



# Genetic Variability Studies 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 one of the oldest oilseed crops cultivated globally and is renowned for its high-quality oil, which possesses excellent resistance to oxidative rancidity. Despite its nutritional and economic importance, genetic improvement in sesame has lagged behind other oilseed crops, primarily due to its narrow genetic base, indeterminate growth habit, and limited research focus. The productivity of sesame remains low and stagnant in many regions, which underscores the need for systematic genetic studies to identify and utilize promising traits for crop improvement. Therefore, assessing

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the extent of genetic variability, heritability, and inter-trait relationships is essential for developing efficient breeding strategies aimed at enhancing seed yield and its contributing traits. The present investigation was undertaken to assess genetic variability, heritability, and genetic advance for yield and its contributing traits in sesame. A total of 30 genotypes (28 genotypes and 2 check varieties) 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 genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from low to high. The lowest GCV and PCV were observed for traits such as oil content, days to maturity, plant height, and number of seeds per capsule; moderate values were recorded for traits like number of capsules per plant, 1000-seed weight, and days to 50% flowering. In contrast, the highest GCV and PCV values were noted for seed yield per plant, number of branches per plant, and capsule length. All traits exhibited high heritability, with the highest values for days to 50% flowering, oil content, capsule length, number of branches per plant, and seed yield per plant. These findings suggest the predominance of additive genetic effects for these traits. Therefore, these traits represent promising targets for direct selection in breeding programs. In conclusion, the genotypes exhibited substantial genetic variability for yield and related traits, offering significant potential for improvement in future breeding efforts.

**Keywords:** Genetic variability; heritability; randomized block design; genetic advance.

## 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 (Dasari et al., 2021). 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, is a self-pollinated crop belonging to the family Pedaliaceae, with a chromosome number of  $2n = 26$  (Kumar & Kumari, 2022). 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.

Improving sesame yield is a complex challenge due to the inheritance patterns of key traits,

which are governed by both additive and non-additive gene actions. Understanding genetic parameters such as variability, heritability, and genetic advance is essential for the development of high-yielding sesame varieties. This study aims to assess the genetic variability, heritability, and genetic advance of key traits related to yield and quality in sesame, with the ultimate goal of enhancing productivity and addressing existing yield gaps.

This research investigates 28+2 genotypes of sesame, selected for their potential to improve seed yield and other critical agronomic traits. The primary traits under investigation include seed yield, oil content, and plant height, all of which are important for improving overall crop productivity. By examining the genetic variability and heritability of these traits, this study seeks to identify superior genotypes that can be utilized in future breeding programs. The results will provide valuable insights into the development of high-yielding sesame varieties, contributing to advancements in breeding techniques and optimizing productivity, particularly in regions such as India, where sesame yield remains suboptimal.

## 2. MATERIAL AND METHODS

### 2.1 Experimental Site and Experimental Design

The present study was carried out at the Oilseeds Research Station, College of Agriculture Latur, during the *Rabi* season of

2024–25 under standard irrigated conditions. The experimental material comprised 28 genotypes along with 2 checks, laid out in a Randomized Block Design (RBD) with two replications. Sowing was done using the line sowing method. Recommended doses of fertilizers and standard agronomic practices were followed to ensure healthy crop growth. Observations for 10 quantitative morphological traits were recorded by randomly selecting 5 plants from each plot in both replications. Each genotype was sown in rows 3 meters long, with a spacing of 30 cm between rows and 10 cm between plants. Border rows were planted around the experimental area to minimize border effects. The plot size was maintained at 4 m × 0.60 m, and all necessary practices were followed to promote optimal crop development.

## 2.2 Characters Studied

Morphological observations for 10 quantitative traits were recorded by randomly selecting 5 plants from each plot in both replications. The traits evaluated 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), harvest index (%), oil content (%), and seed yield per plant (g). Days to 50% flowering were recorded when 50% of the plants in each plot had flowered, while days to maturity were noted when the plants reached physiological maturity. Plant height was measured from the base of the plant to the tip of the tallest stem. The number of branches per plant, number of capsules per plant, and number of seeds per capsule were counted to assess reproductive potential. The 1000-seed weight was obtained by weighing a random sample of 1000 seeds. Harvest index was calculated as the ratio of seed yield to total plant biomass and expressed as a percentage. Oil content was estimated using the Soxhlet extraction method, and seed yield per plant was recorded by weighing the seeds harvested from each selected plant.

