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DISSECTION OF GENETIC VARIABILITY AND TRAITS CONTRIBUTION TO YIELD IN SESAME (*SESAMUM INDICUM* L.) UNDER SUMMER CONDITIONS USING MULTIVARIATE ANALYSIS

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ABSTRACT
Sesame (*Sesamum indicum* L.) is an annual plant of Pedaliaceae family is one major oilseed crop cultivated in India. The present study was conducted to access the variability and relationship between the yield and its component characters in sesame (*Sesamum indicum* L.) during *summer* 2025. The experiment was laid out in randomized block design with three replications in 16 advanced genotypes. The highest genotypic, phenotypic (32.38% and 27.93%) coefficient of variation, heritability (74.40) and GAM (49.64) was observed for number of capsules per plant. The trait number of capsules per plant showed positive correlation (0.746) and positive direct effect (**0.750)** with seed yield. In the Principal component analysis number of capsules per plant (0.454) and test weight (0.430) showed the highest positive coefficients, indicating their major contribution to genetic divergence. These traits are important for improvement through selection.

KEYWORDS: sesame, genetic variability, heritability, genetic advance as per cent of mean, correlation and PCA

INTRODUCTION
Sesame (*Sesamum indicum* L.) is an annual plant of Pedaliaceae family is one major oilseed crop cultivated in India. It is grown for over 5,000 years for cooking and medicinal purposes Umamaheshwari *et al*., (2019). In general, 35% of global production is utilized for confections and 65% is used for the extraction of edible oil Agricultural statistics at glance (2022). The fatty acid composition is rather attractive, due to the high level of unsaturated fatty acids. The only easily accessible source of protein rich in sulfur-containing amino acids is sesame seed Gayathri *et al*., (2025). India plays a vital role in sesame production, the crop is cultivated under rainfed conditions with low inputs. Sesame is grown on 1.531 million hectares in India during the 2023–2024 season, yielding 847,000 tonnes and a productivity of 553 kg/ha. From 0.014 million hectares, Telangana records about 10,000 tonnes of production with a yield level of 740 kilos per hectare Indiastat 2024. Over the past ten years, consumers' growing awareness of the nutritional benefits of sesame seed oil has led to an increase in demand for sesame. It contains protein content of 18-25 %, carbohydrates of 13.5 % and oil content of 44 -58 %. Selection based on its component characters increases yield as they are not only less complex but are also relatively show simple inheritance and less influenced to environmental deviations. Improvement for the yield is normally realised by using genetically diverse parents in the breeding programmes and profound knowledge of genetic variability in crops is very essential for effective selection in development of varieties. Character association among yield and its component characters plays a major role in selection while developing new varieties.

MATERIALS AND METHODS
The experimental trial was conducted during the season summer in the year 2025 in Regional Agricultural Research Station, Polasa, Telnagana, India. Sixteen advanced breeding lines including national check were evaluated in the statistical design of Randomized Block Design with three replications. Each genotype was raised in 3m length with spacing of 30 x 10 cm in ten rows. The crop was grown entirely under summer conditions with irrigation. Recommended agronomic practices were followed uniformly.Observations were recorded on five randomly selected plants per plot for traits including days to 50 % flowering (days), days to maturity (days), plant height (cm), number of branches per plant, number of capsules per plant and seed yield (kg/ha). Statistical analysis was carried out using analysis of variance (ANOVA) as described by Panse and Sukhatme (1961), GCV and PCV were calculated as per (5), heritability (broad sense) and genetic advance and GAM according to Johnson *et al*., (1955) The correlation and path coefficient coefficients were carried out Burton *et al*., (1953).and principal component analysis was performed using PJTAUSTAT, OPSTAT.

RESULTS AND DISCUSSION

The range, mean, variability analysis results were calculated for the seven quantitative traits viz., days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, test weight (g) and seed yield (kg/ha) presented in Table 1. PCV showed higher values than GCV suggesting less effect of environmental factors on the studied traits. GCV and PCV values classification to interpret, where variability is considered low if it is below 10%, moderate between 10% and 20%, and high when it exceeds 20% as per the classification of Sivasubramanian S and Madhavamenon (1973). The little difference between PCV and GCV levels suggests that these traits are largely governed by genetic factors. Previous investigations have revealed similar findings. Padmaja *et al*. (2026), Gayatri *et al*., (2025) and Swapna *et al*., (2024). The range, mean, variability analysis results were calculated for the seven quantitative traits viz., days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, test weight and seed yield presented in Table 1.

