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Heterosis, Inbreeding Depression and Transgressive Segregation for Seed Yield and Component Traits in Sesame (*Sesamum indicum* L.)

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Abstract

Sesame is an essential oilseed crop highly valued for high-quality edible oils. However, sesame has low yields, a lack of genetic variability and is susceptible to many biotic and abiotic stresses which hinder improvements in yield. The current study was performed to estimate heterosis, inbreeding depression and transgressive segregation of seed yield and its component traits in sesame, using a half-diallel mating scheme. The study involves twelve genetically diverse sesame genotypes crossed in half-diallel fashion to generate 66 F₁ and 66 F₂ hybrids. The experiment was laid in a randomized complete block design at Junagadh Agricultural University, India. The analysis of variance (ANOVA) indicated highly significant differences ($P < 0.01$) between the genotypes for all the studied traits, indicating a substantial amount of genetic variability. The results reported significant amounts of heterosis, hybrid vigor as well as multiple traits associated with seed yield and seed yield components. The crosses AT-591 × G. TIL-10, AT-591 × G. TIL-11, G. TIL-10 × G. TIL-11 displayed significant high levels of standard heterosis for seed yield per plant and desirably exhibited positive heterosis for many of the attributes that contribute to seed yield. Moreover, the moderate to great amount of inbreeding depression exhibited for many traits suggested the presence of greater amounts of non-additive gene action within each of the parental genotypes. The crosses AT-556 × AT-591, AT-582 × G.TIL-11, AT-591 × G.TIL-10 and G.TIL-10 × G.TIL-11 can be considered as the most promising combinations for isolating superior transgressive segregants and obtaining high yielding pure lines in sesame.

Keywords: Heterosis breeding, Sesame, Heterosis, Inbreeding depression, segregants, half-diallel, F₂ population

Introduction

Sesame (*Sesamum indicum* L., $2n = 26$) is a very old oilseed crop that is most commonly cultivated second to groundnut, rapeseed and mustard in India. It is commonly referred to as til, gingelly, simsim or gergelim (Biswas *et al.* 2018) [8]. It is a member of the order *Tubiflorae* and family *Pedaliaceae*. Although sesame is generally considered a crop suitable for tropical and sub-tropical conditions, it has also been adopted in temperate regions. Africa is believed to have been the first centre of domestication for sesame with West Asia as a subsequent centre for their introduction into India, China and Japan (Weiss, 1983) [34].

Sesame, the “Queen of Oilseeds” is highly valued for its superior oil quality which is attributed to high concentrations of oleic acid (43%), linoleic acid (35%), palmitic acid (11%), stearic acid (7%). (Ashri, 1998) [5]. Generally, the oil content in sesame ranges from 34 to 63 per cent (Were *et al.* 2006) [35]. It is one of the most important multipurpose oilseeds with a good nutritional, medicinal, and economic value, especially in those areas where there are low-cost, high-quality edible oils available. Sesame's oil has a wide variety of uses due to its stability and versatility in the food processing, medicinal and cosmetic industries (Abbas *et al.* 2022) [1].

In Indian subcontinent, sesame is cultivated on 15.76 lakh hectare of area with an annual production of 8.93 lakh tons and a productivity of 566.9 kg/ha. Approximately 1.72 lakh hectare of Gujarat is devoted to sesame cultivation, yielding about 1.42 lakh tons per year at a productivity of 825.5 kg/ha (Anon, 2025) [3]. Sesame yields in India is lower than other countries, and have been stable for several years due to various climatic limitations. This may be due to asynchronous flower and capsule development, poor capsule retention, and

susceptibility to certain biotic and abiotic stresses, such as diseased crop, insect pests, droughts, and high temperatures. Furthermore, limited yield potential exists because there is no genetic diversity between current cultivated sesame varieties, which reduces their potential to produce genetically improved varieties through breeding programs. To address the low yields and plateau in sesame production in India, the use of hybrid seeds, which have higher seed production and better economic traits, could be a potential solution. This could be achieved through heterosis breeding (Paril *et al.*, 2024)^[21]. In addition to heterosis research, new breeding methods will increasingly rely on the understanding of inbreeding depression effects.

Transgressive segregation is an important genetic phenomenon in crop improvement, wherein segregating generations, particularly the F_2 , produce individuals that exceed both parents for economically important traits. This arises from complementary gene action, accumulation of favorable alleles, and the breakdown of undesirable linkages during segregation and recombination. In self-pollinated crops like sesame, where genetic variability is limited, the identification of transgressive segregants provides an effective approach for developing superior pure lines with enhanced yield and associated traits. Such segregants represent novel and desirable genetic combinations, making F_2 population evaluation crucial for both genetic analysis and practical breeding aimed at sustained yield improvement. Therefore, the present investigation was undertaken to estimate heterosis, inbreeding depression and transgressive segregation for seed yield and its component traits in sesame (*Sesamum indicum* L.) using a half-diallel mating design.

