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Character Association and Path Analysis for Yield and Yield Contributing Traits in Sesame (*Sesamum indicum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Sesame is among the oldest oilseed crop and it is commonly designated as Queen of oilseeds crops owing to the superior quality of its oil, which exhibit strong to oxidative rancidity. Yield is a highly complex quantitative trait governed by multiple genes and markedly influenced by

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environmental factors. Owing to its polygenic nature, direct selection for yield alone may not bring about substantial genetic gain unless the genetic contribution of its component traits is properly considered. Hence, understanding the association between yield and its related attributes is essential for improving selection efficiency. Path coefficient analysis provides a powerful tool in this regard, as it partitions the correlation coefficients into direct and indirect effects, thereby offering deeper insights into the nature of relationships among traits. While correlation analysis measures the strength of association between traits, path analysis reveals the extent to which each trait influences yield directly or through other characters. This approach assists breeders in identifying the most important yield-contributing traits and facilitates effective selection strategies in crop improvement programs. The current study focused on examining the relationship between seed yield and its contributing traits in Sesame. A total of 28+2 genotypes were evaluated at the Oilseeds Research Station, College of Agriculture, Latur during Rabi 2024–2025 using a randomized block design with two replications. The trial was sown on November 28, 2024, at a spacing of 30 × 10 cm. The analysis clearly indicate that number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule and 1000 seed weight demonstrated positive and significant associations with seed yield per plant at either the genotypic level, phenotypic level or both And the study of path coefficient analysis revealed that the characters number of branches per plant and number of capsules per plant exerted positive direct effects on seed yield per plant at the genotypic level. Furthermore, Correlation and path analysis revealed that number of branches per plant, number of capsules per plant, capsule length, and 1000-seed weight are the major yield-contributing traits, and these should be prioritized in selection programs to develop high-yielding sesame genotypes.

Keywords: Correlation coefficient analysis; path coefficient analysis; indirect effect; positive significant; genotypic; phenotypic.

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the oldest cultivated oilseed crops and belongs to the family Pedaliaceae, possessing a diploid chromosome number of 2n = 26. The genus *Sesamum* comprises over 30 species, among which *S. indicum* is the most widely cultivated (Nayar & Mehra, 1970). It holds significant economic value due to its high oil content ranging between 40–60% and protein content of 20–40%. Referred to as the "Queen of Oilseeds," sesame oil is renowned for its superior quality and stability, attributed to a balanced composition of saturated and unsaturated fatty acids, along with natural antioxidants that enhance its shelf life. The crop’s primary center of origin is thought to be in Asia or East Africa, with secondary centers of diversity likely located in Afghanistan and Ethiopia (Vavilov, 1951).

Sesame, also known by various regional names such as Benne, Gingelly, Til, Tila, Simsim and Gergelim. It is primarily cultivated in warm regions across the tropics and subtropics. Sesame is typically grown on plains up to an elevation of 1200 meters, in areas receiving approximately 500 mm of annual rainfall. Optimal conditions for rapid germination, early growth and flower development include temperatures ranging between 25°C and 27°C (ICAR-Indian Institute of Oilseeds Research, 2014).

Seed yield in sesame is a complex quantitative trait that is governed by the cumulative effect of various morphological and yield-attributing characters such as plant height, number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, and 1000-seed weight. Since yield is polygenic and highly influenced by environmental factors, direct selection for yield alone is often misleading and ineffective. Therefore, a better understanding of the association between yield and its related traits is essential for devising efficient selection criteria.

Correlation analysis provides an estimation of the degree and direction of association between different traits, thereby helping to identify key yield-contributing characters. However, correlation alone does not establish the true causal relationship among traits. Path coefficient analysis, an extension of correlation, partitions the correlation coefficients into direct and indirect effects, thus revealing the actual contribution of each trait to yield. This makes it a powerful tool for plant breeders to identify traits with the greatest influence on yield, either directly or through their indirect associations.

Therefore, the study of correlation and path coefficient analysis in sesame is crucial to determine the nature and extent of relationships among yield and yield-attributing traits. This will help in formulating effective selection indices and breeding strategies aimed at genetic improvement and yield enhancement in sesame.

