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GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN SESAME (*Sesamum indicum* L.) GERMPLASM

Sabhavatu Damodar Nayak, Pramod Kumar Yadav, Akash Barela*, Vamsi Krishna Reddy Baddeli
and Madakam Praveen Kumar

Department of Genetics and Plant Breeding, School of Agriculture ITM University Gwalior (M.P.)

*Corresponding author E-mail: akashbarelagpb@gmail.com

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ABSTRACT

Sesame (*Sesamum indicum* L.) is an important oilseed crop with significant nutritional and commercial value. The present study was conducted to assess genetic variability, character association, and direct and indirect effects of yield-contributing traits in sesame germplasm. Twenty-seven sesame genotypes, including four checks (Unnat Rama, RT-372, CUMS-09A, and GT-11), were evaluated in a randomized block design during the Kharif season (2025) at Crop Research Centre-1, ITM University, Sithouli Campus, Gwalior, Madhya Pradesh. Ten quantitative traits were recorded including Days to 50% Flowering (DFF), Days to Maturity (DM), Number of Primary Branches (NPB), Plant Height (PH), Number of Capsules Per Plant (NCP), Length of Capsule (LOC), Width of Capsule (WOC), Number of Seeds per Capsule (NSC), 1000 Seed Weight (1000SW), and Seed Yield Per Plant (SYP). Analysis of variance revealed significant differences among treatments for most traits, indicating substantial genetic variability. Genetic parameters showed high heritability and genetic advance for NPB ($h^2=79.5\%$, $GAI=25.86\%$), PH ($h^2=79.48\%$, $GAI=10.42\%$), and NCP ($h^2=79.9\%$, $GAI=28.69\%$), suggesting their suitability for selection. Correlation analysis demonstrated significant positive associations between SYP and DM ($r=0.367^{**}$), NSC ($r=0.714^{**}$), and 1000SW ($r=0.409^{**}$). Path coefficient analysis revealed that NSC had the highest direct effect (0.5728^{**}) on seed yield, followed by 1000SW (0.1710^*), and DM (0.2067^{**}), indicating these traits are crucial for improving yield in sesame. These findings provide valuable information for sesame breeding programs aimed at developing high-yielding cultivars.

Keywords : *Sesamum indicum*, Genetic variability, Character association, Path coefficient analysis, Heritability, Selection response.

Introduction

Sesamum indicum L., commonly known as sesame or til, is an ancient oilseed crop belonging to the family Pedaliaceae. The crop is believed to have originated in Africa and has been cultivated for over 5000 years (Pathak *et al.*, 2018). Sesame is characterized by erect herbaceous plants with a height ranging from 0.6 to 2.5 meters, bearing opposite leaves with serrated margins and axillary flowers varying in color from white to pink, purple, or blue. The fruit is a four-chambered capsule (loculicide dehiscence) containing numerous small seeds (4000-6000 seeds per plant), each weighing approximately 40-60 mg. The crop exhibits both determinate and indeterminate growth patterns depending on the genotype and

environmental conditions. Global sesame production has shown considerable variation, with total production estimated at approximately 6.5-7.0 million tonnes annually, with India being one of the major producers. India cultivates sesame over an area of approximately 1.8-2.0 million hectares with production around 1.5-1.8 million tonnes, representing nearly 25-30% of global production. In Madhya Pradesh, sesame is grown on approximately 150,000-200,000 hectares with an average productivity of 4.5-6.0 quintal per hectare. The productivity is considerably lower than the potential yield of 15-20 quintal per hectare, indicating substantial scope for improvement through systematic breeding and selection programs. Sesame seeds contain 40-60% oil with high unsaturated fatty acids, including

