expression of different characters including seed yield and would help in proper planning of a successful breeding programme. Several workers used combining ability analysis in sesame and identified superior combining parents [22]; [16]; [13]. Genetic diversity or allelic divergence among the parents is very important in selecting parents for hybridization programme to identifying heterotic crosses and obtaining desirable recombinants in the segregating generations. The mean square for the GCA was higher than the mean square due to SCA for the all the traits [19].

This revealed importance of both additive and non-additive gene actions in the characters. The objectives of the present study are development and identification of superior hybrids. Using Parents with best general and specific combining ability is utilized as donors for improvement of traits. Crosses with specific combining ability and heterosis for seed yield and oil quality with a view to incorporate them in breeding programme for further improvement. The nature of gene action is responsible for controlling genetic expression of the studied traits.

2. MATERIALS AND METHODS

In successive an attempt to genetic improvement of sesame, six genetically diverse parental sesame genotypes namely, NA.80 (P_1), NA.59 (P_2), NA.77 (P_3), NA.78 (P_4), NA.35 (P_5) and NA.40 (P_6) which received from Department of Genetic Resources Research, Field Crop Research Institute. Agricultural Research Center Egypt, were crossed by hand emasculation and pollination using half diallel mating design excluding reciprocals during 2014 summer successive season in an attempt to produce sufficient of seeds for 15 F_1 crosses at kafr-El-Hamam Agricultural Research Station, ARC, Zagazig, Sharkia governorate, Egypt.

In 2015 successive summer growing season, seeds of six parents along with their 15 F_1 crosses were evaluated at Bahteam Agricultural Research Station is located at 30^{O} 14´ N for Latitude and 31^{o} 27´ E for Longitude which is high fertility clay loam soil. The experimental design was arranged as a randomized complete block design with three replications, where each entry either parents or their 15 F_1 hybrids were contiguous sown without leaving separators in three ridges with 4 m long, 0.60 cm broad and plants spaced 20 cm with in ridge. All other agricultural practices for growing sesame either soil preparation, soil fertilization or cultivation followed by recommended packages.

The measurements were recorded for days to 50% flowering and days to physiological maturity (based on all plants/experimental unit), plant height, fruiting zone length, first capsule height, No. of branches/plant, No. of capsules/plant, thousand seed weight and seed yield/plant (based on ten competitive plants/plot). Seed oil content was determined after extraction with soxhelt's apparatus using hexane as an organic solvent according to [1].

Seed yield/plot (kg) was estimated from the plants in the central area being 2.7 m^2 in each experimental plot.

Statistical analysis:

The analysis of variance was detected by [10]. Heterosis was determined for individual hybrids as the percentage deviation of F_1 means performance from either mid parents or better parent's values. The analysis of general and specific combining ability was done according to method 2 model 1 of [3]. The combining ability ratio was calculated according to [18] as follow: $2MS_{gca}/(2MS_{gca}+2Ms_{sca})$. Hayman analysis of variance (ANOVA) was computed according to [4] following [20] modification. Validity of assumptions in [4]; [5] and [6] model was tested using two scaling test i.e. uniformity of Wr-Vr (t^2 test) and regression analysis of Wr/Vr. A graphical analysis [4]; [6] was performed to determine the frequency of dominant and recessive alleles in the parental sesame genotypes. Genetic components along with related genetic parameters were estimated according to [5].

3. RESULTS AND DISCUSSION

Analysis of variance

It is apparent from the results are presented in Table (1), genotypes and its components (parents and their F_1 crosses) mean squares were highly significant and their combined analysis show existence of sufficient genetic variability among genotypes, parents and crosses which allows to improve these characters. Similar results were reported by [19].

The mean squares parents *vs.* crosses were highly significant for all studied trait, indicating presence of sufficient amount of heterosis among hybrids. This was confirmed by the values of mean deviation of F_1's from the mid parents (b_1) [20] in Table (2) which were highly significant for all studied traits.

The significant or highly significant of b_2 values were obtained for all traits, except physiological maturity and number of branches/plant indicating asymmetry of gene distribution for these traits. Finally, item b_3 was highly significant for all studied traits indicating the existence of inconsistent allelic and non-allelic interaction or dominance effects specific to individual crosses for all traits [14]; [7].

(Table 1): Mean squares of six sesame parents and their F_1 season crosses for earliness, yield and its attributes traits in 2015

SOV	Reps	Genotypes	Parents(P)	Crosses©	P. V C.	Error
Df	2	20	5	14	1	40
Days to 50%flowering,day	0.59	29.65**	30.76**	27.10**	59.74**	3.05
Physiological maturity,day	0.51	67.42**	90.40**	59.49**	63.44**	4.24
Plant height, cm	2.24	932.58**	403.26**	600.91**	8222.43**	19.76
First capsule height, cm	55.73	985.72**	2191.30**	594.70**	423.07	143.99
Fruiting zone	11.625	391.973**	716.962**	203.650**	1403.554	5.308
Number of branches/pla-nt	0.67	1.25**	1.43**	0.72*	7.76**	0.32
Number of capsules/pla-nt	10.78	3556.42**	2098.89**	3269.37**	14862.86**	11.03
1000-seed weight,(g)	0.01	0.11**	0.19**	0.08**	0.05**	0.01
Seed yield/plant,(g)	2.73	331.35**	737.08	168.90**	577.02**	5.24
Seed yield/plot. (kg)	4061.03	850302.43*	997318.78*	120656.86*	130258.65*	23714.71
Seed oil content,(%)	0.4	46.00**	82.09**	36.39**	0.03	0.24

Where; *=P<0.05 and **=P<0.01

(Table 2): Jones analysis of combining ability mean squares in six sesame parents and their F_1 crosses for earliness, yield and its attributes in 2015 season

SOV	A	b_1	b_2	b_3	B	Total	Axb	b_1xB	b_2xB	b_3xB	bxB	Total xB
Df	5	1	5	9	15	20	10	2	10	18	30	40
Days to 50%flowering,(day)	25.63**	19.91**	2.85*	3.93**	4.64**	9.88**	0.62	2.74	1.45	0.8	1.15	1.02
Physiological maturity,(day)	72.32**	21.15**	1.93	6.34**	5.86**	22.47**	2.16	0.66	0.99	1.32	1.17	1.41
Plant height,(cm)	204.65**	2740.81**	76.93**	229.83**	346.26**	310.86**	6.47	0.45	9.28	5.84	6.63	6.59
First capsule height,(cm)	665.20**	144.2	283.33**	187.20**	216.36**	328.57**	79.83	121.382	83.87	2.227	37.39	48
Fruiting zone	180.41**	467.85**	132.43**	64.57**	114.07**	130.66**	1.9	1.99	2.14	1.47	1.73	1.77
Number of branches/plant	0.28*	2.59**	0.24	0.35**	0.46**	0.42**	0.09	0.11	0.06	0.15	0.11	0.11
Number of capsules/plant	410.13**	4954.29**	932.11**	1338.22**	1443.92**	1185.47**	2.99	2.88	3.79	4.08	3.9	3.68
1000-seed weight,(g)	0.053**	0.17**	0.034**	0.031**	0.031**	0.036	0.001	0.002	0.004	0.002	0.002	0.002
Seed yield/plant,(g)	2.11.19**	192.34**	100.56**	50.88**	76.87**	110.45**	1.3	1.08	1.95	1.96	1.9	1.75
Seed yield/plot,	138717.29*	376752.88*	50460.03*	79190.03*	42784.22*	16767.48*	5349.03	5927.42	8601.57	9157.52	8756.86	7904.9

(kg)												
Seed oil content, (%)	32.25**	0.01	13.75**	8.25**	9.70**	15.33**	0.05	0.04	0.05	0.12	0.09	0.08

Where; *=P<0.05, **=P<0.01, a=additive effects, b=total non-additive (dominance) effects, b_1=mean deviation of F_1's from their mid-parents, b_2=test if there is equal or unequal distribution among parents and b_3=detect existence of unique dominance of each F_1, i.e., presence of considerable amount of heterotic effect specific to some crosses, B=block.

