



RESEARCH ARTICLE

Combining ability analysis for seed yield and its component traits in sesame (*Sesamum indicum* L.): A genetic study

Sathish Kumar R¹, Manivannan N^{1*}, Mahalingam A^{2*}, Subrahmaniyan K³, Senthil Raja G⁴ & Jayakanthan M⁵

¹Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore 641 003, India

²Department of Genetics and Plant Breeding, Tamil Nadu Agricultural University, Vriddhachalam 606 001, India

³Department of Agronomy, Tamil Nadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai 612 101, India

⁴Department of Plant Pathology, Horticulture Research Station, Tamil Nadu Agricultural University, Ooty 643 001, India

⁵Department of Bioinformatics, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

*Correspondence email - nm68@tnau.ac.in, mahalingam.a@tnau.ac.in

Received: 24 March 2025; Accepted: 12 August 2025; Available online: Version 1.0: 10 November 2025

Cite this article: Sathish KR, Manivannan N, Mahalingam A, Subrahmaniyan K, Senthil RG, Jayakanthan M. Combining ability analysis for seed yield and its component traits in sesame (*Sesamum indicum* L.): A genetic study. Plant Science Today (Early Access). <https://doi.org/10.14719/pst.8477>

Abstract

Sesame (*Sesamum indicum* L.) is a vital oilseed crop cultivated extensively in India. Improving sesame yield requires effective breeding strategies that utilize parents and hybrids with strong combining ability. Line \times Tester analysis was carried out in sesame to study gene action, combining ability of parents and hybrids, mean performance and to select promising hybrids based on mean, gene action and combining ability effects for seed yield and component traits. A set of six lines (EC358033, EC346664, IC129607, IC204840, IC204557 and VS19078) and three testers (TMV 3, VRI 5 and TMV 7) were crossed using a line \times tester mating design. The gene action and combining ability were analysed for ten quantitative traits. All traits showed a preponderance of non-additive gene action. Among lines, IC 129607, IC204557 and VS19078 and testers TMV 3 and TMV 7 had significant and positive GCA effects for seed yield per plant and component traits. The hybrid TMV 7 \times IC204557 exhibited high mean performance, significant GCA and non-significant SCA for seed yield per plant, number of capsules per plant and most of the other traits. Hence, this cross can be further handled through pedigree breeding to obtain high-yielding segregants due to the presence of additive gene action. Hybrids, TMV 3 \times VS19078, TMV 7 \times IC129607, TMV 3 \times IC129607, TMV 3 \times IC204557 and TMV 7 \times VS19078 had high *per se*, good combining parents, but with significant SCA for seed yield or number of capsules per plant and other component traits. Hence, selection should be postponed to later generations in these crosses due to the presence of non-additive gene action.

Keywords: combining ability; gene action; pedigree breeding; seed yield; sesame

Introduction

Sesame is a member of the Pedaliaceae family (*Sesamum indicum* L.; $2n = 2x = 26$). It is primarily a self-pollinating crop (1). Products made from sesame seed oil are used in the food, feed and cosmetics industries all over the world. The seed oil content of sesame is higher than that of soybean (~20 %), rapeseed (~40 %), sunflower (~45 %) and groundnut (45-56 %), with a range of 40 % to 60 % (2). The majority of the fatty acid composition is made up of unsaturated fatty acids, with oleic (35.9-42.3 %) and linoleic (41.5-47.9 %) acids accounting for 80 % of total fatty acids. Less than 20 % of the fatty acid content of sesame seeds is made up of saturated fatty acids, primarily palmitic (7.9-12 %) and stearic (4.8-6.1 %) acids. Due to the presence of natural antioxidants including sesamol, sesamin and sesamol, the seed's 50-60 % oil has exceptional stability (3). The market demand for sesame seeds and oil has been steadily rising as more people become aware of the dietary and health advantages of this crop. Similarly, sesame is ideally suited to replace low-yield crops due to its low irrigation requirements, adaptability to various soil and weather types, minimal labour requirements and high yield, particularly in light of the current situation where crop productivity is being impacted by