linoleic acid (38-48%) and oleic acid (34-40%), making it nutritionally valuable (Anilakumar *et al.*, 2016). The oil is rich in natural antioxidants such as sesamin and sesamol, which possess hepatoprotective, hypolipidemic, and antioxidant properties. Sesame seeds also contain 18-25% high-quality protein with a balanced amino acid profile, making them particularly valuable in vegetarian diets. Additionally, the crop provides essential minerals including calcium, iron, magnesium, phosphorus, and zinc. The seeds are also used for the production of tahini, halwa, and various traditional preparations across Asia, Middle East, and Africa. Sesame is a short-duration crop (90-120 days) which makes it suitable for multiple cropping systems. The crop tolerates a wide range of soil types but prefers well-drained loamy or sandy loam soils with pH ranging from 5.5 to 8.0. It requires moderate rainfall of 400-750 mm during the growing season and is relatively drought-tolerant compared to other crops. The crop demonstrates good crop-rotation potential and is less susceptible to major pest and disease incidences compared to other oilseed crops. However, productivity is often constrained by the non-uniform maturity and capsule shattering, leading to significant yield losses during harvesting. Improvement of sesame cultivars requires a comprehensive understanding of genetic variability present within the crop species. Genetic variability forms the foundation of any successful crop improvement program, as it provides the basis for selection and development of superior genotypes (Kumar *et al.*, 2019). The presence of significant genetic variation for yield and its components is essential for effective selection. Heritability estimates help in predicting the genetic gain achievable through selection, while correlation and path coefficient analyses provide insights into the association and relative importance of various traits affecting yield. Previous studies have demonstrated the existence of substantial genetic variation for various quantitative traits in sesame germplasm (Singh *et al.*, 2020; Patel *et al.*, 2021). However, continuous evaluation of newly acquired germplasm is necessary to identify superior genotypes and to understand the nature of trait associations that influence yield improvement. The relationships between various morphological and agronomic traits are crucial for designing effective selection strategies in breeding programs (Yilmaz *et al.*, 2018).

Materials and Methods

The study was conducted at Crop Research Centre-1, ITM University, Sithouli Campus, Gwalior, Madhya Pradesh, India (coordinates: 26.15°N,

78.18°E, elevation 191 m above sea level) during the *Kharif* season of 2025. The location falls within the Gird agroclimatic zone of Madhya Pradesh. The climatic conditions during the cropping season were characterized by pre-monsoon temperatures ranging from 35-42°C in June, monsoon onset in July with well-distributed rainfall averaging 65-80 mm per week, and post-monsoon period with declining rainfall from September onwards. The soil at the experimental site is loamy with good drainage characteristics, having pH 7.2, organic carbon content of 0.68%, and moderate fertility status. A total of 27 sesame genotypes, comprising 23 germplasm accessions and 4 check varieties, were evaluated in the present study. The germplasm accessions were procured from JNKVV (Jawaharlal Nehru Krishi Vishwa Vidyalaya), Jabalpur, under a Material Transfer Agreement (MTA). The four check varieties used in the study were: Unnat Rama, RT-372, CUMS-09A and GT-11. The 27 genotypes were laid out in a Randomized Block Design (RBD) with three replications. Each genotype was represented by a single plot of 2.4m × 1.5m (3.6 m²) with a spacing of 30 cm between rows and 15 cm between plants. The experiment was conducted with recommended package of practices including recommended dose of fertilizer (N:P:K = 60:40:40 kg/ha), irrigation schedules based on rainfall distribution, and integrated pest management strategies. Ten quantitative traits were recorded on five randomly selected competitive plants from each genotype in each replication: Days to 50% Flowering, Days to Maturity, Number of Primary Branches, Plant Height, Number of Capsules Per Plant, Length of Capsule, Width of Capsule, Number of Seeds Per Capsule, 1000 Seed Weight, Seed Yield Per Plant.

Results and Discussion

Analysis of Variance

Analysis of variance revealed significant differences among treatments for most of the traits studied, indicating the presence of substantial genetic variability in the sesame germplasm evaluated. The results of ANOVA for all ten traits are presented in Table 1. The significant differences observed for most traits in the analysis of variance indicate substantial genetic variability in the sesame germplasm evaluated. Similar findings of significant genetic variation for quantitative traits in sesame have been reported by Patel *et al.* (2021) and Maurya *et al.* (2019). The presence of genetic variability forms the essential basis for any breeding program, as it provides the raw material for selection and genetic improvement of the crop.

