

## Nature of Gene Action for Yield, Yield Components and Major Diseases Resistance in Sesame (*Sesamum indicum* L.)

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**Abstract:** Field experiments were conducted to study the gene action for yield and ten yield components including diseases (Fusarium wilt, Charcoal rot and Alternaria leaf spot) resistance in 6 x 6 half-diallel progenies (F<sub>1</sub>'s) of sesame. These experiments were done at the Experimental Farm, Faculty of Agriculture, Suez Canal University, Egypt, through seasons 2005 and 2006. Highly significant differences among the 15 F<sub>1</sub>'s and their 6 parents for all the investigated Characters were detected. The results indicated preponderance of non-additive genetic variance for all the characters, except for days to maturity and resistance to Alternaria leaf spot disease. Nine traits exhibited overdominance recessive alleles were predominant for fruiting branches/plant, capsules per plant and single plant yield. The distribution of genes with positive and negative effects were symmetrical to nearly symmetrical for 1000-seed weight, charcoal rot disease resistance, fruiting branches/plant, capsules/plant, single plant yield and oil content. Parents possessed mostly negative genes in dominant form for capsules/plant, 1000-seed weight, Charcoal rot, Alternaria leaf spot diseases resistance and oil content, while, the opposite was observed for the rest of the characters. Biparental mating or diallel selective mating and heterosis breeding has been suggested.

**Keywords:** Sesame, gene action, seed yield, yield components, diseases resistance, Fusarium wilt, Charcoal rot and Alternaria leaf spot.

### INTRODUCTION

In Egypt, sesame is a conventional and important oilseed crop next to groundnut. It is probably the first oilseed crop known and used by man, where it dates back to 2130 BC<sup>[39]</sup>. Its recorded history in Egypt returned to 1300 BC<sup>[9]</sup>. The area under sesame cultivation tends to decrease due to diseases infections. The sesame-cultivated area is 32187.92 hectare, which represent about 0.49% of the total cultivated area. The production of sesame reach about 1.15 ton per hectare<sup>[3]</sup>. By 2020, the edible oil requirement will be 20.8 million tonnes, equivalent to 60 million tonnes of oilseeds. The yield potential of sesame is very low and the production can be increased with the available resources by using efficient new agronomic practices in a sustainable way. Nevertheless, one of the main problems in Egypt and other countries is the high infections levels by fungal diseases. Wherever, sesame is growing it is liable to attack at least by eight economically important fungal disease<sup>[28]</sup>. It has been reported that *Fusarium oxysporum*, (Schelt) f. sp. *sesami* Jacz, *Macrophomina phaseolina* (Tassi) Goid and *Alternaria sesami* (Kawamura) Mohanty & Behera,

the causal organism of Fusarium wilt, charcoal rot and leaf spot diseases, respectively, causing great yield losses. Estimated of yield losses according to the references were 25% up to 40% in yield losses 40 %<sup>[18,6,12,11,36,15,16]</sup>. Plants inoculated by *Alternaria sesami* at 8 and 12 weeks of age were most susceptible to the Alternaria leaf spot disease and those inoculated at 4 weeks exhibited the least susceptibility Ojiambo *et al.*<sup>[33]</sup>. On the other hand, great differences of resistance levels for Fusarium wilt, charcoal rot and Alternaria leaf spot diseases on sesame were observed on breeding genotypes<sup>[27,17,36,21]</sup>.

The breeding methodology depends considerably upon the nature and magnitude of gene action controlling the genetic behaviour of most studied characters. An analysis based on large number of progenies from divers parents, particular progenies of diallel set, is expected to give more reliable estimates. However, to have a clear picture of genetic mechanism of the sesame population the absolute value of variances must be partitioned into its genetic components. Furthermore, knowledge regarding the nature and magnitude of gene action governing the inheritance of yield and yield components as well as

major diseases (Fusarium wilt, charcoal rot and Alternaria leaf spot) resistance are essential for formulating efficient breeding strategies for the improvement of a sesame crop. In addition, the additive gene effects are easily fixed, the improvement of the characters with predominant additive effects such as plant height, capsule size, capsules on main stem, capsules per plant, 1000-seed weight and resistance to charcoal rot can be done by single plant selection or the selection of superior segregates in early generations<sup>[42]</sup>. The objective of this study was undertaken to estimate the nature of gene action for different quantitative and qualitative characters including major diseases resistance through genetic component analysis in  $F_1$ 's of a 6 x 6 half-diallel cross of sesame.