global warming in more and more traditional agricultural areas (4). Moreover, recent advancements such as artificial seed technology offer promising opportunities for the clonal propagation and conservation of elite sesame genotypes, thus supporting genetic improvement programs (5). Unfortunately, the absence of high-yielding varieties that are naturally resistant to a variety of biotic and abiotic stressors is the reason for the limited cultivation of sesame. Charcoal rot is one of the most destructive diseases, which usually causes sesame crops to decline by 30 % or even completely lose them. In sesame, charcoal rot generally happens from the end of flowering until maturity. When the weather is hot and dry or there are unfavourable environmental stressors, black spots start to appear on the root or stem (6). Therefore, efforts should be made to create cultivars with high yield potential that can adapt better to various climatic situations. Combining ability analysis is the method used to choose the best parents for hybridization in order to produce elite segregants in recombination breeding (7). With this background, an attempt has been made to assess the combining ability of six *Macrophomina* root rot-resistant genotypes of sesame for seed yield and component traits in a line \times tester mating design. The present study was formulated with the

following objectives: a) to assess the gene action involved for various traits, b) to identify good combining parents for various traits, c) to select promising hybrids based on *per se* performance and d) to formulate a breeding program for the selected hybrids.

Materials and Methods

Experimental materials and sites

The experimental material of the present study consisted of nine genotypes, which were crossed in line \times tester mating design during December to February, 2023-24 at the Regional Research Station, Tamil Nadu Agricultural University, Vriddhachalam. The parental details were presented in Table 1. The male lines were EC 358033, EC346664, IC129607, IC204840, IC204577 and VS19078. All these genotypes are *Macrophomina* root rot resistant. The female testers were TMV 3, VRI 5 and TMV 7. All these genotypes are released varieties in Tamil Nadu. The 18 newly synthesised F_1 crosses, nine parents were evaluated in a randomized complete block design (RCBD) with three replications during June-September, 2024.

Crossing procedure

Each line and tester was raised in an adjacent row manner under field conditions. The crossing was made during Dec-Feb, 2023-24. The recommended agronomic practices were uniformly followed throughout the season. Emasculation was done between 4 PM and 6 PM, one day before anthesis. It was carried out by completely removing the corolla by pulling its tip along with the epipetalous stamens. Other young flowers located close to the emasculated flowers were removed to avoid confusion. Emasculated flowers were covered by a butter paper bag to avoid pollen contamination. In the next day, early morning between 6 AM and 8 AM, the pollen from the desired male flower was dusted on the stigma of the emasculated flower by rubbing the

staminal column of the male parent. After the pollination, the pollinated flowers were tagged and covered with a butter paper cover. After maturity, the hybrid seeds were harvested and stored.

Data collection and statistical analysis

The quantitative traits such as days to 50 % flowering (DFF) (days), days to maturity (DTM) (days), plant height (PH) (cm), number of branches (NBP), number of capsules per plant (NCP), capsule length (CL) (cm), capsule width (CW) (cm), number of seeds per capsule (NSC), 1000-seed weight (TSW) (g) and seed yield per plant (SYP) (g) were recorded on randomly chosen five plants per genotype from each replication. The collected data were subjected to combining ability analysis (8) using $L \times T$ analysis package in TNAU STAT software (9).

Results and Discussions

The ANOVA for combining ability analysis was presented in Table 2. The mean sum of squares due to crosses, lines, testers and hybrids was significant for all traits. This indicated that a considerable amount of variability was present in lines, testers and their hybrids for the studied traits. This variation enhances yield by gathering beneficial genes from genetically diverse genotypes. Research indicates that the results are significant and at par with those reported in previous studies (10).

Gene action

The knowledge of the gene action of the characters is crucial to plan a suitable breeding procedure. The SCA variances were found to be greater than the GCA variances for all the studied quantitative traits (Table 3). This indicated that these traits were governed by predominantly non-additive gene action. Research indicated the predominance of non-additive gene action for seed yield and its contributing traits (11-13).