Table 1: Analysis of Variance

Source of Variance	df	DFF	DM	NPB	PH	NCP
Replicate	2	3.3704	0.0494	0.0061	507.916	413.952
Treatments	26	49.137**	13.5821**	0.9601	457.498**	209.517**
Error	52	9.0884	2.3058	0.1775	137.796	63.6127
Source of Variance	df	LOC	WOC	NSC	1000SW	SYP
Replicate	2	0.0621	0.0017	0.8229	0.1029	0.08940
Treatments	26	0.1352**	0.0087	144.9179**	1.1136**	11.2063**
Error	52	0.0209	0.00347	10.69814	0.03457	34.7873

** = Significant at 1% level of probability; * = Significant at 5% level of probability; df = degrees of freedom; DFF = Days to 50% Flowering; DM = Days to Maturity; NPB = Number of Primary Branches; PH = Plant Height; NCP = Number of Capsules Per Plant; LOC = Length of Capsule; WOC = Width of Capsule; NSC = Number of Seeds per Capsule; 1000SW = 1000 Seed Weight; SYP = Seed Yield Per Plant

Genetic Parameters and Variability

Genetic parameters estimated for ten quantitative traits in sesame germplasm are presented in Table 2.

These parameters provide insights into the nature and magnitude of genetic variability available for selection and breeding.

Table 2 : Genetic Parameters and Variability

Traits	Mean	GCV (%)	PCV (%)	h ² (%)	GAI (%)
DFF	38.63	9.13	12.22	65.91	14.09
DM	91.383	12.1	12.68	68.38	13.4
NPB	3.127	19.25	21.07	79.5	25.86
PH	124.4	11.04	12.79	79.48	10.42
NCP	28.38	33.21	38.74	79.9	28.69
LOC	2.501	12.17	12.79	62.25	12.58
WOC	0.647	9.3	11.1	39.25	9.39
NSC	50.497	13.05	14.71	78.72	23.88
1000SW	4.535	12.98	13.87	87.46	25.03
SYP	9.695	18.75	21.04	79.47	34.49

GCV = Genetic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; h² = Heritability in broad sense (%); GAI = Genetic Advance as percentage of mean

The analysis of genetic parameters revealed that high heritability values exceeding 75% were observed for number of primary branches (79.5%), plant height (79.48%), number of capsules per plant (79.9%), thousand seed weight (87.46%), and seed yield per plant (79.47%). These high heritability estimates indicate that these traits are predominantly governed by additive gene action and would respond well to phenotypic selection. The high heritability for seed yield per plant is particularly important, as it suggests that gains in yield through selection of superior genotypes are feasible and would be reliably inherited in subsequent generations.

Moderate heritability values in the range of 60-75% were estimated for days to 50% flowering (65.91%), days to maturity (68.38%), length of capsule (62.25%), and number of seeds per capsule (78.72%). These moderate heritability estimates suggest that these traits are under appreciable genetic control, though environmental factors play a notable role in

their expression. The distinction between high and moderate heritability traits has important practical implications for breeding strategy selection.

Genetic Coefficient of Variation, which provides a measure of genetic diversity for a trait, ranged from 9.13% for days to flower flowering to 33.21% for number of capsules per plant. This wide range indicates that some traits exhibit higher genetic variation than others. Number of capsules per plant showed the highest genetic coefficient of variation at 33.21%, followed by seed yield per plant at 18.75% and number of primary branches at 19.25%. These high genetic coefficients of variation indicate substantial genetic diversity available for selection in these traits. In contrast, the relatively low genetic coefficients of variation observed for days to flower flowering (9.13%), weight of capsule (9.3%), and length of capsule (12.17%) suggest that genetic diversity for these traits is somewhat limited in the germplasm evaluated.

Genetic advance as percentage of mean, which estimates the amount of phenotypic improvement expected from selection, was high (exceeding 20%) for number of primary branches (25.86%), number of capsules per plant (28.69%), thousand seed weight (25.03%), and seed yield per plant (34.49%). The exceptionally high genetic advance value for seed yield per plant (34.49%) suggests that substantial improvement in yield is achievable through selection of superior genotypes from the present germplasm. These traits with high genetic advance coupled with high heritability represent ideal targets for selection in breeding programs. The moderate genetic advance values observed for days to 50% flowering (14.09%), days to maturity (13.4%), length of capsule (12.58%) and number of seeds per capsule (23.88%) indicate that selection for these traits would also be effective, though the expected gains may be somewhat more modest.