Materials and Methods

Experimental Materials: The experimental material for the present investigation comprised of twelve genetically diverse sesame genotypes viz., AT-371, AT-542, AT-543, AT-547, AT-550, AT-556, AT-582, AT-590, AT-591, AT-593, G. TIL-10 and G. TIL-11. These genotypes were selected on the basis of their genetic diversity and agronomic performance.

Crossing Programme: The twelve parents were crossed in a half-diallel mating design without reciprocals during Summer 2024 to produce 66 F_1 hybrids. Subsequently, F_2 populations were generated from the respective F_1 hybrids during summer 2025. The 66 F_1 hybrids were then used to produce F_2 populations during the summer of 2025. Some of the seeds produced by the 66 F_1 hybrids were sown in separate lines during Kharif 2024 in order to obtain seeds for the respective F_2 populations by selfing.

Experimental Site and Design: The field experiment was conducted during Summer 2024 and 2025 at Sagdividi Farm, Department of Seed Science and Technology, College of Agriculture, Junagadh Agricultural University, Junagadh. The experimental material consisting of 12 parents, 66 F_1 's, 66 F_2 's and one standard check (G. TIL-11) was evaluated in Randomized Block Design (RBD) with three replications. The parents and F_1 's were grown in single row and F_2 's with four rows plot with a spacing 45 × 10 cm.

Characters Studied: Five randomly selected plants from each entry excluding border plants were selected to record

observations on different characters and their average values were used for parents and F_1 and 20 plants in F_2 for statistical analysis. Data were recorded for days to maturity, height up to first capsule (cm), plant height (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, length of capsule (cm), thousand seed weight (g), seed yield per plant (g), biological yield per plant (g), oil content (%) and harvest index (%). The observations on days to 50 per cent flowering, 1000-seed weight, oil content and days to maturity were recorded on plot basis. The oil content was analysed by using Nuclear Magnetic Resonance Spectro Photometer as suggested by Tiwari *et al.* (1974)^[30].

Statistical Analysis

The mean values of recorded observations were finally subject to statistical analysis. The analysis of variance was performed to test the significance of differences among the genotypes for all the characters following fixed effect model as suggested by Panse and Sukhatme (1985)^[20]. The heterotic effects were computed as the percentage increase (+) or decrease (-) of F_1 mean values over better parent (heterobeltiosis) and standard check variety (standard heterosis) for all the characters and crosses following the standard formula. Inbreeding depression (ID) was expressed as per cent reduction in value of F_2 over F_1 generation. Analysis of transgressive segregation in F_2 for seed yield per plant was done with the computation of mean, range, standard deviation, variance, standard error of mean and standard variates following standard statistical methods (Panse and Sukhatme, 1985)^[20].

Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the characters studied indicating the presence of sufficient variability among the genotypes (Table 1). Further, partitioning of mean sum of squares for parents and hybrids, the differences among the parents were also found significant for all the characters except 1000-seed weight and plant height. The differences among the F_1 hybrids were also found significant for all the characters suggesting the presence of sufficient diversity among hybrids themselves for all the characters. The mean squares due to parent's vs hybrids were also found significant for most of the traits except harvest index, indicating the presence of substantial heterosis as group heterosis across the crosses and involvement of non-additive gene action. The range of heterosis in hybrids over their better parent and standard check variety G. TIL-11, number of crosses showing significant and desirable heterosis over better parent and standard check are presented in Table 2. Similar findings for the characters studied were reported by Vavdiya *et al.* (2013)^[33], Joshi *et al.* (2014)^[16], Gaikwad and Lal (2010)^[13], Hassan and Sedeck (2015)^[14], Kumar *et al.* (2015)^[17], Zala *et al.* (2022)^[36] and Tavadare *et al.* (2022)^[29].

Manifestations of heterosis and Inbreeding depression for different characters

For days to 50 per cent flowering, eight crosses showed significant negative heterobeltiosis, indicating earliness. The cross AT-550 × G.TIL-10 recorded the highest desirable heterobeltiosis (-16.22%), followed by AT-590 × AT-593 (-16.07%). The most undesirable cross in terms of lateness

was AT-543 × AT-547 (12.26%), which recorded the maximum positive heterobeltiosis. Significant negative standard heterosis was observed for AT-547 × AT-590 (-16.24%), followed by AT-550 × G.TIL-11 (-15.45%), AT-550 × AT-593 (-14.55%), AT-590 × G.TIL-10 (-14.55%) and AT-547 × AT-591 (-10.91%), indicating their superiority for early flowering. This result agrees with the findings of Sakhiya (2013) [25], Nayak *et al.* (2017) [19], Chaudhary *et al.* (2017) [9], Zala *et al.* (2022) [36] and Chaudhary *et al.* (2024) [10] in sesame. Inbreeding depression in the F₂ generation ranged from -4.10% (AT-542 × AT-591) to 5.91% (AT-543 × AT-593). Among the crosses, only one showed significant positive inbreeding depression, while none exhibited significant negative inbreeding depression.