Table 1. Source/pedigree and features of lines used

| Genotypes | Pedigree | Origin | Features |
|-----------|------------------------------------|--|--|
| TMV 3 | South Arcot local \times Malabar | Oilseeds Research Station, Tindivanam | Black seed coat |
| TMV 7 | SI 250 \times ES 22 | Oilseeds Research Station, Tindivanam | Brown seed coat |
| VRI 5 | VRI 3 \times EC370840 | Regional Research Station, Vriddhachalam | Mono-stem/shy branching, multi-capsule with white seed coat |
| EC358033 | - | Bangladesh | Dark brown with rough seed coat |
| EC346664 | - | Singapore | Brown with rough seed coat |
| IC129607 | - | Jabalpur, Madhya Pradesh | White seed coat |
| IC204840 | - | Cuttack, Odisha | White seed coat |
| IC204557 | - | Cuttack, Odisha | White seed coat |
| VS19078 | TMV 7 \times ORM 14 | Regional Research Station, Vriddhachalam | Profuse branching, small sized capsules with brown seed coat |

Table 2. ANOVA of combining ability for quantitative traits in sesame

| Traits\ Source of variation | Replication | Crosses | Lines | Testers | Hybrids | Error |
|-----------------------------|-------------|-----------|------------|-----------|----------|-------|
| df | 2 | 17 | 2 | 5 | 10 | 34 |
| DFF | 0.42 | 26.34** | 7.89* | 79.37** | 3.51** | 1.12 |
| DTM | 3.59 | 89.86** | 32.66** | 222.30** | 35.07** | 2.78 |
| PH | 18.84 | 1038.07** | 5050.03** | 1163.45** | 172.99** | 15.80 |
| NBP | 0.23 | 8.83** | 48.14** | 5.58** | 2.59** | 0.32 |
| NCP | 3.67 | 5145.03** | 33196.08** | 2647.77** | 783.44** | 12.61 |
| CL | 0.04 | 0.18** | 0.65** | 0.24** | 0.06* | 0.03 |
| CW | 0.01 | 0.01 | 0.04* | 0.00 | 0.01 | 0.01 |
| NSC | 9.12 | 71.45** | 17.04 | 177.57** | 29.27 | 12.81 |
| TSW | 0.00 | 0.51** | 0.71** | 1.33** | 0.07** | 0.01 |
| SPY | 0.41 | 49.67**s | 259.41** | 38.30** | 13.40** | 0.84 |

*, ** - significant at 5 and 1 % respectively

Table 3. Estimates of combining ability variances and contribution of lines, testers and interaction

| Traits | GCA | SCA | SCA/ GCA | Degree of dominance | Proportion contributions (%) | | |
|--------|--------|--------|----------|---------------------|-------------------------------|---------|-------------|
| | | | | | Lines | Testers | Interaction |
| DFF | 0.56 | 0.80 | 1.42 | 1.19 | 3.52 | 88.63 | 7.85 |
| PH | 21.22 | 52.40 | 2.47 | 1.57 | 57.23 | 32.96 | 9.8 |
| NBP | 0.15 | 0.76 | 4.96 | 2.23 | 64.14 | 18.6 | 17.26 |
| NCP | 106.99 | 256.95 | 2.40 | 1.55 | 75.91 | 15.14 | 8.96 |
| CL | 0.00 | 0.01 | 3.47 | 1.86 | 42.12 | 38.94 | 18.95 |
| CW | 0.00 | 0.00 | 0.00 | 0.00 | 36.68 | 10.73 | 52.59 |
| NSC | 1.03 | 5.49 | 5.30 | 2.30 | 2.81 | 73.1 | 24.1 |
| DTM | 1.34 | 10.79 | 8.03 | 2.83 | 4.28 | 72.76 | 22.96 |
| TSW | 0.01 | 0.02 | 1.81 | 1.35 | 16.25 | 76.07 | 7.68 |
| SPY | 0.89 | 33.40 | 37.54 | 6.13 | 61.45 | 22.68 | 15.87 |

Contributions of combining ability variances

The contribution of lines was higher for the traits plant height, number of branches per plant, number of capsules per plant, capsule length and seed yield per plant. The testers' contribution showed higher for the traits such as days to 50 % flowering, capsule width, number of seeds per capsule, days to maturity and thousand seed weight. The line × tester interaction contributed more to capsule width alone. These results indicated that both lines and testers had more variability for their general combining ability effects for various traits. However, hybrids had more variation for their specific combining ability for capsule width only than the combining ability effects of the parents. Research indicated the significant at par results in previous studies (12, 14).

