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Genetic Variability and Trait Association Analysis 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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Short Research Article

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Abstract

This study is important for the scientific and plant breeding community as it provides clear evidence of substantial genetic variability among sesame genotypes under field conditions. The research provides dependable selection criteria for enhancing sesame yield by pinpointing essential traits that contribute to yield and possess high heritability and genetic gain. Variance analysis, PCV, GCV, heritability, genetic gain, and correlation provide insights into the relationships between two variables, enabling breeders to choose superior genotypes for development of varieties. The current study aimed to examine the phenotypic and genotypic variability among various genotypes, as well as to evaluate genetic advancement, correlation coefficients among traits, and sesame yield. The research took place in summer 2024 at RARS, Polasa, Jagtial, to assess genetic

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variability among fifteen sesame (Sesamum indicum L.) genotypes. Variance analysis showed significant differences across all traits examined among the genotypes. The number of capsules per plant showed the highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The count of branches per plant and the quantity of capsules per plant showed significant heritability and high genetic advance (GAM), indicating that these characteristics are mainly influenced by additive gene effects. Consequently, phenotypic selection for these characteristics may be beneficial for upcoming breeding programs.

Keywords: Genetic variability; heritability; genetic advance as percent of mean; Sesamum.

1. Introduction

"Sesame (*Sesamum indicum* L.) is an ancient oilseed crop and an economically very important crop, but it has been neglected and underutilized compared with other crop species; consequently, there is still much room for its genetic improvement" (Pandey et al., 2021; Burton (1952). "It is the oldest oilseed crop, is widely grown during the rainy season with inadequate management and is often subject to the vagaris of rainfall. Sesame is renowned for its exceptional oil quality. The crop is primarily grown for its seeds, which have the highest oil content (44–55%), protein content (22-25%), and are rich in antioxidants like sesamin (0.4–1.1%), sesamolin (0.3–0.6%), and are resistant to oxidation because they contain tocopherols and lignans, which are endogenous antioxidants" (Sonia et al., 2024; Fisher & Yates, 1938). "Sesame seeds are the rich source of fat, proteins, minerals, Ca and Fe. High percentage of unsaturated fatty acids are found in sesame oil i.e. oleic acid and linoleic acid. Keeping quality of sesame oil is more due to the high percentage of antioxidant present in it. Sesame oil is used in industrial purpose like insecticides, pharmaceutical and paints" (Sharma and Chauhan, 1984; Panse & Sukhatme, 1985). "Sesame is very famous food additive in Indian household to enhance food flavor (For improvement in a particular trait of the sesame crop, the genetic variability present in the crop needs to be assessed and exploited. Analysis of variance, PCV, GCV, heritability, genetic advance, and Correlation gives the information about mutual association between two variables on the basis of which breeders can select superior genotypes for seed yield. This study is important for the scientific and plant breeding community as it provides clear evidence of substantial genetic variability among sesame genotypes under field conditions. By identifying key yield contributing traits with high heritability and genetic advance, the study offers reliable selection criteria for improving sesame productivity. The findings contribute to a better understanding of the genetic architecture of economically important traits in sesame and can directly support the development of high yielding varieties through efficient breeding strategies" (Pandey et al., 2021). The present investigation was conducted to study the phenotypic and genotypic variability among the genotypes and to estimate genetic advance, correlation coefficient among the characters and on yield of sesame.

2. Materials and Methods

The study was conducted at Regional Agricultural Research Station, Polasa, Jagtial, during *summer* 2024. A total of fifteen sesame genotypes of diverse origin were taken for the present study. "The fifteen genotypes were raised in Randomized Block Design (RBD) with three replications. Each genotype was sown in three metres length with inter-row spacing of 30 cm and intra row spacing of 15 cm. Sowing was done by dibbling the seed at 2-3 cm depth. Recommended agronomic practices and need based plant protection measures were undertaken. Observations were recorded on five randomly selected plants per replication. The following characters were observed and recorded. Days to 50 percent flowering, Plant height at maturity (cm), number of branches per plant, number of capsules per plant, 1000 seed weight (g) and Seed yield (kg/ha). Data from five plants of each genotype were averaged replication wise and mean data was used for statistical analysis. Mean, range and coefficient of variation were also estimated. GCV and PCV were calculated" as per Burton and de Vane (1953), heritability (broad sense) as per Allard (1960) and genetic advance and GAM according to Johnson et al. (1955), and correlation coefficient analysis by Johnson et al. (1951). 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. (1955) as low (0–30%), medium (30–60%), and high (>60%). Similarly, genetic advance as a percentage of mean was categorized by Johnson et al. 1995 as low (<10%), moderate (10–20%), and high (>20%). All statistical analyses were conducted using statistical package at Computer Centre, PJTAU, Rajendranagar, Hyderabad, Telangana, India.