2. MATERIAL AND METHODS

2.1 Experimental Site and Experimental Design

The present investigation was conducted at the Oilseeds Research Station, Latur, Maharashtra, India, during the *Rabi* season of 2024-25 under normal irrigated conditions. The experimental material consisted of 28 Genotypes and 2 checks, which were analyzed using a Randomized Block Design with two replications. The crop was sown using the line sowing method. Recommended fertilizers and cultural practices were followed to ensure the growth of healthy crops. Morphological observations of 10 quantitative characters were recorded by randomly selecting 5 plants from each plot and replication. Each genotype was sown in rows, each 3 meters in length, with a spacing of 30 cm between rows and 10 cm between plants. Border rows were planted on all sides of the experimental plots to prevent border effects. All recommended practices were adhered to for optimal crop growth, and the plot size was 4 x 0.60 m².

2.2 Characters Studied

Morphological observations for 10 quantitative traits were recorded by randomly selecting 5 plants from each plot and replication. The traits measured included days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000-seed weight (g), length of capsule (cm), oil content (%), and seed yield per plant (g). The number of days to 50% flowering was recorded when half the plants in each plot had flowered, while the days to maturity were noted when the plants reached physiological maturity. Plant height was measured from the base to the tip of the tallest stem, and the number of branches per plant, number of capsules per plant, and number of seeds per capsule were counted to evaluate reproductive potential. 1000-seed weight was determined by weighing a random sample of 1000 seeds, and the Oil content was determined using the Soxhlet extraction method, and seed yield per plant was measured by weighing the seeds harvested from each plant.

2.3 Statistical Analysis

Genotypic and phenotypic correlation coefficients were estimated using variance and covariance components following the procedure described by Al-Jibouri et al. (1958). Path coefficient analysis, employed to partition the direct and indirect effects of different traits on the dependent variable, was performed according to the method proposed by Dewey and Lu (1959). All statistical analyses were executed using R software (version 4.5.1).

3. RESULTS AND DISCUSSION

3.1 Correlation Coefficient Analysis

Genetic associations between traits may result from either pleiotropy or linkage. Pleiotropy occurs when a single gene governs multiple traits, while linkage arises from the proximity of different genes controlling separate traits on the same chromosome. In both situations, the resulting correlations can be either positive or negative, depending on whether the genes involved promote or suppress the expression of the related traits. The correlation coefficient measures the magnitude and direction of these associations, thereby providing insights into trait interrelationships and their collective impact on yield.

The present study, genotypic correlation coefficients were generally higher than their corresponding phenotypic correlation coefficients for most traits, indicating their significant influence on seed yield (Tables 1 and 2). As suggested by Singh *et al.* (2024), indirect selection is particularly effective for traits with low heritability. Such correlation analyses serve as an important tool for breeders, offering guidance in identifying and selecting traits that can enhance both yield and quality in sesame.

The trait seed yield per plant exhibited positive and highly significant genotypic correlations with all major yield-contributing traits, indicating its polygenic nature and strong dependence on multiple agronomic characters. At the genotypic level, strong positive correlations were recorded with number of branches per plant (r_g = 0.7827), number of capsules per plant (r_g = 0.8354), number of seeds per capsule (r_g = 0.9204), length of capsule (rg = 0.936), 1000 seed weight (rg = 0.9486) and oil content (rg = 0.9793).

At the phenotypic level, the trait also showed strong and significant positive correlations with number of branches per plant (rp = 0.6991), number of capsules per plant (rp = 0.7586), number of seeds per capsule (rp = 0.7796), capsule length (rp = 0.7501), 1000 seed weight (rp = 0.8647) and oil content (rp = 0.9802). These consistent and significant associations at both genotypic and phenotypic levels confirm the direct contribution of these component traits to seed yield.

