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HETEROTIC GROUPING WITH COMBINING ABILITY AND GENE ACTION IN *SESAMUM INDICUM* L. USING LINE × TESTER ANALYSIS

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SUMMARY

Line × tester analysis is an efficient method to evaluate many entries for GCA (general combining ability) and SCA (specific combining ability) effects. Fifteen lines and three testers of sesame (*Sesamum indicum* L.) gained evaluation for shattering, yield, and oil quality traits. Crossing selected tolerant and sensitive accessions in line × tester fashion ensued, with the resultant F_1, parent material, and commercially cultivated varieties sown in the field to ascertain the genetic mechanisms to assess heterosis manifestation and generation turnover. Combining ability analysis exhibited variable direction and magnitude of GCA effects among line and testers and SCA effects among crosses. The lines SG-41, G-43, and SG-50 and testers SG-60 and SG-1 were the best general combiners. Crosses SG-44 × SG-60, SG-50 × SG-60, SG-103 × SG-14, SG-103 × SG-60, SG-110 × SG-14, SG-50 × SG-1, and SG-113 × SG-60 had a positive significant SCA effect for maximum yield-related traits. SG-39 × SG-60, SG-44 × SG-60, and SG-50 × SG-60 had positive significant SCA effects for maximum oil-related qualities. Crosses SG-41 × SG-1, SG-41 × SG-60, SG-43 × SG-60, SG-50 × SG-14, and SG-50 × SG-60 had positive and significant heterosis over the mid-parent, a better parent, and commercial hybrids for most of the traits. Conditioning on secondary branches, flower initiation, capsule length, and 1000-seed weight were by non-additive genetic effect, with all the other parameters under the control of additive gene action. The variance ratio of GCA to SCA showed less than unity; in contrast, the additive genetic variance was more than the dominant variance for all traits except for secondary branches, flower initiation, capsule length, and 1000-seed weight. The association of traits based on correlation and path analyses suggested that plant height, oil content, and 1000-seed weight can serve as criteria for selecting sesame for a future breeding program.

Keywords: Sesame (*Sesamum indicum* L.), heterosis, line × tester analysis, GCA and SCA, gene action, correlation

Key findings: Crosses SG-44 × SG-60, SG-50 × SG-60, SG-103 × SG-14, SG-103 × SG-60, SG-110 × SG-14, SG-50 × SG-1, and SG-113 × SG-60 had the positive significant SCA effects for maximum yield-related traits; these crosses were best specific combiners for most of the traits.

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is a traditional oilseed crop cultivated since ancient times for its edible oil and seed in the Indo-Pak subcontinent. It is known as the king of oilseeds due to the presence of seed-oil of 60%, high protein, and antioxidant contents (Morris, 2002; Koca *et al*., 2007; Anilakumar *et al*., 2010; Toan *et al*., 2010; Ke *et al.*, 2011; Wang *et al.*, 2014) and therefore, its extensive use in food, nutraceutical, and pharmaceutical industries. It reduces the blood glucose level significantly and improves the conditions of type 2 diabetes (Lin *et al*., 2018) and has anti-inflammatory properties (Hsu and Parthasarathy, 2017) and has wide use for medicinal purposes (Salunkhe *et al.*, 1991; Suja *et al.*, 2004; Quasem *et al*., 2009).

Europe is a growing market that imports a large amount of sesame seed worth USD 235.25 (€216) million. The major importing countries are Germany, Netherlands, Poland, Greece, and the United Kingdom. About 80% of the import is from Latin America, Africa, and Asia (Eurostat, 2017). There is an overall annual growth of around 4.0% in value on the import of sesame. Pakistan, at present, is facing a severe shortage of edible oil of about 80%. The foremost reason for this shortage is poor cultivars, lack of policy, and an ever-increasing population. Though Pakistan grows sesame, unfortunately, its production is low, attributable to the conventional varieties used with shattering and indeterminate growth habit that cause severe harvesting issues. It therefore results in yield loss and poor adaptation to mechanized harvesting. Most of the world's sesame, probably more than 98%, suffers from shattering issues; thus, most harvest is manual (Myint *et al.,* 2019). It is one of the main reasons the country's breeding programs aimed to increase plant yield (Hamid *et al.,* 2003). Hence, enhanced sesame production may contribute toward bridging the gap between domestic production and consumption of edible oil in the country. It will help reduce the import, on the one hand, and increase the magnitude of exports to the European and international sesame markets, on the other. Therefore, shattering and low yield need proper addressing to earn more through export and become self-sufficient in production. For this purpose, the sesame crop's genetic improvement is very crucial. Knowledge about heritability helps plant breeders to predict the nature of the further generation for appropriate selection and to assess the degree and magnitude of genetic improvement through selection (Schmidt *et al*., 2019).

Sesame is a self-pollinated crop and highly suitable for applying variability via heterosis (Andrade *et al*., 2014). Heterosis usage has been successful for seed and oil yield. Hybrid vigor in sesame has reports from Pal as early as 1945. Subsequent studies have stressed the importance of heterosis as a means for crop improvement in sesame. Results on the F_1 sesame hybrids showing heterosis for seed yield components came from California, the USA, India, and Venezuela (Riccelli and Mazzani, 1964; Delgado, 1972; Murty, 1975; Dixit, 1976). With its uniformity, quality, and high yield, farmers prefer hybrids developed via heterosis. In any breeding program, it is essential to identify superior parents for hybridization and crosses to expand the genetic variability for selecting superior genotypes.

The performance of a heterotic hybrid combination depends upon the combining abilities of its parents. Recognizing the best parental combination is the most critical challenge for breeders, since general combining ability and specific combining ability are very influential (Bajaj *et al*., 1997). GCA is a highly effective tool for the selection of parents. It is extremely useful as it indicates that one parent of a poor combination could make the best combination of selecting the other parent properly. Meanwhile, SCA determines the type of gene action. Higher SCA indicates the best general combiners that may result from additive by additive gene action (Ramakrishnan and Soundarapandian, 1990; Reddy *et al.,* 1984; Krishnadoss *et al.*, 1986, 1987). Various use of analyses, such as Diallel, North Carolina, and line × tester, determine the combining abilities. Extensive mating patterns and requirements of genetic assumptions in diallel are limitations. Similarly, North Carolina design requires a more number of flowers to make all possible combinations. Line by tester analysis is an efficient method to evaluate many entries for GCA and SCA effects and helps interpret the genetic basis of plant characters (Kempthorne, 1957; Rani *et al*., 2015; Aristya *et al*., 2017; Khuimphukhieo and Khaengkhan, 2018).

Moreover, it is more efficient and easier to compute. For the success of any breeding program, the nature and magnitude of variability and heritability are prime factors. Heritability calculates genetic advance, indicating the degree of gain in character obtained under selection pressure. Therefore, genetic advance is an essential selection

parameter that helps in the breeding program. High genetic advance, coupled with high heritability estimates, offers the most suitable condition for selection. It also indicated the presence of additive genes in the trait and further suggested reliable crop improvement for selecting such traits (Johnson *et al.,* 1955; Panse, 1957). Therefore, breeders must know about the heritability of agronomic traits to improve crop yield. An attempt aimed to study the heterotic effect, general and specific combining abilities, and genetic advancement on *Sesamum indicum* L. transpired. New findings for breeders would include a better understanding of the genetic systems governing the inheritance of characters to improve, as well as, the potential of different crosses. It would enable them to develop higher yields and market-value varieties. Additionally, assessing is better in predicting performance in subsequent generations.