## 2.3 Statistical Analysis

The overall mean values for various traits were subjected to statistical analysis. Analysis of variance (ANOVA) was performed using the Randomized Block Design (RBD) method, as described by Panse and Sukhatme (1985). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formula proposed by Burton

and Devane (1953). Estimates of heritability and genetic advance as a percentage of the mean (GAM) were also computed. According to the classification by Sivasubramanian and Madhavamenon (1973), both phenotypic and genotypic coefficients of variation are categorized as high (>20%), moderate (10–20%), and low (<10%). Heritability ( $h^2$ ) estimates were classified by Johnson et al. (1995) as low (0–30%), medium (30–60%), and high (>60%). Similarly, genetic advance as a percentage of mean was categorized by Johanson et al. as low (<10%), moderate (10–20%), and high (>20%). All statistical analyses were conducted using R software version 4.5.1

## 3. RESULTS AND DISCUSSION

### 3.1 Analysis of Variance

The analysis of variance and the mean performance of the sesame genotypes for various traits are presented in Table 1. The results revealed that the mean sum of squares due to genotypes was highly significant for all the traits studied. This indicates the presence of substantial genetic variability among the genotypes.

Significant differences were observed among genotypes for all characters, including 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), capsule length, oil content (%), and seed yield per plant (g). The wide range of variability found for yield and its component traits highlights considerable potential for genetic improvement, where selection for one trait could lead to simultaneous enhancement of others. Similar findings were reported by Rajitha et al. (2021), Akkiligunta et al., (2024).

### 3.2 Mean Performance

Based on the mean performance, the highest seed yield per plant was recorded in genotypes JLS-1411-1-1 (14.60 g) and TS-13 (14.60 g), followed by TLT-13-1 (13.95 g), JLS-1417-4-3 (13.60 g), and JLS-1512-35-2 (13.55 g), highlighting their potential as high-yielding genotypes for future varietal improvement programs. Similarly, the highest oil content was noted in JLS-1512-35-2 (48.50%), followed by TLT-10 (48.25%), JLS-1411-1-1 (47.65%), and TS-13 (47.65%), suggesting these genotypes as promising candidates for improving oil quality in sesame.

Notably, early flowering was observed in LT-109 (41.50 days), TLT-12 (43 days), LT-105 (47 days), and LT-111 (47 days). These early flowering genotypes are particularly valuable in regions prone to terminal drought stress, as they allow the crop to complete its reproductive phase before adverse environmental conditions set in, thereby contributing to yield stability under moisture-limited environments.

Regarding maturity, genotypes such as TS-50 (91.50 days), TS-110 (91.50 days), TLT-09 (93 days), TLT-05-2 (93 days), and TLT-13-1 (93 days) exhibited early maturity. These genotypes are suitable for early harvesting and can support double cropping systems or post-rainy season cultivation, ultimately enhancing cropping intensity and farm profitability.

Additionally, dwarf plant height was recorded in TS-113 (79.50 cm), TLT-7 (90 cm), LT-107 (92 cm), LT-111 (92.50 cm), and JLT-408 (93.60 cm). Dwarf genotypes are beneficial as they offer better lodging resistance under high-input conditions and are more suitable for dense planting, improving plant stand stability and potentially increasing yield per unit area.

### 3.3 Genotypic and Phenotypic coefficient of Variation

Variance is a statistical measure that reflects the extent of variability observed in quantitative traits within a population. While phenotypic variance represents the total observed variation, it does not accurately indicate the portion that can be fixed in subsequent generations. In contrast, genotypic variance accounts for the heritable portion of variation that can be passed on and fixed through selection. Environmental variance, however, varies across locations and cannot be inherited or fixed.

