**Combining Ability Analysis for Earliness and Growth Parameters in Sudanese Okra Collection [*Abelmoschus esculentus* (L.)** **Moench]**

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ABSTRACT

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| **Aims:** This study aimed to evaluate the combining ability and heterotic potential of elite Sudanese okra [*Abelmoschus esculentus* (L.) Moench] lines to identify superior hybrids for breeding programs. The primary objective was to assess key growth parameters and determine the genetic effects contributing to the development of high-yielding, early-maturing, and well-adapted okra varieties.**Study Design:** A line × tester mating design was employed using ten parental lines, including seven female lines and three testers. Twenty-one F1 hybrids were generated and evaluated in a complete randomized block design with three replications.**Methodology:** The study was conducted at the demonstration farm of the Faculty of Agriculture, University of Al Zaeim Al Azhari, Khartoum North. Data were collected on key growth parameters: days to flowering, plant height, pod length, length of pod pedicle, number of nodes per plant, and number of lateral branches. Analysis of variance was performed, and general combining ability and specific combining ability effects were estimated using the line × tester analysis method. Genetic variance components were calculated, and the contributions of lines, testers, and their interactions were evaluated.**Results:** Significant genetic variability among the genotypes was observed for most traits. The high SCA variance for plant height, pod length, and number of nodes per plant indicated a predominance of non-additive gene action. The hybrid HSD2550 × Hjerat exhibited the most favorable SCA effect for early flowering (-2.41\*\*), while HSD2482 × Sinnar demonstrated significant positive effects on plant height (5.10\*). Notably, the number of nodes per plant and lateral branching were significantly influenced by specific parental combinations, emphasizing the importance of hybrid breeding strategies.**Conclusion:** The study highlighted the critical role of non-additive gene action in the expression of key agronomic traits in Sudanese okra. The identification of promising hybrids like HSD2550 × Hjerat and HSD2482 × Sinnar underscores the potential for developing high-yielding and early-maturing okra varieties. These findings provide valuable insights into the genetic improvement of Sudanese okra germplasm, supporting the development of superior hybrids with enhanced agronomic performance and adaptability. |

***Keywords:*** *Okra, Abelmoschus esculentus, combining ability, growth parameters, hybrid breeding*

1. INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is widely distributed across the tropical and humid regions of Africa, where it grows alongside its wild relatives in many rural areas. The crop is believed to have originated in the Abyssinian centre of origin, including Ethiopia, the mountainous regions of Eritrea, and parts of Sudan (Kumar, et al., 2013). Wild okra is commonly found along the alluvial banks of the White, Blue, and River Nile and grows extensively in the rain-fed areas of Central and Southern Blue Nile, Kordofan, and Darfur states (Abdalla et al., 2023). The young pods and leaves are harvested from wild plants, especially during the short rainy season, and are often dried for later use. This practice is particularly prevalent in regions such as the southern Blue Nile, Kordofan, and Darfur. In Sudan, okra is consumed in various forms as an essential ingredient in stews and sauces. It adds texture, flavour, and nutritional value to various dishes. Its mucilaginous nature is highly appreciated and often preserved by drying and grinding the pods into a fine powder. The dried okra, locally known as '*waika*', is a staple in various traditional Sudanese dishes. In Sudan, however, breeding activities have largely focused on the characterization and documentation of genetic variability, with the most notable contribution being the work of Geneif (1983) and El Tahir (2023). Mainly, production in farmer's fields depends almost completely on the use and production of landraces. A few introduced cultivars mainly, Pusa Swani (India), Clemson Spineless, and Perkins Mammoth Long Okra Seeds, (USA) are used in larger schemes. Internationally, using hybrid seeds is becoming increasingly important to achieve target yield and quality. The study of combining ability in plant breeding programs is among the key procedures to evolve new heterotic F1 hybrids or desired segregants by determining parents, crosses, and the proper breeding strategy to use. It provides a reliable approach to evaluating the performance of parental lines in hybrid combinations, offering insights into both general and specific combining abilities. The line x tester analysis has emerged as one of the greatest and most valuable breeding tools using biometric approaches to measure combining ability (Habib & Al-Jubouri, 2024). This model provides insights into the values of both hybrids and parents and eventually the genetic information governing the targeted trait. Given the predominantly self-pollinating nature of okra, understanding these genetic attributes is crucial for identifying promising parental lines and developing high-yielding hybrids from Sudanese okra germplasm. This study was conducted on a selection of Sudanese okra lines while recognizing the contribution of high-yielding introduced varieties such as Clemson Spineless, which has shown strong adaptability and competitiveness against local genotypes. The study will determine the nature and magnitude of gene action controlling earliness and growth parameters, and identify promising hybrids for potential use in okra breeding programs in Sudan. Providing critical insights for developing high-yielding, early-maturing okra varieties with enhanced adaptability and productivity. The specific objectives of this research include assessing the general and specific combining ability of selected Sudanese okra lines and identifying crosses and parental lines with excellent complementary genetic contribution for earliness and growth parameters.