MATERIALS AND METHODS

The experimental site, plant material, and procedure

The research took place in the field area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, during the summer, autumn, and spring of 2019–2020, with the sesame germplasm collected from the said institution. It comprised 120 accessions screened for shattering tolerance and shattering sensitivity. Accessions SG-39, SG-40, SG-41, SG-43, SG-44, SG-50, SG-103, SG-105, SG-109, SG-110, SG-111, SG-112, SG-113 SG-115, and SG-117 performed well for shattering and yield-related traits and thus, used in this experiment. Accessions SG-1, SG-14, and SG-60 served as testers as these were weak.

The geographical coordinates of Faisalabad are the rolling flat plains of Northeast Punjab, between longitude 73° 74 East and latitude 30° 315 North with an elevation of 184 masl. The climate of Faisalabad is arid due to its high evapotranspiration. The average recorded yearly rainfall is almost 300 mm. The average temperature in summer ranges from 30 °C–45 °C, while during winter, the average temperature falls between 6 °C–17 °C.

The experimental layout used a randomized complete block design with three replications keeping one-foot plant-to-plant and two feet row-to-row distances. Three seeds sown per hole were with the help of the dibbler. Later, thinning application left one plant per hole. Following all the cultural practices performed in the field was for optimum crop production. Fertilizer application consisted of one bag of diammonium phosphate and half a bag of urea per acre at the time of sowing, with another half bag of urea applied in the first irrigation of three irrigations.

Crossing

Emasculation is the elimination of anthers from bisexual flowers without influencing the female reproductive part (pistil). Such a process obtains the desired cross-plant needed for further evaluation. Three flowers of each genotype got emasculated during the crossing season. Mother plants underwent the hand emasculation method, with the anthers removed from florets using forceps without injuring the stigma. Self-pollination can occur by emasculating florets that are too mature. Hand emasculation in florets was at the middle part of the flowers to minimize the risk.

Evaluation of breeding material

Parent material, F_1, and commercially cultivated varieties sown in the field ascertained the genetic mechanism to assess heterosis manifestation and generation turnover. Then, performing the selection of single plants segregated generation F_2. Selected F_2 plants further grown raised F_3 in a progeny row trial. Choosing the best plants from the best families followed for further analysis and selection of the germplasm with better yield, oil quality, and shattering tolerance.

Data recording were for the following traits: days to flower initiation (days to 50% flowering), flowering completion (days to maturity), number of secondary branches, plant height (cm), capsule formation, 1000-seed weight (g), seed per capsule (g), capsule length, oil percentage, protein percentage, palmitic acid (%), stearic acid (%), oleic acid (%), linoleic acid (%), and linolenic acid (%).

Statistical analysis

Combining ability estimates, effects, and proportional contribution of lines, testers, and their interaction to total variance computations used the line × tester analysis (Kempthorne 1957). Calculating heterosis was at all mid-parent, better-parent, and commercial levels, as Falconer and Mackay (1996) described.

Correlation coefficients at genotypic and phenotypic levels followed Kwon and Torrie's (1964) method of computations. Path analysis followed that of Dewey and Lu (1959). Heritability in a broad sense estimates followed Poehlman (1987), using an arbitrary scale of magnitude of heritability to express the results. Genetic Advance calculation was according to the formula by Singh and Chaudhury (1985).

RESULTS AND DISCUSSION

Genetic variability among lines and testers

Mean square values from the analysis of variance for field traits are available in Table 1. Genetic variation among these entries for most field traits occurred to improve the yield and oil-related traits. This result indicated that the tested breeding material can benefit future breeding programs to enhance sesame yield, oil quality, and shattering-related traits. Genetic variability among parents vs. crosses for most traits under study indicated that heterosis is present among crosses that may be useful for hybrid development. Reports on genetic variability in sesame populations for yield-related traits also came from Sudhakar *et al*. (2007), Parameshwarappa *et al*. (2009), Sumathi and Muralidharan (2010), Gidey *et al.* (2013), Teklu *et al.* (2014), Iqbal and Dasgupta (2015), and Stavridou *et al*. (2021).

Based on the performance or crosses, SG-41 × SG-60, SG-43 × SG-60, SG-41 × SG-1, and SG-50 × SG-60 revealed high yielding, lower shattering indices, with better oil quality. These crosses may need further evaluation as a source of developing shattering resistance and high-yielding sesame hybrids.

Mean performance of parents and hybrids

General combing ability effects for the field traits appear in Table 2. The lines and the testers had different magnitudes and direction of GCA effects. Parent SG-50, followed by SG-110, showed the highest positive and significant GCA effects for plant height. SG-50 performed well for plant height and flower completion. SG-39 showed the highest positive GCA effects for 1000-seed weight and seeds per capsule. SG-44 had positive, significant GCA effects. Likewise, tester SG-1 had the highest positive effect for GCA for flower initiation, flower completion, 1000-seed weight, and seeds per capsule.

Table 3 also presents GCA effects for oil quality-related traits, differing in magnitude and direction within lines and testers. Among lines, SG-40 had positive significant GCA effects for oil and protein percentage, and palmitic, stearic, and linoleic acids, whereas SG-105 had positive significant GCA effects for oil content, protein content, palmitic acid, and stearic acid. Meanwhile, SG-110 recorded positive significant GCA effect for oil, protein, and linolenic acid contents. Among testers, SG-1 had the highest significant values for all the traits related to oil quality (Table 3), followed by SG-60, which had positive significant GCA effects for oil content, palmitic acid, stearic acid, and linolenic acid.

Specific combining ability effects for the crosses for yield and oil-related traits are in Tables 4 and 5. The results showed variable direction and magnitude of SCA for field traits among crosses. For oil-related traits, results indicated variation in the magnitude and direction of the crosses. Positive and significant SCA effects showed for the cross, SG50 × SG60, noted for oil content, protein content, palmitic acid, stearic acid, oleic acid, and linolenic acid. Positive significant SCA effects also emerged for SG103 × SG1 for protein content, palmitic acid, stearic acid, oleic acid, and linolenic acid.

Heterosis

Observed heterosis was among the crosses over the better parent and commercial hybrids for field traits. Crosses SG-41 × SG-1, SG-41 × SG-60, SG-43 × SG-60, SG-50 × SG-14, and SG-50 × SG-60 had positive and significant heterosis over the commercial hybrids under study, as shown in Table 6. Significant positive heterosis was also in various populations for the said traits in *Sesamum indicum* L. (Sankar and Kumar, 2001; Anuradha and Reddy, 2008; Raghunaiah *et al*., 2008; Praveenkumar *et al*., 2012; Padma and Kamala, 2012; Imran *et al.,* 2017).

Estimation of genetic components

The phenotypic coefficient of variance was more than the genotypic coefficient of variance (Table 7), indicating more environmental effects for these traits. The genotypic coefficient of variation ranged from 0.72% to 81.92%, and the phenotypic coefficient of variation ranged from 1.78% to 83.91%. The phenotypic coefficient of variation was

Table 1. Analysis of variance for various morphological traits and fatty acid profile in sesame.