Heterobeltiosis for days to maturity ranged from -20.07% (AT-590 × AT-593) to 10.07% (AT-547 × G.TIL-11). Eighteen crosses showed significant negative heterobeltiosis, indicating earlier maturity. The most promising crosses for earlier maturity were AT-590 × AT-593

(-20.07%), AT-547 × AT-591 (-11.48%), AT-547 × G.TIL-10 (-11.41%) and AT-550 × G.TIL-10 (-9.13%). The standard heterosis values across all crosses ranged from -15.30% to 11.94%, with 15 crosses showing significant negative standard heterosis. The cross AT-590 × AT-593 recorded the highest desirable standard heterosis (-15.30%), followed by AT-547 × G.TIL-10 (-13.06%) and AT-547 × AT-590 (-12.31%). Significant negative heterosis for days to maturity was also reported by Gaikwad and Lal (2010) [13], Zala *et al.* (2022) [36], and Chaudhary *et al.* (2024) [10] in sesame. Inbreeding depression for days to maturity ranged from -4.85% to 5.60% and was generally low in magnitude, indicating relative stability of the trait in segregating generations. Only one cross, AT-371 × AT-556, exhibited significant positive inbreeding depression. Similar findings have been reported by Anuradha and Reddy (2008) [4], Toprope (2009) [31], Banerjee and Kole (2009) [6], and Zala *et al.* (2022) [36].

A high degree of heterosis was observed for height up to the first capsule among the hybrids studied. Heterobeltiosis ranged from -66.98% (AT-543 × AT-593) to 45.90% (AT-582 × G.TIL-11). A total of 52 crosses exhibited significant negative heterobeltiosis, indicating reduced height up to the first capsule. The crosses AT-543 × AT-593 (-66.98%), AT-543 × AT-591 (-63.12%), AT-542 × AT-593 (-56.92%), and AT-371 × AT-550 (-49.13%) were identified as desirable combinations. Standard heterosis ranged from -43.64% to 63.64%, with 16 crosses showing significant negative standard heterosis. Inbreeding depression for height up to the first capsule ranged from -54.87% to 11.64%. Significant negative inbreeding depression was observed in nine crosses, with AT-550 × AT-591 (-54.87%), G.TIL-10 × G.TIL-11 (-37.00%) and AT-547 × AT-582 (-32.99%) showing the greatest reduction from the F₁ to F₂ generation. These results are consistent with the findings of Banerjee and Kole (2009) [6], Zala *et al.* (2022) [36] and Ramana *et al.* (2024) [23].

The magnitude of heterosis for plant height was quite variable. Heterobeltiosis for the hybrids ranged from -21.33% for AT-556 × G.TIL-11 to 8.65% for G.TIL-10 × G.TIL-11, while standard heterosis ranged from -16.04% to 15.92%. The hybrids G.TIL-10 × G.TIL-11 (15.92%), AT-591 × G.TIL-10 (14.93%), and AT-371 × AT-591 (10.18%)

exhibited statistically significant positive standard heterosis for height at the first capsule. These findings are comparable to those reported by Banerjee and Kole (2009) [6], Zala *et al.* (2022) [36] and Ramana *et al.* (2024) [23]. The range for inbreeding depression for height at the first capsule was -13.00% to 6.39%, with none of the hybrids showing significant inbreeding depression.

For number of branches per plant, heterobeltiosis ranged from -73.17% (AT-547 × AT-550) to 25.58% (AT-542 × AT-556). Only two crosses, AT-542 × AT-556 (25.58%) and AT-591 × G.TIL-10 (14.67%), exhibited significant positive heterobeltiosis. Standard heterosis ranged from -75.00% to 95.45%, with five crosses showing significant positive standard heterosis. The crosses AT-591 × G.TIL-10 (95.45%), AT-591 × G.TIL-11 (61.36%) and G.TIL-10 × G.TIL-11 (36.36%) were identified as promising hybrids for this trait. Significant positive heterosis for number of branches per plant in sesame has been reported by Nayak *et al.* (2017) [19], Sapara *et al.* (2018) [26], Zala *et al.* (2022) [36], Chaudhary *et al.* (2024) [10] and Srinivas *et al.* (2025) [28]. Inbreeding depression for number of branches per plant ranged from -121.71% (AT-547 × AT-550) to 42.27% (AT-591 × G.TIL-10). Significant positive inbreeding depression was observed in AT-591 × G.TIL-10 (42.27%) and AT-591 × G.TIL-11 (29.26%), whereas several crosses exhibited significant negative inbreeding depression. The crosses AT-547 × AT-550 (-121.71%) and AT-593 × G.TIL-10 (-68.86%) recorded the greatest induction in branch number from F₁ to F₂ generation.

