Plant Archives Vol. 26, No. 2, 2026 pp. 2664-2668 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.365

GENETIC VARIABILITY AND TRAIT ASSOCIATION ANALYSIS IN ADVANCED GENOTYPES OF SESAME (*Sesamum indicum* L.)

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(Date of Receiving-29-07-2026; Date of Revision-14-10-2026; Date of Acceptance-19-10-2026)

ABSTRACT

Sesame (*Sesamum indicum* L.) is one of the oldest oilseed crops cultivated in tropical and subtropical areas of the world. Thirteen advanced genotypes of sesame were assessed for variability, heritability, genetic advancement, phenotypic correlation and genotypic correlation. The number of branches per plant showed moderate heritability and high genetic advance, indicating the predominance of additive genetic effects and the potential for effective improvement through selection. Correlation analysis revealed that seed yield showed a significant positive correlation with the number of capsules per plant, suggesting that these trait can serve as criteria for selecting new varieties aimed at higher seed yield. These traits should be prioritized in breeding programmes aimed at yield enhancement and quality improvement in sesame.

Key words : Sesame, Yield attributing traits, Variability, Correlation.

Introduction

Sesame (*Sesamum indicum* L.) is an ancient oilseed crop belonging to family Pedaliaceae with diploid (2n = 26) chromosome. The genus Sesamum contains more than 30 species of which *Sesamum indicum* is the most cultivated species (Nayar and Mehra, 1970). It is economically very important crop as it contains high oil of about 40-60% and good quality of 20-40% protein are rich in antioxidants like sesamin (0.4–1.1%), sesamolin (0.3–0.6%) and it is resistant to oxidation due to the presence of endogenous antioxidants like tocopherols and lignans (Sonia *et al*., 2024). High percentage of unsaturated fatty acids are found in sesame oil (oleic acid and linoleic acid) (Padmaja *et al*., 2026). In India, sesame is grown in diverse agro-ecological zones and holds a crucial place in dryland farming systems. Telangana state, in particular, is known for the cultivation of sesame during the *summer* and late *kharif* seasons. In India, during the 2023-24 cropping season, sesame cultivation spanned nearly 1.531 million hectares, resulting in an estimated output of 8,47,000 tonnes and an average productivity of 553 kilograms per hectare. Telangana made a notable contribution, recording approximately 10,000 tonnes of production with a yield level of 740 kilograms per hectare from 0.014 million hectares (Indiastat, 2024). To improve sesame yield, identification and utilization of genetically superior genotypes is imperative. Understanding genetic parameters such as genotypic and phenotypic variation coefficients (GCV and PCV), heritability estimates, 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 to 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.

Materials and Methods

The present investigation was carried out at Professor Jayashankar Telangana Agricultural University, Polasa, Jagtial in 2025 (*summer* season). The experiment was laid in Randomized Block Design with 13 genotypes

including three checks Swetha, JCS 3202 and JCS 1020 varieties were used as local checks, Plot area was 3.6m^2 with plant-to-plant distance of 15 cm and row to row distance of 30 cm. Data of seven traits has been recorded, it was recorded on five randomly selected plants in each genotype in all two replications. Recommended agronomic practices were uniformly applied throughout the crop growth period. Observations were recorded on seven quantitative traits from five randomly chosen plants per genotype for phenological traits (days to 50% flowering and maturity), plant architecture (height and number of branches), yield attributes (capsule count, 1000-seed weight and yield per plant), Statistical analysis was performed as per the standard methods. Analysis of variance was used to assess genotypic variability following Federer (1956), with significance tested using F-values (Fisher and Yates, 1963). GCV and PCV were calculated as per Burton and de Vane (1953), heritability (broad sense) as per Allard (1960) and genetic advance, GAM and The correlation coefficients according to Johnson *et al.* (1955).

Results and Discussion

Understanding the nature and extent of genetic variability in the experimental material is essential for planning effective crop improvement strategies. The degree of phenotypic variability observed in the traits provides an indication of the potential for improvement through selection. To evaluate this, an analysis of variance was conducted for each trait, which revealed highly significant differences among genotypes, indicating ample genetic variation across all studied traits. This variation serves as a promising foundation improving yield potential through recombination and selection in future breeding efforts. Key genetic parameters were estimated to gain deeper insights, including broad-sense heritability, genetic advance (GAM) and the genotypic and phenotypic coefficients of variation (GCV and PCV). These results are summarized in Table 1. Together, heritability and genetic advance (GAM) offer valuable insights into the genetic control of quantitative traits and help guide effective selection decisions. Based on adjusted mean values, considerable variability was observed among the genotypes, with plant height ranging from 107. 6 to 139.5 cm, capsules per plant varying between 78.5 and 124, seed yield recorded in the ranging from 844 to 1113 kg/ ha. Many researchers have documented wide variations for various yield-contributing features in sesame, including Revathi *et al*. (2012) and Gayatri *et al*. (2025). Sivasubramanian and Menon (1973) provided a classification to interpret GCV and PCV values, where variability is considered low if it is below 10%, moderate between 10%, 20% and high when it exceeds 20%. In present investigation, the phenotypic coefficient of variation was found to be slightly higher than the genotypic coefficient of variation for most of the traits, suggesting that environmental influence was minimal. The narrow gap between PCV and GCV values indicates that these traits are largely governed by genetic factors. Similar trends have been reported in earlier studies by Padmaja *et al*. (2026), Gayatri *et al*. (2025) and Swapna *et al*. (2024), Plant height showed a moderate extent of variation for both phenotypic and genotypic coefficients, which was on par with the results observed by Thouseem *et al*. (2022) and Vamshi *et al*. (2021). Low PCV and GCV values were recorded for days to 50% flowering days to maturity and 1000 seed weight which were in agreement with the results reported by Padmaja *et al*. (2022) for 1000 seed weight, Mahla *et al*. (2024) for days to maturity and days to 50% flowering. Number of branches per plant recorded high PCV and moderate GCV, which was on par with the findings reported by Vamshi *et al*. (2021). The traits number of capsules per plant recorded moderate PCV and low GCV. Similar observations were recorded by Takele and Abera (2023) for number of capsules per plant for moderate GCV. Low PCV and moderate GCV for plant height. These results are similar with the findings of Zahran *et al*. (2020) and Takele and Abera (2023). According to them, heritability estimates are categorized as low when below 30 percent, moderate when ranging between 30 and 60 percent and high when the value is above 60 percent. Similarly, genetic advance as percent of mean is categorized as low when it is below 10%, moderate between 11%, 20% and high when it is 20% or more. When heritability is high but the corresponding genetic advance as percent of mean is low, it typically suggests the role of non-additive gene effects, indicating that direct selection may not lead to substantial improvement due to possible environmental interactions. Conversely, traits exhibiting high values for both heritability and genetic advance as percent of mean are generally influenced by additive gene action, thus offering better scope for genetic enhancement through selection (Nadarajan *et al*., 2018). In contrast, when both heritability and genetic advance are low, it suggests a strong environmental influence on the trait, and selection in such cases would likely be ineffective. Heritability values in the present investigation ranged from 22% to 87%, while GAM (genetic advance as percent of mean) spanned from 3.73% to 24.33%. Trait number of branches per plant exhibited moderate heritability along with a high genetic advance as a percent of the mean. Saxena and Bisen (2017), Tripathy *et al*. (2016) recorded