High values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for seed yield per plant (GCV = 19.01%, PCV = 19.98%), indicating substantial genetic variability with minimal environmental influence, making this trait highly amenable to improvement through simple selection methods similar finding reported by Saravanan et al. (2020), Kumhar and Bisen (2021). Similarly, the number of branches per plant recorded high GCV (19.31%) and PCV (20.40%), suggesting sufficient scope for effective selection Vinishree et al. (2013), Patil and Loksha (2018), Capsule length also exhibited high variability, with GCV and PCV

values of 18.20% and 18.78%, respectively, indicating strong genetic diversity and stability across environments Singh et al. (2024)). Moderate estimates of GCV and PCV were noted for the number of capsules per plant (GCV = 12.21%, PCV = 13.17%), suggesting a moderate level of variability suitable for genetic enhancement similar findings reported by Vamshi et al., (2021). Likewise, 1000-seed weight displayed moderate variability (GCV = 12.28%, PCV = 13.34%), indicating good potential for improvement through selection (Sasipriya et al. (2022). Days to 50% flowering showed moderate GCV (11.91%) and PCV (12.16%), reflecting stable inheritance and limited environmental influence similar findings reported Pavani et al., (2020).

In contrast, relatively low GCV and PCV values were recorded for plant height (GCV = 9.36%, PCV = 9.91%), oil content (GCV = 8.14%, PCV = 8.31%), number of seeds per capsule (GCV = 6.3%, PCV = 7.8%), and days to maturity (GCV = 4.96%, PCV = 5.46%). These lower values indicate greater stability but limited potential for immediate improvement through simple selection similar findings reported by Thiyagu et al., (2023).

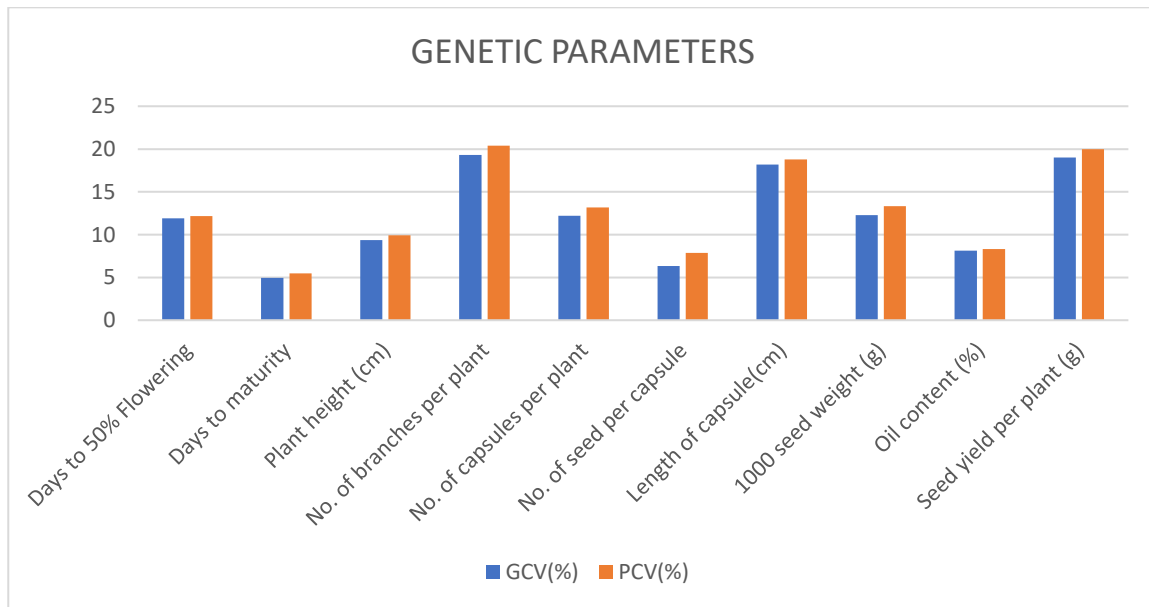
### 3.4 Heritability and Genetic Advance as Percent of Mean

Heritability reflects the proportion of total phenotypic variation that can be attributed to genetic factors, whereas genetic advance estimates the expected improvement in a trait through selection. Together, these parameters provide valuable insights for plant breeders in designing effective strategies to develop improved crop varieties. Broad-sense heritability helps determine the extent to which observed variation is genetically controlled. Genetic advance, on the other hand, predicts the level of improvement achievable in future generations through selection and serves as a useful tool for enhancing genetic gain in breeding programs.