3. Results and Discussion

The statistical evaluation of the numerical data obtained on quantitative traits showed highly significant differences among the genotypes studied across all nine characteristics, such as days to 50 percent flowering, days to maturity plant height (cm), number of branches per plant, number of capsules per plant, 1000 seed weight (g), and seed yield (kg/ha), signifying notable genetic variability within the examined experimental material. PCV slightly surpassed GCV for all traits, suggesting the influence of environmental factors on the manifestation of these traits under study (Table 1). A high genotypic and phenotypic coefficient of variation was noted for the number of capsules per plant (21.83 and 23.7). It demonstrates significant genetic variability with limited environmental impact, rendering this characteristic particularly suitable for enhancement via straightforward selection techniques, akin to observations noted by Padmaja et al. (2026), Gayathri et al. (2025) and Ashfaq et al. (2025).

Moderate GCV (17.69) and high PCV (23.00) was observed in number of branches per plant. Similar findings were recorded by Vamshi et al. (2021). Low GCV and moderate PCV were observed for plant height (5.72, 11.07) and seed yield (8.29, 12.75). Similar results were found by Rajitha et al. (2021) and Mahla et al. (2024) for plant height and Pavani et al. (2020) for seed yield. Low GCV and PCV was observed for days to 50% flowering (5.01, 6.70) and days to maturity (2.43, 2.63) and test weight (5.94, 6.63). The small difference between these two estimates might be due to less environmental influence on this character This is in consonance with the findings of Padmaja et al., 2026, Gayathri et al., (2025), Ashfaq et al. (2025) for days to 50% flowering and days to maturity and Pavani et al. (2020) for test weight.

3.1 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 programmes.

High heritability with (85.0) accompanied by high genetic advance as a percentage of the mean (41.36) indicate that additive gene action is predominant, making them highly responsive to selection for number of capsules per plant. These results are similar with the findings of Swapna et al. 2024 and Padmaja et al., 2026. Moderate heritability with high genetic advance as per cent of mean for number of branches per plant (59.0, 35.90). Swapna et al. (2024) and Ashfaq et al. (2025) reported high genetic advance as per cent of mean. Moderate heritability was reported by Rajitha et al. (2021) and Mitkari et al. (2023). It indicates direct selection for the number of branches per plant would be highly effective for improving yield. Similar results with the findings of Menzir (2012). Moderate heritability with moderate genetic advance as per cent of mean for seed yield (42.0, 11.12). Significant heritability accompanied by a moderate genetic improvement relative to the mean for 1000 seed weight (80.0, 10.95). These findings aligned with Mitkari et al. (2023).

Moderate heritability with a low genetic advance as percentage of mean for days to maturity (56.0, 7.73) and plant height (27, 6.10). The findings of the current study aligned with those of Abate et al. (2015). Thouseem et al. (2022) reported days to maturity and plant height findings that aligned with the results of Saxena and Bisen (2017) and Mahla et al. (2024). Moderate heritability with minimal genetic gain as a percentage of the average for days to 50% flowering (56.0, 7.73). The moderate heritability and low genetic gain as a percentage of the mean for this trait suggest that non-additive gene effects significantly influence the expression of this attribute.

Table 1. Variability parameters, heritability and genetic advance as per cent of mean for yield and yield component traits

S. No.	Character	Range	General Mean	Vg	Vp	Coefficient of variation		Heritability (%)	Genetic advance as per cent of mean
						GCV (%)	PCV (%)	(Broad Sense)	
1	Days to 50% flowering	31-39	35.76	3.21	5.74	5.01	6.7	56.00	7.73
2	Plant height (cm)	86-119	99.85	32.65	122.13	5.72	11.07	27.00	6.1
3	Days to maturity	87-95	90.8	4.85	5.71	2.43	2.63	85.00	4.61
4	Number of branches per plant	3-6	3.89	0.47	0.8	17.69	23	59.00	28.01
5	Number of capsules per plant	53-105	72.04	247.25	292.12	21.83	23.72	85.00	41.36
6	Seed yield (Kg/ha)	812-1091	916.71	5779.29	13652.57	8.29	12.75	42.00	11.12
7	Test weight (g)	2.93-3.57	3.16	0.04	0.04	5.94	6.63	80.00	10.95