The trait days to 50% flowering exhibited negative correlations of flowering time with yield traits These findings are in line with the reports of Pohekar *et al.* (2023) and Takele *et al.* (2021), The character days to maturity exhibited a negative correlation with most of the yield-contributing traits suggesting that early maturing genotypes tend to be more productive Similar results have been reported by Ahmed *et al.* (2022) and Takele *et al.* (2021) The trait number of branches per plant exhibited positive and highly significant genotypic correlations with key yield-contributing traits The findings are supported by earlier reports from Ahmed *et al.* (2022) and Kehie *et al.* (2020); Kalaiyarasi *et al.(*2019).

3.2 Path Analysis

The association between yield and its component traits may at times be misleading, as simple correlation does not always reflect the true nature of their relationship. This is because multiple traits simultaneously influence yield, which can either inflate or mask the actual strength of association. To address this, path coefficient analysis is employed to partition the total correlation into direct and indirect effects. The combined use of correlation and path analysis thus provides a clearer understanding of the contribution of individual traits to yield, thereby facilitating more precise and effective selection in breeding programs.

The greater direct effects observed in phenotypic path coefficients compared to genotypic path coefficients indicate a considerable influence of genotype–environment interactions on the expression of traits. This observation is further substantiated by the results of the path analysis presented in Tables 3 and 4 and Figs. 1 and 2.

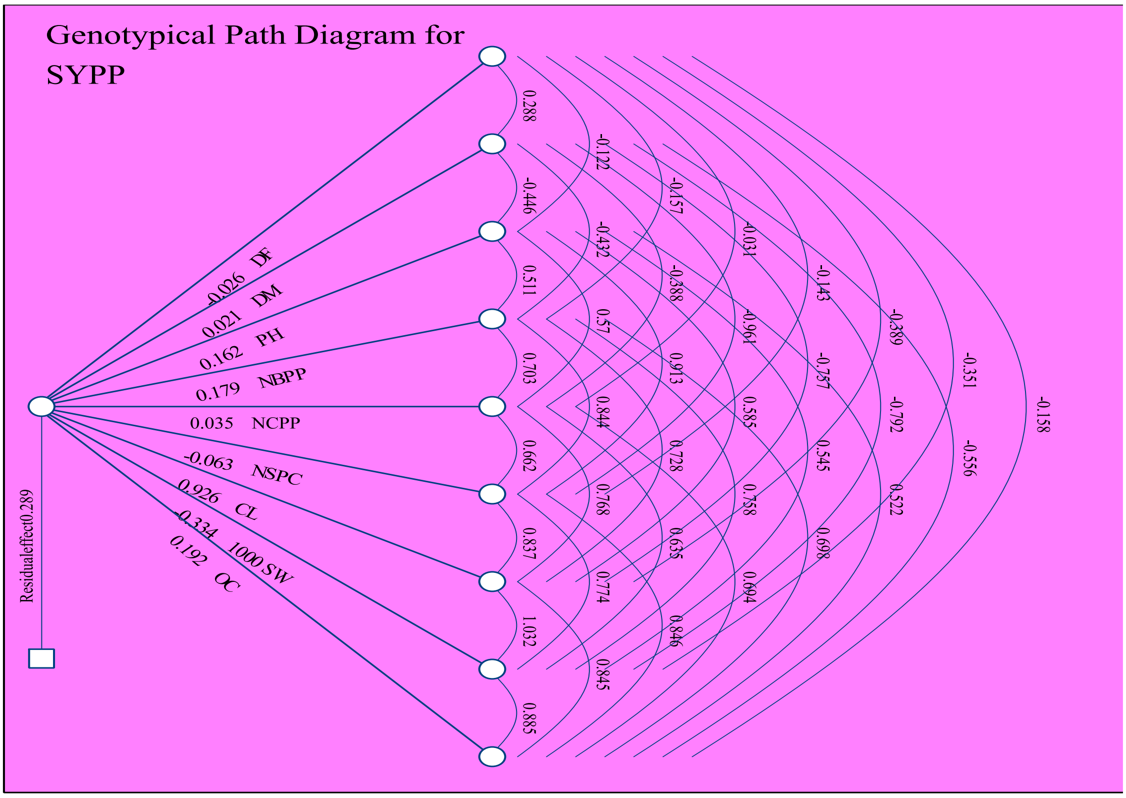

Fig. 1. Genotypic path analysis for direct (diagonal) and indirect (off diagonal) effects of yield components on seed yield in sesame