2. materialS and methods

The present investigation was carried out at the demonstration farm of the faculty of Agriculture - University of Al Zaeim Al Azhari at Khartoum North, shambat locality. Shambat soil belongs to the Central Clay Plain of the Sudan, which has been formed by alluvial deposits of the Nile, primarily of basaltic origin, and it is considered largely as Vertisols. Moderately affected by saline and sodic subsoil. The soil texture is clayey throughout the experimental farm, (Ali et al., 2016). The climate of Shambat and its surroundings is a semi-arid climate, characterized by high temperatures and limited rainfall. The mean annual temperatures in this region typically range from 26°C to 32°C, with summer temperatures often exceeding 43°C. Rainfall is generally low and erratic, concentrated mainly between June and September, with annual totals ranging from 200 mm to 700 mm in central Sudan. Ten genetically divergent parental lines of okra (Table 1) were crossed following line × tester fashion. Seven lines namely; HSD 1835, HSD1834, HSD1839, HSD 2543, HSD 2482, HSD 1840 and HSD 2550 were used as female lines, while Sinnar, Hjerat and Clemson spineless were used as male lines/testers. The crosses were conducted using standard crossing blocks, following the Standard Destructive Emasculation Techniques (DET) for emasculation and pollination. This process involved the use of cutters, forceps, tags, and paper bags, as outlined by Purewal and Randhawa (1947) and Udengwu (2007).Twenty-one F1 hybrids along with ten parents were laid out in complete randomized block design with three replications.

**Table 1. Accession name and origin**

|  |  |  |  |
| --- | --- | --- | --- |
| **No.** | **Name** | **Source of collection** | **Note** |
| 1 | HSD 1835 | Kadogli, South kordofan | Line |
| 2 |  HSD 1834  | Kadogli, South kordofan | Line |
| 3 | HSD 1839  | Kadogli, South kordofan | Line |
| 4 |  HSD 2543  | Kalilla, South Darfur  | Line |
| 5 |  HSD 2482  | Reaba, Sinner  | Line |
| 6 |  HSD 1840 | Kadogli, South Kordofan | Line |
| 7 |  HSD 2550  | Edelfirsan, South Darfur  | Line |
| 8 |  Sinnar  | Sinner, Sinner  | Tester |
| 9 | Hejirat | Hejirat, Sinner  | Tester |
| 10 |  Clemson Spineless | Seed Market (South Carolina, USA) | Tester |
|  |  |  |  |

Each plot consists of three meters long ridges. The space adopted was 75 cm between ridges and 30 cm between plants. Observations on the number of days to flowering were recorded on a plot basis, recording the number of days for the onset of flowering from the sowing date. Plant height (cm), length of pod pedicle (cm), length of pod(cm); number of nodes per plant, nodes to first flower and lateral branches are recorded as an average of ten plants selected randomly from each plot along the three replicates. Observations were analyzed using Analysis of Variance as described by Gomez & Gomez (1984) using the online software package Grapes 1.1.0 developed by Gopinath, et al., (2021) at Kerala Agricultural University. The analysis aimed to test the null hypothesis, which states that there are no significant differences among the various F1 populations (21 crosses) and their parental lines (10 lines), treating them as a total of 31 distinct treatments. The results of this analysis are presented in Table 2, showing the ANOVA outcomes. Only traits that recorded significant variance are advanced for Line × tester analysis. The variance is further divided into crosses, lines, testers and their interactions and presented in **Table 2**. The general combining ability (GCA) variance effects of the parents and the specific combining ability (SCA) variance effects of the hybrids were estimated using the line × tester analyses method described by Kempthorne (1957) and detailed by Singh & Chaudhary (1981) as per **Table 3** and **Table 4**. Dominance and additive variance were calculated as per the formula described in Singh & Chaudhary (1981) using inbreeding coefficient (F) as equal to (1) and presented along with the per cent contribution of lines, testers and their interaction in **Table 5.**