Low PCV (3.87) and GCV (2.82) for days to 50% flowering and days to maturity (1.61, 1.46). These results are similar with the findings Gayatri *et al*., (2025) and Swapna *et al*., (2024). High heritability (82.20) coupled with low genetic advance (2.73) as percent of mean for days to maturity indicates the effect of non-additive gene action suggesting limited gain from selection despite genetic control. These results are similar with the findings Padmaja *et al*. (2026), Gayatri *et al*., (2025). Moderate PCV (14.98%) and GCV (11.00%) were noticed for seed yield. These results are similar with the findings Monpara and Khairnar (2016). Moderate PCV (10) and low GCV was noticed for test weight (10.86, 9.11) which was on par with the findings reported by Rajitha (2019) for moderate PCV and low GCV by (17). High PCV and moderate GCV was noticed for number of branches per plant (20.82, 13.52). These results are similar with the findings of Divya *et al*., (2018) for high PCV and moderate GCV by Rajitha (2019). Seed yield per plant recorded moderate PCV (14.98) and low GCV (11.00). These results are similar with the findings Monpara and Khairnar (2016). High PCV and GCV number of capsules per plant (32.38% and 27.93%). Similar results were reported by earlier workers Mitkari *et al*., (2023) and Ashfaq *et al*., (2015). Number of branches per plant recorded high PCV (20.82%) and moderate GCV (13.52%), which was on par with the findings reported by Abate and Mekbib (2015). Moderate heritability with a low genetic advance as percentage of mean for days to 50% flowering (53.3, 4.24). The findings of the current study aligned with those of Takele and Abera (2023). Number of branches per plant (42.2, 18.08) and seed yield (53.90, 16.64) recorded moderate heritability and genetic advance as per cent of mean. These results are similar with the findings of Abate and Mekbib (2015) for seed yield.

High heritability (74.4) coupled with high genetic advance as per cent of mean (49.64) for number of branches per plant. These reports were in accordance with findings of (18) and (19). It indicates the involvement of additive type of gene action in controlling this trait, confirming that opting for capsule number would be effective for selection. High heritability (70.4) coupled with moderate genetic advance as per cent of mean (15.74) for test weight showing that selection will be effective and that additive gene action governs this trait. These recordings were on par with reports of Ashfaq *et al*., (2025).

The high magnitude of PCV, GCV, heritability and genetic advance as percent of mean for number of capsules per plant indicating the presence of ample amount of variation for these characters and that this character was controlled by additive gene action in controlling this trait. This trait would be effective for crop improvement as suggested by earlier workers Ashfaq *et al*., (2025) and Gayathri *et al*., (2025).

High heritability values indicate as a measure of genetic advancement through phenotypic selection. In the present study, higher heritability followed by genetic advance as per cent of mean for the number of capsules per plant were recorded. This suggested that selection for this trait would be effective for crop improvement as suggested by earlier workers Padmaja *et al*., (2026) Gayathri *et al*., (2025). for the improvement in seed yield.

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

Traits	Range	Genetic variance (Vg)	Phenotypic variance (Vp)	Phenotypic Coefficient of Variance	Genotypic Coefficient of Variance	Heritability h^2 (Broad Sense)	Genetic advance as percent of mean 5%
Days to 50% flowering	40-45	1.47	2.76	3.87	2.82	53.30	4.24
Days to maturity	89-94	1.81	2.20	1.61	1.46	82.20	2.73
Number of branches per plant	46145	0.23	0.56	20.82	13.52	42.20	18.08
Number of capsules per plant	48-129	478.93	643.56	32.38	27.93	74.40	49.64

Test weight (g)	3.01-3.84	0.09	0.13	10.86	9.11	70.40	15.74
Seed yield (Kg/ha)	641-1074	10136.19	18798.09	14.98	11.00	53.90	16.64

The estimates of correlation coefficients between seed yield and other yield contributing traits were given in Table 2. Relative higher magnitude of correlation coefficients indicating a strong heritable association among various yield contributing characters. Therefore, selection based on the phenotype would be effective for yield improvement. The number of capsules per plant had positive significant correlation with seed yield (0.746). This was in accordance with earlier studies (21). Days to maturity exhibited significant negative association with test weight (-0.333). These results are similar with the findings Disowja *et al*., (2020).

Table 2. phenotypic correlation coefficients of component characters with seed yield

	Days to 50% flowering	**Days to maturity**	**No.of primary branches**	**Number of capsules**	**Test weight (g)**	**Seed yield kg/ ha**
Days to 50% flowering	**1.000**	-0.0952	0.0253	-0.1499	0.1275	-0.1491
Days to maturity		**1.000**	-0.1375	0.1268	-0.333 **	0.0136
No.of primary branches			**1.000**	0.0683	0.2296	0.0225
Number of capsules				**1.000**	0.1608	0.746 ***
Test weight (g)					**1.000**	0.1512
Seed yield kg/ ha						**1.000**

In sesame, seed yield is a quanititative trait which is highly influenced by a number of inter-related factors Moosavi *et al*., (2015) revealed that, when many traits are affecting an assumed character, splitting the total correlation into direct and indirect effects of cause would give more meaningful understanding to the cause of association between the dependent trait like yield and independent trait like yield component trait Srikanth and Ghodke (2022). The direct and indirect effects of various characters on seed yield are given in Table 3. Number of capsules per plant had the maximum positive direct effects (0.750) on seed yield. which was similar to the findings of results reported by Moosavi *et al*., (2015) and Srikanth and Ghodke (2022). This indicated that direct selection of this trait would improve the seed yield per plant . While days to maturity (-0.086) showed the negative direct effect i.e. early maturing genotypes were also higher yielders. Similar results were observed in previous results Bamrotiya *et al*., (2016). The results suggests that traits like number of capsules per plant have a positive and significant impact on seed yield and make them valuable criteria for selection criteria. Hence greater emphasis must be given on these associated traits as criteria for selection to target improvement of seed yield.