For length of capsule, heterobeltiosis ranged from -29.83% (AT-543 × AT-547) to 23.16% (AT-582 × G.TIL-10). Twenty-four crosses exhibited significant negative heterobeltiosis, whereas only two crosses showed significant positive heterobeltiosis, namely, AT-582 × G.TIL-10 (23.16%) and AT-547 × AT-550 (14.86%). Standard heterosis ranged from -27.92% to 20.84%, with AT-547 × AT-550 (20.84%), AT-582 × G.TIL-10 (20.10%) and AT-542 × AT-591 (19.11%) showing significant positive standard heterosis. The results are consistent with the findings of Reddy *et al.* (2015) [24], Imran *et al.* (2017) [15], Nayak *et al.* (2017) [19], Sapara *et al.* (2018) [26], Zala *et al.* (2022) [36] and Chaudhary *et al.* (2024) [10]. Inbreeding depression for capsule length ranged from -15.84% (AT-371 × AT-542) to 17.42% (AT-582 × G.TIL-10). Only one cross, AT-582 × G.TIL-10, exhibited significant positive inbreeding depression, whereas AT-371 × AT-542 (-15.84%), AT-543 × AT-547 (-15.24%) and AT-591 × G.TIL-11 (-13.64%) showed significant negative inbreeding depression. These results are in agreement with the findings of Banerjee and Kole (2009) [6], Zala *et al.* (2022) [36] and Ramana *et al.* (2024) [23].

Heterosis over the better parent for number of capsules per plant ranged from -52.08% (AT-542 × G.TIL-10) to 34.09% (AT-582 × AT-593). Significant and positive heterobeltiosis was recorded in AT-582 × AT-593 (34.09%), followed by AT-547 × AT-582 (31.10%), G.TIL-10 × G.TIL-11 (21.97%), AT-591 × G.TIL-10 (18.09%) and AT-582 × G.TIL-11 (14.41%), suggesting the presence of favourable non-additive gene interactions governing capsule number. Standard heterosis ranged from -52.67% to 25.44%, with G.TIL-10 × G.TIL-11 (25.44%), AT-591 × G.TIL-10 (23.13%), AT-550 × AT-591 (16.19%) and AT-582 × G.TIL-11 (14.41%) showing significant positive standard heterosis. Similar results for significant positive heterosis

for number of capsules per plant in sesame were reported by Das *et al.* (2000)^[12], Praveenkumar *et al.* (2012)^[22], Zala *et al.* (2022)^[36], Chaudhary *et al.* (2024)^[10] and Srinivas *et al.* (2025)^[28]. Inbreeding depression in the F₂ generation ranged from -65.76% (AT-556 × AT-591) to 34.75% (AT-547 × AT-591). The cross AT-556 × AT-591 manifested the highest magnitude of negative inbreeding depression (-65.76%), indicating substantial increase in performance due to inbreeding. These observations agree with the findings of Toprope (2009)^[31], Banerjee and Kole (2009)^[6], Zala *et al.* (2022)^[36] and Ramana *et al.* (2024)^[23].

Heterobeltiosis for number of seeds per capsule ranged from -59.35% (AT-371 × G.TIL-10) to 11.87% (AT-556 × G.TIL-10). Significant positive heterobeltiosis was observed in AT-556 × G.TIL-10 (11.87%) and AT-550 × AT-556 (9.39%), whereas AT-371 × G.TIL-10 (-59.35%) and AT-371 × G.TIL-11 (-57.00%) recorded the highest negative heterobeltiosis. No cross showed significant positive standard heterosis for this trait. The absence of significant positive standard heterosis for this trait agrees with the findings of Banerjee and Kole (2009)^[6], Vavdiya *et al.* (2013)^[33], Reddy *et al.* (2015)^[24] and Zala *et al.* (2022)^[36]. In the F₂ generation, inbreeding depression ranged from -46.13% (AT-547 × AT-591) to 33.96% (AT-547 × AT-582). The most desirable cross was AT-547 × AT-591 which recorded the highest negative inbreeding depression (-46.13%). The undesirable and significant and positive inbreeding depression was recorded in AT-547 × AT-582 (33.96%), AT-547 × AT-550 (23.90%), AT-556 × G. Til-10 (17.53%), AT-550 × AT-556 (12.71%) and AT-547 × AT-556 (12.32%). The occurrence of significant inbreeding depression in these crosses indicates breakdown of favorable heterotic combinations due to segregation, thereby reflecting the predominance of non-additive gene action in the inheritance of number of seeds per capsule. Similar results for significant inbreeding depression for yield and its component traits in sesame were also reported by Singh (2002)^[27], Toprope (2009)^[31], Banerjee and Kole (2009)^[6], Zala *et al.* (2022)^[36], and Ramana *et al.* (2024)^[23].