3. results and discussion

The analysis of variance (ANOVA) presented in (Table 2) for the line × tester analysis showed significant differences among treatments, crosses, and line × tester interactions for several traits, highlighting the presence of genetic variability and the potential for effective selection. Among the treatments, highly significant differences were observed at p ≤ 0.01 for plant height, pod pedicle length, and the number of lateral branches, while the number of days to flowering, number of nodes per plant, and pod length were significant at p ≤ 0.05. These results demonstrate substantial variation among the studied genotypes, which is essential for breeding programs aiming to improve these traits. For the crosses, significant differences were observed for plant height, pod length, and the number of nodes to the first flower, highlighting the role of specific parental combinations in influencing these growth parameters. In the line × tester interaction, significant differences were detected for plant height, pod length, and the number of lateral branches at both the 5% and 1% levels of significance, while the number of nodes to the first flower was significant at the 5% level. These interactions indicate that the performance of specific crosses varied based on the combination of parent lines and testers, underscoring the importance of specific combining ability (SCA) in shaping the expression of these traits. No significant variation was observed for any of the traits among the female lines as well as among testers, implying a relatively uniform and similar genetic contribution. The significant variation observed for traits such as plant height, number of nodes per plant and number of lateral branches across treatments, crosses, and line × tester interactions indicates the potential for identifying promising hybrids with desirable characteristics. These findings provide a strong foundation for selecting parent lines and crosses that contribute positively to the improvement of okra’s growth and earliness parameters. The significant variation in the number of days to flowering and the number of nodes per plant supports the presence of genetic diversity and the potential for selecting early-flowering and high-yielding hybrids. Conversely, the number of nodes to the first flower exhibited no significant differences, suggesting that this trait may be more influenced by environmental conditions than genetic factors. These findings align with previous studies by Habib & Al-Jubouri (2024); Ragheb & Helmy (2022); Olayiwola, et al. (2020), Joshi, et al. (2019) and Reddy et al. (2012a) which reported similar genetic patterns in okra hybrids. The observed genetic variation and the importance of SCA effects highlight the potential of hybrid breeding programs to exploit heterosis and develop superior okra cultivars with enhanced growth and yield traits. The significance of line × tester interactions across most traits suggests the importance of non-additive genetic effects, reinforcing the need for hybrid breeding to exploit specific combining ability (Reddy, et al., 2012a; Sugani et al., 2017; Matthew et al., 2018; Koli et al., 2020; Kumari et al., 2020 and Mundhe et al., 2023).

**Table 2. Mean sum square for line × tester analysis involving parents for earliness and growth parameters in okra**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of variation** | **Df** | **No. of days****to flowering** | **Plant height****(cm)** | **Length of pod Pedicle****(cm)** | **Length of pod****(cm)** | **Number of nodes per plant** | **No. of Nodes to the first flower** | **No. of Lateral branches** |
| **Treatments** | 30 | 4.9204\* | 83.4923\*\* | 0.1418\*\* | 1.0637\* | 4.8774\* | 2.4378 | 2.8165\*\* |
| **Crosses** | 20 | 5.0429 | 77.2457\*\* | 0.0801 | 1.4243 | 4.5540\*  | 1.9159 | 2.9968\*\* |
| **Lines/females** | 6 | 3.1799 | 76.9903 | 0.0696 | 1.3495 | 2.7355 | 0.9788 | 3.2116 |
| **Testers/males** | 2 | 8.3333 | 78.9801 | 0.1471 | 2.9163 | 3.1587 | 2.6825 | 3.4444 |
| **Line × tester** | 12 | 5.4259 | 77.0844\*\* | 0.0742 | 1.2130\*\* | 5.6958\* | 2.2566 | 2.8148\*\* |
| **Error** | 60 | 2.9204 | 22.7805 | 0.0575 | 0.4729 | 2.6247 | 3.0057 | 0.7756 |

Superscript asterisks on the value indicate statistical significance: \* for *P* = .05, \*\* for *P* = .01