General combining ability

Good parents are necessary for the hybridization breeding program in order to create more variability. The average performance of a genotype in a set of hybrids is used to estimate the general combining ability (GCA). The GCA effects result from additive gene action and are fixable. Hence, it is used to choose the good parents (15). For earliness, negative GCA is ideal for days to 50 % flowering and days to maturity traits. Among the lines, IC 129607, IC204557 and VS19078 and the testers TMV 3 and TMV 7 had significant and positive GCA effects for seed yield per plant (Table 4). Hence, these genotypes can be considered as good combiners for seed yield per plant. Among these genotypes, line IC 129607 had good combining ability for plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule and 1000-seed weight. The line IC204557 had good combining ability for days to 50 % flowering, plant height, number of capsules per plant, capsule length and days to maturity. The line VS19078 had good combining ability for the number of capsules per plant and 1000-seed weight. In the case of testers, TMV 3 had good combining ability for the number of capsules per plant, while TMV 7 had good combining ability for plant height, number of branches per plant, number of capsules per plant and 1000-seed weight. Hence, lines IC 129607, IC204557 and VS19078 and testers TMV 3 and TMV 7 could be used in hybridization programme to

generate high genetic variability. Research indicates significant GCA effects in lines for plant height, number, number of capsules per plant and seed yield per plant (11, 16-18).

Mean performance of hybrids

The *per se* performance of hybrids is one of the important criteria for the selection of superior crosses (11). Among hybrids, seven hybrids, viz., TMV 3 × IC129607, TMV 3 × IC204557, TMV 3 × VS19078, TMV 7 × EC358033, TMV 7 × IC129607, TMV 7 × IC204557 and TMV 7 × VS19078 recorded superior mean performance for seed yield than the general mean (Table 5). Hybrids TMV 3 × IC129607, TMV 7 × EC358033, TMV 7 × IC129607, TMV 7 × IC204557 and TMV 7 × VS19078 recorded superior mean performance for five or more traits, especially for plant height, number of branches per plant and number of seeds per capsule. Hybrids, TMV 3 × IC204557, TMV 7 × IC204557 and TMV 7 × VS19078 showed superior performance for earliness in addition to the above traits. Hence, considering the superior performance for seed yield and other traits, hybrids TMV 3 × IC129607, TMV 7 × EC358033, TMV 7 × IC129607, TMV 7 × IC204557 and TMV 7 × VS19078 may be considered as superior. Research also indicated some superior hybrids based on the hybrids' *per se* performance.

Specific combining ability

Specific combining ability effects help the breeder to assess the nature of the gene involved in the particular cross. The specific combining ability effects are the deviation from the predicted value based on their parents' GCA effects (18). The non-significant and significant SCA effects indicate the presence of additive and epistatic effects, respectively. Hybrids with high mean performance, good combining parents and non-significant SCA effects for seed yield and component characters are desirable for a pedigree breeding programme (11). Due to the presence of additive gene action in these types of crosses, selection can be practised in the early generation itself. The crosses with high mean, good GCA parents with significant SCA can also be utilised to evolve varieties. However, the selection should be postponed for generations till to attain homozygosity