The magnitude of heterosis over the better parent for thousand seed weight was relatively low among the crosses studied. Heterobeltiosis ranged from -14.48% (AT-543 × AT-582) to 5.37%, and no cross exhibited significant positive heterobeltiosis. Standard heterosis ranged from -13.44% (AT-542 × AT-590) to 8.20% (AT-582 × G.TIL-11). The estimate of standard heterosis ranged from -13.44% in AT-542 × AT-590 to 8.20% in AT-582 × G.TIL-11. Only two crosses, AT-582 × G.TIL-11 (8.20%) and AT-582 × AT-591 (8.00%), showed significant and positive standard heterosis. This finding confirms the findings of Vavdiya *et al.* (2013)^[33], Reddy *et al.* (2015)^[24], Imran *et al.* (2017)^[15], Beniwal (2018)^[7], Zala *et al.* (2022)^[36], Chaudhary *et al.* (2024)^[10], and Srinivas *et al.* (2025)^[28]. Inbreeding depression in the F₂ generation for thousand seed weight ranged from -8.81% (AT-371 × AT-542) to 10.30% (AT-556 × AT-591). Significant positive inbreeding depression was observed in AT-556 × AT-591 (10.30%) and AT-582 × AT-591 (8.53%), while AT-371 × AT-542 (-8.81%) showed the highest negative inbreeding depression. The presence of significant inbreeding depression in these crosses indicates the breakdown of heterotic gene combinations due to segregation, reflecting the role of non-additive gene action in the inheritance of thousand seed weight. Similar observations were reported by Toprope

(2009)^[31], Banerjee and Kole (2009)^[6], Zala *et al.* (2022)^[36], and Ramana *et al.* (2024)^[23].

Seed yield per plant showed considerable heterosis among the crosses studied. Heterobeltiosis ranged from -45.35% (AT-547 × AT-556) to 14.08% (AT-591 × G.TIL-11). Significant and positive heterobeltiosis was recorded only in AT-591 × G.TIL-11 (14.08%). The highest negative heterobeltiosis was observed in AT-547 × AT-556 (-45.35%), followed by AT-542 × AT-593 (-38.52%). The estimate of standard heterosis ranged from -45.43% (AT-547 × AT-556) to 20.51% (AT-591 × G.TIL-10). The crosses AT-591 × G.TIL-10 (20.51%), AT-591 × G.TIL-11 (18.90%), and G.TIL-10 × G.TIL-11 (17.86%) exhibited desirable and significant positive standard heterosis. Similar findings for this trait in sesame were reported by Vavdiya *et al.* (2013)^[33], Reddy *et al.* (2015)^[24], Imran *et al.* (2017)^[15], Tripathy *et al.* (2017)^[32], Beniwal (2018)^[7], Sapara *et al.* (2018)^[26], Zala *et al.* (2022)^[36], Chaudhary *et al.* (2024)^[10], and Srinivas *et al.* (2025)^[28]. Inbreeding depression in the F₂ generation for seed yield per plant ranged from -48.88% (AT-556 × AT-591) to 24.32% (AT-543 × AT-590). The most desirable cross was AT-556 × AT-591 followed by G. TIL-10 × G. TIL-11 (-27.67%) which recorded the highest negative inbreeding depression. Significant positive inbreeding depression was observed in AT-543 × AT-590 (24.32%), AT-542 × AT-590 (23.93%), AT-547 × AT-591 (23.03%), and AT-590 × AT-593 (22.14%), indicating breakdown of heterotic gene combinations in segregating generations. Similar observations were also reported by Banerjee and Kole (2009)^[6], Vavdiya *et al.* (2013)^[33], Reddy *et al.* (2015)^[24], Zala *et al.* (2022)^[36], and Ramana *et al.* (2024)^[23].

Heterobeltiosis for biological yield per plant ranged from -38.67% (AT-547 × G.TIL-10) to 21.70% (AT-542 × G.TIL-11). Among the twenty-four significant crosses, three exhibited significant and positive heterobeltiosis, while twenty-one showed significant and negative heterobeltiosis. The significant and positive heterobeltiosis, arranged in descending order, was observed in AT-542 × G. TIL-11 (21.70%), followed by AT-591 × G.TIL-11 (19.12%) and AT-371 × AT-547 (18.18%). Standard heterosis ranged from -36.83% to 28.08%, with AT-543 × AT-556 (28.08%), AT-582 × G.TIL-10 (27.07%) and AT-556 × G.TIL-10 (24.45%) showing significant positive standard heterosis. Similar findings were reported by Nayak *et al.* (2017)^[19], Sapara *et al.* (2018)^[26], Anandan *et al.* (2019)^[2], Chauhan *et al.* (2019)^[9], Chaudhary *et al.* (2024)^[10] and Srinivas *et al.* (2025)^[28] in sesame. In the F₂ generation, inbreeding depression ranged from -32.78% (G.TIL-10 × G.TIL-11) to 21.15% (AT-543 × AT-590). Significant positive inbreeding depression was observed in AT-543 × AT-590 (21.15%) followed by AT-590 × AT-593 (18.06%). In contrast, G.TIL-10 × G.TIL-11 (-32.78%) and AT-591 × G.TIL-10 (-23.00%) showed significant negative inbreeding depression, indicating comparatively greater stability across generations. Similar trends were also reported by Banerjee and Kole (2009)^[6], Toprope (2009)^[31], Reddy *et al.* (2015)^[24], Zala *et al.* (2022)^[36] and Ramana *et al.* (2024)^[23].