1-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 (3). Combining ability analysis has been utilized to know the nature and extent of gene action controlling expression of different characters including seed yield and its attributes would help in proper planning of a successful breeding programme, these results agreement with [22].

(Table 3): Combining ability mean squares of six sesame parents and their F_1 crosses for earliness, yield and its attributes traits in 2015 season

S.O.V	GCA	SCA	Error
Df	5	15	40
Days to 50%flowering,(day)	25.63**	4.64**	1.02
Physiological maturity,(day)	72.32**	5.86**	1.41
Plant height,(cm)	204.65**	346.26**	6.59
First capsule height,(cm)	665.20**	216.36**	48
fruiting Zone	180.41**	114.07**	1.77
Number of branches/plant	0.28	0.46**	0.11
Number of capsules/plant	410.13**	1443.92**	3.68
1000-seed weight,(g)	0.05**	0.03**	0.002
Seed yield/plant,(g)	211.19**	76.87**	1.75
Seed yield/plot . (kg)	138717.24*	142784.22**	7904.9
Seed oil content, (%)	32.25**	9.70**	0.08

Where; *=P<0.05 and **=P<0.01

2-Heterotic effects:

To draw the valid conclusions respecting the amount of heterosis for various traits, the percentage of deviation of F_1 mean performance from the mid parents (average heterosis) and better parents (heterobeltiosis) were computed as shown in Table (4). Significant negative direction of heterosis and heterobeltiosis are desirable goal for the earliness traits, days to 50% flowering and days to physiological maturity to produce high yield in a short period especially intensive cropping systems.

The early physiological maturity character is dependent on a minor gene complex. These are also very valuable source for plant breeding programmes aiming for adaptation of sesame to different environments as well as for studied on thermo and photo-period sensitivity. These results are in agreement with [15].

Also, short plant height and first capsule height are suitable for mechanical harvesting and lodging resistance. Several hybrids had high negative heterosis values over both mid
The highest proportion of seed oil was achieved by (P_4 X P_6) in mid parent, while the hybrid (P_1 X P_3) the batter

and better parents for earliness characters. The most promising hybrids for earliness in flowering were (P_1 X P_2) in mid parent, while hybrid (P_2 X P_6) is better parent. While for earliness in maturity, the best hybrids were (P_2 X P_5) as seen in (Table4). The desirable hybrids for plant height were (P_5 x P_6) and (P_1 X P_5), in mid parent and batter parent. For first capsule height, the best hybrids were (P_4 X P_6) and (P_1 X P_4) respectively. The best hybrids for fruiting zone length were (P_4 X P_5). For yield and its components as well as seed oil content characters, the significant positive heterotic values over mid and better parent are preferred.

As shown from the results in Table (4), the best hybrids for number of branches/plant were (P_3 X P_5). The desirable hybrids for number of capsules/plant were (P_1 X P_5) and (P_2 X P_5). The hybrid of (P_4 X P_5) was the best one for thousand seed weight. For seed yield/plant, the superior hybrids were (P_1 X P_5) in mid parent and (P_1 X P_6) in better parent, in case of seed yield/plot the hybrids of (P_1 xP_5).

parent. Several investigators reported high heterotic effect of sesame [2]; [12]; [11]; [9]; [13] and [19].

3-*Per se* performance associated with combining ability:

3-1-Performance and general combining ability effects (GCA):

It is clear from the results in Tables (5) and (6), that the earliest parents for days to 50% flowering and days to physiological maturity were P_1. This is finding confirmed by negative and highly significant GCA effects of the parent, indicating the parent possessed more decreasing alleles towards earliness.

(Table 4): Heterosis (%) of fifteen sesame F_1 crosses over both mid parent (M.P.) and better parent (B.P.) for earliness, yield and its attributes in 2015 season

Crosses		P_1 X P_2	P_1 X P_3	P_1 X P_4	P_1 X P_5	P_1 X P_6	P_2 X P_3	P_2 X P_4	P_2 X P_5	P_2 X P_6	P_3 X P_4	P_3 X P_5	P_3 X P_6	P_4 X P_5	P_4 X P_6	P_5 X P_6	LSD 5%
Days to 50%flowering	M. P	-12.96**	2.80*	-6.57**	-5.80**	-10.65	0.32	0.63	-6.25**	-7.45**	-2.97*	-1.64	-4.89**	-4.55**	-0.65	-3.21*	2.5
	B. P	3.68*	8.09**	-0.74	-4.41**	1.47	5.33**	4.58**	-3.23*	-5.10**	-2	0	-2.67	-3.92**	0.65	-2.58	2.88
Physiological maturity	M. P	0.6	3.77*	3.99**	-0.44	-0.08	3.89*	-0.25	-1.79	3.79*	2.91	3.54*	0.8	5.14**	1.4	2.03	2.94
	B. P	1.91	8.45**	8.73**	6.22**	2.4	7.92**	3.67*	0.05	10.06**	2.95	5.54**	2.82	7.72**	3.39	6.13**	3.4
Plant height	M. P	14.14**	11.93**	11.35**	26.04**	7.64*	14.72**	19.63**	10.94**	20.70**	8.43*	6.09	26.79**	15.10**	-2.43	28.05**	6.35
	B. P	16.64**	15.86**	17.24**	29.1	11.55**	16.18**	23.19**	17.57**	26.41**	10.23**	13.94**	34.54**	25.80**	5.36	29.51**	7.34
First capsule height	M. P	13.31	46.00**	-15.12	16.91	0.19	10.13	7	3.56	21.64*	-18.43*	1.11	38.87**	-11.32	-19.79*	34.52**	17.15
	B. P	-5.25	33.77**	-36.96**	11.78	-6.66	-0.46	-7.88	-7.88	5.65	-35.43**	-0.69	32.80**	-30.73**	-38.56**	19.8	26.5
Fruiting Zone	M. P	1.02	-10.89**	14.59**	2.59	-7.75**	5.56**	14.57**	17.41**	25.99**	19.62**	9.26**	14.80**	41.23**	14.16**	3.29	4.41
	B. P	-16.49**	-16.21**	-1.72	-12.14**	-20.63**	-8.06**	9.61**	11.91**	20.72**	8.39**	-0.65	3.87*	40.68**	13.98**	3.8	5.09
Number of branches/plant	M. P	6.40**	6.28**	28.76**	21.21**	46.89**	35.92**	29.31**	36.36**	13.04**	-0.85*	62.22**	11.11**	14.56**	-8.46**	0.81	1.09
	B. P	5.88**	4.76**	14.50**	8.53**	27.45**	33.33**	14.50**	18.81**	0.78	10.69**	39.05**	0.78	-9.92**	-9.16**	0.94	1.26
Number of capsules/plant	M. P	5.81*	-13.80**	53.09**	90.05**	50.80**	23.78**	0.28	82.11**	26.03**	16.15**	-20.90**	6.22*	10.95**	48.92**	4.75	6.35
	B. P	-3.08	-32.38**	41.31**	76.59**	44.31**	4.21	-0.56	73.95**	24.09**	-2.87	-35.82**	-11.69**	6.84*	47.86**	5.48	7.33