SOV	Df	PH	FI	FC	SB	1000-SW	CF	CL	SPC
Morphological traits									
Replications	2	0.2ns	0.7ns	0.20ns	1.1ns	0.4ns	0.0ns	0.12 ns	11ns
Entries	62	1408.4**	235.6**	1408.42**	4.4ns	4.1	166.6**	3.5	570**
Parents	17	17.0**	15.9**	206.81**	6.2ns	2.5	51.9**	2.1	1112**
Parents vs. Crosses	1	85927.1**	13808.5**	79283.15**	56.75**	39.1**	8606.4**	152.8**	31151**
Crosses	44	25.1**	11.9**	102.80**	2.5ns	3.9	18.3**	0.7	52**
Lines	14	41.7**	35.1**	74.81**	6.7**	6.5*	41.2**	1.0	44
Testers	2	3.1	0.2	65.65**	1.4	3.6	0.6	0.1	74**
Lines × Testers	28	18.4**	1.3	119.44**	0.5	2.6	8.1**	0.5	55**
Error	124	2.3	0.9	2.0	0.1	0.1	0.4	0.1	1
SOV	Df	OP	PP	PA	OA	SA	LA	LIA	
Fatty acid profile									
Replications	2	0.7	0.2	0.0	0	0.0	0.0	0.00	
Entries	62	513.8**	40.0**	88.3**	1137**	47.5**	14.6*	0.64	
Parents	17	99.3**	3.6*	32.7**	45**	23.0**	1.5	0.09	
Parents vs. Crosses	1	28984.2**	2310.8**	4870.5**	68298**	2294.8**	864.6**	37.25*	
Crosses	44	26.9*	2.5*	1.1	33*	5.8*	0.3	0.02	
Lines	14	40.1*	3.6*	1.6	50**	9.3*	0.4	0.02	
Testers	2	9.8*	5.7**	0.5	35**	7.9*	0.2	0.05	
Lines x Testers	28	21.5**	1.7	0.9	24**	3.9*	0.3	0.01	
Error	124	1.3	0.4	0.6	2	0.4	0.3	0.05	

ns = non-significant, *, ** = significant at 0.05 and 0.01 probability levels, respectively; df = degree of freedom, PH= Plant Height, FI=Days to 50%Flowering, FC=Flower Completion, CF=Capsule Formation, SB=Secondary Branches, CL=Capsules Length, SPC=Seeds Per Capsule, and 1000SW=Thousand Seed Weight, OP=Oil Percentage, PP=Protein Percentage, PA=Palmitic Acid, OA=Oleic Acid, SA=Stearic Acid, LA=Linoleic Acid, and LIA=Linolenic Acid.

Table 2. General combining ability effects of parental lines and testers for various morpho-phenological traits.

Lines/Testers	PH	FI	FC	SB	1000-SW	CF	CL	SPC
Lines								
SG-39	0.38	-2.24**	1.06	0.13	1.66	-0.98**	0.28	2.16
SG-40	2.45	-1.98**	-1.67**	0.15	1.09	1.36	0.50	1.61
SG-41	-2.27**	-1.17	2.93	0.28	0.46	3.91	-0.39	1.49
SG-43	-1.72**	-0.42**	-4.41**	1.00	0.04	1.24	0.52	-1.96**
SG-44	-3.30**	-0.95**	0.04	1.20	-0.68**	4.13	-0.18**	2.42
SG-50	4.17	-0.82**	4.66	0.99	-0.10**	0.36	-0.19**	0.58
SG-103	2.07	-0.45**	-1.69**	1.16	-0.39**	-0.76**	0.30	-1.72**
SG-105	-1.52**	-0.49**	2.88	-0.02**	-0.07	-3.42**	-0.04**	-4.29**
SG-109	-0.46**	-0.89**	1.02	-0.25**	1.15	-1.09**	0.02	1.37
SG-110	2.70	-0.93**	0.73	-0.52**	0.73	0.91	0.19	0.40
SG-111	1.02	-1.57**	-3.36**	-0.61**	-0.43**	-1.09**	0.14	-2.60**
SG-112	-2.61**	1.76	-0.58**	-0.12**	-0.81**	0.58	-0.12**	-3.56**
SG-113	0.02	2.73	-5.43**	-0.72**	-0.55**	-1.31**	0.03	0.93
SG-115	-0.57**	3.71	1.04	-0.72**	-0.82**	-0.87**	-0.38**	1.29
SG-117	-0.35**	3.70	2.79	-1.95**	-1.29**	-2.98**	-0.67	1.89
S.E.	0.51	0.31	0.47	0.12	0.13	0.22	0.09	0.37
Testers								
SG-1	-0.10	0.08**	0.91**	0.04**	0.20**	-0.07	-0.05	0.92**
SG-14	-0.20	-0.01	0.46**	0.16**	0.12**	0.13**	0.02**	-1.46
SG-60	0.30**	-0.07	-1.37	-0.19	-0.32	-0.07	0.04**	0.54**
S.E.	0.51	0.31	0.47	0.12	0.13	0.22	0.09	0.37

*, ** = significant at 0.05 and 0.01 probability levels, respectively, PH = Plant height, FI = Days to 50% flowering, i.e., Flowering initiation, FC = Flowering completion, SB = Secondary branches, 1000-SW = 1000 Seed weight, CF = Capsule formation, CL= Capsule length, and SPC = Seeds per capsule.

Table 3. General combining ability effects of parental lines and testers for various oil quality traits.

Lines/Testers	OP	PP	PA	SA	OA	LA	LIA
Lines							
SG-39	-3.91**	0.38	0.02	1.21	-0.97**	-0.11**	0.04
SG-40	2.67	0.16	0.31	0.69	-0.10**	-0.11**	0.01
SG-41	1.72	-0.20	0.34	1.31	0.13	0.20	0.03
SG-43	-2.36**	-0.48**	0.33	0.07	-2.26**	0.28	-0.01**
SG-44	2.70	0.33	0.87	1.25	-0.99**	0.31	-0.04**
SG-50	2.12	-0.19**	-0.01**	-0.55**	-1.23**	0.22	-0.13**
SG-103	0.53	-0.04**	0.11	-0.32**	1.13	013	0.01
SG-105	-1.91**	-0.25**	-0.01**	-0.89**	-0.87**	0.07	-0.03**
SG-109	1.42	-0.33**	-0.29**	-1.69**	0.04	-0.20**	-0.03**
SG-110	1.13	0.79	-0.55**	-1.05**	-2.26**	0.10	0.07
SG-111	-0.78**	0.08	-0.37**	-0.53**	-0.99**	0.06	0.07
SG-112	-1.70**	0.13	0.14	-0.45**	2.37	-0.24**	-0.01**
SG-113	-2.16**	1.16	-0.70**	0.88	7.23	-0.18**	0.02
SG-115	-1.16**	0.16	-0.48**	1.21	-1.76**	-0.25**	-0.04**
SG-117	1.71	-1.70**	0.25	-1.15**	0.52	-0.28**	0.03
S.E.	0.37	0.20	0.25	0.49	0.13	0.17	0.07
Testers							
SG-1	0.33**	0.41**	0.10**	0.39**	0.73**	0.08**	0.03**
SG-14	-0.53	-0.25	-0.10	-0.44	0.26**	-0.03	-0.04
SG-60	0.21**	-0.15	0.01**	0.05**	-0.99	-0.06	0.01**
S.E.	0.37	0.20	0.25	0.49	0.13	0.17	0.07

OP = Oil Percentage, PP = Protein Percentage, PA = Palmitic Acid, SA = Stearic Acid, OA = Oleic Acid, LA = Linoleic Acid, and LIA= Linolenic Acid.

Table 4. Specific combining ability effects of F_1 hybrids for various morphological traits.

