Hayman’s diallel analysis for yield and attributing traits in sesame (Sesamum indicum L.)

R. A. Gami¹, B. B. Chauhan² and R. N. Patel³

¹Sorghum Research Station,
²Department of Genetics and Plant Breeding, CPCA,
³Potato Research Station, S.D. Agricultural University, Deesa-385 535 ,Gujarat, India
E-Mail: ramangami@gmail.com

Abstract
Eight sesame (Sesamum indicum L.) genotypes were crossed in a half diallel mating fashion. The analysis of variance for combining ability revealed that the mean sum of squares are due to the general combining ability were highly significant for all the traits. The t² test specified the fulfillment of assumptions required under diallel analysis for all the traits studied except the number of effective branches per plant, capsule length (cm) and harvest index (%). The component D measures the additive effects of genes. It was significant for all the traits except seed yield per plant and harvest index. The components H₁ and H₂ were significant for all the traits except days to maturity revealing the importance of fixable and non-fixable component. Greater values of H₁ than H₂ and the ratio of H₁/4H₂ (< 0.25) confirmed the unbalanced distribution of gene at the loci in the parents’ implying dominance for all the traits. It was also confirmed by greater than one value of KD/KR components for all the traits which suggested the higher frequency of dominant genes than recessive genes in the parents. The component F was significant for days to flowering, days to maturity, capsule length, oil content and leaf area per plant. The graphical analysis showed the regression line intercepted Wr axis below the origin indicating over dominance for plant height, the number of seed per capsule, oil content and leaf area per plant. The regression line intercepted the positive side of Wr axis for days to maturity which implies the presence of partial dominance.

Keywords
Sesame, Hayman’s diallel analysis, fixable and non-fixable components

INTRODUCTION
Sesame (Sesamum indicum L.; 2n = 2x = 26) globally known as ‘sesame’ and in India as ‘Til’ belongs to an order Lamiales and family Pedaliaceae. It is one of the oldest and the most important traditional oilseed crops of the world. The genus Sesamum comprises most of wild species believed to be originated in Africa while the cultivated type i.e., S. indicum originated in India (Bedigian, 2010 and Zohary et al., 2012). Recent archeological remnants suggest that the cultivated sesame evolved from wild species in the Indian subcontinent during Harappan civilization and spread west to Mesopotamia before 2000 B.C (Fuller, 2003). Some report claims sesame was first cultivated in Africa and later spread to India at a very early time (Alegbejo et al., 2003; Purseglove, 1969). According to Tunde-Akintunde et al. (2012), sesame was grown as a main oil crop in Indus valley civilization and then spread to Mesopotamia around 2500 B.C. Sesame is an important source of high quality oil and protein (IPGRI and NBPGR, 2004). Due to excellent qualities of the seed, oil and meal, sesame is called as the “Queen of oilseeds”. Sesame seeds have nutritional as well as medicinal value due to its rich protein, carbohydrate, fat, fiber, vitamins E, A and B complex and minerals viz., calcium, phosphorus, iron, copper, magnesium, zinc and potassium with high-unsaturated fatty acid (linolenic and tocopherol).

During breeding of high yielding varieties of crop plants, breeders are continually challenged with the problem of parent selection. Though elimination of poor crosses on the basis of their performance in initial generation has been suggested; but information on the genetic architecture of yield and its components will help to sort out the improved crosses more competently. Several reports in the past indicate that the diallel analysis...
is the hastiest method of understanding the genetic nature of quantitatively inherited traits and to ascertain the prepotency of parents. Kearsley (1965) noted that Hayman and Jink’s diallel analysis (1953) deliver more evidence than other methods, but has more necessary assumptions. The studies anticipated by Griffing (1956) do not afford any test to detect epistasis or linkage. Hayman and Jink’s analysis do provide such test. When using Griffing’s analysis to estimate variance components, it has been suggested that simple tests, such as the Wr-Vr evaluation found in Hayman (1954b) model, may be used to ascertain the presence of epistasis and/or linkage disequilibrium (Pooni et al., 1984; Wright, 1985). This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The validity of the hypothesis of additive-dominance model was tested by confirming unit slope of regressions of Wr and Vr and by non-significant value of t² as prescribed by Hayman (1954b). The diallel analysis given by Jinks and Hayman (1953) and Hayman (1954a) was employed to find out the genetic constitution of the parents with respect to various traits in the sesame.