1000-seed weight	M.P	3.06**	2.30**	-0.50**	1.57**	2.86****	-7.39**	-8.07**	1.68**	0.39**	3.49**	2.80**	3.89**	4.10**	-1.34**	0.11	0.15
	B.P	-1.48**	-1.34**	-7.85**	1.49**	0.34**	-8.23**	-11.08**	-0.41**	-4.69**	-0.77**	1.59**	-0.50**	-1.31**	-9.23**	0.13	0.17
Seed yield/plant	M.P	13.01**	-18.01**	63.93**	82.77**	31.12**	-11.75**	-2.18	60.46**	-15.02**	20.91**	7.09**	5.93**	69.47**	-1.24	3.27	4.38
	B.P	-27.22**	-50.49**	4.46*	28.56**	30.70**	-24.03**	-4.49*	2.87	-27.43**	6.25**	-35.55**	-19.97**	7.52**	-17.31**	3.78	5.05
Seed yield/plot	M.P	15.66	-15.84	66.91	79.69	29.58**	-9.4	1	65.12	-10.41	22.25	11.49	8.19	70.21	1.14	22.01	29.45
	B.P	-24.4	-48.59	7.55*	26.86	29.18	-22.01	-2.04	7.41	-21.8	8.07	-32.15	-16.79	9.18	-13.99	8.11	25.41
Seed oil content	M.P	-8.05**	-5.10**	0.05	7.72**	0.17	-6.74**	-8.17**	3.79**	0.3	0.51	-0.42	11.27**	-12.07**	11.93**	9.41	0.7
	B.P	-13.93**	7.15**	-1.10**	-4.66**	0.16	-10.86	-13.10**	-2.85**	-5.56*	-0.54	-2.58**	0.43	-13.09**	0.08	-3.17**	0.81

Where; *=P<0.05 and **=P<0.01

There was a close correspondence between *per se* performance and GCA effects, relative to P_5 was the shortest parents and identified as desirable ones for both plant height and first capsule height, showed the P_1 the near surface of soil. Fruiting zone length the analysis revealed that the p_1 the tallest plant. The first order of parents were P_4 and P_6 for number of branches/plant, and P_3 for number of capsules/plant, P_4 and P_2 for thousand seed weight, P_2 for seed yield/plant, and P_3 and P_4 for seed yield/plot and P_5 and P_1 seed oil content. However, the considerable positive GCA effects were achieved by P_4 for number of branches/plant, P_3 for number of capsules/plant, P_4 and p_2 for thousand seed weight, P_2 for seed yield/plant, P_3 and P_4 for seed yield/plot, P_5 and P_1 for seed oil content. To determine combining ability of parents in the early generation, the genetic diversity or allelic divergence among the parents is very important in selection parents for hybridization programme to identifying heterotic crosses and obtaining desirable recombinants in the segregating generation. Significant variation for yield and yield related traits were reported by [23] and [8].

Table 5: Mean performance of sesame parents and their F_1 crosses for earliness, yield and its attributes traits in 2015 season

Crosses	Days to 50%flowerig,day	Physiologic-al maturity, day	Plant height, cm	First capsule height, cm	Fruiting Zone	Number of branches/ Plant	Number of capsules/ plant	1000-seed weight, (g)	Seed yield/plant, (g)	Seed yield/plot (kg)	Seed oil content, (%)
P_1	45.33	106.31	171.30	68.99	117.36	3.40	99.00	3.69	10.18	814.67	57.33
P_2	55.00	107.54	178.80	102.61	76.67	3.37	119.00	4.05	53.36	2651.75	50.00
P_3	50.00	115.89	183.33	82.88	103.33	3.50	174.00	3.98	48.99	3674.25	54.85
P_4	51.00	116.00	189.43	142.14	83.93	4.37	117.00	4.33	37.11	2821.61	56.02
P_5	51.67	111.58	159.71	79.94	84.95	2.50	108.33	3.88	9.98	798.13	57.35
P_6	52.33	120.53	163.36	75.63	83.67	4.30	115.33	3.64	25.03	1977.45	44.16
P_1 X P_2	43.67	107.57	199.80	97.22	98.0	3.60	115.33	3.99	25.73	2004.66	49.35
P_1 X P_3	49.00	115.29	198.47	110.87	98.33	3.67	117.67	3.92	24.26	1888.85	53.23
P_1 X P_4	45.00	115.59	200.84	89.60	115.33	5.00	165.33	3.99	38.76.	3034.57	56.70
P_1 X P_5	43.33	108.86	178.16	74.61	93.15	4.33	156.33	3.90	41.45	3191.65	57.44
P_1 X P_6	46.00	112.93	210.90	84.54	103.11	4.67	203.67	4.24	32.18	2508.60	54.66
P_2 X P_3	52.67	116.06	207.72	102.14	95.00	4.67	181.33	3.72	37.22	2865.68	48.90

P_2 X P_4	53.33	111.49	220.26	130.94	92.00	5.00	118.33	3.85	35.44	2764.04	48.68
P_2 X P_5	50.00	109.60	187.78	94.52	94.67	4.00	207.00	4.03	36.37	2848.25	55.71
P_2 X P_6	49.67	118.36	206.50	108.40	101.00	4.33	147.67	3.86	25.66	2073.76	47.22
P_3 X P_4	49.00	119.32	202.10	91.78	112.00	3.90	169.00	4.30	52.05	3970.65	55.72
P_3 X P_5	50.00	117.76	181.98	82.31	102.67	4.87	111.67	4.04	31.57	2493.07	55.87
P_3 X P_6	48.67	119.16	219.78	110.06	107.33	4.33	153.67	3.96	39.21	3057.26	55.09
P_4 X P_5	49.00	119.64	200.92	98.46	119.00	3.93	125.00	4.28	39.90	3080.61	49.84
P_4 X P_6	51.33	119.93	172.11	87.33	95.67	3.97	173.00	3.93	30.69	2426.88	56.06
P_5 X P_6	50.33	118.43	206.85	109.64	103.33	4.97	196.57	3.87	26.62	2137.33	53.53
LSD 5%	1.29	1.52	3.28	8.86	1.7	0.42	2.45	0.07	1.69	113.65	0.36
LSD 1%	1.72	2.03	4.39	11.85	2.28	0.56	3.28	.0.1	2.26	152.08	0.48

Where; *=P<0.05 and **=P<0.01

(Table 6): General combining ability effects of six sesame parents for earliness yield and its attributes in 2015 season