F_1 hybrids	PH	FI	FC	SB	SPC	1000-SW	CF	CL
39 × 1	-0.34	-0.09	-5.55	-0.41	5.48**	2.33**	-1.38	0.19**
39 × 14	0.99**	-0.03	3.03**	0.13**	-0.45	-1.27	-2.24	0.32**
39 × 60	-0.64	0.12**	2.53**	0.28**	-5.03	-1.06	3.62**	-0.50
40 × 1	-1.09	-0.02	9.58**	0.16**	-2.42	1.40**	1.29**	0.03**
40 × 14	0.37**	-0.16	-5.17	0.11**	2.52**	-0.80	0.76**	-0.17
40 × 60	0.71**	0.19**	-4.41	-0.27	-0.09	-0.60	-2.04	0.14**
41 × 1	2.03**	-0.43	-4.49	0.40**	0.71**	-0.74	0.07**	-0.01
41 × 14	-4.07	0.79**	6.89**	-0.42	-0.38	0.11**	-0.13	-0.08
41 × 60	2.03**	-0.36	-2.41	0.03**	-0.33	0.62**	0.07**	0.10**
43 × 1	1.89**	-1.25	2.65**	-0.92	2.73**	0.52**	2.73**	-0.72
43 × 14	4.62**	0.35**	11.76**	-0.27	-0.15	-0.30	1.87**	-0.60
43 × 60	-0.71	-0.10	-6.67	0.66**	-3.48	0.42**	0.07**	-0.08
44 × 1	-1.90	0.05**	-5.00	-0.06	0.12**	0.47**	-2.82	-0.42
44 × 14	-1.77	-0.09	4.18**	-0.04	3.16**	-0.76	2.31**	0.90**
44 × 60	3.67**	0.03**	0.81**	0.10**	-3.28	0.29**	0.51**	-0.48
50 × 1	-0.07	0.09**	0.71**	0.49**	-6.29	0.12**	1.96**	0.22**
50 × 14	-1.17	0.18**	-5.77	-0.17	-3.16	-0.21	-0.91	-0.52
50 × 60	1.23**	-0.27	5.06**	-0.32	9.45**	0.09**	-1.04	0.30**
103 × 1	1.40**	-0.21	0.40**	-0.05	-1.49	-0.09	-1.60	-0.23
103 × 14	1.03**	0.28**	-2.68	0.40**	1.98**	-0.36	0.53**	0.53**
103 × 60	0.53**	0.33**	-0.85	0.75**	-0.03	0.09**	0.73**	0.51**
105 × 1	-2.78	0.39**	1.09**	0.70**	-0.95	-0.89	-0.93	-0.24
105 × 14	2.05**	-0.25	-4.33	-0.46	4.31**	0.56**	-0.80	0.23**
105 × 60	-0.81	-0.73	-4.30	-0.11	6.90**	0.96**	3.73**	0.28**
109 × 1	0.19**	0.12**	-1.91	0.83**	-1.63	1.66**	-0.27	-0.20
109 × 14	0.29**	0.21**	-1.46	0.71**	0.76**	1.73**	-0.47	-0.27
109 × 60	1.19**	0.27**	6.17**	-0.61	-1.62	-0.96	-0.93	-0.04
110 × 1	-2.03	-0.23	9.78**	-0.10	-0.36	-0.80	0.73**	0.28**
110 × 14	1.20**	0.39**	-5.24	-0.02	1.26**	1.52**	0.53**	-0.13
110 × 60	0.83**	-0.16	-4.54	0.13**	-0.91	-0.72	-1.27	-0.15
111 × 1	2.91**	0.33**	-2.73	-0.01	1.71**	-0.08	0.73**	-0.01
111 × 14	-0.76	-0.41	2.52**	0.00	-0.22	-0.52	-1.13	0.52**
111 × 60	-2.15	0.08**	0.21**	0.01**	-1.49	0.60**	0.40**	-0.50
112 × 1	-1.95	0.64**	-3.51	-0.24	5.37**	-0.45	-0.93	0.12**
112 × 14	4.31**	-1.43	4.74**	0.24**	-11.12	0.39**	1.87**	-0.15
112 × 60	-2.35	0.79**	-1.23	-0.01	5.75**	0.07**	-0.93	0.03**

Table 4. (cont'd).

F_1 hybrids	PH	FI	FC	SB	SPC	1000-SW	CF	CL
113 × 1	2.25**	-0.37	-7.27	-0.24	-1.32	-0.31	-0.04	-0.43
113 × 14	-0.89	-0.71	2.65**	0.18**	-0.20	-0.19	-0.24	0.43**
113 × 60	-1.35	1.08**	4.61**	0.06**	1.51**	0.51**	0.29**	0.01**
115 × 1	-0.37	-0.05	-4.13	-0.17	0.77**	0.26**	-0.16	0.51**
115 × 14	1.06**	1.41**	9.72**	0.11**	2.81**	-0.43	-0.02	-0.50
115 × 60	-0.70	-1.37	-5.59	0.06**	-3.58	0.17**	0.18**	-0.01
117 × 1	-1.12	0.13**	4.51**	-0.20	0.35**	-0.07	-0.38	0.23
117 × 14	0.54**	0.36**	-3.71	0.01**	0.67**	-0.11	-0.24	-0.22
117 × 60	0.58**	-0.49	-0.81	0.19**	-1.01	0.18**	0.62**	0.00
S.E.	0.88	0.54	0.81	0.20	0.65	0.22	0.38	0.15

PH = Plant height, FI = Days to 50% flowering, i.e., Flowering initiation, FC = Flowering completion, SB = Secondary branches, 1000-SW = 1000 Seed weight, CF= Capsule formation, CL= Capsule length, and SPC = Seeds per capsule.

Table 5. Specific combining ability effects of F_1 hybrids for the fatty acid profile.