Table 1. Phenotypic correlation coefficients among seed yield and yield contributing traits in sesame

Characters	Days to 50 % Flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of capsules per plant	No. of seed per capsule	Length of capsule (cm)	1000 Seed weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50 % flowering	1 **	0.255 *	-0.1232	-0.1575	-0.0019	-0.0947	-0.3718 **	-0.308 *	-0.2742 *	-0.301
Days to maturity		1 **	-0.4214 **	-0.344 **	-0.1849	-0.535 **	-0.5873 **	-0.5415 **	-0.5327 **	-0.5744 **
Plant height (cm)			1 **	0.4395 **	0.4467 **	0.6103 **	0.4674 **	0.4386 **	0.562 **	0.6099 **
No. of branches per plant				1 **	0.5932 **	0.4706 **	0.6796 **	0.6035 **	0.6282 **	0.6991 **
No. of capsules per plant					1 **	0.4583 **	0.6375 **	0.5473 **	0.6999 **	0.7586 **
No. of seed per capsule						1 **	0.5471 **	0.5424 **	0.7037 **	0.7796 **
Length of capsule (cm)							1 **	0.8155 **	0.8038 **	0.8647 **
1000 seed weight(g)								1 **	0.7458 **	0.8488 **
Oil content (%)									1 **	0.8336 **
Seed yield per plant										1 **

** and ** Significance at 5 and 1 per cent level, respectively*

Table 2. Genotypic correlation coefficients among seed yield and yield contributing traits in sesame

Characters	Days to 50% Flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of capsules per plant	No. of seed per capsule	Length of capsule (cm)	1000 seed weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50% flowering	1 **	0.2876	-0.1216	-0.1569	-0.0313	-0.1426	-0.3892 *	-0.3531	-0.3324	-0.3326
Days to maturity		1 **	-0.4462 *	-0.4321 *	-0.3882 *	-0.9609 **	-0.7571 **	-0.8007 **	-0.634 **	-0.6314 **
Plant height (cm)			1 **	0.5114 **	0.57 **	0.913 **	0.5853 **	0.5504 **	0.6692 **	0.6692 **
No. of branches per plant				1 **	0.7034 **	0.8439 **	0.7283 **	0.7542 **	0.7813 **	0.7827 **
No. of capsules per plant					1 **	0.6624 **	0.7676 **	0.6353 **	0.8349 **	0.8354 **
No. of seed per capsule						1 **	0.8369 **	0.7835 **	0.922 **	0.9204 **
Length of capsule(cm)							1 **	1.0357 **	0.9348 **	0.936 **
1000 seed weight(g)								1 **	0.9793 **	0.9802 **
Oil content (%)									1 **	0.8511 **
Seed yield per plant (g)	-									1 **

** and ** Significance at 5 and 1 per cent level, respectively*

Table 3. Phenotypic direct and indirect effects of various traits on seed yield per plant in sesame

Characters	Days to 50 % Flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Number of seed per capsule	Length of capsule (cm)	1000 seed weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50 % flowering	**-0.1459**	-0.0392	0.0179	0.0229	0.0022	0.0164	0.0554	0.0476	0.0226	-0.301
Days to maturity	0.0268	**0.0997**	-0.0431	-0.0381	-0.027	-0.0686	-0.0659	-0.0643	-0.0522	-0.5744 **
Plant height (cm)	0.003	0.0105	**-0.0242**	-0.0114	-0.0121	-0.0175	-0.0126	-0.0117	-0.0119	0.6099 **
Number of branches per plant	0.0091	0.0221	-0.0273	**-0.0579**	-0.0372	-0.0354	-0.0407	-0.0389	-0.0378	0.6991 **
Number of capsules per plant	-0.0049	-0.0866	0.1604	0.2058	**0.3205**	0.1704	0.2229	0.1868	0.2084	0.7586 **
Number of seed per capsule	-0.0432	-0.2648	0.2772	0.2348	0.2045	**0.3846**	0.2516	0.2401	0.2675	0.7796 **
Length of capsule (cm)	0.001	0.0017	-0.0013	-0.0018	-0.0018	-0.0017	**-0.0025**	-0.0023	-0.002	0.8647 **
1000 seed weight (g)	-0.1274	-0.2519	0.1887	0.2627	0.2277	0.2439	0.3558	**0.3906**	0.3133	0.8488 **
Oil content (%)	-0.0195	-0.0659	0.0617	0.0821	0.0818	0.0875	0.1008	0.1009	**0.1258**	0.8336 **