Parents	P_1	P_2	P_3	P_4	P_5	P_6	LSD gi 5%	LSD gi 1%	LSD gi-gj 5%	LSD gi-gj 1%
Days to 50% flowering	- 3.47**	1.74**	0.49	0.53	0.07	0.65	0.66	0.88	1.81	2.49
Physiological maturity	-3..64**	-3.22**	2.18**	2.00**	-0.81**	3.49**	0.78	1.04	2.13	2.85
Plant height	-1.99*	4.12**	3.75**	3.55**	-8.95**	-0.48	1.67	2.24	4.6	6.15
First capsule height	-9.80**	8.15**	-1.29	13.65**	-7.35**	-3.37	4.52	6.05	12.41	16.61
Fruiting zone	6.16**	-7.42**	3.58**	1.06*	-1.42**	-1.95**	0.87	1.16	2.38	3.19
Number of branches/plant	-0.1	-0.07	-0.06	0.21	-0.22*	0.25	0.21	0.29	0.59	0.79
Number of capsules/plant	- 8.56**	-2.14**	7.07**	-5.01**	--1.43*	10.07**	1.25	1.67	3.43	4.6
1000-seed weight	-0.05**	0.03*	0.01	0.15**	0.01	-0.08**	0.03	0.04	0.08	0.11
Seed yield/plant	-5.65**	0.4	6.80**	5.39**	4.01**-	2.94**	0.86	1.15	2.37	3.17
Seed yield/plot	-429.63**	20.64	491.16**	403.15**	-293.38**	-191.94**	58	77.61	159.28	213.14
Seed oil content	1.60**	-2.92**	0.66**	0.72**	1.98**	-2.04**	0.18	0.25	0.51	0.68

Where; *=P<0.05 and **=P<0.01

3-2-Performance and specific combining ability effects (SCA):

It is worthy to appear as shown in Tables 5 and 7 that some correspondence between performance and SCA effects for the most traits. Concerning the performance of all genotypes (Table 5), the data show that the earliest cross combinations were (P_1 x P_5) and (p_1 x p_2) for days to 50% flowering and (P_1 x P_2) for days to physiological maturity, respectively the hybrids in (p_1 xp_2) the earliest in days to 50% flowering and physiological maturity is dependent on a minor gene complex.

The shortest hybrids were (P_4 x P_6) for plant height and (P_1 x P_5) for first capsule height and (p_4 x p_5) for the fruiting zone length. The best cross combinations were (P_1 x P_4) and for number of branches/plant, (P_2 x P_5) and (P_1 x P_6) for number of capsules/plant, (P_3 x P_4) and (P_4 x P_5) for thousand seed weight, (P_3 x P_4) for seed yield/plant, (p_1 x p_4) and (p_1 x p_5) also seed yield/plot the best crosses (P_1 x P_5) for seed oil content. The specific combining ability values (SCA) of hybrids are presented in Table (7). The earliest crosses due to SCA effects were (P_1 x P_2) for days to 50% flowering, (P_2 x P_5) for days to physiological maturity respectively.

The shortest crosses were (P_4 x P_6) for plant height and (P_4 x P_6) for first capsule height, respectively. The valuable positive SCA effects were detected in (P_4 x P_5) in fruiting zone length and (P_3 x P_5) and (P_1 x P_4) for number of branches/plant, (P_2 x P_5) and (P_1 x P_6) for number of capsules/plant, (P_3 x P_4) and (P_4 x P_5) for thousand seed weight, (P_1 x P_5) for seed yield/plant, (P_1 x P_5) for seed yield/plot and (P_2 x P_5) for seed oil content, in respective order. The SCA represents the dominance and epistasic, which can be associated with heterobeltiosis [21].

It is therefore suggested that SCA performance might be considered as acriterion for selecting the best crosses. A perusal of F_1's hybrids revealed that (P1 x P5) for seed/plant, (P_1 x P_5) for seed yield/plot and (P_1 x P_2) for earliness and yield attributing traits were identified as the best crosses since they possessed desirable *per se* performance, SCA effects along with mid and better parent heterosis.

(Table 9): Specific combining ability effects of fifteen sesame F_1 crosses for earliness, yield and its attributes across in 2015 season

Crosses	Days to 50%flowering	Physiological maturity	Plant height	First capsule height, cm	Fruiting Zone	Number of branches/plant	Number of capsules/plant	1000-seed weight	Seed yield/plant	Seed yield/plot	Seed oil content
P_1 X P_2	-3.95**	-0.14	5.29**	2.69	0.21	-0.35	-20.37**	0.10**	-.58	-114.17	-2.65**
P_1 X P_3	2.64**	2.18*	4.33*	25.78	-10.46**	-0.30	-27.24**	-0.01	-9.45**	-700.49**	-2.35**
P_1 X P_4	-1.40	2.66*	6.90**	-10.42	9.06**	0.77**	32.51**	-0.08*	6.46**	533.23**	1.06**
P_1 X P_5	-2.61**	-1.25	-3.29	-4.42	-10.64**	0.53*	19.92**	0.04	18.54**	1386.85**	0.54**
P_1 X P_6	-0.53	-1.49	20.98**	1.54	0.15	0.40	55.78**	0.40**	8.21**	602.35**	1.78**
P_2 X P_3	1.10	2.54**	7.47**	0.90	-0.21	0.67**	30.01**	-0.23**	-2.54*	-173.94*	-2.16**
P_2 X P_4	1.72*	-1.86*	20.21**	12.96*	-0.69	0.74**	-20.91**	-0.24**	-2.91**	-187.58**	-2.45**
P_2 X P_5	-1.15	-2.93**	0.22	-2.46	4.46**	0.17	64.17**	0.08	7.42**	593.17**	3.33**
P_2 X P_6	-2.07**	3.53**	10.47**	7.45	11.32**	0.03	-6.66**	0.00	-4.36**	-287.76**	-1.13**
P_3 X P_4	-1.36	0.57	2.41	-16.76	8.31**	-0.38	20.55**	0.17**	7.30**	548.52**	1.01**
P_3 X P_5	0.10	1.83	-5.21**	-5.23	1.46	1.02**	-40.37**	0.05	-3.78**	-232.52**	-0.09
P_3 X P_6	-1.82*	-1.07	24.12**	18.55**	6.65**	0.02	-9.87**	0.06	2.79**	230.22**	3.15**
P_4 X P_5	-0.95	3.89**	13.94**	-4.01	20.31**	-0.18	-14.95**	0.14**	5.95**	443.02**	-6.18**
P_4 X P_6	0.80	0.13	-23.34**	-19.12**	-2.50*	-0.61	21.55**	0.11**	-4.33**	-312.15**	4.06**
P_5 X P_6	0.26	1.18	23.89**	19.18**	7.65**	0.82**	41.63**	-0.63**	-9.46**	-719.13**	-7.39**
LSD $_{Sij\ 5\%}$	1.49	1.76	3.80	10.25	1.97	0.49	2.84	0.07	1.95	131.52	0.42
LSD $_{Sij\ 1\%}$	2.00	2.35	5.08	13.71	2.63	0.65	3.80	0.09	2.62	175.99	0.56
LSD $_{sij-sik}$ 5%	2.70	3.18	6.86	18.52	3.56	0.88	5.13	0.12	3.53	237.71	0.75
LSD $_{sij-sik}$ 1%	3.61	4.25	9.18	24.79	4.76	1.17	6.86	0.16	4.73	318.08	1.01
LSD $_{sij-skl}$ 5%	2.50	2.94	6.35	17.15	3.29	0.81	4.75	0.11	3.27	220.08	0.70
LSD $_{sij-skl}$ 1%	3.34	3.94	8.50	22.95	4.41	1.09	6.35	0.15	4.38	294.49	0.93

Where; *=P<0.05 and **=P<0.01

4-Types of gene action and heritability

4-1-Validity of hypothesis

For testing the validity of the major assumption, uniformity of Wr-Vr (t^2 test) and regression analysis were conducted underlying the genetic models seen in Table (8).