F_1 hybrids	OC	PC	SA	PA	OA	LA	LIA
39 × 1	4.44**	-0.56	-1.09	-0.44	-2.42	0.16**	-0.02
39 × 14	1.02**	0.04**	0.70**	-0.06	2.62**	-0.17	-0.01
39 × 60	-5.46	0.52**	0.39**	0.50**	-0.20	0.02**	0.03**
40 × 1	-2.86	0.16**	-1.01	-0.59	-1.19	-0.24	-0.08
40 × 14	-1.75	-0.39	0.29**	0.21**	-0.40	-0.01	0.04**
40 × 60	4.61**	0.24**	0.72**	0.37**	1.59**	0.25**	0.04**
41 × 1	-1.31	0.50**	-0.52	0.01**	-0.89	0.09**	0.06**
41 × 14	-0.49	-0.66	-0.94	-0.03	-0.88	-0.32	-0.03
41 × 60	1.81**	0.16**	1.46**	0.02**	1.77**	0.24**	-0.03
43 × 1	5.76**	-0.11	2.36**	-0.06	2.45**	0.02**	-0.01
43 × 14	3.12**	1.35**	2.23**	0.60**	0.00	0.56**	0.10**
43 × 60	-5.23	-0.81	-1.24	-0.50	1.84**	-0.37	-0.04
44 × 1	-0.89	0.62**	1.93**	0.61**	0.67**	0.19**	-0.02
44 × 14	2.07**	0.27**	0.93**	0.42**	-0.09	0.24**	0.09**
44 × 60	-1.18	-0.89	-2.85	-1.03	-0.58	-0.42	-0.07
50 × 1	2.32**	-0.23	0.09**	0.18**	0.67	0.02**	0.00
50 × 14	-4.00	0.07**	-0.36	-0.32	-0.84	0.16**	-0.04
50 × 60	1.68**	0.16**	0.27**	0.14**	0.17**	-0.18	0.05**
103 × 1	-0.51	0.16**	0.78**	0.89**	-1.35	0.08**	0.11**
103 × 14	0.06**	-0.43	0.25**	-0.81	2.34**	-0.01	-0.06
103 × 60	-0.68	-0.53	-0.24	-0.92	3.58**	0.02**	-0.10
105 × 1	1.10**	0.04**	0.22**	-0.37	0.19**	-0.31	-0.10
105 × 14	0.58**	0.39**	-0.91	-0.04	-0.16	0.12**	0.07**
105 × 60	1.56**	0.34**	0.28**	0.37**	1.76**	0.00	0.08**
109 × 1	-0.77	-0.12	-1.07	-0.30	0.29**	0.10**	-0.13
109 × 14	0.10**	0.54**	-0.24	-0.10	0.76**	0.21**	-0.06
109 × 60	1.80**	-0.40	-0.51	-0.49	0.10**	-0.34	0.00
110 × 1	1.40**	0.76**	1.03**	-0.32	1.64**	-0.25	-0.05
110 × 14	1.87**	-0.32	0.15**	-0.10	1.45**	0.28**	0.00
110 × 60	-3.27	-0.44	-1.18	0.41**	-3.09	-0.03	0.05**
111 × 1	-1.49	-0.28	-2.04	0.14**	-6.07	-0.13	0.02**
111 × 14	-0.57	0.29**	0.96**	-0.09	5.66**	-0.04	0.01**
111 × 60	2.06**	-0.01	1.08**	-0.06	0.41**	0.17**	-0.03
112 × 1	-0.31	0.32**	-0.53	0.12**	-0.56	0.04**	0.03**
112 × 14	0.50**	-1.19	0.72**	-0.34	-0.59	-0.23	-0.07
112 × 60	-0.19	0.88**	-0.19	0.21**	1.15**	0.18**	0.05**
113 × 1	0.53**	-1.09	-0.97	-0.63	1.42**	-0.11	0.05**
113 × 14	0.76**	0.92**	0.30**	0.32**	-1.35	-0.19	-0.03
113 × 60	-1.29	0.17**	0.68**	0.31**	-0.07	0.30**	-0.02
115 × 1	-2.41	0.61**	0.00	0.01**	7.21**	0.24**	0.02**
115 × 14	2.26**	0.26**	-0.37	-0.32	-4.32	0.30**	0.03**
115 × 60	0.15**	-0.87	0.37**	0.31**	-2.88	-0.53	-0.05
117 × 1	-0.37	-1.56	-0.02	-0.61	2.02**	-0.37	-0.10
117 × 14	0.96**	0.13**	0.05**	0.79**	-0.23	0.18**	0.01**
117 × 60	-0.59	1.43**	-0.02	-0.19	-1.79	0.19**	0.10**
S.E.	0.65	0.35	0.35	0.43	0.86	0.29	0.13

OC = Oil content, PC = Protein content, PA = Palmitic acid, SA = Stearic acid, OA = Oleic acid, LA = Linoleic acid, and LIA= Linolenic acid.

Table 6. Heterosis in F_1 hybrids over commercial hybrid TH-6 for various field-related traits.

F_1 hybrids	PH	CH	FI	CH	FC	CH	1000-SW	CH	CL	CH	SPC	CH
39 × 1	-1.80	-4.01	-8.19	-4.01	-7.98	-13.7	-25.29	011**	-17.56	-0.6	14.08**	1.09**
39 × 14	-0.59	-2.83	-8.99	-2.83	-2.50	-15.0	-5.06	-0.06	-14.48	-0.1	-2.37	-3.73
39 × 60	1.33**	-0.74	-9.24	-3.63	-2.76	-15.7	-17.24	-0.07	-34.07	-0.1	-17.63	-5.23
40 × 1	1.75**	1.01**	-7.48	-2.66	-6.26	-12.9	20.69**	0.15**	18.16**	0.01	4.86**	1.16**
40 × 14	0.71**	-0.07	3.54**	-1.35	7.76**	-14.7	32.91**	0.15**	16.05**	0.00	7.73**	2.32**
40 × 60	0.45**	-0.17	2.96**	-0.17	6.97**	-14.9	-26.44	0.15**	24.58**	0.01	-4.99	1.74**
41 × 1	1.37**	1.01**	4.67**	-4.28	3.75**	-11.9	3.45**	-0.09	52.67**	0.06	8.87**	1.74**
41 × 14	-10.02	-10.61	9.04**	-10.61	-2.36	-10.4	13.92**	0.11**	49.75**	0.05	6.45**	1.16**
41 × 60	-3.30	-3.59	8.43**	-3.59	5.77**	-14.2	3.45**	0.11**	21.56**	-0.01	-4.79	1.16**
43 × 1	1.49**	-1.21	-2.95	-1.21	-0.03	-8.43	3.45**	0.11**	12.40**	0.01	3.45**	1.74**
43 × 14	2.68**	-0.07	-4.99	-6.17	7.94**	-10.9	14.79**	0.11**	10.50**	0.00	4.56**	2.32**
43 × 60	2.85**	0.27**	7.83**	-9.44	8.97**	-11.8	-9.77	-0.08	29.54**	0.04	-5.99	2.32**
44 × 1	2.53**	1.01**	-4.82	-9.29	6.64**	-10.2	-0.57	0.06**	58.94**	0.06	4.30**	1.16**
44 × 14	1.49**	-0.07	-6.16	-9.33	7.55**	-12.1	12.03**	0.06**	55.78**	0.05	3.70**	1.16**
44 × 60	2.67**	1.28**	-6.51	-2.99	-11.26	-12.8	-1.72	0.06**	26.32**	-0.01	-7.00	1.16**
50 × 1	4.75**	2.02**	11.65**	0.10**	9.20**	-9.82	-1.08	0.06**	55.17**	0.06	9.17**	1.74**
50 × 14	4.71**	1.95**	10.77**	-1.18	10.07**	-11.13	-9.73	0.06**	52.16**	0.05	12.08**	2.90**
50 × 60	5.91**	3.29**	10.14**	2.08**	10.20**	-13.2	13.51**	-0.10	23.46**	-0.01	0.21**	2.90**
103 × 1	5.71**	3.03**	11.41**	-0.54	4.15**	-9.66	20.69**	0.11**	30.72**	0.01	3.18**	1.16**
103 × 14	2.62**	-0.07	10.53**	-4.08	2.17**	-10.9	32.91**	0.11**	28.15**	0.00	6.01**	2.32**
103 × 60	1.78**	-0.74	-2.66	-0.74	3.30**	-10.9	20.69**	0.11**	24.74**	-0.01	-6.36	1.74**
105 × 1	1.15**	0.00	-1.84	-8.38	9.28**	-8.27	-10.67	-0.12	-23.88	-0.10	-17.34	-6.38
105 × 14	-2.45	-3.67	-4.52	-3.67	10.17**	-11.3	-28.09	-0.06	-11.11	-0.08	-12.80	-4.72
105 × 60	-3.13	-4.16	-4.88	-4.16	-4.31	-12.1	-30.34	-0.09	-18.61	-0.11	-30.75	-8.00
109 × 1	-3.22	-5.99	-5.00	-5.99	-10.59	-11.3	-39.05	-0.06	-8.25	-0.07	-5.49	-2.05
109 × 14	-1.56	-4.38	-4.18	-4.38	-8.07	-11.2	-25.71	0.06**	-23.39	-0.10	-10.32	-3.49
109 × 60	-1.83	-2.62	-4.47	-2.62	-11.42	-12.1	-39.08	-0.09	-20.92	-0.11	-20.42	-3.71
110 × 1	-3.00	-3.94	-0.79	-3.94	-25.73	-7.6	-40.23	-0.06	6.99**	-0.04	-12.60	-4.31
110 × 14	0.67**	-0.27	-3.58	-0.27	-21.45	-10.8	-20.25	0.03**	-17.09	-0.09	-11.48	-3.76
110 × 60	-2.30	-3.09	-5.51	-3.09	-5.84	-13.0	-31.03	-0.08	-11.04	-0.09	-19.39	-3.32
111 × 1	0.78**	-0.07	-5.31	-0.07	-14.94	-11.0	-31.03	-0.10	-23.44	-0.08	-10.47	-3.86
111 × 14	-3.01	-3.94	-8.21	-3.94	-10.50	-14.3	-21.52	-0.12	-10.97	-0.06	-18.47	-6.36
111 × 60	-3.75	-4.50	-7.61	-4.50	-14.17	-14.2	-34.48	-0.09	-35.58	-0.12	-25.75	-5.93
112 × 1	-4.76	-5.18	-7.94	-5.18	-17.77	-12.7	-10.34	-0.08	-21.85	-0.08	-8.62	-5.66
112 × 14	-2.68	-3.01	-3.08	-3.01	-5.38	-8.79	-7.59	-0.10	-31.09	-0.10	-33.80	-13.24
112 × 60	-8.62	-9.28	1.92**	-9.28	-12.43	-4.55	-26.44	-0.13	-28.19	-0.11	-9.59	-2.29
113 × 1	0.00	-1.75	3.37**	-1.75	-23.54	-2.21	-36.78	-0.12	-32.34	-0.10	-5.60	-3.57
113 × 14	-3.29	-5.09	1.46	-5.09	-14.56	-4.68	-20.25	-0.11	-10.93	-0.07	-8.47	-4.30
113 × 60	-4.30	-5.91	0.90**	-5.91	-8.54	-5.67	20.69**	-0.11	-13.18	-0.08	-13.38	-2.54
115 × 1	-5.28	-5.87	4.93**	-5.87	-18.40	0.98**	3.45**	-0.10	-17.96	-0.08	1.91**	-2.15
115 × 14	-3.99	-4.51	7.59**	-4.51	-5.20	2.82**	-21.52	-0.14	-42.51	-0.13	0.65**	-2.35
115 × 60	-5.08	-5.80	-0.13	-5.80	-21.93	-5.03	3.45**	-0.13	-31.81	-0.13	-17.75	-4.89
117 × 1	-6.26	-7.51	3.16**	-7.51	-6.13	1.39**	20.69**	-0.14	-30.32	-0.11	-1.47	-2.05
117 × 14	-4.76	-5.90	2.73**	-5.90	-14.57	0.24**	32.91**	-0.15	-41.30	-0.14	-5.79	-3.25
117 × 60	-3.21	-3.40	-1.74	-3.12	-18.09	-2.95	20.69**	-0.15	-0.99	-0.01	-9.07	1.16**