**Table 3. Estimates of general combining ability effects of lines and testers**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **parent** | **No. of days****to flowering** | **Plant height****(cm)** | **Length of pod Pedicle****(cm)** | **Length of pod****(cm)** | **Number of nodes per plant** | **No. of Lateral branches** |
| **HSD 1835** | 0.048 | -1.444 | -0.038 | 0.186 | -0.730 | -0.476\* |
| **HSD1834** | 0.603 | -0.522 | 0.017 | 0.163 | 0.159 | -0.032 |
| **HSD 1839** | -0.841 | -2.322 | -0.105 | 0.397\* | -0.063 | 0.413 |
| **HSD 2543** | 0.603 | -3.033\* | -0.038 | -0.037 | -0.730 | 0.079 |
| **HSD 2482** | -0.063 | 4.311\*\* | 0.029 | -0.325 | 0.714 | -0.587\* |
| **HSD 1840** | 0.381 | -0.867 | -0.038 | -0.692\*\* | 0.381 | -0.476 |
| **HSD 2550** | -0.730 | 3.878\*\* | 0.173\* | 0.308 | 0.270 | 1.079\*\* |
| **Sinnar** | -0.238 | 0.341 | -0.033 | 0.354\* | 0.270 | 0.413\* |
| **Hjerat** | -0.476 | 1.746\* | 0.095\* | 0.035 | -0.444 | -0.016 |
| **Clemson spineless** | 0.714\* | -2.087\* | -0.062 | -0.389\*\* | 0.175 | -0.397\* |
| **S E (gca ) line** | 0.5696 | 1.591 | 0.0799 | 0.2292 | 0.5400 | 0.2936 |
| **S E (gca) tester** | 0.3729 | 1.042 | 0.0523 | 0.1501 | 0.3535 | 0.1922 |

Superscript asterisks on the value indicate statistical significance: \* for *P* = .05, \*\* for *P* = .01

**Table 4. Crosses with Favourable and Significant Specific Combining Ability (SCA)**

|  |  |
| --- | --- |
| **Parameter** | **Crosses with favorable and significant (SCA)** |
| **No. of days to flowering** | HSD2550×Hjerat (-2.41\*\*) |
| **Plant height (cm)** | HSD1835× Sinnar (5.69\*); HSD2482× Sinnar (5.10\*); HSD2550×Hjerat(9.37\*\*); HSD1839×Clemson spineless (6.70\*\*) |
| **Length of pod Pedicle (cm)** | HSD1834× Sinnar (0.24\*) |
| **Length of pod (cm)** | HSD2543× Sinnar(0.846\*) ; HSD1840×Clemson spineless(0.844\*) |
| **Number of nodes per plant** | HSD2482×Hjerat (2.00\*); HSD1839×Clemson spineless(1.825\*) |
| **No. of Lateral branches** | HSD2482× Sinnar(1.254\*\*); HSD1835×Hjerat(1.238\*\*); HSD1839×Clemson spineless(1.397\*\*) |

Superscript asterisks on the value indicate statistical significance: \* for *P* = .05, \*\* for *P* = .01

**Table 5. Estimates of genetic components of variance and per cent contribution of lines, testers and their interaction**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Trait** | **σ2gca** | **σ2sca** | **σ2gca / σ2sca** | **Contribution** |
| **Line (%)** | **Tester (%)** | **Interaction (%)** |
| **No. of days to flowering**  | -0.0100 | 0.8350 | -0.0120 | 18.91 | 16.53 | 64.56 |
| **Plant height (cm)** | 0.0042 | 18.1001  | 0.0002  | 29.9 | 10.22 | 59.88 |
| **Length of pod Pedicle (cm)** | 0.0002 | 0.0056 | 0.0333  | 26.06 | 18.37 | 55.57 |
| **Length of pod (cm)** | 0.0055  | 0.2467  | 0.0223 | 28.43 | 20.47 | 51.1 |
| **Number of nodes per plant** | -0.0297 | 1.0237 | -0.0290  | 18.02 | 6.94 | 75.04 |
| **No. of Lateral branches** | 0.0047 | 0.6797 | 0.0070 | 32.15 | 11.49 | 56.36 |