Residual (P): 0.3024 (dark figure denotes direct effect)

Table 4. Genotypic direct and indirect effects of various traits on seed yield per plant in sesame

Characters	Days to 50 % Flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Number of seed per capsule	Length of capsule (cm)	1000 seed weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50 % flowering	**-0.0256**	-0.0074	0.0031	0.004	0.0008	0.0036	0.01	0.009	0.004	-0.3326
Days to maturity	0.0061	**0.0212**	-0.0094	-0.0091	-0.0082	-0.0203	-0.016	-0.0168	-0.0118	-0.6314 **
Plant height (cm)	-0.0197	-0.0723	**0.1621**	0.0829	0.0924	0.148	0.0949	0.0883	0.0845	0.6692 **
Number of branches per plant	-0.0281	-0.0773	0.0915	**0.1789**	0.1258	0.1509	0.1303	0.1355	0.1249	0.7827 **
Number of capsules per plant	-0.0011	-0.0136	0.02	0.0246	**0.035**	0.0232	0.0269	0.0222	0.0243	0.8354 **
Number of seed per capsule	0.009	0.061	-0.0579	-0.0535	-0.042	**-0.0635**	-0.0531	-0.0491	-0.0537	0.9204 **
Length of Capsule(cm)	-0.3604	-0.7011	0.542	0.6744	0.7107	0.7749	**0.926**	0.9556	0.7828	0.936 **
1000 seed weight(g)	0.1174	0.2646	-0.182	-0.2531	-0.2121	-0.2585	-0.3448	**-0.3341**	-0.2957	0.9802 **
Oil content (%)	-0.0303	-0.1065	0.1	0.1338	0.133	0.162	0.162	0.1696	**0.1916**	0.8511 **

Residual (G): 0.2886 (dark figure denotes direct effect)