### MATERIALS AND METHODS

At Suez Canal University, Experimental Farm, Fac. of Agric., Ismailia, Egypt, a field experiments were conducted during two summer seasons. In May 2005, all possible single crosses excluding reciprocals were made using six diverse sesame genotypes (Table1). The six parents and 15  $F_1$ 's in May 2006 were grown in a randomized complete block design with four replications in four-row plots of 4 m row length and a spacing of 45 cm x 10 cm. Recommended agriculture practices were applied at the proper time as usual in the local sesame growing. Some of qualities and quantities characters were subjected as following. Days to 50% from flowering character measured by number of days from sowing until 50% of the plant had been flowered. Days to maturity was recorded, however, observations on 10 random competitive plants for contributing characters namely plant height, fruiting branches/plant, capsules per plant, 1000-seed weight and single plant yield. The oil content were extracted and determined according to the methods described by A.O.A.C.<sup>[4]</sup> using soxhlet apparatus.

In separated trials, during the same seasons, root rot severity and wilt diseases percentage were individually tested under greenhouse conditions. The inoculums of the pathogens were prepared by growing each tested fungus on sand: barley: water medium (1:3:3, w:w:w) for two weeks at  $28 \pm 2^\circ$  C. Soil infested was carried out using of each fungus of *F. oxysporum f. sp. sesami* and *M. phaseolina* at the rate of 3% (w : w) barley medium : pot according Pastor-Corrales and Abawi<sup>[34]</sup> and Nawar<sup>[32]</sup>. Control pots were filled with the same amount of sterilized barley medium. Sesame seeds were surface-sterilized with 3% sodium hypochlorite solution for 3 min, 15 seeds were sown in each pot. A set of four replicates were used for each treatment. Charcoal rot was recorded after 60 days from planting according to

Ahmed<sup>[1]</sup>. Wilted plants were counted and disease severity was assessed daily, starting 15 days after planting, by using the scale outlined by Marlatt *et al.*<sup>[29]</sup>. *Alternaria sesami* fungal growth on PDA plates (15 days old) were used to prepare spore suspension ( $2 \times 1000$  spore /ml) sesame plants (45 days old ) grown in greenhouse were sprayed with the spore suspension, then covered with plastic bags in order to high humidity around the plant leaves for 72hr. after spraying. Plants sprayed with water were used as control Ragab, *et al.*<sup>[35]</sup>. The development of disease was assessed one week after inoculation according to Karunanithi<sup>[25]</sup>. Genetic analysis of the data was done as per Hayman<sup>[23]</sup>.

### RESULTS AND DISCUSSIONS

Sesame improvement programme heavily leaning on the magnitude of genetic variability and the extend to which it is heritable. Unless the amount of genetic gain measured as a percentage of mean is substantial, heritability alone cannot depict the possible improvement of character achievable through selection. Further estimates of total genetic variance with separate out to its constituents as well as various ratios between the genetic components in  $F_1$  generations of 6 x 6 diallel based on the approach proposed by Hayman<sup>[24]</sup> could be feasible for improving a different traits. In addition, they would help and assistant the breeder to infer, to certain extent, about the nature of gene action involved for a characters studied that can be achieved through selection.

The analysis of variance (Table 2) revealed that there were highly significant variations among the 21 genotypes (15  $F_1$ 's + six parents) for all the investigated characters, indicating considerable genetic diversity among the parents and their respective crosses. These findings suggested the presence of fair amount of genetic variability considered adequate for further biometrical assessment in yield and the ten yield components including resistance of diseases (Fusarium wilt, charcoal rot and Alternaria leaf spot). In addition, these genotypes seem to have different genes controlling the investigated traits. These results are confirmed by the works of some authors scientists<sup>[19,13,22,40,41,37,38,21,20,14,15,2,17]</sup> where, significant genetic variations were detected among sesame genotypes for yield and its attributes as well as major diseases resistance.

On the other hand, the analysis of variance to test the consistency of  $W_r$ ,  $V_r$  for the all studied traits as presented in Table 2 reflects the validity of assumptions reported by Hayman<sup>[24]</sup>. The mean squares from the analysis of variance for the six parental arrays if all the assumptions were met. In other words, significant values indicate failure of the hypothesis.