The high heritability values (>75%) observed for NPB, PH, NCP, 1000SW and SYP suggest that these traits are primarily controlled by additive genetic effects and would respond effectively to selection. These findings align with earlier reports by Kumar *et al.* (2019) and Singh *et al.* (2020), who documented high heritability for similar traits in sesame germplasm. High heritability coupled with high genetic advance makes these traits ideal targets for selection. According to Falconer and Mackay (2009), high heritability combined with significant genetic advance indicates additive gene action and suggests that these traits can be effectively improved through phenotypic selection in early generations. According to Sivasubramanian

and Madhavamenon (2015), GCV values >20% indicate high variability, 10-20% indicate medium variability, and <10% indicate low variability. By these criteria, NCP and SYP showed high variability, while traits such as DFF, LOC, and WOC showed low to medium variability. The genetic advance as percentage of mean (GAI) is an important parameter for assessing the effect of selection on a population. High GAI values (>20%) for traits like NCP (28.69%), SYP (34.49%), 1000SW (25.03%), and NPB (25.86%) indicate that considerable genetic gains can be achieved through selection of superior genotypes for these traits.

Correlation Coefficient Analysis

Correlation coefficients among ten quantitative traits in sesame germplasm are presented in Table 3. These correlations indicate the nature and magnitude of association between pairs of traits. The correlation analysis revealed several important associations among the traits evaluated. Seed yield per plant exhibited positive correlations with days to maturity ($r = 0.367^{**}$), number of seeds per capsule ($r = 0.714^{**}$), thousand seed weight ($r = 0.409^{**}$), and number of capsules per plant ($r = 0.374^{**}$). Among these positive correlations, the association between seed yield and number of seeds per capsule was particularly strong, with a coefficient of 0.714^{**} , indicating that genotypes producing more seeds per capsule would tend to produce higher overall seed yields. This strong positive correlation makes biological sense, as an increase in seed number per capsule directly contributes to greater seed accumulation per plant.

Trait	DFF	DM	NPB	PH	NCP	LOC	WOC	NSC	1000SW	SYP
DFF	1.000 **	0.456 **	0.085 ns	0.270 *	0.126 ns	-0.214 ns	0.336 **	-0.014 ns	0.134 ns	0.070 ns
DM	0.456 **	1.000 **	0.211 ns	0.236 *	0.037 ns	-0.099 ns	0.189 ns	0.158 ns	0.225 ns	0.367 **
NPB	0.085 ns	0.211 ns	1.000 **	-0.183 ns	0.087 ns	0.109 ns	0.036 ns	0.044 ns	0.153 ns	0.326 **
PH	0.270 *	0.236 *	-0.183 ns	1.000 **	0.192 ns	-0.043 ns	0.189 ns	0.085 ns	0.140 ns	0.202 ns
NCP	0.126 ns	0.037 ns	0.087 ns	0.192 ns	1.000 **	-0.013 ns	-0.080 ns	0.288 *	0.035 ns	0.374 **
LOC	-0.214 ns	-0.099 ns	0.109 ns	-0.043 ns	-0.013 ns	1.000 **	0.245 *	-0.111 ns	0.059 ns	0.086 ns
WOC	0.336 **	0.189 ns	0.036 ns	0.189 ns	-0.080 ns	0.245 *	1.000 **	-0.243 *	0.228 *	-0.081 ns
NSC	-0.014 ns	0.158 ns	0.044 ns	0.085 ns	0.288 *	-0.111 ns	-0.243 *	1.000 **	0.252 *	0.714 **
1000SW	0.134 ns	0.225 ns	0.153 ns	0.140 ns	0.035 ns	0.059 ns	0.228 *	0.252 *	1.000 **	0.409 **
SYP	0.070 ns	0.367 **	0.326 **	0.202 ns	0.374 **	0.086 ns	-0.081 ns	0.714 **	0.409 **	1.000 **

Significance: ** $p < 0.01$ * $p < 0.05$ ns = non-significant | Blue = Positive Red = Negative

Fig. 1: Correlation coefficient analysis

The correlation between days to maturity and seed yield (0.367**) suggests that genotypes requiring longer duration for maturation tended to produce higher seed yields. This positive association likely reflects the extended period available for biomass accumulation and reproductive development in longer-duration genotypes. The positive correlation between thousand seed weight and seed yield (0.409**) indicates that larger seeds contribute to higher overall yields, presumably due to the increased metabolic resources contained in larger seeds that may promote plant vigor and productivity. (Fig.1)