* = Significant at 5% level of probability, ** = Significant at 1% level of probability, CH= Commercial heterosis over Check
PH = Plant height, FI = Days to 50% flowering, FC = Flowering completion, 1000SW = 1000-Seed weight, CL= Capsule length, SPC = Seeds per capsule.

Table 7. Coefficients of variability, broad sense heritability, and genetic advance for various traits.

Traits	Genotypic coefficient of variation	Phenotypic coefficient of variation	Broad sense heritability (%)	Broad sense heritability	Genetic advance
PH	65.9	66.0	99.8	0.99	16.9
FI	32.8	38.2	85.9	0.85	67.6
FC	81.9	83.9	97.6	0.97	21.7
SB	3.1	3.6	87.0	0.87	6.4
1000-SW	3.1	3.1	99.4	0.99	16.1
CF	27.4	29.4	93.2	0.93	11.9
CL	5.7	46.1	12.4	0.12	2.9
SPC	8.6	35.5	24.1	0.24	3.2
OC	39.0	45.7	85.4	0.85	1.7
PC	0.7	1.8	66.7	0.66	1.4
OA	12.1	12.3	98.4	0.98	15.9
PA	54.2	56.6	95.8	0.95	4.3
SA	16.4	16.7	97.8	0.97	13.1
LA	41.1	42.7	92.7	0.92	3.7
LIA	11.9	12.6	94.9	0.94	6.9

PH = Plant height, FI = Days to 50% flowering, i.e., Flowering initiation, FC = Flowering completion, SB = Secondary branches, 1000-SW = 1000 Seed weight, CF= Capsule formation, CL= Capsule length, SPC = Seeds per capsule, OC = Oil content, PC = Protein content, OA = Oleic acid, PA = Palmitic acid, SA = Stearic acid, LA = Linoleic acid, and LIA = Linolenic acid.

maximum for flower initiation, followed by plant height and palmitic acid. The maximum genotypic coefficient of variance among the accessions resulted for leaf area, followed by flower initiation, plant height, and palmitic acid, with the lowest value for protein content. Heritability for various traits ranged from 0.12–0.99. The highest heritability occurred for plant height, followed by flower completion, stearic acid, and 1000-seed weight, indicating that the contribution of genotypes was more in the expression of traits. Similar findings also surfaced from studies by Kandamoorthy and Govindarasu (2005); Banerjee and Kole (2009); Banumathy *et al.* (2010), and Saha *et al.* (2012). The characters with high heritability can serve as selection criteria for a future breeding program. These findings follow the results from Sumathi and Muralidharan (2010).

Genetic components came out in sesame accessions for variance in the considered traits of the experiment, as shown in Table 8. A non-additive genetic effect conditioned the secondary branches, flower initiation, capsule length, and 1000-seed weight, with all the other parameters controlled by an additive gene action. The result gained strength by the variance ratio of GCA to SCA as less than unity. The additive genetic variance was more than the dominant variance for all traits except for secondary branches, flower initiation, capsule length, and 1000-seed weight. These findings are for consideration for selection purposes. Reddy *et al.* (2001) and Krishnaiah *et al.* (2002) reported similar findings.

According to Johnson *et al.* (1955), high heritability estimates, along with high genetic advance, are usually more helpful in predicting gain under selection than heritability estimates alone. Genetic advance (GA) under selection refers to improving characters in genotypic value for the new population compared with the base population under one selection cycle at a given selection intensity. Heritability for various traits ranged from 0.12–0.99. The characters with high heritability can benefit as selection criteria for a future breeding program. The genetic advance was highest for the oleic acid, followed by plant height and flower completion, while the lowest was for linolenic acid. High heritability and genetic advance revealed for traits like oleic acid, plant height, and flower completion.

Other traits showed high heritability and moderate or low genetic advance, which can get upgraded by inter-mating superior genotypes of segregating populations derived from combination breeding. Reports by Kandamoorthy and Govindarasu (2005), Banerjee and Kole (2009), Banumathy *et al.* (2010), and Saha *et al.* (2012) gave similar findings. The research results proposed that the present breeding material may help to improve yield, shattering indices, and oil quality in sesame**.** Accessions cross SG-41 × SG-1, SG-41 × SG-60, SG-43 × SG-60, SG-50 × SG-14, and SG-50 × SG-60 could be valuable in future breeding programs for further improvement.