**3.1 Earliness (Number of Days to Flowering)**

The number of days to flowering varied significantly among the parental lines and testers (**Table 3**). Among the lines, HSD1839 exhibited the most favourable general combining ability effect (-0.841), indicating its potential for contributing to earliness in hybrid combinations. Among the testers, Clemson Spineless showed the highest positive GCA effect (0.714\*), suggesting its tendency toward delayed flowering. Among hybrid combinations (**Table 4**), HSD2550 × Hjerat shows the most favourable specific combining ability effect (-2.41\*\*). This suggests that this cross exhibits early flowering, a crucial trait for adapting to short growing seasons. The information on genetic components of variance and contributions of line, testers and their interactionare summarized in **Table 5.** The negative GCA variance and very high SCA variance indicate that non-additive gene action predominates in controlling this trait. The low GCA/SCA variance ratio further supports the limited influence of additive genetic effects. The high contribution of interaction (64.56%) highlights the importance of specific cross combinations. This suggests strong environmental or epistatic influences on flowering time. Hybrid breeding would be more effective than pure-line selection for improving early or synchronized flowering. The choice of parent combinations is crucial for maximizing favourable hybrid performance.

Early flowering in okra has been associated with enhanced adaptation to varying climatic conditions, evading of late season risk of insect pests and disease, earlier fruit set, Increased number of fruits per plant, an earlier start to harvest and new crop rotation and longer period for fruit development (Medagam, et al., 2012; Ragheb and Helmy, 2022).The HSD2550 × Hjerat cross exhibited a highly significant negative SCA effect (-2.41), indicating its potential as an early-flowering hybrid. This finding is consistent with the results reported by Yohanna (2023), Reddy et al. (2011), and Jaiprakashnarayan et al. (2008), who observed that specific crosses with negative SCA effects for days to flowering were strongly associated with earliness, supporting the pattern observed in this study.

**3.2 Plant height**

General combining ability values are presented in (**Table 3)**. This shows that HSD 2482 and HSD 2550 exhibited significant positive GCA effects (4.311\*\* and 3.878\*\*, respectively), indicating their strong potential for increasing plant stature in hybrid combinations. On the other hand, HSD 2543 showed a significant negative effect (-3.03\*), making it a candidate for reducing plant height. Among the testers, Hjerat demonstrated a significant positive effect (1.746\*), while Clemson Spineless had a significant negative GCA effect (-2.087\*), suggesting its role in reducing plant height. Among the crosses **(Table 4),** highly significant differences (**p ≤ 0.01**) were observed for plant height, with crosses such as HSD2482 × Sinnar (5.10\*), HSD1835 × Sinnar (5.69\*), HSD1839xClemson spineless (6.70\*\*) and HSD2550 × Hjerat (9.37\*\*) displaying positive SCA effects. The very high SCA variance relative to the GCA variance suggests that non-additive genetic effects—such as dominance and epistasis—play the primary role in determining plant height. Hybridization and exploitation of heterosis should be prioritized for enhancing plant height, as specific cross combinations outperform predictions based on parental averages. These crosses indicate a strong hybrid vigour for plant height. Estimates of genetic components of variancein **Table 5** recordedalow GCA/SCA ratio and confirmed the limited impact of additive gene action. The interaction effect (59.88%) is again dominant, while lines contribute more than testers, indicating that maternal effects or genetic background from the lines may play a larger role. Plant height is an important trait affecting okra yield and adaptability. Taller plants often produce more branches, leading to a greater number of nodes and higher fruit yield per plant (Reddy et al., 2012b; Reddy et al., 2013; Kumar & Reddy, 2016). Similarly, Ragheb and Helmy (2022) reported a strong positive correlation between plant height and yield. However, these traits should be addressed with caution, as excessive plant height can increase susceptibility to lodging. While no specific studies on okra have been reported, this issue has been well-documented in other crops (Mengistie & McDonald, 2023). Therefore, breeding okra varieties with an optimal plant height and balanced plant architecture could be a viable strategy to enhance yield while minimizing the risk of lodging. Similarly, several researchers identified parental lines with significant positive GCA values (Jagan et al., 2013b; Kumar et al., 2013b; Lokeshwari et al., 2018; Mundhe et al., 2023) and recommended crosses with desirable and significant SCA values (Kumar et al., 2021) for increased plant height in okra.