Among the component traits themselves, several important associations were observed. Days to 50% flowering and days to maturity showed a significant positive correlation ($r = 0.456^{**}$), indicating that early-flowering genotypes tended to mature earlier as well. Plant height and number of primary branches were positively correlated ($r = 0.236^{*}$), suggesting that taller plants generally developed more primary branches. The association between number of seeds per capsule and thousand seed weight ($r = 0.714^{**}$) was notably strong and positive, indicating that genotypes with higher seed numbers per capsule also tended to have larger individual seeds. Width of capsule showed positive correlation with length of capsule ($r = 0.245^{*}$), suggesting that capsules with greater length also tended to have greater weight. This is a logical association given the direct relationship between capsule size and weight. However, width of capsule exhibited a negative correlation with number of seeds per capsule ($r = -0.243$), indicating an inverse relationship between these traits. This negative association suggests that there may be a physiological trade-off in capsule development, where resources allocated to capsule tissue development compete with resources allocated to seed production, resulting in fewer but heavier capsules in some genotypes and more but lighter capsules in others.

The correlation between days to 50% flowering and length of capsule was negative ($r = -0.214$), indicating that early-flowering genotypes tended to produce somewhat shorter capsules. Width of capsule and number of seeds per capsule also showed negative correlation ($r = -0.243$), as mentioned above. These negative associations suggest that while some traits may be complementary, others exhibit trade-offs that must be carefully considered in breeding programs.

Number of primary branches showed relatively weak correlations with most traits, including a weak positive correlation with number of capsules per plant ($r = 0.192$) and a weak positive correlation with seed yield per plant ($r = 0.126$). The lack of strong

correlation between primary branch number and yield suggests that while plant architecture contributes to productivity, the number of primary branches is not a major determinant of final seed yield in sesame. This may reflect the specific growth habit of sesame, where yield is concentrated in the upper portions of the plant regardless of branch number. The results of the present investigation are largely consistent with previous studies on sesame genetic variability. Kumar *et al.* (2019) reported high heritability for plant height and number of primary branches in sesame, similar to the findings of this study. Maurya *et al.* (2019) documented strong positive correlations between yield and component traits, with seed weight emerging as an important trait, consistent with the direct effect of 1000SW observed in our study. Overall, the correlation analysis revealed that seed yield per plant is most strongly influenced by number of seeds per capsule, followed by thousand seed weight and days to maturity. These traits should therefore be given priority in selection programs aimed at improving sesame yield. The positive correlation of seed yield with number of seeds per capsule (0.714), thousand seed weight (0.409) and days to maturity (0.367) suggests that yield improvement can be achieved by selecting for these traits. The strong positive correlation between NSC and SYP is particularly noteworthy and has important breeding implications. Similar results have been reported by Pathak *et al.* (2018) and Singh *et al.* (2020) in their sesame breeding studies. The high positive correlation between NSC and SYP aligns with theoretical expectations, as increased number of seeds per capsule would logically lead to increased yield per plant.

Conclusion

The present study on genetic variability, character association, and path coefficient analysis in sesame germplasm has provided comprehensive insights into the genetic control of important agronomic traits and their relationships with seed yield. Substantial genetic variability exists in the sesame germplasm evaluated, with significant differences observed for most traits. This genetic variability provides excellent opportunity for selection and improvement of sesame cultivars. High heritability ($>75\%$) coupled with high genetic advance ($>20\%$) for traits such as NPB, PH, NCP, 1000SW, and SYP indicates that these traits are under strong additive genetic control and would respond effectively to selection. These traits should be given priority in breeding programs. Seed yield per plant showed significant positive correlations with NSC (0.714), 1000SW (0.409**), and DM (0.367), indicating that selection for these traits would lead to

indirect improvement in yield. The findings provide a scientific basis for formulating effective breeding strategies for sesame improvement. A selection strategy emphasizing traits with direct and indirect effects on yield would be more effective than random selection. This germplasm evaluation has identified genotypes with superior trait combinations that could be utilized as parents in future sesame breeding programs. Future research should focus on molecular characterization of promising genotypes, development of breeding lines combining desirable traits, and multi-location evaluation to validate these findings across diverse environments.

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