Table 2. Correlation of seed yield with other yield component traits in sesame

	Days to 50% flowering	Plant height (cm)	Days to maturity	Number of branches per plant	No. of capsules/ Plant	Test weight	Seed yield
Days to 50% flowering	1.000	-0.097	0.802 ***	0.057	-0.058	-0.111	0.032
Plant height (cm)		1.000	-0.133	-0.019	0.123	0.100	0.140
Days to maturity			1.000	-0.131	0.010	0.023	0.054
Number of branches per plant				1.000	-0.095	-0.038	-0.053
No. of capsules/Plant					1.000	0.016	0.705***
Test weight						1.000	0.127
Seed yield							1.000

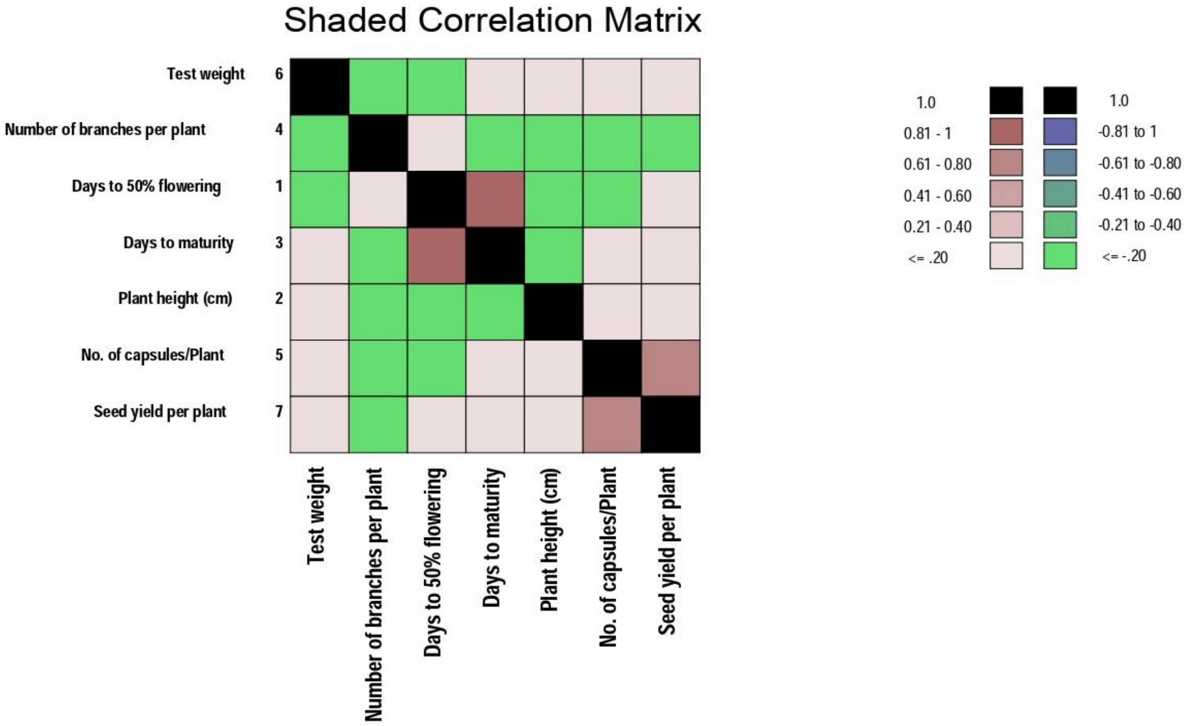

Fig. 1. Shaded correlation matrix

Consequently, the findings suggested limited potential for additional enhancement via individual plant selection. These outcomes align with the results of Bindu et al. (2014) and Mahla et al. (2024).

3.2 Correlation Coefficients

Table 2 presents the estimates of correlation coefficients among seed yield and other traits that contribute to yield. Relatively larger correlation coefficients show a strong hereditary link among different yield-related traits. Consequently, choosing based on phenotype would be beneficial for enhancing yield. The number of capsules per plant showed a strong positive correlation with seed yield (0.705). These outcomes align with the results reported by Padmaja et al., 2026 and Maheetha et al., 2025. Days to maturity showed a strong positive correlation with days to 50% flowering (0.802). These results align with the conclusions drawn by Maheetha et al., 2025. This kind of character relationship suggests that enhancing seed yield can be accomplished by increasing traits such as the number of capsules per plant.

4. Conclusion

The study revealed that traits viz., number of capsules per plant are to be given more importance during selection programme and direct selection for seed yield through these traits could be effective for seed yield improvement in 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 writing or editing of this manuscript.

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Competing Interests

Authors have declared that no competing interests exist.

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