Table 3. Direct effects and indirect effects of component characters on seed yield

	Days to 50% of flowering	**Days to maturity**	**Number of branches per plant**	**Number of capsules per plant**	**Test weight (g)**	**Seed yield kg/ha**
Days to fifty per cent of flowering	**0.046**	0.004	-0.001	0.007	-0.006	-0.149
Days to maturity	0.008	**-0.086**	0.012	-0.011	0.029	0.014
Number of branches per plant	-0.001	0.006	**-0.044**	-0.003	-0.010	0.023
Number of capsules per plant	-0.113	0.095	0.051	**0.750**	0.121	0.746***
Test weight (g)	0.002	-0.006	0.004	0.003	**0.018**	0.151

R square = 0.567 Residual Effect = 0.658

Principal Component analysis (PCA)

The canonical root analysis revealed that the first three canonical vectors accounted for 82.95% of the total divergence among the genotypes. The first vector (Vector I) exhibited the highest eigenvalue (25.38) and explained 45.95% of the total variation. Canonical root analysis is an effective multivariate technique for identifying the traits responsible for genetic divergence among genotypes. In the present study, the first three canonical vectors explained more than 80% of the total variation, indicating that these vectors adequately represented the genetic diversity present in the material. The predominance of Vector I suggests that the variation among genotypes was primarily governed by differences in yield-contributing traits. In this vector, number of capsules per plant (0.454) and test weight (0.430) showed the highest positive coefficients, indicating their major

contribution to genetic divergence. Similar with the earlier reports (26) for number of capsules per plant. The high positive loadings of number of capsules per plant and test weight in Vector I indicate that these traits were the major determinants of genetic divergence and therefore represent important selection criteria for yield improvement. Days to maturity (-0.774) recorded the highest negative loading, suggesting an inverse association with the variation captured by this vector. The second vector (Vector II) had an eigenvalue of 13.88 and accounted for 25.12% of the total variation. In Vector II, the large negative loading for number of capsules per plant and moderate negative contribution of seed yield indicate that these traits differentiated genotypes in a direction opposite to that represented by flowering time and test weight. This suggests the existence of diverse genetic groups with contrasting combinations of yield components.The largest positive contributions were from test weight (0.330) and days to 50% flowering (0.169), whereas number of capsules per plant (-0.821) and seed yield (-0.302) exhibited substantial negative loadings. The strong negative contribution of days to maturity further suggests that divergence was associated with variation in crop duration, providing opportunities for selecting both early- and late-maturing genotypes depending on breeding objectives. Together, the first and second vectors explained 71.07% of the cumulative variation. The third vector (Vector III) contributed 11.88% of the total variation with an eigenvalue of 6.56, increasing the cumulative variance explained to 82.95%. In this vector, test weight (0.753) and days to maturity (0.516) showed the highest positive coefficients, followed by number of primary branches (0.324). Seed yield contributed only marginally (0.010), indicating a limited role in the divergence represented by this vector. The third vector emphasized the role of test weight, days to maturity, and number of primary branches, indicating that these traits contributed additional independent variation beyond that explained by the first two vectors. The consistently high contribution of test weight across all three vectors demonstrates its stability as a discriminating trait and underscores its importance in parent selection. Therefore, genotypes exhibiting superior performance for number of capsules per plant, test weight, and desirable maturity duration may be considered promising parents for hybridization programmes to exploit genetic diversity and achieve greater genetic gain in sesame breeding.

Table 4: Eigen value per cent of total variation

	1 Vector	2 Vector	3 Vector
Eigene Value (Root)	25.383	13.879	6.563
% Var. Exp.	45.949	25.124	11.879
Cum. Var. Exp.	45.949	71.072	82.952
Days to 50% flowering	0.071	0.169	0.179
Days to maturity	-0.774	-0.305	0.516
No.of primary branches	-0.050	0.071	0.324
Number of capsules	0.454	-0.821	0.172
Test weight (g)	0.430	0.330	0.753
Seed yield kg/ ha	0.045	-0.302	0.010

CONCLUSION

The present number of capsules per plant recorded high GCV, PCV coupled with a high broad sense heritability and genetic advance as per cent of mean. The number of capsules per plant is positively correlated and showed high direct effects on seed yield indicating selection of number of capsules per plant can be used as selection criteria for developing new varieties for higher seed yield. In PCA number of capsules per plant contributed more variations in the study. Therefore, more importance should be given during the selection in the breeding programme.

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Authors' contributions

DPJ conducted the whole experiment and collected the data. BR supported in the field trial and prepared manuscript preparation.

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