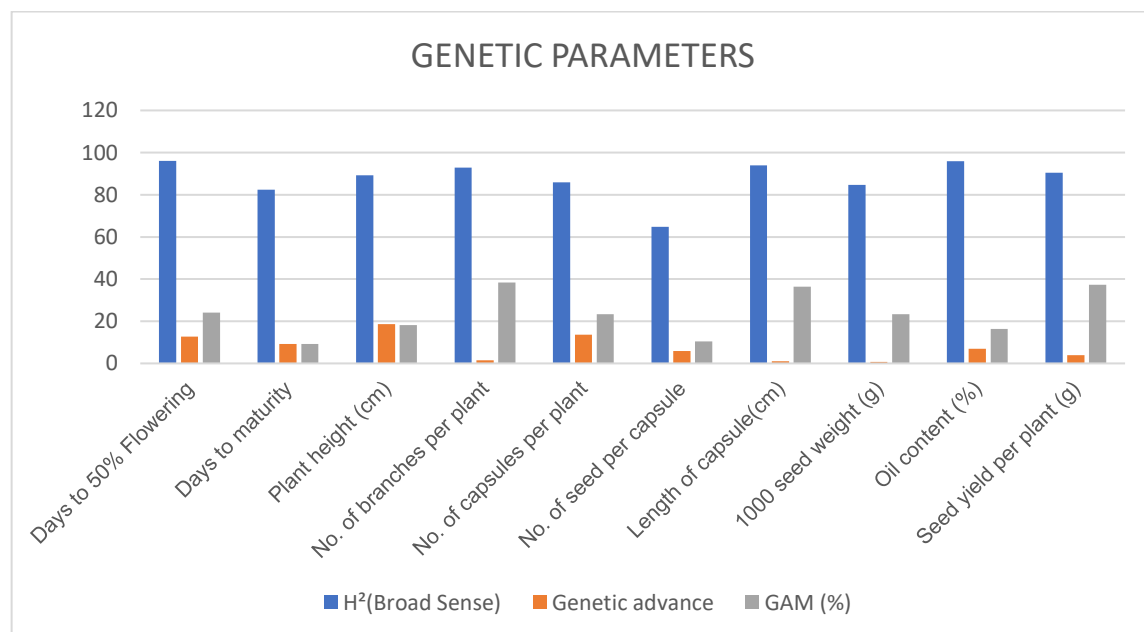
All the traits listed in Table 2 and Fig. 2 exhibited high heritability. Traits with high heritability accompanied by high genetic advance as a percentage of the mean indicate that additive gene action is predominant, making them highly responsive to selection. Notably, days to 50% flowering showed a heritability of 96.05% with a genetic advance of 24.06%, oil content had a heritability of 95.92% with a genetic advance of

16.41%, and capsule length showed 93.33% heritability and 36.34% genetic advance. Likewise, the number of branches per plant and seed yield per plant showed heritability values of 92.86% and 90.50%, respectively, with corresponding genetic advances of 38.35% and 37.25%, respectively, as detailed in Table 2. These results suggest that simple phenotypic

selection would be effective for improving these traits. Similar findings have been reported Takele and Abera (2023) and Thouseem et al. (2022) who also noted high heritability with high genetic advance in sesame, supporting the conclusion that such traits are primarily governed by additive gene action and are amenable to improvement through selection.



**Fig. 1. Genotypic and phenotypic coefficient of variation for yield and yield contributing character**



**Fig. 2. Heritability, Genetic Advance and Genetic advance as per cent of mean for yield and yield contributing character**