Table (8): Validity of hypothesis through t^2, Regression coefficient (b), t-values for b=0 and b=1, Wr+Vr and Wr-Vr of six sesame parents and their F_1's crosses for earliness, yield and its attributes traits in 2015 season

Character	t^2	Regression coefficient (b)±SE	b=0	b=1	Wr+Vr	Wr-Vr
Days to 50%flowering	0.04	0.74+_0.29	2.50	0.90	815.17**	80.02
Days to physiological maturity	13.95**	0.80+_0.05	17.21**	4.25*	3909.89**	14.01
Plant height	11.85**	-0.10+_0.13	-0.74	8.23**	154699.95*	20869.64**
first capsule height	2.21	1.23+_0.46	2.67	-0.50	1967594.74	87342.42*
Fruiting zone length	0.002	0.55+_0.43	1.27	1.05	96889.52**	19197.86**
No. of branches	0.18	0.98+_0.25	3.89*	0.08	2.14**	0.70
No. of Capsule/plant	0.14	-0.47+_0.36	-1.30	4.08*	810315.03*	44189.43**
Thousand seed weight	0.46	0.49+_0.83	0.59	0.62	0.01**	0.002**
Seed yield/plant	1.06	0.21+_0.43	0.50	1.83	70297.24**	11701.32**
Seed yield/plot	0.02	0.19+_0.39	0.50	2.10	38684.7701	92784836.78**
Seed oil content	1.45	1.17+_0.34	3.46*	-0.49	1804.51**	126.01**

Where; *=P<0.05 and **=P<0.01

The highly significant differences among twenty one sesame genotypes indicated that the parents possessed widely diverse traits and this diversity could be transmitted to the off spring and it permitted the genetic analysis of the data. The non-significance of t^2 test validated the use of simple additive dominance model for genetic analysis of all studied traits except days to physiological maturity and plant height in which uniformity of Wr-Vr (t^2 test) was significant or highly significant, except first capsules height and seed yield/plot indicating the presence of non-allelic interaction in the inheritance of these traits.

4-2-Graphical analysis:

Graphical analysis of the parent off spring covariance (Wr) and array variance (Vr) and their related statistics was made to get a clear picture about the inheritance for all studied traits (Table 8 and Figures 1-11). Additive-dominance model of inheritance was observed as regression coefficient (b) of (Wr/Vr) in significant departed from unity in first capsule height and seed yield/plot, 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 days to 50% flowering, days to physiological maturity seed yield/plant and seed oil content, 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, over dominance model was pronounced as the regression line touched the Wr axis below origin point for days to 50% flowering, physiological maturity, plant height, thousand seed weight, fruiting zone length and seed yield per plant. In contrast, regression line cut the Wr axis above the origin point for the rest of traits, indicating the presence of partial dominance.

Over dominance was found for all traits, except days to physiological maturity, number of branches/plant and seed oil content. This was supported by significant or highly significant differences in the magnitude of the Wr-Vr values over arrays in all studied traits, except for days to 50% flowering, days to physiological maturity and number of branches, indicating the presence of either non-allelic gene interaction or epistatic effects. In the contrary, the analysis of the variance revealed highly significance (Wr+Vr) value (Table 9) for all studied traits, confirming the presence of non-additive genetic variation for all traits.

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 $(H_1/D)^{1/2}$ and distorted the (Vr, Wr) graphs [5]; [7]. 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, P_1 for earliness and physiological maturity first capsules height and fruiting zone, P_6 the tallest plant height whereas, P_2 for thousand seed weight and seed yield/plant, P_3 and P_4 seed yield/plot, P_1 and P_5 for seed oil content, 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 parent following genotype, which might be due to be farthest ones from the origin of regression graph.