**MATERIAL AND METHODS**

The experimental material comprised of eight parents (including check G.TIL 4) and their 28 half-diallel crosses. The half diallel crosses were made during Khairi - 2017 at Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar by manual crossing. The seeds of parental lines were maintained through selfing. A set of 36 genotypes comprising of eight parents (including check G.TIL 4) and their 28 F₁ hybrids were sown in Randomized Block Design (RBD) with three replications, during Khairi - 2018. Each entry was sown in 3.0 m length in two rows with 45 × 15 cm spacing. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. The observations were recorded both as visual assessment (days to flowering and days to maturity) and measurement on randomly selected five competitive individual plants (plant height, the number of effective branches per plant, the number of capsules per plant, capsule length, the number of seeds per capsule, 1000 seed weight, seed yield per plant, harvest index and oil content. The replication wise mean values of each entry for the 12 traits were analyzed using Randomized Block Design (RBD) as suggested by Panse and Sukhatme (1985). Genetic components of variance were computed by employing diallel cross method suggested by Hayman (1954a) for the traits where additive – dominance model fitted well. Adequacy of the additive dominance model was tested with the help of ‘ t²’ test as proposed by Hayman (1954a). The graphical analysis was made according to Hayman (1954b). The replicated mean data were analyzed statistically using the software WINDOSTAT version 8.1. The material used in this experiment was tested for the treaty with assumptions basic to Hayman diallel analysis. Sesame is normally self-pollinated. The parents in the study were homozygous and diverse in their origin, while the maternal effects were presumed to be absent in the studied material. For testing other assumptions, two general tests i.e., t² test and regression of Wr on Vr were used.

**RESULTS AND DISCUSSION**

The analysis of variance from the mean data was carried out as per Randomized Block Design of the field experiment. The results (Table 1) revealed highly significant differences due to the genotypes for all the traits. This supports that the parents and their hybrids under study possessed sufficiently high amount of genetic variability. Further, partitioning of mean sum of square due to genotypes implied that the differences among the parents were significant for all the traits excluding harvest index. Significant differences among parents showed greater diversity in the parental lines.

| Sources of variation | d.f. | Days to flowering | Days to maturity | Plant height | Number of effective branches per plant | Number of capsules per plant | Capsule length | Number of seeds per capsule | 1000 seed weight | Seed yield per plant | Harvest index | Oil content |
|----------------------|------|------------------|------------------|--------------|---------------------------------------|------------------------------|----------------|----------------------------|-----------------|---------------------|--------------|-------------|
| Replications         | 2    | 0.56             | 1.44             | 143.59       | 0.56                                  | 37.39                       | 0.03*          | 2.06                       | 0.00            | 5.90                | 9.41         | 0.05        |
| Genotypes            | 35   | 14.28**          | 3.99**           | 246.26**     | 0.95**                                | 223.06**                    | 0.10**         | 165.19**                   | 0.42**          | 17.59**             | 25.11**      | 32.43**     |
| Parents              | 7    | 26.99**          | 11.23**          | 343.21**     | 1.31**                                | 290.68**                    | 0.23**         | 234.32**                   | 0.48**          | 8.35**              | 3.02         | 63.09**     |
| Hybrids              | 27   | 8.11**           | 2.18             | 221.54**     | 0.78**                                | 211.20**                    | 0.07**         | 147.38**                   | 0.39**          | 20.38**             | 31.15**      | 24.62**     |
| Parents Vs Hybrids   | 1    | 92.02**          | 2.15             | 234.93**     | 2.97**                                | 70.03                       | 0.13**         | 162.00**                   | 0.68**          | 7.08                | 16.74*       | 28.45**     |
| Error                | 70   | 1.74             | 1.59             | 57.24        | 0.25                                  | 53.13                       | 0.01           | 0.80                       | 0.00            | 3.06                | 3.69         | 0.26        |

* P ≤ 0.05,  ** P ≤ 0.01

The results of t² test specified the fulfillment of assumptions required under diallel analysis for all the traits under study except the number of effective branches per plant, capsule length and harvest index (Table 2). The non fulfillment of assumption in these traits shows the unjustifiability of the hypothesis of simple additive-dominance model of gene action and involvement of epistasis and/or linkage disequilibrium. Non-significant t² value in sesame diallel analysis has been reported by Vekaria et al. (2015) for days to flowering, days to maturity, plant height, the number of capsules per plant, seed yield per plant and oil content. The non-significant t² values have also been
reported by Fahmy et al. (2015) for days to flowering, days to maturity, plant height, the number of capsules per plant, 1000 seed weight, seed yield per plant and oil content. El-Kadar et al. (2017) observed non-significant t² values for days to flowering, the number of capsules per plant, 1000 seed weight and seed yield per plant.