Table 8. Dominance variance, additive variance, and potency ratio of field-related traits in Sesame.

Genetic Components	PH	FI	FC	SB	1000-SW	CF	CL	SPC
$Б^2D$	3.40	0.48	56.60	0.44	133.27	10.23	0.62	121.51
$Б^2H$	37.51	18.14	99.40	13.55	143.45	20.78	11.49	124.19
Potency ratio	0.09	0.02	0.56	0.03	0.92	0.49	0.05	0.97

PH = Plant height, FI = Days to 50% flowering, i.e., Flowering initiation, FC = Flowering completion, SB = Secondary branches, 1000-SW = 1000 Seed weight, CF = Capsule formation, CL= Capsule length, and SPC = Seeds per capsule.

Table 9. Dominance variance, additive variance, and potency ratio of oil-related traits in sesame.

Genetic components	OC	PC	OA	SA	PA	LA	LIA
When F = 0, 6^2D	27.03	1.83	28.59	4.82	0.40	0.02	47.59
When F = 1, 6^2D	6.76	0.46	7.15	1.20	0.10	0.00	11.90
When F = 0, 6^2H	19.93	2.18	26.84	5.10	0.78	0.20	18.95
When F = 1, 6^2H	4.98	0.54	6.71	1.28	0.19	0.05	4.74
Potency Ratio	0.98	1.08	0.96	1.03	1.37	3.15	0.63

OC = Oil percentage, PC = Protein percentage, OA = Oleic acid, SA = Stearic acid, PA = Palmitic acid, LA = Linoleic acid, and LIA = Linolenic acid.

Table 10. The proportional contribution of lines, testers, and line × tester interactions to the total variance for different morphological and oil-related traits in sesame.

Traits	Contribution (%)		
	Lines	Testers	Line × tester
Morphological traits			
PH	52.9	0.6	46.6
FI	93.3	0.1	6.6
FC	23.2	2.9	73.9
SB	85.7	2.6	11.7
1000 - SW	53.3	4.2	42.5
CF	71.6	0.2	28.2
CL	48.0	0.7	51.3
SPC	26.7	6.4	66.8
Oil-related traits			
OP	47.4	1.7	50.9
PP	46.1	10.2	43.7
OA	48.9	4.9	46.2
PA	46.9	2.0	51.2
SA	50.5	6.2	43.3
LA	40.6	3.6	55.8
LIA	39.5	12.8	47.7

PH = Plant height, FI = Days to 50% flowering, i.e., Flowering initiation, FC = Flowering completion, SB = Secondary branches, 1000-SW = 1000 Seed weight, CF = Capsule formation, CL = Capsule length, SPC = Seeds per capsule, OP = Oil percentage, PP = Protein percentage, OA = Oleic acid, PA = Palmitic acid, SA = Stearic acid, LA = Linoleic acid, and LIA= Linolenic acid.

The proportional contribution of genotypes

Comparative participation of lines, testers, and line into testers for the field and oil-related traits, respectively, through line × tester mating design by hybridizing the 15 female lines with the three testers are in Tables 9 and 10. Table values indicate the maternal effects are more, indicating lines contributed the most for the traits under study. Conversely, testers have less involvement in trait appearance, signifying less paternal impact than the lines among the traits. Although, the line into tester interaction (maternal and paternal) increased in most of the traits.

CONCLUSIONS

The hybrids SG-41 × SG-60, SG-43 × SG-60, SG-41 × SG-1, and SG-50 × SG-60 showed as high yielding, with lower shattering indices, and had better oil quality. The highest heritability emerged for plant height, followed by flower completion, stearic acid, and 1000-seed weight, indicating that the contribution of genotypes was more in the expression of

traits. Conditioning of secondary branches, flower initiation, capsule length, and 1000-seed weight was by non-additive genetic effect, with all the other parameters under the control of additive gene action. SG-50 × SG-60 needs further testing across multiple locations and years on larger scales to evaluate their yield potential and stability.

REFERENCES

Andrade PBD, Freitas BM, Rocha EEDM, Lima JAD, Rufino LL (2014). Floral biology and pollination requirements of sesame (*Sesamum indicum* L.). *Acta Scien. Anal. Sci. 36*: 93-99.

Anilakumar KR, Pal A, Khanum F, Bawas A (2010). Nutritional, medicinal, and industrial uses of sesame (*Sesamum indicum* L.) seeds. *Agric. Conspec. Sci.* 75:159-168.

Anuradha T, Reddy LK (2008). Study of heterosis and inbreeding depression in sesame. *Agric. Sci. Dig*. 28: 157-164.

Aristya VE, Taryono T, Wulandari RA (2017). Evaluation of genetic parameters in M4 and M5 generations of sesame mutant lines. *SABRAO J. Breed. Genet.* 49(2): 201–210.

Bajaj RK, Aujla KK, Chalal GS (1997). Combining ability studies in sunflower (*Helianthus annuus* L.). *J. Crop Improv.* 24:50-54.

Banerjee PP, Kole PC (2009). Analysis of genetic architecture for some physiological characters in sesame (*Sesamum indicum* L.). *Euphytica* 168(1): 11-22.

Banumathy SR, Manimaran A, Sheeba N, Manivannan B, Ramya D, Kumar G, Ramasubramanian V (2010). Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electr. J. Plant Breed.* (1)500-504.

Delgado M (1972). Yield components of sesame (*S. indicum* L.) under different plant population densities. M.Sc. Thesis. University of California, USA.

Dewey DR, Lu KHA (1959). Correlation and path coefficient analysis of a component of crested wheat grass seed production. *Agron. J.* 51: 515-518.

Dixit RK (1976). Heterosis and inbreeding depression in sesame. *Indian J. Agric. Sci*. 46, 514-517.

Eurostat (2017). European Bureau Statistics. European database. Agriculture and Fisheries Statistics. Available at: http://ec.europa.eu/eurostat/web/transport/publications.

Falconer DS, Mackay TFC (1996). Introduction to Quantitative Genetics. *Addison Wesley Longman Ltd.* Edinburgh Gate. Harlow, Essex CM20 2JE, England.

Gidey YT, Kebede SA, Gashawbeza GT (2013). Assessment of genetic variability, genetic advance, correlation, and path analysis for morphological traits in sesame genotypes, *Int. J. Plant Breed. Gent*. 7(1): 21:34.

Hamid KA, Ibrahim AS, Taha MB, Ahmed ME (2003). Performance, interrelationship, and path analysis of some yield components in sesame. *U. J. Agric. Sci*. 11: 305-320.

Hsu E, Parthasarathy S (2017). Anti-inflammatory and antioxidant effects of sesame oil on atherosclerosis: A descriptive literature review. *Cureus* 9(7): 1438. http://doi.org/10.7759/cureus.

Imran M, Dash M, Das TR, Kabi M, Baisakh B, Lenka B (2017). Studies on heterosis for yield and yield attributes in sesame (*Sesamum indicum* L.). *Studies* 15:107-116.

Iqbal A, Dasgupta T (2015). Genetic estimates of morphological traits and phenotypic diversity in core collections of sesame (*Sesamum indicum* L.). *Indian Agric.* 5: 61-69.

Johnson HW, Robinson HF, Comstock RE (1955). Estimates of genetic and environmental variability in soybeans. *Agron. J*. 47: 314-318.