Heterosis over the better parent for harvest index ranged from -32.66% (AT-582 × G.TIL-10) to 18.80% (AT-543 × G.TIL-11). Of the 45 significant crosses, thirteen exhibited significant and positive heterobeltiosis, with AT-543 × G.TIL-11 (18.80%), AT-547 × G.TIL-10 (16.83%) and AT-543 × AT-582 (16.07%) identified as superior cross

combinations. Standard heterosis ranged from -29.93% to 25.59%. Of the 43 significant crosses, six showed significant and positive standard heterosis, with the cross AT-591 × G.TIL-10 (25.59%) recording the highest desirable and significant standard heterosis, followed by G.TIL-10 × G.TIL-11 (23.15%) and AT-547 × G.TIL-10 (23.04%). Similar findings have been reported by Nayak *et al.* (2017)^[19], Sapara *et al.* (2018)^[26], Anandan *et al.* (2019)^[2], Chauhan *et al.* (2019)^[11], Chaudhary *et al.* (2024)^[10], and Srinivas *et al.* (2025)^[28] in sesame. In the F₂ generation, inbreeding depression ranged from -22.50% (AT-593 × G.TIL-10) to 26.96% (AT-543 × AT-591). AT-593 × G.TIL-10 (-22.50%) and AT-547 × G.TIL-11 (-21.62%) exhibited significant negative inbreeding depression. Whereas, Significant and positive inbreeding depression was observed in AT-543 × AT-591 (26.96%), AT-371 × G.TIL-11 (19.14%), and AT-542 × AT-550 (19.70%). Similar findings for inbreeding depression in harvest index were also reported by Toprope (2009)^[31], Zala *et al.* (2022)^[36], and Ramana *et al.* (2024)^[23].

Heterosis over the better parent for oil content ranged from -19.81% in AT-547 × G.TIL-11 to 4.69% in AT-543 × AT-590. Among the 19 significant crosses, all exhibited significant and negative heterobeltiosis, and no cross showed desirable, significant, and positive heterobeltiosis. The lowest heterobeltiosis was recorded in AT-547 × G.TIL-11 (-19.81%), followed by AT-547 × AT-593 (-15.76%). Standard heterosis ranged from -19.81% to 3.30%, and all significant crosses recorded negative standard heterosis. No significant and desirable positive standard heterosis was observed for this trait. The absence of significant and positive heterobeltiosis, as well as standard heterosis for oil content, closely agrees with earlier reports by Banerjee and Kole (2009), Reddy *et al.* (2015), and Zala *et al.* (2022), who also observed negligible or non-significant positive heterotic effects for oil content. Inbreeding depression for oil content ranged from -14.84% (AT-547 × G.TIL-11) to 10.18% (AT-543 × G.TIL-10). Significant positive inbreeding depression was observed in AT-543 × G.TIL-10 (10.18%), AT-543 × AT-547 (9.44%), and AT-550 × AT-582 (8.39%), whereas AT-547 × G.TIL-11 (-14.84%) and AT-547 × AT-590 (-7.29%) exhibited significant negative inbreeding depression. Similar findings for inbreeding depression in harvest index and related yield traits in sesame were also reported by Banerjee and Kole (2009)^[6], Misra *et al.* (2008)^[18], Zala *et al.* (2022)^[36], and Ramana *et al.* (2024)^[23].

Overall, the magnitude and direction of heterosis and

inbreeding depression varied considerably among the traits and cross combinations, indicating differential genetic control of the characters studied. Significant positive heterosis, along with moderate to high inbreeding depression observed for seed yield and several yield-contributing traits, suggests the predominance of non-additive gene action. Crosses such as AT-591 × G.TIL-10, AT-591 × G.TIL-11, and G.TIL-10 × G.TIL-11 consistently exhibited desirable heterotic effects for seed yield and associated traits, and may be utilised in future breeding programmes for the isolation of superior segregants in sesame. A comparative assessment of these three bests standard heterobeltiotic crosses for seed yield, along with their standard heterotic effects for yield components, is presented in Table 3.