Table 4. General combining ability (GCA) effect for various quantitative traits

| Traits | DFF | PH | NBP | NCP | CL | CW | NSC | DTM | TSW | SPY |
|----------------|----------|-----------|----------|-----------|----------|---------|----------|----------|----------|----------|
| Testers | | | | | | | | | | |
| TMV 3 | 0.65 * | -6.92 ** | 0.04 | 11.34** | -0.05 | 0.02 | -0.62 | 0.65 | -0.07** | 0.59 ** |
| VR1 5 | -0.67 * | -12.18 ** | -1.65 ** | -47.48 ** | 0.21 ** | -0.05 * | 1.12 | -1.55 ** | -0.16 ** | -4.06 ** |
| TMV 7 | 0.02 | 19.10 ** | 1.62 ** | 36.13 ** | -0.16 ** | 0.04 | -0.50 | 0.89 * | 0.22 ** | 3.47 ** |
| Lines | | | | | | | | | | |
| EC358033 | -0.55 | -0.37 | 0.69 ** | -1.40 | 0.15 ** | -0.02 | 3.70 ** | 1.97 ** | 0.09 ** | 0.41 |
| EC346664 | 0.26 | -12.49 ** | -0.59 ** | -23.30 ** | -0.05 | -0.01 | 0.68 | -2.25 ** | -0.34 ** | -3.32 ** |
| IC129607 | 2.93 ** | 19.13 ** | 1.02 ** | 3.85 ** | 0.09 | 0.03 | 4.83 ** | 2.71 ** | 0.25 ** | 1.55 ** |
| IC204840 | -3.64 ** | -10.65 ** | -1.11 ** | -15.41 ** | -0.11 * | -0.02 | -2.99 * | -7.33 ** | -0.31 ** | -1.67 ** |
| IC204557 | -2.77 ** | 2.98 * | -0.07 | 20.96 ** | 0.16 ** | 0.03 | 0.95 | -2.10 ** | -0.30 ** | 1.15 ** |
| VS19078 | 3.77 ** | 1.41 | 0.06 | 15.31 ** | -0.25 ** | -0.01 | -7.17 ** | 7.01 ** | 0.61 ** | 1.88 ** |

*, ** - significant at 5 and 1 % respectively

Table 5. Mean performance of hybrids for various quantitative traits

| Hybrids | DFF | PH | NBP | NCP | CL | CW | NSC | DTM | TSW | SPY |
|--------------------|-------|--------|------|--------|------|------|-------|--------|------|-------|
| TMV 3 × EC358033 | 34.67 | 108.00 | 5.00 | 98.67 | 2.83 | 0.69 | 62.00 | 99.33 | 2.73 | 5.60 |
| TMV 3 × EC346664 | 35.11 | 105.78 | 3.89 | 70.22 | 2.52 | 0.69 | 58.45 | 85.00 | 2.13 | 3.29 |
| TMV 3 × IC129607 | 37.00 | 126.33 | 6.44 | 121.00 | 2.58 | 0.79 | 61.56 | 98.56 | 2.90 | 12.07 |
| TMV 3 × IC204840 | 33.33 | 90.33 | 4.56 | 97.11 | 2.73 | 0.76 | 58.44 | 89.44 | 2.38 | 5.59 |
| TMV 3 × IC204557 | 32.33 | 118.33 | 5.22 | 144.22 | 2.68 | 0.69 | 61.11 | 95.22 | 2.48 | 11.52 |
| TMV 3 × VS19078 | 38.33 | 116.24 | 4.00 | 100.44 | 2.47 | 0.71 | 51.56 | 102.11 | 3.23 | 8.72 |
| VRI 5 × EC358033 | 32.00 | 109.17 | 4.39 | 48.72 | 3.08 | 0.72 | 63.44 | 93.11 | 2.63 | 4.86 |
| VRI 5 × EC346664 | 34.67 | 86.78 | 2.67 | 40.89 | 2.95 | 0.63 | 62.22 | 94.33 | 2.23 | 1.58 |
| VRI 5 × IC 129607 | 37.67 | 132.78 | 2.56 | 50.22 | 3.12 | 0.68 | 65.33 | 95.67 | 2.63 | 2.58 |
| VRI 5 × IC 2045840 | 29.50 | 104.00 | 2.33 | 31.33 | 2.57 | 0.61 | 52.33 | 84.67 | 2.40 | 2.85 |
| VRI 5 × IC 204557 | 31.44 | 99.22 | 3.22 | 51.56 | 3.06 | 0.65 | 64.89 | 88.33 | 2.17 | 2.76 |
| VRI 5 × VS19078 | 37.56 | 101.56 | 3.78 | 56.00 | 2.57 | 0.62 | 55.33 | 100.33 | 3.25 | 4.27 |
| TMV 7 × EC358033 | 35.11 | 135.00 | 7.11 | 130.22 | 2.58 | 0.65 | 64.08 | 96.33 | 3.03 | 12.39 |
| TMV 7 × EC346664 | 34.44 | 123.24 | 6.11 | 100.78 | 2.43 | 0.77 | 59.78 | 96.78 | 2.75 | 6.78 |
| TMV 7 × IC129607 | 37.55 | 151.55 | 8.50 | 122.11 | 2.63 | 0.72 | 66.00 | 96.78 | 3.35 | 11.63 |
| TMV 7 × IC204840 | 29.67 | 127.00 | 4.22 | 107.11 | 2.41 | 0.69 | 58.67 | 86.78 | 2.42 | 8.17 |
| TMV 7 × IC204557 | 31.33 | 144.66 | 5.78 | 148.89 | 2.80 | 0.88 | 55.26 | 93.00 | 2.58 | 10.78 |
| TMV 7 × VS19078 | 38.83 | 139.72 | 6.84 | 171.29 | 2.27 | 0.74 | 50.02 | 101.44 | 3.47 | 14.27 |
| GMean | 34.48 | 117.76 | 4.81 | 93.93 | 2.68 | 0.71 | 59.47 | 94.29 | 2.71 | 7.21 |
| S.E. | 0.61 | 2.29 | 0.32 | 2.05 | 0.10 | 0.05 | 2.07 | 0.96 | 0.05 | 0.53 |
| C.D.(5 %) | 1.74 | 6.52 | 0.92 | 5.83 | 0.27 | 0.14 | 5.87 | 2.74 | 0.14 | 1.50 |