The component D measures the additive effects of genes; it was significant for all the traits except seed yield per plant and harvest index (Table 2). This implies that these traits can be easily fixed in early generation. These results are in harmony with those reported by Mohilal and Manoharan (2005), Lavanya et al. (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Aldaji et al. (2014), Vekaria et al. (2015), El-Kadar et al. (2017) for seed yield per plant and one or more component traits, and Tripathy et al. (2016a, 2016b) for oil content and Tripathy et al. (2016b) for seed yield per plant in sesame.

The estimates H₁ and H₂ were significant for all the traits except days to maturity in which only H₁ component confirmed significant effects (Table 2). The significant H₁ component denotes non-additive (dominance or epistatic) genetic effects, which plays a major role in the inheritance of these traits. This finding is in agreement with the results reported by Mohilal and Manoharan (2005), Lavanya et al. (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Aldaji et al. (2014), Vekaria et al. (2015), Tripathy et al. (2016a), El-Kadar et al. (2017) for seed yield per plant and one or more attributes in sesame.

Significant values of additive (D) and non-additive components (H₁ and H₂) clearly assert the predominance role of both fixable and non-fixable components. Further, the magnitude of non-additive (H₁) component was higher than additive (D) component for all the traits except days to maturity showing more important role of over dominance for these traits. This was also evident from the mean degree of dominance (1/4) for all the traits except days to maturity demonstrating over dominance for most of the traits (Table 2). Similar results were reported by Mohilal and Manoharan (2005), El-Bramawy and Shaban (2007), El-Kadar et al. (2017), Aldaji et al. (2014), Sedeck and Shafie (2013), Vekaria et al. (2015) for seed yield per plant and its contributing traits in sesame. However, the over-dominance observed may not be considered as index of true over-dominance as the degree of dominance could be biased due to linkage, epistasis or both (Comstock and Robinson, 1952).

### Table 2. Estimation of genetic components of variance and other parameters for 12 traits in sesame

| Parameters | Days to flowering | Days to maturity | Plant height (cm) | Number of effective branches per plant | Capsule length (cm) | Number of seeds per capsule | 1000 seed weight (g) | Seed yield per plant | Harvest index | Oil content |
|------------|------------------|------------------|-------------------|----------------------------------------|--------------------|-----------------------------|---------------------|-------------------|--------------|-------------|
| b (Wr, Vr) | 0.78             | 0.89             | 0.51              | 0.25                                   | 1.4                | 0.5                         | 0.22                 | -0.13             | -0.11        | 0.83        |
| t₀       | -5.91**          | -2.59*           | -1.51             | -1.09                                  | -1.30              | -5.73**                     | -1.11                | -0.45             | 0.61         | 2.15        |
| t₁       | 1.68             | 0.35             | 1.43              | 3.85**                                 | 1.64               | 1.13                        | 1.60                 | 5.68**            | -2.17**      | 0.65        |
| F        | 1.2              | 0.47             | 0.003             | 14.67**                                | 7.33**             | 0.24                        | 0.25                 | 3.23              | 90.85**      | 0.05        |
| D        | 8.43**           | 3.22**           | 94.53**           | 0.35**                                 | 79.32*             | 0.07**                      | 77.82*               | 0.16              | 1.74         | -0.28       |
| H₁       | 9.91**           | 2.27**           | 181.83*           | 0.69*                                  | 268.45**           | 0.10**                      | 256.96**             | 0.53**            | 23.35**      | 34.41**     |
| H₂       | 7.06**           | 1.11             | 144.45*           | 0.55*                                  | 184.77*            | 0.07**                      | 200.92**             | 0.35*             | 19.87**      | 28.06**     |
| F        | 6.82**           | 3.22**           | 54.82**           | 0.22                                  | 116.42             | 0.08**                      | 118.23               | 0.21              | 2.57         | 1.20        |
| h²       | 14.84**          | 0.12             | 29.85             | 0.45*                                  | 3.81*              | 0.02*                       | 26.45                | 0.11              | 0.70         | 2.16        |
| E        | 0.57             | 0.53*            | 19.88*            | 0.09*                                  | 17.56              | 0.03                        | 0.28                 | 0.00              | 1.05         | 1.28        |
| (H₁/D)₀.5 | 1.08             | 0.84             | 1.39              | 1.40                                  | 1.84               | 1.19                        | 1.82                 | 1.82              | 3.67         | 11.19       |
| H₁/4H₂   | 0.18             | 0.12             | 0.20              | 0.17                                  | 0.17               | 0.17                        | 0.20                 | 0.17              | 0.21         | 0.20        |
| KD/KR    | 2.19             | 3.96             | 1.53              | 1.58                                  | 2.33               | 2.77                        | 2.43                 | 2.13              | 1.51         | 1.49        |
| h²/H₁    | 2.10             | 0.11             | 0.21              | 0.81                                  | 0.02               | 0.28                        | 0.13                 | 0.32              | 0.04         | 0.08        |
| r (P,Wr+Vr) | 0.92**           | 0.73             | 0.52              | 0.41                                  | 0.47               | 0.92                        | 0.41                 | 0.18              | -0.24        | -0.66       |
| Heritability | 0.49             | 0.42             | 0.40              | 0.37                                  | 0.27               | 0.37                        | 0.13                 | 0.41              | 0.18         | 0.23        |