Transgressive Segregation in F₂ for seed yield per plant

The range, mean, frequency distribution, proportion of desirable transgressive segregants, threshold value and normal deviation value for five crosses in F₂ generation for seed yield per plant are presented in Table 4. Substantial transgressive segregation was observed for seed yield per plant in the F₂ populations, indicating the presence of considerable genetic variability among the segregants. The occurrence of transgressive segregants beyond the increasing parent in all the five crosses suggested that favourable alleles governing seed yield were contributed by both the parents. Considerable variation was observed among the crosses with respect to frequency and intensity of transgressive segregation, indicating that both parameters were not necessarily associated with each other. Among the crosses, AT-556 × AT-591 recorded the highest frequency of desirable transgressive segregants, whereas the cross G.TIL-10 × G.TIL-11 exhibited the highest intensity of transgression despite a comparatively lower frequency of transgressive segregants, suggesting the occurrence of few recombinants with exceptionally high yield potential. Higher normal deviation values observed in certain crosses further indicated greater scope for genetic improvement through selection. The simultaneous occurrence of high frequency and high intensity of transgressive segregants suggested the involvement of additive × additive gene interactions arising from recombination of favourable alleles from both parents. Among the crosses, AT-556 × AT-591, AT-582 × G.TIL-11, AT-591 × G.TIL-10 and G.TIL-10 × G.TIL-11 were identified as promising combinations for isolating superior transgressive segregants and developing high yielding pure lines in sesame.

Table 1: Analysis of variance (mean square) for the experimental design for different characters in sesame

Source	Mean square							
	d. f.	Days to 50 per cent flowering	Days to maturity	Height up to First capsule (cm)	Plant height (cm)	No. of branches per Plant	Length of capsule (cm)	No. of capsules per Plant
Replication	2	0.697	5.210	6.582	86.802*	0.384	0.111	45.834**
Genotypes	143	15.511**	112.640**	221.397**	60.690**	1.520**	0.194**	210.101**
Parents	11	5.950**	71.907**	268.385**	38.790	1.788**	0.149**	104.201**
F ₁ 's crosses	65	16.472**	108.914**	153.524**	87.417**	2.067**	0.288**	152.622**
P vs. F ₁ 's	1	11.470*	71.571**	1170.846**	317.196**	7.817**	0.327**	64.090*
F ₂ 's crosses	65	16.464**	125.623**	256.819**	31.100**	0.822**	0.108**	167.995**
P vs. F ₂ 's	1	10.860**	49.931*	964.657**	48.531	2.533**	0.090**	72.091**
Error	286	1.995	9.075	8.045	23.068	0.128	0.037	9.852
Source	Mean square							
	d. f.	No. of seeds per capsule	1000-seed weight (g)	Seed yield per Plant (g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)	
Replication	2	45.833**	0.201	2.310	28.461	0.954	0.860	

Genotypes	143	210.101**	0.091**	10.439**	107.300**	35.963**	9.646**
Parents	11	212.102**	0.039	10.021**	94.927**	17.624**	3.943*
F ₁ 's crosses	65	273.380**	0.087**	7.659**	139.826**	38.715**	11.017**
P vs. F ₁ 's	1	992.328**	0.700**	8.878**	54.606*	1.156	30.312**
F ₂ 's crosses	65	16.464**	0.094**	11.634**	71.004**	32.730**	9.008**
P vs. F ₂ 's	1	10.860	0.800**	69.732**	347.755**	103.984**	32.779**
Error	286	9.852	0.041	0.856	15.283	2.545	2.534

*, ** Significant at 5% and 1% levels, respectively

Table 2: Range of heterobeltiosis and standard heterosis with number of significant crosses in positive and negative direction over better parent and standard check for various characters in sesame

Sr. No.	Characters	Desirable aspect	Range		Number of crosses with significant heterosis			
			H (%)	SH (%)	H (%)		SH (%)	
					+ ve	-ve	+ ve	-ve
1	Days to 50 per cent flowering	Early	-16.22 to 12.26	-16.24 to 18.18	8	8	10	6
2	Days to maturity	Early	-20.07 to 10.07	-15.30 to 11.94	7	18	20	15
3	Height up to first capsule	Low	-66.98 to 45.90	-43.64 to 63.64	2	52	22	16
4	Plant height (cm)	High	-21.33 to 8.65	-16.04 to 15.92	0	20	3	15
5	Number of branches per plant	High	-73.17 to 25.58	-75.00 to 95.45	2	41	5	28
6	Length of capsule (cm)	Long	-29.83 to 23.16	-27.92 to 20.84	2	24	3	25
7	Number of capsules per plant	High	-52.08 to 34.09	-52.67 to 25.44	5	28	4	42
8	Number of seeds per capsule	High	-59.35 to 11.87	-62.33 to 3.67	2	46	0	57
9	1000-seed weight (g)	High	-14.48 to 5.37	-13.44 to 8.20	0	26	2	26
10	Seed yield per plant (g)	High	-45.35 to 14.08	-45.43 to 20.51	1	31	3	40
11	Biological yield per plant (g)	High	-38.67 to 21.70	-36.83 to 28.08	3	21	6	19
12	Harvest index (%)	High	-32.66 to 18.80	-29.93 to 25.59	13	32	6	37
13	Oil content (%)	High	-19.81 to 4.69	-19.81 to 3.30	0	19	0	36