**Table 1:** Number, genotypes name and sources of the sesame parental used in the present investigation.

No.	Genotypes name	Sources
1	Taka 1	Nuclear Research Center, Atomic Energy Authority
2	Taka 2	Nuclear Research Center, Atomic Energy Authority
3	Taka 3	Nuclear Research Center, Atomic Energy Authority
4	Mutant 48	Faculty of Agriculture, Cairo University, Giza
5	Mutant 3	Faculty of Agriculture, Cairo University, Giza
6	Giza 32	Agriculture Research Center, Giza

**Table 2:** Analysis of variance and uniformity of  $W_r$ ,  $V_r$  in the  $F_1$ 's to test the validity of the assumptions of diallel model of studied traits.

S.OV.	D.F	Days to 50% flowering	Days to maturity	Plant height	fruiting branches per plant	Capsules per plant	1000 -seed weight	Fusarium wilt	Charcoal rot	Alternaria leaf spot	Single plant yield	Oil content
Rep.	3	1.56	1.29	3.12	1.01	2.31	0.49	4.14	3.11	1.25	1.99	1.28
Genotypes	20	19.14**	26.89**	410.25**	6.18**	365.17**	1.01**	49.14**	35.10**	21.09**	8.10**	12.56 **
Error	60	1.68	1.87	10.28	1.98	3.29	0.28	3.99	2.78	2.08	1.19	0.95
Testing the validity												
Rep.	3	4.08	3.29	51.18	0.98	10.29	0.04	3.95	3.28	1.28	0.69	1.15
Parents	5	8.1	19.58**	29.1	5.28**	17.82	0.44	15.29	11.25	10.91*	4.98	2.98
Error	15	5.98	4.25	69.48	1.29	11.28	0.24	6.41	4.58	3.59	4.25	1.95

**Table 3:** Estimates of components of genetic variance and related parameters in  $F_1$ 's for yield and its attributing characters as well as Fusarium wilt, Charcoal rot and Alternaria leaf spot diseases resistance in sesame.

Component	Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Capsules per plant	1000 -seed weight	Fusarium wilt	Charcoal rot	Alternaria leaf spot	Single plant yield	Oil content
D	0.81	12.11**	266.94**	0.19	71.45**	0.16**	21.29**	2.88*	5.08**	0.39	8.69**
H1	8.53**	8.99	319.95**	9.88**	14643.03**	0.21**	42.69**	8.91**	3.7	120.13*	16.28**
H2	6.59**	7.92	290.41**	8.86**	13959.39**	0.19**	19.61**	5.88**	2.48	106.12	12.17**
F	0.57	2.04	67.04**	-0.68	-345.12	0.05	17.18**	2.67	2.46	0.47	5.29**
H2	4.92**	5.18	150.12**	5.33**	11680.70**	0.02	-0.28	0.7	0.67	89.59**	38.19**
E	0.49	1.96*	12.97**	0.11	47.17	0.06*	1.43	0.23	1.30*	0.26	2.49
$\sqrt{H_1} / D$	2.91	0.86	1.96	9.48	13.13	1.31	1.41	2.01	1.69	18.99	1.32
uv	0.21	0.22	0.22	0.24	0.23	0.25	0.11	0.25	0.17	0.23	0.24
KD/KR	1.35	1.42	1.26	0.72	0.82	1.26	2.13	2.15	195	0.89	1.59
K	0.69	0.66	0.54	0.57	0.9	-0.04	-0.05	0.16	0.31	0.97	0.89
$r(Y_i, W_i+V_i)$	-0.21	-0.59	-0.43	-0.47	0.31	0.5	-0.2	0.41	0.23	-0.32	0.8

\*, \*\* Denote significant at 5% and 1% levels, respectively.

The significant array mean squares for days to maturity, fruiting branches per plant and disease resistance to Alternaria leaf spot suggest that one or more of Haymans's assumptions of adequate additive dominance model for these traits were not valid. While, non-significant variation was found of  $W_r$ ,  $V_r$  among the arrays for the other traits (Table 2), indicating that at least some of the assumptions of these traits were valid.