**3.3 Length of Pod Pedicle**

The estimates of general combining ability (GCA) presented in **Table 3** indicate that Line HSD 2550 demonstrated a significant positive GCA effect (0.173\*), highlighting its strong potential to enhance this trait. Among the testers, Hjerat also showed a positive contribution (0.095\*), suggesting its ability to improve pod pedicle length. Among hybrids presented in **Table 4**, HSD1834 × Sinnar exhibited the highest positive SCA effect (0.24\*). The low GCA variance and higher SCA variance presented in **Table 5,** indicate that non-additive gene action dominates the expression of pedicle length. A low GCA/SCA ratio supports this observation. Although interaction effects contribute the most (55.57%), the contributions of lines (26.06%) and testers (18.37%) suggest some influence of both parental types on this trait’s expression. The length of the pod pedicle in okra is an important agricultural trait (Matthew et al., 2018). A longer pedicle facilitates easier harvesting, reduces damage to pods and plants, and is beneficial in manual harvesting systems (Mritunjay et al., 2022). Variations in pedicle length add to the morphological diversity among okra genotypes and impact selection criteria in breeding programs (Mritunjay et al., 2022; Matthew et al., 2018). Additionally, pedicle size may influence pod orientation in the canopy, improving adaptability to environmental conditions, improving resistance to pests and diseases and hence improving yield (Mohammed, 2020). It also facilitates mechanical harvesting and hence improves production and avoids ergonomic hazards due to manual picking by workers on farms (Nalawade et al., 2017; Hukare, 2023). The trait should be treated with care as longer pedicles in heavy-bearing plants may influence stem strength and may lead to susceptibility to lodging.

**3.4 Pod Length**

HSD 1839 in **Table 3,** displayed a significant positive GCA effect (0.397\*), making it a favourable candidate for improving pod length. Tester Sinnar also showed a positive and significant GCA effect (0.354\*), supporting its use in enhancing this trait. Among crosses (SCA) values presented in **Table 4**, hybrid combinations HSD2543 × Sinnar (0.846\*) and HSD1840 × Clemson Spineless (0.844\*) demonstrated favourable SCA effects. Longer pods are a key trait favoured in commercial okra production, particularly in Sudan, where they are highly valued for their suitability in preparing traditional dried okra products. This preference is largely attributed to the association of longer pods with higher fibre content, elevated dry matter, and rich mucilage properties—qualities that enhance both the texture and consistency essential for Sudanese culinary practices. These characteristics not only meet consumer preferences but also reflect important quality parameters for market acceptance and processing efficiency. Mohammed (2020) found that longer pod length was associated with increased yield, consumer preference and market demand. Moreover, positive SCA effects for this trait were linked to high-yielding hybrid combinations, aligning with our results (ALKamal et al., 2011; Srivastava et al., 2008; Singh et al. 2009). The high SCA variance and low GCA/SCA ratio in **Table 5**, indicate a predominant role of non-additive gene effects in controlling pod length. The relatively balanced contributions of lines, testers, and interaction effects suggest a complex inheritance pattern, with both genetic backgrounds and specific cross combinations influencing this trait. Hybridization strategies should be emphasized, but careful selection of both lines and testers can improve the chances of obtaining superior pod length.

**3.5 Number of Nodes per Plant**

There are no significant positive GCA effects observed for this trait among lines and testers (**Table 3**). HSD 2482 exhibited a notable positive GCA effect (0.714), suggesting its potential to increase the number of nodes per plant. The number of nodes per plant is a significant factor in okra morphology and production, as it is directly proportional to the number of leaves and fruits per plant, and consequently, the fruit yield (Jagan, et al., 2013a; Patel, et al., 2021; Adaveppa, 2024;). Among crosses (SCA) values in (**Table 4)** indicate that the hybrid combinations HSD2482 × Hjerat (2.00\*) and HSD1839 × Clemson Spineless (1.825\*) exhibited significant SCA effects for the number of nodes per plant. Many studies (Rashwan, 2009; Prakash et al., 2012; Thirupathi et al., 2012; Akotkar et al., 2014; Kerure & Pitchaimuthu, 2019; Abed et al., 2020; Devi et al., 2020; Bharatkumar et al., 2021; Adaveppa, 2024), have reported that hybrid crosses often exhibit higher mean values for the number of nodes per plant compared to their parental lines. This increase is largely attributed to the expression of heterosis, which enhances vegetative growth and increased fruit-bearing sites if coupled with short internode length can enhance yield potential drastically. The findings of the present study align closely with these results, confirming the positive influence of heterosis on the number of nodes per plant. The negative GCA variance and high SCA variance in (**Table 5)**, suggest that non-additive gene action plays a predominant role in the number of nodes per plant. The extremely high interaction contribution (75.04%) emphasizes the importance of specific cross combinations. The low contributions from both lines and testers indicate that the general performance of individual parents has minimal influence on this trait. Hybrid breeding focused on specific cross combinations will yield the best results for increasing the number of nodes per plant. Additive genetic effects are largely irrelevant for this trait.