*P ≤ 0.05, **P ≤ 0.01

The equal distribution of positive and negative alleles in the parents aids the breeder in choosing precise desirable traits without losing any desirable traits. The value of H₁ was greater than H₂ for all the traits indicating that the frequency of gene distribution in the parental lines was unequal and this was also proved by the ratio of H₁/4H₂ (< 0.25) which confirmed the unbalanced distribution of gene at the loci in the parents implying dominance for all the traits (Table 2). The results are in accordance with Mohilal and Manoharan (2005), Sedeck and Shafie (2013), Vekaria et al. (2015), Mather and Jinks (1971) while discussing the short comings of numerical component analysis suggested that (H₁/D)₀.5 at each locus is true for major degree of dominance only, where the distribution of dominance and recessive genes is symmetrical. Asymmetrical distribution of genes may influence over estimation of mean degree of dominance.

The values of estimates of F component was significant for days to flowering, days to maturity, capsule length, oil content and leaf area per plant, while for rest of the traits it was positive indicating the presence of an excess of asymmetrical distribution of genes.
dominant alleles than recessive alleles. This was also confirmed by greater than one value of KD/KR components for all the traits suggesting higher frequency of dominant genes than recessive genes in the parents. The present findings are in accordance with those of Mothilal and Manoharan (2005), Lavanya et al. (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Vekaria et al. (2015), El-Kadar et al. (2017) for seed yield per plant and one or more components in sesame. The information of number of gene/group of gene responsible for particular trait is vital for the genetic progress through selection. The value $h^2/H^2$ indicated that at least one group of gene operated for seed yield per plant and most of other traits in the present study. These result are analogous with the results reported by Mothilal and Manoharan (2005), El-Bramawy and Shaban (2007), Lavanya et al. (2006) and Vekaria et al. (2015).

The values of $h^2/H^2$ did not provide any valid interpretation for all the traits about the group 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 are correlated (Jinks 1956) or when complementary gene interaction occur (Liang et al. 1968; Marlatt et al. 1996). Environment component (E) was significant for days to maturity, plant height and the number of effective branches per plant (Table 2). This signifies the considerable role

![Fig. 1 Vr, Wr graph for days to flowering in sesame](image1)

![Fig. 2 Vr, Wr graph for days to maturity in sesame](image2)
Estimated narrow sense heritability was low for seed yield per plant and most of the other traits except days to flowering, days to maturity and plant height which registered moderate heritability. Moderate to low levels of heritability indicated that all the traits were controlled by additive and non-additive genes with preponderance by non-additive genes. This shows that selection would be rewardable at late generation.

The correlation between parental order of dominance (Vr + Wr) and parental mean (Y) was positive and significant for days to flowering and oil content, explicating contribution of recessive alleles for increasing the mean values (Fig 1.). Thus, recessive genes are accountable for early flowering and increasing oil content. El-Bramawy and Shaban (2007) also reported recessive genes for oil content. In case of seed yield per plant the negative correlation indicates role of dominant genes for increasing mean values.