The estimates of the components of genetic variance (Table 3) revealed that the additive component (D) was significant for days to maturity, plant height, capsules/plant, and 1000-seed weight, Fusarium wilt, Charcoal rot and Alternaria leaf spot resistance. On the other hand, the dominance genetic variances ( $H_1$  and  $H_2$ ) were significant for all the studied characters, except for days to maturity and disease resistance to Alternaria leaf spot. This indicated the importance of

both additive and non-additive genetic variances in the expression of these characters. However, non-additive component of genetic variance was predominant in all the characters, except days to maturity and oil content. These results are in harmony with results reported by El-Shakhess<sup>[21]</sup>; Bakheit *et al.*<sup>[7]</sup>; El-Bramawy<sup>[15]</sup>.

Concerning F component, it was significant and positive for plant height, Fusarium wilt resistance and oil content, indicating presence of an excess of dominant alleles. Recessive alleles were of greater frequency for capsules/plant. For the remaining characters, there might be a symmetrical distribution of dominant and recessive alleles. The environmental component of variance (E) possessed little effect of the environmental factors, since, the component of variance (E) in all cases was not significant (except days to maturity, plant height and 1000-seed weight) as presented in Table (3). Similar results were detected by El-Bramawy<sup>[15]</sup>.

It's worthy to mention that value  $h^2$  as a measure of over all dominance effects of heterozygous loci, was significant and positive estimates for days to flowering, plant height, branches/plant, capsules/plant and single plant yield. These results indicated that the mean direction of dominance was positive for these characters. The non-significant values of  $h^2$  for the remaining characters did not indicate any direction of dominance. This finding was in agreement with the results reported by Bayoumy<sup>[8]</sup>.

The average degree of dominance ( $\sqrt{H_1/D}$ ) indicated over-dominance for nine traits (days to 50% flowering, branches/plant, capsules/plant, 1000-seed weight, Fusarium wilt, Charcoal rot and Alternaria leaf spot diseases resistance as well as single plant yield). The values indicated partial to nearly complete dominance for days to maturity and slightly over-dominance to complete dominance for plant height. The over dominance observed in most of the traits might not be an index of real over dominance, because the degree of dominance might be biased due to linkage, epistasis or both<sup>[10]</sup>.

The gene frequency among parental sesame that estimates of  $\bar{u} \ v$  ( $H_2/4H_1$ ) indicated a symmetrical distribution of genes with positive and negative effects for 1000-seed weight and charcoal rot disease resistance. The distribution seemed also to be nearly symmetrical for days to maturity, fruiting branches/plant, capsules/plant, single plant yield and oil content.

The quantity of KD/KR was greater than the unity for all the traits, except for fruiting branches/plant (0.72) and capsules/plant (0.82), indicating preponderance of dominant genes in the parents. For fruiting branches/plant and capsules/plant, an excess of recessive genes was evident. These results were in harmony with those reported by El-Bramawy<sup>[15]</sup>.

The value of K ( $h^2/H_2$ ) was greater than the unity only for capsules on main stem, suggesting that one group of genes exhibiting dominance governed that character. For the remaining characters, K value was lower than one. Thus, the values of K did not provide any valid interpretation for all the traits about the groups of genes exhibiting dominance. The ratio could be underestimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes is correlated<sup>[25]</sup>, or when complementary gene interactions occur<sup>[29,31]</sup>.

The correlation between parental performance ( $Y_i$ ) and parental order of dominance ( $W_i+V_i$ ) was positive for capsules/plant, 1000-seed weight and diseases resistance to Charcoal rot and Alternaria leaf spot as well as oil content, indicating that parents possess mostly negative genes in dominant form for these traits. For the remaining traits, positive genes were mostly dominant.

**Conclusion:** The study indicated that both additive and non-additive components of genetic variances were involved with predominance of dominance variances for all the traits, except for days to maturity and disease resistance to Alternaria leaf spot. Pedigree selection is an appropriate method to improve each of days to maturity and oil content as additive variance is predominant for both the characters. As selection based on progeny performance exploits only additive component of genetic variances, bi-parental mating or diallel selective mating, which allows intermating among the selected segregates in the different cycles, would be useful to recover superior homozygotes in later generations. Besides, the greater contribution of dominance and over dominance indicated the scope of heterosis breeding in sesame, which exploits non-additive gene action.

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