Kandamoorthy S, Govindarasu R (2005). Genetic divergence in extra early rice (*Oryza sativa* L.) under two culture systems, *Indian J. Genet.* (65): 43-44.

Ke T, Dong C, Han M, Zhao Y, Chen H, Liu H (2011). Analysis of expression sequence tags from a full-length-enriched cDNA library of developing sesame seeds (*Sesamum indicum*). *BMC Plant Biol.* 11(180): 1-12.

Kempthorne O (1957). An Introduction to Genetic Statistics. *John Wiley and Sons Inc*. New York, USA.

Khuimphukhieo I, Khaengkhan P (2018). Combining ability and heterosis of sesamin and sesamolin content in sesame. *SABRAO J. Breed. Genet*. 50(2): 180-191.

Koca H, Bor M, Ozdemir F, Turkan I (2007). The effect of salt stress on lipid peroxidation, antioxidative enzymes, and proline content of sesame cultivars. *Environ. Exp. Bot*. 60:344-351.

Krishnadoss D, Kadambavan M, Sundaram R, Sethupathi R, Rajasekaran S (1987). Combining ability in *Sesamum*. *Ind. J. Agric. Sci*. 57(2): 85-88.

Krishnadoss D, Kadamhavanasundaram M (1986). Correlation between yield and yield components in sesame. *Oilseeds Res*. 3(2): 205-209.

Krishnaiah G, Reddy KR, Sekhar MR (2002). Variability studies in Sesame. *Crop Res*. 24: 501- 504.

Kwon SH, Torrie JH (1964). Heritability and interrelationship of traits of two soybean populations. *Crop Sci.* 4(1): 196-198.

Lin TK, Zhong L, Santiago JL (2018). Anti-inflammatory and skin barrier repair effects of topical application of some plant oils. *Int. J. Mol. Sci*. 19: 70.

Morris JB (2002). Food, industrial, nutraceutical, and pharmaceutical uses of sesame genetic resources. *Janick J, Whipkey VA.* 153-156.

Murty DS (1975). Heterosis, combining ability and reciprocal effects for agronomic and chemical characters in sesame. *Theor. Appl. Genet.* 45: 294-299.

Myint TE, Mon K, Kyaw T (2019). Assessment of supply chain management of sesame seed in Pakokku Township, Magway Region, Myanmar. *Int. J. Agric. Marketing* 6: 215-224.

Padma SM, Kamala T (2012). Heterosis in *Sesamum indicum* L. *Asian J. Agric.* Sci. 4(4): 287-290.

Pal BP (1945). Studies in hybrid vigor of sesame (*Sesamum indicum* L.). *Ind. J. Genet. Plant Breed.* 5:106-121.

Panse VG (1957). Genetics of quantitative characters concerning plant breeding. *Ind. J. Genet. Plant Breed.* 17: 318-328.

Parameshwarappa SG, Palakshappa MG, Salimath PM, Parameshwarappa KG (2009). Evaluation and characterization of germplasm accessions of sesame (*Sesamum indicum* L.). *Karnataka J. Agric. Sci*. 22(5): 1084-1086.

Poehlman J (1987). Reproduction in Crop Plants. 10.1007/978-94-015-7271-2_2.

Praveenkumar K, %Laxuman P, Guddadamath S, Adigera S (2012) Heterosis, combining ability and gene action in inter-mutant hybrids of sesame (*S. indicum* L.). *Bioinfolet* 9(3): 316-322.

Quasem JM, Mazahreh AS, Abu-Alruz K (2009). Development of vegetable-based milk from decorticate sesame (*Sesamum indicum*). *Am. J. Appl. Sci*. 6(5): 888-896.

Raghunaiah E, Kishand AG, Ansari NA (2008). Combining ability and heterosis for yield and yield components in sesame (*Sesamum indicum* L.). *J. ANGRAU* 36: 9-16.

Ramakrishnan M, Soundrapandian (1990). Association studies in sesame. *Madras Agric. J.* 77: 580-581.

Rani TS, S. Laxman S, Thippeswamy S, Kiranbabu T, Venkataiah M, Rao MP (2015). Genetic studies for the exploitation of heterosis in sesame (*Sesamum indicum* L.). *SABRAO J. Breed. Genet*. 47(3): 231-237.

Reddy MB, Reddy MV, Rana BS (1984). Combining ability studies in sesame. *Indian J. Genet*. 44(2): 314.

Reddy PAV, Sekhar MR, Rangnatha ARG, Dhanraj A (2001). Genetic variability and heritability for seed yield and its components in sesame. *J. Oilseeds Res.* 18:173-175.

Riccelli M, Mazzani B (1964). Manifestacion de heterosis en desarrollo, precocidad y rendimiento de los cruces diadelos de 32 cultivares de Ajonjoli. *Agron. Trop. (Venezuela)* 14(2): 101-125.

Saha S, Begum T, Dasgupta T (2012). Analysis of genotypic diversity in sesame based on morphological and agronomic traits. Conference on Int. Research on Food Security, Natural Resource Management, and Rural Development organized by Georg August Universitat Gottingen and University of Kassel-Witzenhausen, Germany.

Salunkhe DK, Chavan JK, Adsule RN, Kadam SS (1991). Sesame. In: World oilseeds: History, technology, and utilization. Van Nostrand Reinhold, New York: 371-402.

Sankar PD, Kumar CRA (2001). Heterosis for yield and yield components in sesame (*Sesamum indicum* L.). *Sesame Safflower Newsletter* (16): 6-8.

Schmidt P, Hartung J, Bennewitz J, Piepho HP (2019). Heritability in plant breeding on a genotype-difference basis. *Genetics* 212(4): 991-1008.

Singh RK, Chaudhary BD (1985). Biometrical Method in Quantitative Genetics Analysis. Kalyani Publishers, New Delhi, India.

Stavridou E, Lagiotis G, Kalaitzidou P, Grigoriadis I, Bosmali I, Tsaliki E, Tsiotsiou S, Kalivas A, Ganopoulos I, Madesis P (2021) Characterization of the genetic diversity present in a diverse sesame landrace collection based on phenotypic traits and EST-SSR markers coupled with an HRM analysis. *Plants* 10(4): 656. https://doi.org/10.3390/plants10040656.

Sudhakar N, Sridevi O, Salimath P (2007). Variability and character association analysis in sesame (*Sesamum indicum* L.). *J. Oilseeds Res*. 24(1): 56-5.

Suja KP, Abraham JT, Thamizh SN, Jayalekshmy A, Arumughan C (2004). Antioxidant efficacy of sesame cake extract in vegetable oil protection. *Food Chem*. 84:393-400.

Sumathi P, Muralidharan V (2010). Inheritance of branching and important biometrical traits in sesame (*Sesamum indicum* L.). *Indian J. Genet. Plant Breed.* 69: 97-101.

Teklu DH, Kebede SA, Gebremichael DE (2014). Assessment of genetic variability, genetic advance, correlation, and path analysis for morphological traits in sesame genotypes. *Asian J. Agric. Res.* 8: 181-194.

Toan DP, Thuy-Duong TNA, Carlsson S, Bui TM (2010). Morphological evaluation of sesame (*Sesamum indicum* L.) varieties from different origins. *Aust. J. Crop Sci*. 4: 498-504.

Wang L, Yu J, Li D, Zhang X (2014). Sinbase: An integrated database to study genomics, genetics, and comparative genomics in *Sesamum indicum. Plant Cell Physiol.* 56(1): .e2-e2. doi:10.1093/pcp/pcu175.