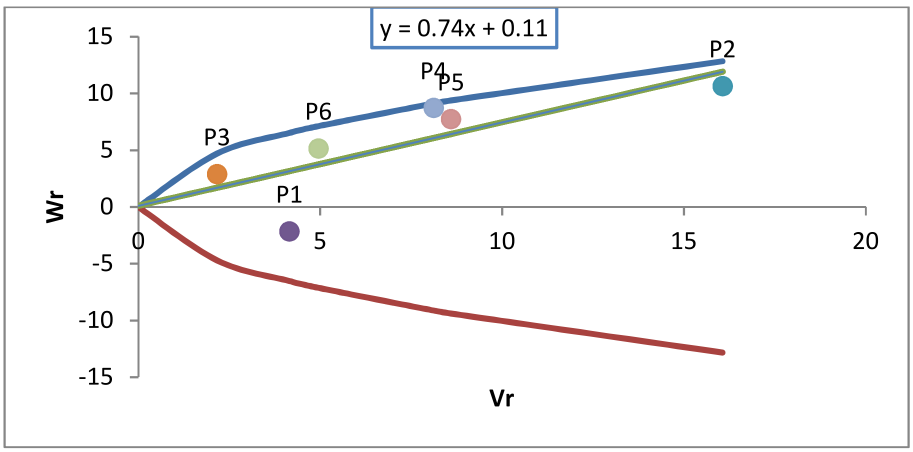

Fig (1) wr/vr graphs for days to 50% flowering

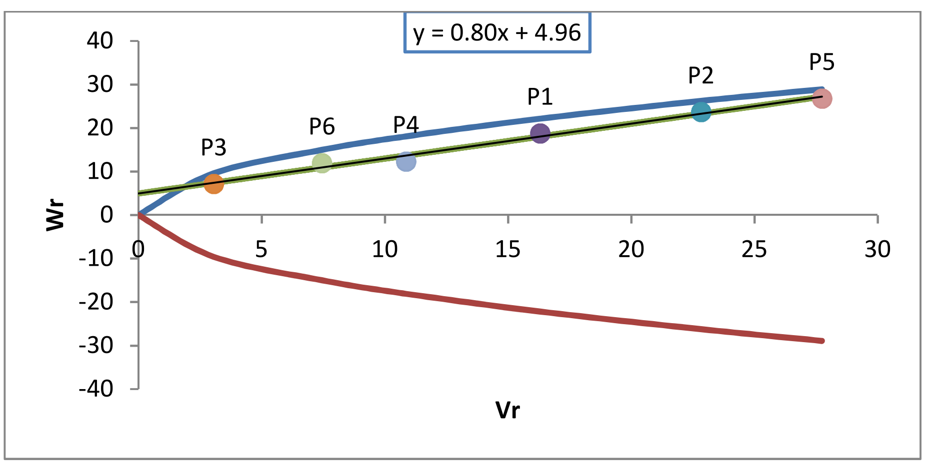

Fig (2) wr/vr graphs for days to physiological maturity

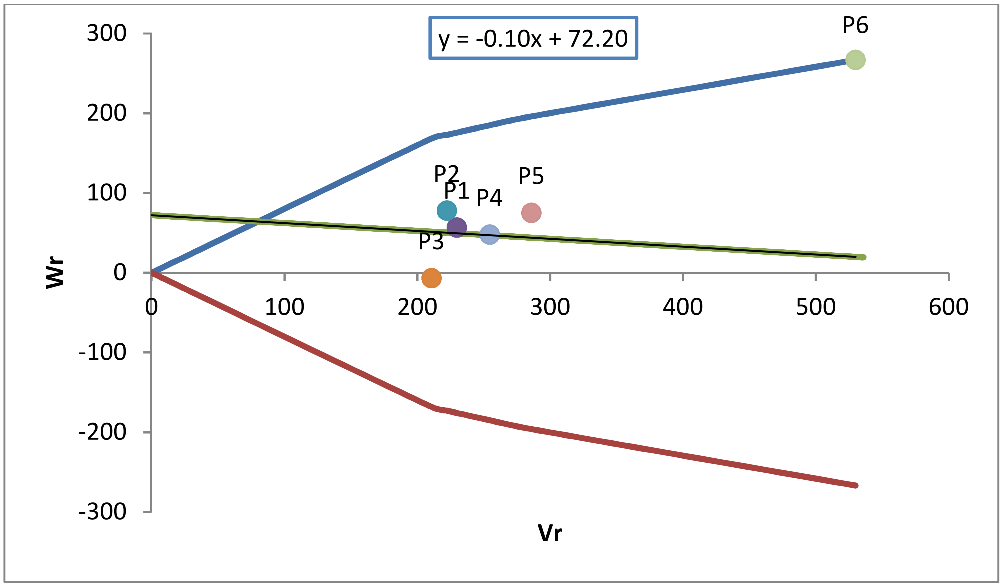

Fig (3) wr/vr graphs for plant height

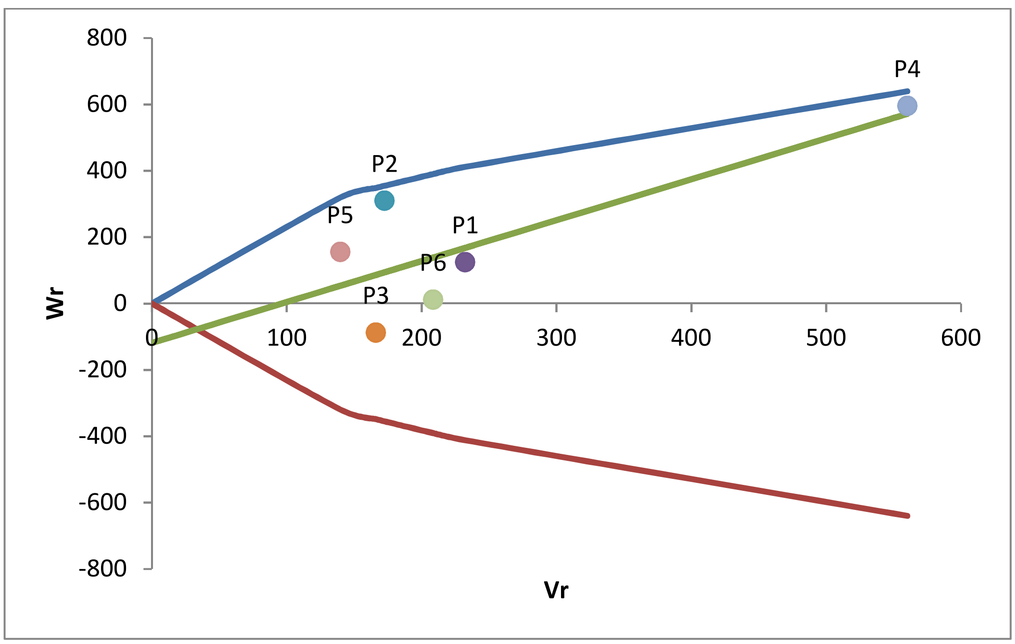

Fig (4) wr/vr graphs for first capsule height

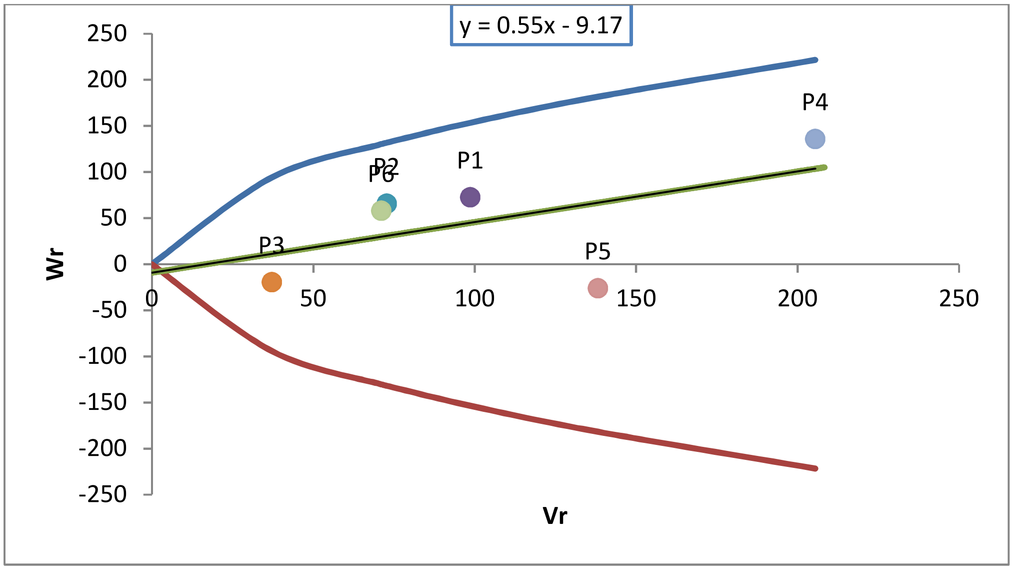

Fig (5) wr/ vr graphs for fruiting zone length

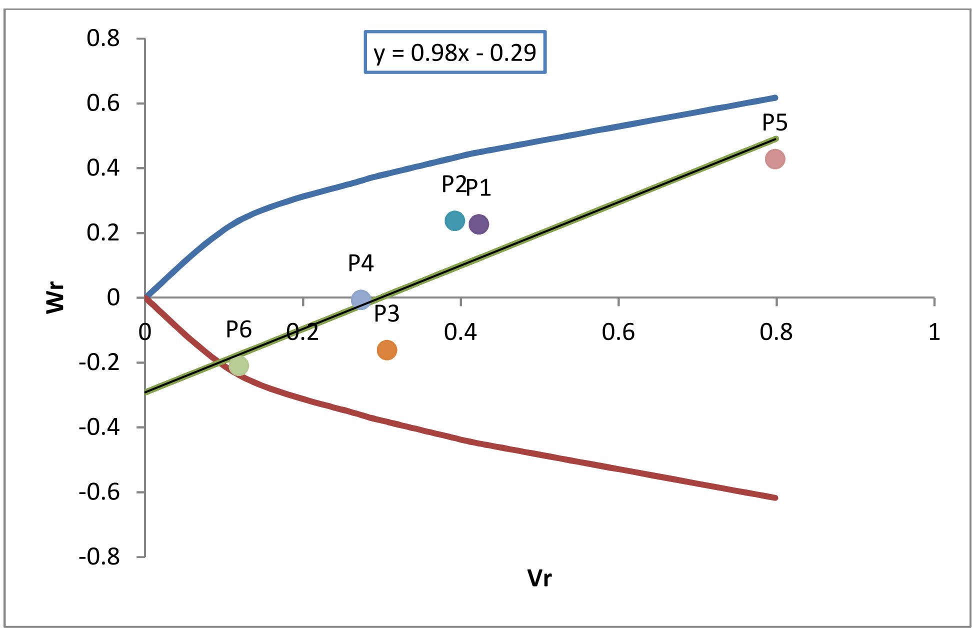

Fig (6) wr/vr graphs for No. of branches/plant

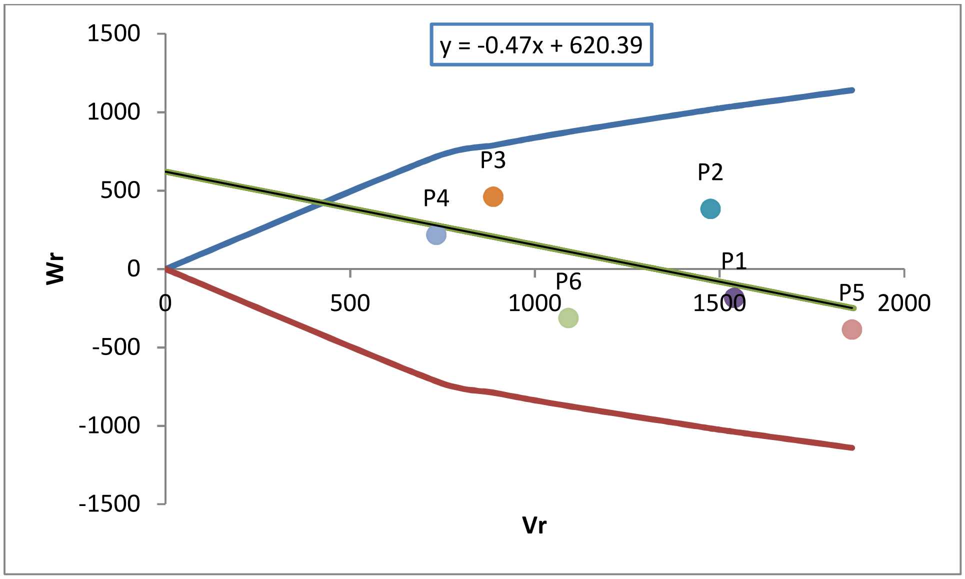

Fig (7) wr/vr graphs for No. of capsules/plant

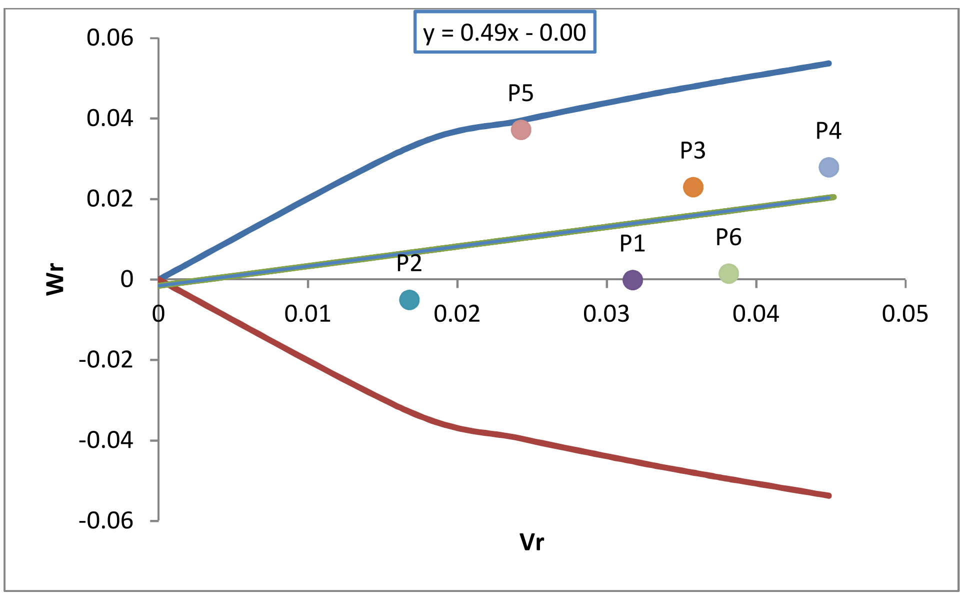

Fig (8) wr/vr graphs for 1000 seed weight

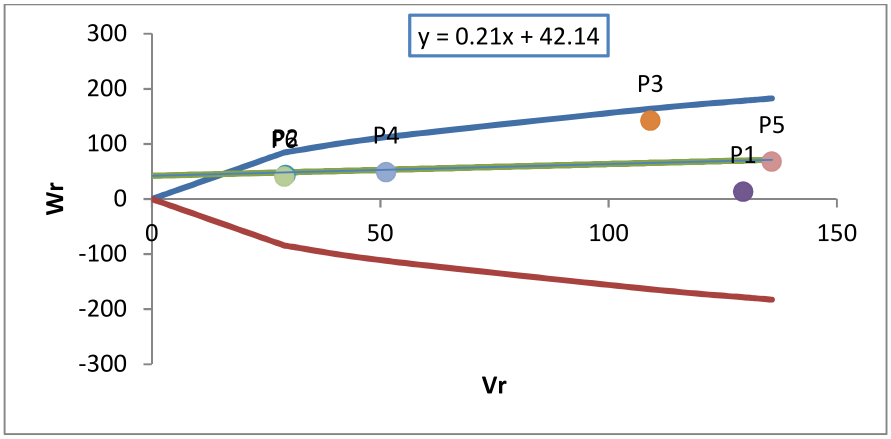

Fig (9) wr/vr graphs for seed yield/plant

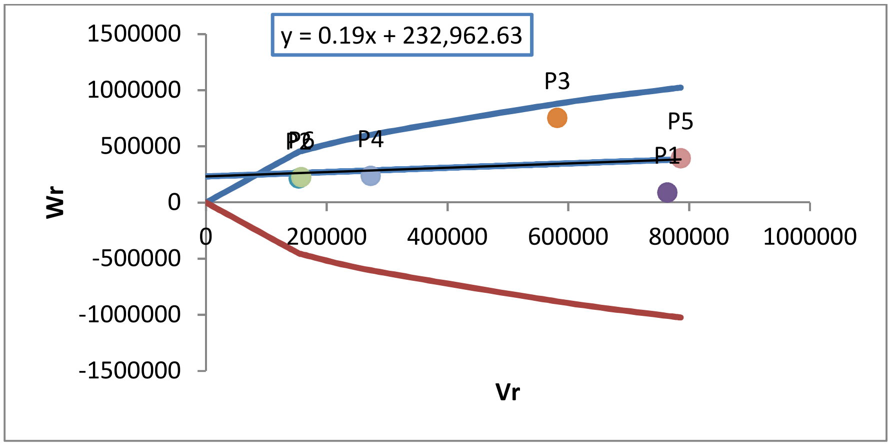

Fig (10) wr/vr graphs for seed yield/plot

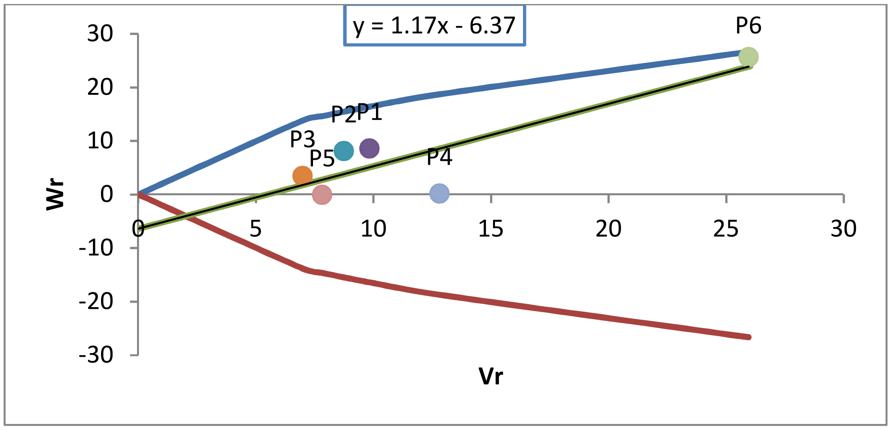

Fig (11) wr / vr graphs for seed oil content %

4-3- Genetic components and related genetic parameters

With respect to genetic components estimated by the Hayman’s diallel analyses as presented in Table (9). The data revealed that the components of additive (D) and dominance (H_1& H_2) effects were positive and significant or highly significant either in days to 50% flowering, days to physiological maturity, number of branches. 1000 seed weight and seed oil content, indicating that important of both additive and non-additive components in the inheritance of above traits.

The magnitude of dominance (H_1& H_2) was significant or highly significant higher than additive components (D) for all traits except plant height, fruiting zone length, No. of capsules/plant, seed yield/plant and seed yield/plot, indicating that the presence of over-dominance for the previous traits. Value of H_1 was greater than H_2 except seed yield/plant and seed yield/plot indicating that frequency of gene distribution in the parents was unequal and that was also supported by the ratio of $H_2/4H_1$ (<0.25) which showing asymmetrical gene distribution at the loci in the parents showing dominance for all the traits.