is attained to avoid biased selection due to the influence of non-additive gene action (16). Among the high-yielding hybrids, TMV 3 × VS19078, TMV 7 × IC129607 and TMV 7 × IC204557 had non-significant SCA for seed yield with good combining parents (Table 6). The cross TMV 7 × IC204557 also had non-significant SCA for days to 50 % flowering, number of branches per plant, number of capsules per plant, capsule length, days to maturity and 1000-seed weight. Hybrids TMV 3 × VS19078 and TMV 7 × IC129607 had non-significant SCA for days to 50 % flowering, plant height, capsule length, capsule width, number of seeds per capsule and days to maturity. Hence, these crosses can be used in a pedigree breeding programme. High-yielding hybrids, TMV 3 × IC129607, TMV 3 × IC204557 and TMV 7 × VS19078 had significant SCA for seed yield with good combining parents. All these hybrids had significant SCA for the number of capsules per plant. However, these hybrids had non-significant SCA for most of the other traits. Hence, these crosses can also be used for breeding programmes, but the selection needs to be postponed to the later generations. Research indicates the good specific combinations for the number of branches per plant, the number of capsules per plant and seed yield per plant (15, 19-22).

Conclusion

To conclude, the present study found a predominance of non-additive gene action for seed yield and other yield components. Among the lines IC 129607, IC204557 and VS19078 and the testers TMV 3 and TMV 7 had significant and positive GCA effects for seed yield per plant and component traits. Among hybrids, TMV 7 × IC204557 had high *per se* performance, significant GCA and non-significant SCA for seed yield per plant, number of capsules per plant and most of the other traits. Hence, this cross can be further advanced through pedigree breeding to obtain high-yielding segregants due to the presence of additive gene action. Hybrids, TMV 3 × VS19078, TMV 7 × IC129607, TMV 3 × IC129607, TMV 3 × IC204557 and TMV 7 × VS19078 had high *per se*, good combining parents but with significant SCA for seed yield or number of capsules per plant and other component traits. Hence, selection should be postponed for generations in these crosses due to the presence of non-additive gene action.

Table 6. Specific combining ability effects (SCA) of crosses for various quantitative traits