**Table 1. Analysis of variance for ten yield-contributing characters in sesame.**

S. No	Characters	Mean sum of squares		
		Replications (df=1)	Treatments (df=29)	Error (29)
1	Days to 50% flowering	12.50	<b>83.15**</b>	3.8
2	Days to maturity	12.15	<b>58.45 **</b>	10.28
3	Plant height (cm)	93.20	<b>205.48**</b>	22.11
4	Number of branches per plant	0.322	<b>1.158 **</b>	0.08
5	Number of capsules per plant	17.28	<b>118.95**</b>	16.75
6	Number of seeds per capsule	3.6	<b>38.43**</b>	13.50
7	Length of capsule	0.1406	<b>0.5819**</b>	0.035
8	1000-seed weight (g)	0.013	<b>0.330**</b>	0.050
9	Oil content (%)	0.36	<b>24.72**</b>	1
10	Seed yield per plant (g)	0.24	<b>9.12**</b>	0.866

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

**Table 2. Parameters of genetic variability for yield and yield contributing character in sesame**

Sr. No.	Name of the Character	Range	Mean	GV ( $\sigma^2g$ )	PV ( $\sigma^2p$ )	GCV	PCV	Heritability (Broad sense) (%)	Genetic advance (1%)	Genetic advance as % Mean
1	Days to 50% flowering	41.5-64.5	53.016	39.93	41.57	11.91	12.16	96.05	12.75	24.06
2	Days to maturity	91.5-110	98.85	24.08	29.22	4.96	5.46	82.4	9.17	9.28
3	Plant height(cm)	92-118.25	102.21	91.68	102.4	9.36	9.91	89.2	18.63	18.20
4	No. of Branches per plant	2.5-4.95	3.79	0.538	0.57	19.31	20.40	92.86	1.4560	38.35
5	No. of capsules per plant	44.5-70.5	58.53	51.09	59.47	12.21	13.17	85.91	13.64	23.31
6	No. of Seed per capsule	49-63	55.80	12.46	19.12	6.326	7.8562	64.85	5.85	10.49
7	Length of capsule	2.1-3.55	2.87	0.273	0.291	18.20	18.78	93.93	1.0437	36.34
8	1000 seed wt. (g)	2.45-3.75	3.04	0.139	0.165	12.28	13.34	84.73	0.7092	23.28
9	Oil content (%)	36.4-48.5	42.32	11.85	12.36	8.136	8.3074	95.92	6.9480	16.41
10	Seed yield per plant (g)	8.05-14.6	10.69	4.130	4.56	19.01	19.98	90.50	3.98	37.25

GV = Genotypic variance, PV = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient variation

In contrast, high heritability combined with moderate to low genetic advance often points to the involvement of non-additive gene effects such as dominance and epistasis, or to environmental influences that mask genetic potential. This situation may reduce the effectiveness of direct selection, especially in early generations. This trend was observed in traits such as plant height (heritability 89.2%, genetic advance 18.20%), number of capsules per plant (85.91%, 23.31%), 1000-seed weight (84.73%, 23.28%), days to maturity (82.4%, 9.28%), and number of seeds per capsule (64.85%, 10.49%). These results suggest limited prospects for immediate improvement through direct selection. Similar observations were made by Hika et al. (2015) for days to maturity.

#### 4. CONCLUSION

The present investigation highlights considerable variability among all the genotypes for each of the traits studied. The highest values of genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for seed yield per plant (g), number of branches per plant, and capsule length. In contrast, lower GCV and PCV values were noted for oil content, days to maturity, number of capsules per plant, and plant height. The presence of substantial genetic variability in the breeding material provides a strong foundation for effective selection and plays a crucial role in identifying suitable parental lines for use in hybridization programs aimed at crop improvement. High heritability accompanied by high genetic advance as a percentage of the mean was recorded for traits such as days to 50% flowering, oil content, capsule length, number of branches per plant, and seed yield per plant. Furthermore, moderate heritability combined with moderate genetic advance was observed for plant height, number of capsules per plant, and 1000-seed weight. These results indicate that these traits are largely governed by additive gene action, suggesting that selection based on these characteristics would be effective for achieving genetic improvement.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