Fig. 3. Vr, Wr graph for plant height in sesame

Fig. 4. Vr, Wr graph for number of seeds per capsule in sesame

of environmental factor in the expression of these traits.
The regression of Wr on Vr was desirable and near unity for days to flowering, days to maturity, plant height, the number of seeds per capsule, 1000 seed weight, oil content and leaf area per plant. Hence, the graphical analysis was performed for these traits only. For the remaining traits including seed yield per plant, the Wr-Vr graph was much distorted and failed to give much information.

In graphical analysis, the regression line intercepted Wr axis below the origin indicating over dominance for plant height (Fig 3.), the number of seeds per capsule (Fig 4.) and oil content (Fig 6.). The regression line intercepted the positive side of Wr axis for days to maturity implying the presence of partial dominance (Fig 2.), while the regression line intercepted at near origin of Wr axis for 1000-seed weight showing the presence of dominance gene action (Fig 5.). The results are in agreement with El-Kadar et al. (2017) for plant height, days to maturity, 1000 seed weight and oil content. The wide scattering of parental array points along the regression line in the Wr-Vr graph for days to maturity, the number of seeds per capsule, 1000 seed weight and leaf area per plant suggests considerable
genetic diversity among the parents for these traits. The parental line G.TIL 4 had maximum recessive genes for early maturity and dwarfness. Similarly, the parent G.TIL 10 had maximum recessive genes for early flowering and increased oil content, while it also possessed maximum dominant genes for the number of seed per capsule and 1000 seed weight.

**REFERENCE**

Aldaj, A. M. M. I.; Noubissie, T. J. B.; Njintang, Y. N.; Nguimbou, R. M. and Bell, J. M. 2015. Diallel analysis of seed oil content in sesame. *Journal of Global Bioscience*, 4 (3): 1735-1746.

Aldaj, A. M. M. I.; Noubissie, T. J. B. and Njintang, Y. N. 2014. Genetic analysis of seed yield components in *Sesamum indicum*. *Scholars Academic Journal of Biosciences*, 2 (6): 318-325.

Alegbejo, M. D.; Iwo, G. A.; Abo, E. M. and Idowu, A. A. 2003. Sesame: a potential industrial and export oilseed crop in Nigeria. *Journal of Sustainable Agriculture*, 23 (1): 59-76. [Cross Ref]

Bedigian, D. 2010. Introduction and early use of sesame in America: medicine, cookery and folkways. In: Bedigian, D. (Ed.), *Sesame; The Genus Sesamum*, Medicinal and aromatic plants–Industrial profiles series, Boca Raton, Florida, CRC Press, Taylor and Francis Group, pp. 389-421.

Comstock, R. E. and Robinson, H. F. 1952. Estimation of the average dominance of genes. In: “Heterosis” (Ed. Gowen, J. W.), Iowa State College Press, America, pp. 494-516.

El-Bramawy, M. A. S. and Shaban, W. I. 2007. Nature of gene action for yield, yield components and major diseases resistance in sesame (*Sesamum indicum* L.). *Research Journal of Agriculture and Biological Science*, 3 (6): 821-826. [Cross Ref]

El-Kadar, M. T. M.; Fahmy, R. M.; El-Shaer, H. F. A. and El-Rahman, M. A. 2017. Genetic analysis of six parental sesame genotypes for yield and its attributes in F₂ crosses. *Journal of Basic and Environmental Sciences*, 2: 190-209.

Fahmy, R. M.; El-Satar, M. A. and Hassan, T. H. A. 2015. Heterosis, combining ability and gene action for yield and its attributes of F₂ crosses in sesame. *Egypt Journal of Plant Breeding*, 19 (3): 917-943. [Cross Ref]

Fuller, D. Q. 2003. Further evidence on the prehistory of sesame. *Asian Agri-History*, 7: 127-137.

Griffing, B. 1956. A general treatment of the use of diallel cross in quantitative inheritance. *Hereditiy*, 10: 31-50. [Cross Ref]

Hayman, B. I. 1954a. The analysis of variation of diallel tables. *Biometrics*, 10: 235-244. [Cross Ref]

Hayman, B. I. 1954b. The theory and analysis of diallel crosses. *Genetics*, 39: 789-809.