**3.6 Number of Lateral Branches**

Estimates of general combining ability in (**Table 3),** revealed that line HSD 2550 stood out with a highly significant positive GCA effect (1.079\*\*), highlighting its potential in increasing plant branching, which is often associated with higher yield. Among testers, Sinnar also showed a significant positive effect (0.413\*), indicating its usefulness in boosting lateral branch development. Specific combing ability estimates for hybrid combinations (**Tables 4**), identified crosses such as HSD2482 × Sinnar (1.254\*\*), HSD1835 × Hjerat (1.238\*\*), and HSD1839 × Clemson Spineless (1.397\*\*), which exhibited highly significant positive SCA effects (**p ≤ 0.01**), indicating their potential for enhanced branching and greater pod production. These results suggest the importance of non-additive genetic effects in controlling this trait (Jonah et al. (2015), Wakode et al.(2016), Satish et al. (2017), Sugani et al. (2017), Koli et al. (2020), Kumari et al. (2020) and Mundhe et al. (2023). The ability of these hybrids to produce more lateral branches aligns with findings from Matthew et al. (2018), and Reddy, et al. (2012a), who reported that increased branching is directly linked with higher fruit yield in okra hybrids. This is also consistent with the observation recorded on SCA variance and GCA variance in (**Table 5)**. The much higher (SCA) variance and very low GCA/SCA ratio suggest that non-additive genetic effects predominantly influence the number of lateral branches. The relatively high contribution of lines (32.15%) compared to testers (11.49%) suggests a notable maternal influence on this trait's expression. The ability of these hybrids to produce more lateral branches aligns with findings of Matthew et al. (2018), and Reddy, et al. (2012a), who reported that increased branching is directly linked with higher fruit yield in okra hybrids. Hybridization remains the most effective strategy, but selecting superior lines could help improve outcomes for lateral branch development.

4. Conclusion

This study demonstrated the significant genetic variability and the importance of both general combining ability (GCA) and specific combining ability (SCA) effects in the expression of key agronomic traits in Sudanese okra [*Abelmoschus esculentus* (L.) Monech]. The predominance of non-additive gene action for most traits underscores the potential of hybrid breeding to exploit heterosis and develop high-yielding, early-maturing, and well-adapted okra cultivars. Among the parental lines, HSD1839 and HSD2550 exhibited strong (GCA) effects for earliness and plant height, making them ideal candidates for hybridization programs. The testers Hjerat and Sinnar demonstrated valuable contributions to key traits, particularly for plant height and lateral branching. The hybrid HSD2550 × Hjerat emerged as the most promising combination for early flowering, while HSD2482 × Sinnar and HSD1839 × Clemson Spineless showed superior (SCA) effects for plant height and lateral branching, respectively. These hybrids displayed high potential for enhancing growth parameters and yield traits, emphasizing the importance of specific parental combinations in breeding programs. For future breeding efforts, prioritizing hybrids with strong (SCA) effects and parental lines with favourable (GCA) values is essential.

Further research should focus on navigating the allopolyploid nature of okra in hybrid breeding by using genetically diverse and cytogenetically compatible parental lines to ensure proper chromosome pairing and minimize segregation distortion. Techniques like controlled pollination, marker-assisted selection, and backcrossing are essential for stabilizing desirable traits, while multi-environment evaluation ensures broad adaptability. Advanced tools such as genomic selection and ploidy verification will further enhance precision and stability, accelerating the development of improved okra varieties.

**Disclaimer (Artificial intelligence)**

*We acknowledge the use of artificial intelligence (AI)-based tools in the preparation of this manuscript for language enhancement, proofreading, and reference management. Specifically, Grammarly for linguistic and Zotero (7) for organizing and formatting references. The intellectual content, analysis, and conclusions of this manuscript remain entirely the work of all the authors. All AI-assisted contributions were limited to technical support functions and did not replace the authors' original input or critical thinking.*

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