- Akkiligunta, P., Jatothu, J., B., U. K., & C. V., S. K. (2024). Unveiling the sesame germplasm – A study of genetic variability for yield (*Sesamum indicum* L.). *Journal of Experimental Agriculture International*, 46(8), 693–699. <https://doi.org/10.9734/jeai/2024/v46i82752>
- Burton, G. W., & Devane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 45(10), 478–481. <https://doi.org/10.2134/agronj1953.00021962004500100005x>
- Dasari, R., Srikanth, T., Padmaja, D., & Kiran Babu, T. (2021). Genetic variability and heritability studies among genotypes of sesame (*Sesamum indicum* L.). *Journal of Oilseeds Research*, 38(1), 31–35. <https://doi.org/10.56739/jor.v38i1.136>
- Hika, G., Geleta, N., & Jaleta, Z. (2015). Genetic variability, heritability and genetic advance for the phenotypic traits in sesame (*Sesamum indicum* L.) populations from Ethiopia. *Science, Technology and Arts Research Journal*, 4(1), 20–26.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47(7), 314–318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Kumar, S., & Kumari, P. (2022). Assessment of genetic variability and correlation studies in sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and Phytochemistry*, 11(6), 2243–2246.
- Kumhar, S. R., & Bisen, R. (2021). Genetic analysis and diversity studies in sesame (*Sesamum indicum* L.). *Journal of Oilseeds Research*, 38(4), [page range if available]. <https://doi.org/10.56739/jor.v38i4.137205>
- Nayar, N. M., & Mehra, K. L. (1970). Sesamum—its uses, botany, cytogenetics, and origin. *Economic Botany*, 24(1), 20–31. <https://doi.org/10.1007/BF02860629>
- Panse, V. G., & Sukhatme, P. V. (1985). *Statistical methods for agricultural workers* (2nd ed.). ICAR, New Delhi, India.

- Patil, M., & Lokesh, R. (2018). Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy & Natural Products*, 4(1), 1–5.
- Pavani, K., Lal Ahamed, M., Ramana, J. V., & Sirisha, A. B. (2020). Studies on genetic variability parameters in sesame (*Sesamum indicum* L.). *International Journal of Chemical Studies*, 8(4), 101–104.
- Saravanan, M., Kalaiyarasi, R., & Viswanathan, P. L. (2020). Assessment of genetic variability, character association and path analysis in F<sub>2</sub> population of sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, 11(2), 447–450. Retrieved from <https://www.ejplantbreeding.org/index.php/EJPB/article/view/3457>
- Sasipriya, S., Parimala, K., Eswari, K. B., & Balram, M. (2022). Studies on genetic variability in sesame (*Sesamum indicum* L.). *Journal of Oilseeds Research*, 39(2), [page range if available]. <https://doi.org/10.56739/jor.v39i2.141707>
- Singh, A. K., Sinha, S., Satyendra, S., Sinha, S., Dinkar, D., & Singh, P. K. (2024). Genetic variability, correlation and path analysis for selection in elite breeding material of sesame (*Sesamum indicum* L.). *Journal of Oilseeds Research*, 41(2), 132–137. <https://doi.org/10.56739/1m3c6f57>
- Sivasubramanian, S., & Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, 60, 1093–1096.
- Takele, F., & Abera, G. (2023). Variability study in Ethiopian sesame (*Sesamum indicum* L.) genotypes at Western Oromia. *International Journal of Precision Farming*, 1(1), 1–7.
- Thiyagu, K., Kumar, S., & Jeyakumar, P. (2023). Estimation of genetic variability and association analysis in sesame (*Sesamum indicum* L.) genotypes. *Electronic Journal of Plant Breeding*, 14(1), 164–169.
- Thouseem, N., Arya, K., & Gayathri, G. (2022). Genetic variability, heritability and genetic advance for seed yield and yield-associated traits in white seeded sesame (*Sesamum indicum* L.). *The Pharma Innovation Journal*, 11(6), 385–388.
- Vamshi, K., Reddy, K. H. P., & Kumar, V. S. (2021). Genetic variability, heritability and genetic advance studies in sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and Phytochemistry*, 10(4), 1754–1758.
- Vavilov, N. I. (1951). *The origin, variation, immunity and breeding of cultivated plants* (K. S. Chester, Trans.). *Chronica Botanica*, 13, 1–366.
- Vinishree, L., Lokesh, R., Goudappagoudar, R., & Banakar, C. N. (2013). Analysis of genetic variability for yield and its components in sesame (*Sesamum indicum* L.). *International Journal of Plant Sciences*, 8(1), 91–93.

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