The F value was positive for all traits except days to 50% flowering and physiological maturity. That 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 except the above traits as shown in Table (10), for which negative value indicated presence of higher number of recessive than dominants genes. The overall dominance effects of heterozygous loci (h^2) were found to be positive and significant or highly significant for all studied traits except, seed oil content, first capsules height and 1000 seed weight indicating that most of the dominant genes had positive effects. All estimates of environmental variance (E) were insignificant for all studied character, indicating that all character have not been greatly affected by environmental factors.

Table (9): Estimation of genetic components for earliness, yield and its attributes traits in 2015 season

Genetic components	E	D	F	H_1	H_2	h^2
Days to 50% flowering	0.98+_0.92	9.27+_2.43**	-2.82+_5.93	14.98+_6.16**	13.11+_5.50*	2.36+_3.70*
Physiological maturity	1.35+_0.59*	8.78+_1.57*	-8.56+_3.84	8.32+_3.9	7.51+_3.35*	2.95+_2.40*
Plant height	6.31+_39	8.11+_0.43	5.67+_555.57	7.88+_265	3.71+_237.20	2.95+_159.67
First capsule height	5346.60+_43.21	84+_114..317*	7.21+_279.2	51.12+_290.2	20.34+_59.21	67.46+_174.4
Fruiting zone length	21.870+_16	17.12+_44.58	24.17+_108.910	23.18+_113.18	21.71+_101	4.42.20+_68
Number of branches/plant	80.110.03**	36+_0.09**	46+_0.22	37+_0.22**	24+_0.20**	61+_0.13
Number of capsules/plant	3.67+_203	95.96+_537	75.93+_1312	9.69+_1364	3.60+_1218	9.07+_820.3
1000-seed weight	1.000+_0.01	0.06+_0.01**	0.07+_0.03	0.13+_0.03	0.10+_0.03*	0.01+_0.02
Seed yield/plant	1.71+_16.77	3.99+_44.36	1.56+_108.390	5.26+_112.6	8.01+_100.5	23.72+_67.7
Seed yield/plot	2.94+_9485	6.65+_2509	90.73+_6130	5.41+_6370	9.57+-5691	1.53+_3830S
Seed oil content	0.08+_1.42	728+_3.77**	4.04+_9.21**	4.67+_9.57**	2.51+_8.55**	-0.04+_5.75

Where; *=P<0.05 and **=P<0.01

Table (10): Estimation of genetic parameters for earliness, yield and its attributes traits in 2015 season