| Crosses | DFF | PH | NBP | NCP | CL | CW | NSC | DTM | TSW | SPY |
|--------------------|---------|----------|----------|-----------|---------|--------|---------|----------|----------|----------|
| TMV 3 × EC358033 | 0.09 | -2.46 | -0.54 | -5.21 * | 0.05 | -0.01 | -0.55 | 2.42 * | -0.00 | -2.61 ** |
| TMV 3 × EC346664 | -0.28 | 7.44 ** | -0.37 | -11.75 ** | -0.07 | -0.02 | -1.08 | -7.69 ** | -0.17 ** | -1.19 * |
| TMV 3 × IC129607 | -1.06 | -3.63 | 0.57 | 11.88 ** | -0.15 | 0.04 | -2.12 | 0.90 | 0.00 | 2.71 ** |
| TMV 3 × IC204840 | 1.85 ** | -9.85 ** | 0.81 * | 7.25 ** | 0.21 * | 0.05 | 2.58 | 1.83 | 0.05 | -0.54 |
| TMV 3 × IC204557 | -0.02 | 4.52 | 0.44 | 17.99 ** | -0.12 | -0.07 | 1.31 | 2.38 * | 0.14 ** | 2.58 ** |
| TMV 3 × VS19078 | -0.56 | 3.99 | -0.91 ** | -20.15 ** | 0.08 | 0.01 | -0.13 | 0.16 | -0.02 | -0.96 |
| VRI 5 × EC358033 | -1.26 * | 3.95 | 0.54 | 3.66 | 0.04 | 0.08 | -0.85 | -1.60 | -0.01 | 1.30 * |
| VRI 5 × EC346664 | 0.60 | -6.31 ** | 0.10 | 17.74 ** | 0.10 | -0.01 | 0.95 | 3.85 ** | 0.02 | 1.75 ** |
| VRI 5 × IC 129607 | 0.93 | 8.07 ** | -1.62 ** | -0.08 | 0.14 | 0.01 | -0.08 | 0.22 | -0.17 ** | -2.12 ** |
| VRI 5 × IC 2045840 | -0.66 | 9.07 ** | 0.28 | 0.29 | -0.21 * | -0.02 | -5.27 * | -0.75 | 0.16 ** | 1.37 * |
| VRI 5 × IC 204557 | 0.41 | -9.34 ** | 0.14 | -15.85 ** | 0.00 | -0.04 | 3.35 | -2.30 * | -0.09 | -1.54 ** |
| VRI 5 × VS19078 | -0.01 | -5.44 * | 0.56 | -5.77 ** | -0.07 | -0.02 | 1.91 | 0.59 | 0.09 | -0.76 |
| TMV 7 × EC358033 | 1.17 | -1.49 | -0.00 | 1.55 | -0.09 | -0.07 | 1.41 | -0.82 | 0.01 | 1.31 * |
| TMV 7 × EC346664 | -0.31 | -1.13 | 0.27 | -5.99 ** | -0.04 | 0.04 | 0.13 | 3.85 ** | 0.15 ** | -0.57 |
| TMV 7 × IC129607 | 0.13 | -4.44 | 1.05 ** | -11.80 ** | 0.01 | -0.05 | 2.21 | -1.12 | 0.17 ** | -0.59 |
| TMV 7 × IC204840 | -1.18 | 0.79 | -1.10 ** | -7.54 ** | 0.00 | -0.03 | 2.69 | -1.08 | -0.21 ** | -0.83 |
| TMV 7 × IC204557 | -0.39 | 4.82 * | -0.58 | -2.13 | 0.12 | 0.10 * | -4.66 * | -0.08 | -0.05 | -1.04 |
| TMV 7 × VS19078 | 0.58 | 1.45 | 0.35 | 25.91 ** | -0.00 | 0.01 | -1.78 | -0.75 | -0.07 | 1.72 ** |

*, ** - significant at 5 and 1 % respectively

Acknowledgements

We extend our sincere thanks to the Regional Research Station, Vriddhachalam, Tamil Nadu Agricultural University, for doing the research.

Authors' contributions

SKR drafted the manuscript. MN and MA supervised and worked on the manuscript. SK, SRG and JM were involved in planning and provided critical feedback on the manuscript. All authors read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