Table 3: Comparative study of three most standard heterotic crosses for seed yield per plant with their standard heterotic effects for yield components in sesame

Sr. No.	Crosses	Mean Seed yield per plant (g)	Per cent of standard heterosis (SH%)						
			Seed yield per plant (g)	Plant height (cm)	Number of branches per plant	Number of capsules per plant	1000- seed weight (g)	Biological yield per plant (g)	Harvest index (%)
1	AT-591 × G. TIL-10	13.49	20.51 **	14.93 **	95.45 **	23.13 **	-4.55	-3.79	25.59 **
2	AT-591 × G. TIL-11	13.31	18.90 **	5.79	61.36 **	4.98	-6.23	19.12 *	-0.05
3	G. TIL-10 × G. TIL-11	13.20	17.86 **	15.92 **	36.36 **	25.44 **	2.96	-4.32	23.15 **

*, **Significant at 5% and 1% levels, respectively

Table 4: Range, mean, frequency distribution, proportion of desirable transgressive segregants, threshold value and normal deviation value for 5 crosses in sesame

Generation	Range	Mean + SE	Frequency distribution in standard deviation							Frequency total	TS (%)	Threshold value	ND value
			-3	-2	-1	0	1	2	3				
[1] Cross 38 (AT-547 x G. TIL-11)													
P ₁	7.57-10.18	9.02 ± 0.090	-	-	-	-	-	-	-	-	-	-	-
P ₂	8.97-13.27	11.19 ± 0.120	-	-	-	-	-	-	-	-	-	-	-
F ₂	11.20-14.46	12.91 ± 0.090	-	1	9	41	6	3	-	60	15.00	11.27	4.33
[2] Cross 48 (AT-556 x AT-591)													
P ₁	8.62-13.27	11.04 ± 0.141	S-	-	-	-	-	-	-	-	-	-	-
P ₂	10.26-13.84	11.73 ± 0.123	-	-	-	-	-	-	-	-	-	-	-
F ₂	9.82-14.66	12.43 ± 0.170	-	-	12	35	13	-	-	60	21.67	12.51	1.94
[3] Cross 56 (AT-582 x G. TIL-11)													
P ₁	6.81-10.55	8.87 ± 0.112	-	-	-	-	-	-	-	-	-	-	-
P ₂	8.97-13.27	11.19 ± 0.120	-	-	-	-	-	-	-	-	-	-	-
F ₂	10.11-12.90	11.50 ± 0.082	-	1	9	38	11	1	-	60	20.00	11.14	2.56
[4] Cross 62 (AT-591 x G. TIL-10)													
P ₁	10.26-13.84	11.73 ± 0.123	-	-	-	-	-	-	-	-	-	-	-
P ₂	11.47-14.62	13.13 ± 0.083	-	-	-	-	-	-	-	-	-	-	-
F ₂	12.10-17.75	15.02 ± 0.189	-	-	14	36	10	-	-	60	16.67	12.81	3.51
[5] Cross 66 (G. TIL-10 x G. TIL-11)													
P ₁	11.47-14.62	13.13 ± 0.083	-	-	-	-	-	-	-	-	-	-	-
P ₂	8.97-13.27	11.19 ± 0.120	-	-	-	-	-	-	-	-	-	-	-
F ₂	13.27-19.83	16.88 ± 0.182	-	2	10	40	6	2	-	60	13.33	12.7	4.96

Conclusion

The present investigation demonstrated the existence of substantial genetic variability among the parental lines and their F₁ and F₂ populations for all the thirteen quantitative traits studied. This implies that there exists wide scope for genetic improvement through hybridization and selection. Significant heterosis observed for seed yield and its contributing traits revealed the importance of non-additive gene action in the inheritance of these characters. Among the evaluated crosses, AT-591 × G. Til-10, AT-591 × G. Til-11, and G. Til-10 × G. Til-11 exhibited superior performance for seed yield and contributing traits. Therefore, they are identified as promising combinations for further use in the breeding programs of sesame plants. Also, in some crossed combinations of certain lines, there was evidence of positive heterosis, which could lead to the development of high-yielding early-maturing sesame varieties.

The extent of inbreeding depression varied among traits and crosses, showing that both additive and non-additive effects contributed differently to the yield and related traits. Lower inbreeding depression associated with traits for earliness, thousand seed weight, and oil content suggest that these traits have a relatively stable expression during inheritance and hence have greater potential for effective selection in early generations of segregation, while higher degree of inbreeding depression associated with seed yield and biological yield suggest that the effect of dominance is greater for these traits than for others. The results of this study support the notion that selecting for transgressively superior segregants from advanced generations of segregation will allow for successful breeding of high yielding sesame cultivars with improved agronomic performance.

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