Characters	Days to50% flowe-ring	Physiological maturity	Plant heig-ht	First capsule heig-ht	Fruit-ing zone length	Num-ber of bran-ches	Numb-er of capsul-es /plant	1000-seed weight	Seed yield /plant	Seed yield /plot	Seed oil content
$(H1/D)^{0.5}$	1.27	0.80	2.93	1.12	1.39	1.94	2.84	1.45	1.16	1.18	1.28
$H_2/4H_1$	0.22	0.24	0.24	0.19	0.19	0.22	0.21	0.20	0.18	-.0.18	0.18
KD/KR	0.79	0.69	1.26	2.51	2.52	1.97	1.95	2.26	2.61	2.57	2.05
R	0.86	-0.68	0.66	0.91	-0.33	0.88	0.05	0.41	0.09	-0.05	-0.87
h^2/H_2	o.94	0.74	1.72	0.11	0.88	1.30	0.67	0.10	0.52	0.65	-0.001
$h^2_{(n.s)}$	0.62	0.77	0.17	0.38	0.28	0.04	0.09	0.28	0.40	0.39	0.48
$h^2_{(b.s)}$	0.91	0.95	0.98	0.86	0.98	0.74	1.00	0.95	0.98	0.99	0.99

The average degree of dominance over all loci Table (10), as estimated by $(H_1/D)^{½}$ ratio was found to be more than unity for all traits except days to physiological maturity indicating the role of over dominance gene effects in the inheritance of this traits, for which less than unity indicating the presence of partial dominance in the control of the traits. Correlation of (Wr+Vr) and Yr as seen in Table (10), which was lower than zero showed that all studied traits except No. of branches and thousand seed weight, indicating the dominance genes had considerable effects on the these traits.

The h^2/H_2 values Table (10) were less than unity for all studied traits except plant height implied to be governed by one gene. Estimates of broad sense heritability, for all traits in Table (10) were very high and varied from 1.00 to 0.74. On the other hand, narrow sense heritability was found to be low for all studied traits except days to 50% flowering, days to physiological maturity with values ranging from 0.04 to 0.77, indicating that selection should be delayed to late segregating generations. However, three traits had relatively high narrow sense heritability such as days to 50% flowering (0.62), days to physiological maturity (0.77) as well as first capsule height (0.38) and seed oil content (0.48) suggesting that selection would be effective for improving these traits.

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