Table 1 : Genetic parameters for yield components in sesame genotypes.

	Range	Genotypic variance (Vg)	Genotypic Coefficient of variation (GCV %)	Phenotypic variance (Vg)	Phenotypic Coefficient of variation (PCV%)	Broad sense heritability (%)	Gen. Adv as % of Mean 5 %
Days to 50% flowering	37.5-43.5	2.45	3.85	3.25	4.43	0.75	6.88
Days to maturity	87.5-94.5	4.14	2.24	4.76	2.40	0.87	4.30
Number of branches per plant	1.5-4.5	0.35	17.38	0.75	25.59	0.46	24.33
Plant height (cm)	107.5-139.5	39.77	5.03	178.45	10.66	0.22	4.89
Number of capsules per plant	78.5-124.4	72.10	8.62	222.40	15.14	0.32	10.11
Test weight (g)	3.145-3.45	0.01	2.58	0.02	3.69	0.49	3.73
Seed Yield (Kg/ha)	844-1113	2961.08	5.65	10983.22	10.87	0.27	6.04

Table 2 : Analysis of correlation between quantitative attributes.

	Days to 50% flowering	Days to maturity	Number of branches per plant	Plant height (cm)	Number of capsules per plant	Test weight (g)	Seed yield (Kg/ha)
Days to 50% flowering	11.000	0.933 ***	0.265	-0.214	0.501 **	0.013	0.309
Days to maturity		1.000	0.283	-0.252	0.377	0.051	0.291
Number of branches per plant			1.000	0.230	0.039	-0.045	-0.001
Plant height (cm)				1.000	-0.147	-0.274	-0.160
Number of capsules per plant					1.000	-0.030	0.711**
Test weight (g)						1.000	-0.131
Seed Yield (Kg/ha)							1.000

moderate heritability and Divya *et al*. (2018) reported high GAM. High heritability along with low GAM was shown by days to 50% flowering and days to maturity. Similar results were obtained by Mitkari *et al*. (2023) and Bharathi *et al*. (2014) for days to 50% flowering. High heritability coupled with low GAM was observed for days to maturity, which align with the findings observed by Hamoud *et al*. (2016) and Chandramohan *et al*. (2014) Moderate heritability with low GAM for test weight. Similar observation was recorded by Sahu *et al*. (2022). Low heritability coupled with low GAM for seed yield and Plant height, which align with the findings observed by Padmaja *et al*. (2022) for seed yield and plant height by Begum *et al*. (2017).

The correlation coefficient estimates between seed yield and other traits contributing to yield are presented in Table 2. Relatively higher values of correlation coefficients suggest a robust heritable link between

several yield contributing traits. Days to maturity showed a strong positive correlation with days to 50% flowering (0.933). This suggests that genotypes that flower early generally reach maturity sooner. These findings are consistent with earlier research (Mitkari *et al*., 2023 and Padmaja *et al*., 2026). Days to 50% flowering had strong positive significant correlation with number of capsules per plant (0.501). Similar results were reported by earlier workers (Navaneetha *et al*., 2019). Seed yield was positively significant correlation with number of capsules per plant (0.711). Such strong association is highly desirable since improvement in any of these yield-contributing characters will have a direct positive effect on seed yield per plant. This suggests that selection focusing on this trait would likely lead to a substantial improvement in seed yield. Similar results were reported by previous studies (Kalaiyarasi *et al*., 2019 and Disowja *et al*., 2020; Padmaja *et al*., 2026).

Conclusion

The present experiment revealed substantial genetic variability in the studied sesame genotypes. Traits such as number of branches per plant exhibited substantial heritability coupled with moderate genetic advance as percent of mean, indicating the predominance of additive genetic effects and the potential for effective improvement through selection. Correlation analysis indicated that the characters *viz*., number of capsules per plant, days to maturity and days to 50% flowering are inter correlated among themselves. Therefore, these traits are to be given priority during selection for improvement of yield. The study revealed that the traits number of productive branches, number of capsules per plant to be given more importance during selection programme for seed yield improvement in sesame

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