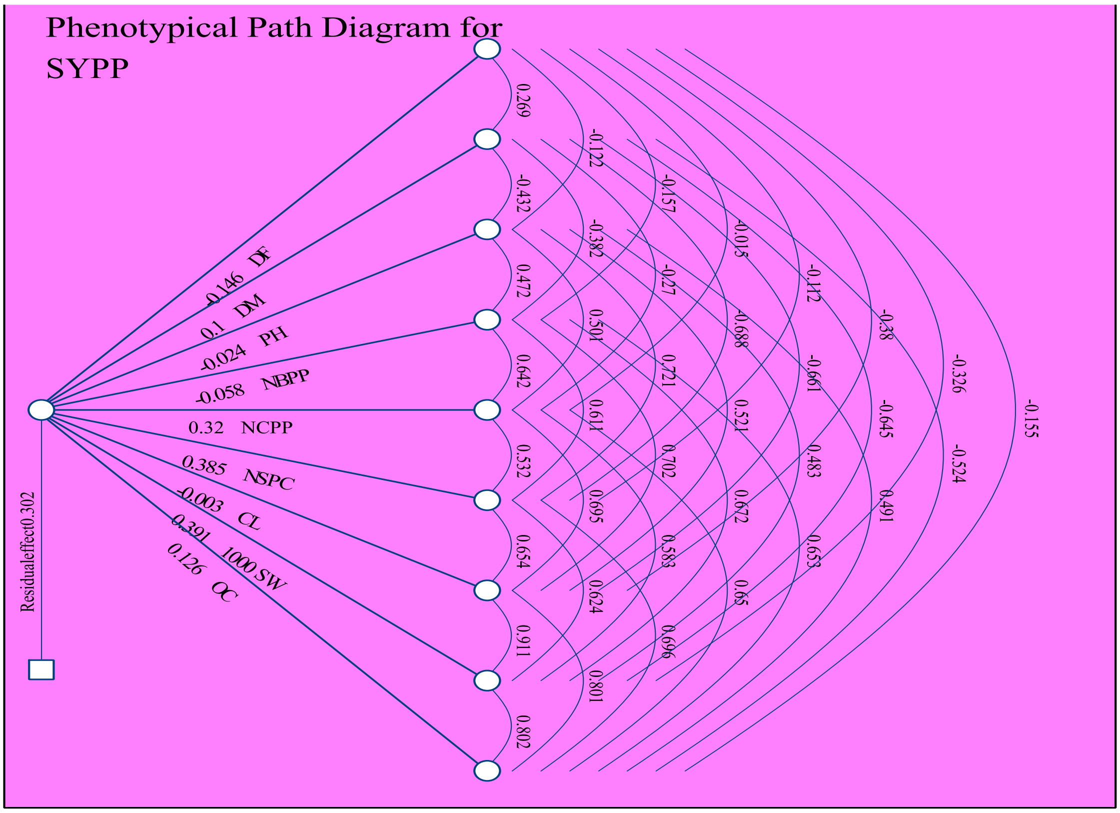

Fig. 2. Phenotypic path analysis for direct (diagonal) and indirect (off diagonal) effects of yield components on seed yield in sesame

The direct effect of the phenotypic path coefficient value is found to be greater for the majority of the traits when compared to the genotypic path coefficient value. This suggests a significant genotype × environment interaction for the traits expressed. The findings of the path analysis are presented in Tables 3 and 4 and Figs. 1 and 2 revealed that, at the genotypic level, the trait exerting the maximum positive direct effect on seed yield per plant was the length of capsule (0.926), oil content (0.1916), number of branches per plant (0.1789), plant height (0.1621),Traits such as days to maturity (0.0212), number of capsule per plant (0.035) had smaller positive direct effects. These results are in agreement with the findings of Kumar *et al.* (2022), Sasipriya *et al.* (2018); Nevani *et al.* (2022); Disowja *et al.* (2020); Kante *et al.* (2022).

At the phenotypic level, the highest direct effect was recorded for the 1000-seed weight (0.3906) followed by number of seeds per capsule (0.3846), number of capsules per plant (0.3205), oil content (0.1258), and Smaller direct effects were observed for days to maturity (0.09).

The character days to 50 per cent flowering exhibited a negative direct effect on seed yield per plant at both genotypic (-0.3326) and phenotypic (-0.3010) levels These results are in agreement with the findings of Kumar *et al.* (2022), Sasipriya *et al.* (2018) and Nevani *et al.* (2022); The character number of branches per plant exhibited a highly significant and strong positive correlation with seed yield per plant at both genotypic (0.7827) and phenotypic (0.6991) levels Similar findings were also reported by Kumar *et al*. (2022), Sasipriya *et al.* (2022) and Nevani *et al.* (2022). The character capsule length showed a highly significant and strong positive correlation with seed yield per plant at both genotypic (0.9360) and phenotypic (0.8647) levels with residual effect (G): 0.2886 and(P): 0.3024. These results are supported by earlier findings of Disowja *et al.* (2020); Reddy *et al*. (2020) and Madhu *et al.* (2023).

4. CONCLUSION

The present study reveals that Seed yield per plant exhibited a positive association with traits such as capsule length, number of seeds per capsule, plant height, number of branches per plant, number of capsules per plant and 1000-seed weight. These traits can therefore be considered as reliable selection criteria for improving yield. Hence, applying selection pressure on any of these characters could lead to the development of high-yielding genotypes. The traits number of branches per plant and number of capsules per plant exhibited a strong positive direct influence on seed yield per plant and can therefore be simultaneously targeted in selection strategies aimed at enhancing seed yield.

From the present study, it can be concluded that the characters number of branches per plant, number of capsules per plant, length of capsule, and 1000 seed weight are major yield contributing characters. Therefore, due emphasis should be given to these traits in formulating the criterion in the selection programme to evolve high yielding genotypes of sesame.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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