- Ashri A. Sesame breeding. In: Janick J, editor. Plant Breeding Reviews, Vol. 16. New York: John Wiley & Sons, Inc., 1998. p. 179–228. <https://doi.org/10.1002/9780470650110.CH5>
- Teklu DH, Shimelis H, Abady S. Genetic improvement in sesame (*Sesamum indicum* L.): Progress and outlook: A review. *Agronomy (Basel)*. 2022;12(9):2144. <https://doi.org/10.3390/agronomy12092144>
- Kefale H, Wang L. Discovering favorable genes, QTLs and genotypes as a genetic resource for sesame (*Sesamum indicum* L.) improvement. *Front Genet*. 2022;13:1002182. <https://doi.org/10.3389/fgene.2022.1002182>
- Dossa K, Diouf D, Wang L, Wei X, Zhang Y, Niang M, et al. The emerging oilseed crop *Sesamum indicum* enters the “Omics” era. *Front Plant Sci*. 2017;8:1154. <https://doi.org/10.3389/fpls.2017.01154>
- Al-Jaf IHM, Mubarak AK, Abed BM, Al-Dulaimy AFZ. Artificial seeds technology: a review. *Anbar J Agric Sci*. 2023;21(2):396–407. <https://doi.org/10.32649/ajas.2023.181869>
- Wang L, Zhang Y, Zhu X, Li D, Zhang X. Development of an SSR-based genetic map in sesame and identification of quantitative trait loci associated with charcoal rot resistance. *Sci Rep*. 2017;7(1):8349. <https://doi.org/10.1038/s41598-017-08858-2>
- Fasahat P, Rajabi A, Rad JM, Derera JJ. Principles and utilization of combining ability in plant breeding. *Biomet Biostat Int J*. 2016;4(1):1–24. <https://doi.org/10.15406/bbij.2016.04.00085>
- Kempthorne O. An introduction to genetic statistics. New York: Wiley; 1957.
- Manivannan N. TNAU-STAT-Statistical package [Internet]. 2014 [cited 2025 Aug 14]. Available from: <https://sites.google.com/site/tnaustat>
- Gore BD, Rathod ST, Naik GH, Sarvade PB. Combining ability studies in sesame (*Sesamum indicum* L.) for seed yield and its contributing traits. *Int J Adv Biochem Res*. 2024;8(4):448–51. <https://doi.org/10.33545/26174693.2024.v8.i4f.986>
- Vidhyavathi R, Manivannan N, Muralidharan V. Line × tester analysis in sesame (*Sesamum indicum* L.). *Indian J Agric Res*. 2005;39(3):225–8.
- Kumari BM, Manivannan N, Ganesamurthy K. Combining ability analysis in sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2015;6(3):700–8.
- Priya R, Thiagarajan K, Bharathi SP, Krishnasamy V. Combining ability studies through Line × Tester analysis in sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2016;7(4):883–7. <https://doi.org/10.5958/0975-928X.2016.00120.4>
- Deshmukh AS, Misal AM, Tavadare PL, Dasari R. Combining ability analysis in sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2019;10(3):1283–91. <https://doi.org/10.5958/0975-928X.2019.00164.9>
- Sprague GF, Tatum LA. General vs. specific combining ability in single crosses of corn. *J Am Soc Agron*. 1942;34(10):923–32. <https://doi.org/10.2134/agronj1942.00021962003400100008x>
- Manivannan N, Ganesan J. Line × tester analysis over environment in sesame. *Indian J Agric Res*. 2001;35(4):255–8.
- Chaudhari GB, Anarase SA, Ban YG. Combining ability and gene action over environments in Sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2016;7(1):71–7. <https://doi.org/10.5958/0975-928X.2016.00010.7>
- Disowja A, Parameswari C, Gnanamalar RP, Vellaikumar S. Heterosis and combining ability studies in sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2021;12(2):347–52. <https://doi.org/10.37992/2021.1202.051>
- Allard RW. Biometrical approach to plant breeding. In: Genetics in plant breeding: report of symposium held May 21 to 23, 1956. Brookhaven Symposia in Biology, No. 9. Upton (NY): Brookhaven National Laboratory; 1956. p. 66–8.
- Thiyagu K, Kandasamy G, Manivannan N, Muralidharan V. Studies in combining ability for economic traits in cultivated sesame (*Sesamum indicum* L.). *Madras Agric J*. 2007;94:168–73. <https://doi.org/10.29321/MAJ.10.100659>
- Suganthi S, Abdigafar A, Satheeshkumar P, Kamaraj A, Bhuvaneswari R. Estimation of combining ability in sesame (*Sesamum indicum* L.) through diallel analysis. *Plant Arch*. 2020;20(SP):3614–8.
- Gadhiya CJ, Patil SS, Kalaria RK, Parsaniya TA, Baria KG, Bhoya BJ, et al. Genetic studies on yield and yield attributing traits in sesame (*Sesamum indicum* L.). *Electron J Plant Breed*. 2023;14(1):209–16. <https://doi.org/10.37992/2023.1401.030>

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonpublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc. See https://horizonpublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.