IGPRI and NBPRG 2004. Descriptors for sesame (*Sesamum spp.*). International Plant Genetic Resources Institute, Rome, Italy and National Bureau of Plant Genetic Resources, New Delhi, India.

Jinks, J. L. and Hayman, B. I. 1953. The analysis of diallel crosses. *Maize Genetics Newsletter*, 27: 48-54.

Jinks, J.L. 1956. The F₂ and backcross generation from a set of diallel crosses. *Hereditiy.*, 10 : 1-30. [Cross Ref]

Kearsey, M. J. 1965. Biometrical analysis of a random mating population; a comparison of five experimental designs. *Heredity*, 20: 205-235. [Cross Ref]

Lavanya, M. S.; Kumar, S. T.; Gokulakrishnan, J.; Kumar, N. S.; Eswaran, R. and Anandan, A. 2006. Genetic analysis for seed yield and its component characters in sesame (*Sesamum indicum* L.). *Research on Crops*, 7 (2):171-173.

Liang, G. H. L.; Heyne, E. G. and Chung, J. M. 1968. The analysis of heritable variation for three agronomic traits in a six-variety diallel of grain sorghum (*Sorghum vulgare Pers.*). *Canadian Journal of Genetics and Cytology*, 10: 460-469. [Cross Ref]

Marlatt, M. L.; Correll, J. C. and Kaufmann, P. 1996. Two genetically distinct populations of *Fusarium oxysporum* f. sp. *lycopersici* race 3 in the United States. *Plant Disease*, 80 (12): 1336-1342. [Cross Ref]

Mather, K. and Jinks, J. L. 1971. Biometrical genetics. Chapman and Hall Ltd., London, pp. 382. [Cross Ref]

Mothilal, A. and Manoharan, V. 2005. Diallel analysis for the estimation of genetic parameters in sesame (*Sesamum indicum* L.). *Agriculture Science Digest*, 25 (2): 133-135.

Pooni, H. S.; Jinks, J. L. and Singh, R. K. 1984. Methods of analysis and the estimation of the genetic parameters from a diallel set of crosses. *Heredity*, 52: 243-253. [Cross Ref]

Purseglove, J. W. 1969. Tropical crops dicotyledons. Volume 1, Longman, London.

Sedec, F. Sh. and Shafie, W. W. M. 2013. Estimates of gene action and interrelationship among yield characters in diallel crosses of sesame (*Sesamum indicum* L.). *Assiut Journal of Agricultural Science*, 44 (3): 15-31.
Gami et al.,

Sukhatme, P. V. and Panse, V. G. 1985. Statistical methods for agricultural workers. 4th ed. ICAR, New Delhi.

Tripathy, S. K.; Mishra, D. R.; Mishra D.; Mohanty, S. K.; Dash, S.; Swain, D.; Mohapatra, P. M. and Pradhan, K. C. 2016a. Inheritance pattern of oil content in sesame (Sesamum indicum L.). Plant Gene and Trait, 7 (7): 1-6.

Tripathy, S. K.; Mishra, D. R.; Mohapatra, P. M.; Pradhan, K.; Mishra, D.; Mohanty, S. K.; Dash, S.; Reshmi Raj, K. R.; Swain, D.; Mohanty, M. R. and Panda, S. 2016b. Genetic analysis of seed yield in sesame (Sesamum indicum L.). International Journal of Agricultural Sciences, 6 (9): 1128-1132.

Tunde-Akintunde, T. Y.; Oke, M. O. and Akintunde, B. O. 2012. Sesame seed, Oilseeds, 5: 81-97. Uduak, G. A. (Ed.), In Tech. ISBN: 978-953-51-0665-4. Available at http://www.intechopen.com/books/oilseeds/sesameseed.

Vekaria, D. M.; Dobaria, K. L.; Rajani, C. J. and Patel, M. B. 2015. Nature and magnitude of gene action and genetic components of variation for yield and yield contributing characters in F2 generation of sesame (Sesamum indicum L.). An International Quarterly Journal of Life Science, 10 (2): 857-861.

Wright, A. J. 1985. Diallel designs, analysis and reference populations. Heredity, 54: 307-311. [Cross Ref]

Zohary, D.; Hopf, M. and Weiss, E. 2012. Domestication of plants in the old world: The origin and spread of domesticated plants in southwest Asia, Europe and the Mediterranean Basin. 4th Edition. Oxford University Press, pp. 243. [Cross Ref]