



# Plant Archives

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

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.118>

## ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY STUDIES IN SESAME (*SESAMUM INDICUM*. L)

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(Date of Receiving : 18-08-2024; Date of Acceptance ; 13-10-2024)

### ABSTRACT

Sesame (*Sesamum indicum* L.), commonly known as Till or Gingelly, is India's third most important oilseed crop, valued for its high-quality oil with long shelf life due to compounds like sesamin and sesamol. However, sesame production in India faces challenges, particularly low productivity, largely due to a lack of cultivars that can thrive in diverse growing conditions. To address this issue, understanding the genetic diversity and assessing the variability by studying the components of phenotypic variance, genotypic variance and its derived genetic estimates such as phenotypic coefficient of variation, Genotypic coefficient of variation and heritability are crucial. This study focused on evaluating the genetic variation of 40 sesame genotypes. By studying the analysis of variance significant genetic differences among the genotypes were observed for the characters chosen. The characters *viz.*, days to maturity, number of primary branches per plant and number of capsules per plant observed to have high GCV value and signifies the impact of genotype and environmental interaction. Thereby elucidate the chance of selecting the traits for breeding program. The other characters recorded moderate and thousand seed weight recorded low GCV. Traits like days to fifty percent flowering, plant height and days to maturity had high heritability, meaning they are less affected by the environment. The characters which show high GCV value coupled with high heritability increases the dependability on selection of traits. Other traits, like the number of primary branches and capsule length showed moderate to low heritability. To study the genetic diversity, Cluster analysis were performed and dendrogram was constructed which revealed five distinct groups of genotypes, providing useful information for selecting genetically diverse parents for breeding program.

**Keywords:** Sesame, Genetic estimates, coefficient of variation, Heritability, Diversity

### Introduction

Sesame (*Sesamum indicum*. L) is the third most important oil seed crop in India. It is commonly known as Till or Gingelly. It is adapted to various climatic conditions and thrives well in well-drained soil. Sesame has a relatively superior oil quality in

comparison to many major oil seed crops and it is known as king of oils seeds. Tigabu.E *et al.*, (2021). The seed oil has long shelf life due to the presence of lignans (Sesamin, Sesamol, Sesamolin) Kiruthika *et al.* (2018). Sesame crop earns higher contribution to export among the oil seed crop grown in India.

Therefore, the attention towards increasing the production and productivity is greatly warranted. One of the reasons attributed for lower productivity of this crop is non availability of cultivars responsive to different agro ecological situations and management conditions (Hedge *et al.*, 2004). To overcome this issue, it is essential to screen and document the variation exists in the germplasm. A study on analyzing the variability present in the germplasm is prerequisite for initiating a varietal development programme. As the economic characters are highly influenced by environment, analyzing the nature and magnitude of heritable genetic variation is highly demanded. Moreover, understanding the knowledge on genetic divergence is a key component in selecting the parents for hybridization, to identify heterotic crosses with good combining ability and to obtain desirable segregants. In this context, the present study is focused on the objective to investigate the genetic

diversity of the germplasm and its relative contribution of each character towards genetic divergence.

### Materials and Methods

The experiment was carried out at Pandit Jawaharlal Nehru college of Agriculture and research institute, Karaikal during summer, April 2022. The topography of the soil in the experimental area was consistent and had a clayey loam texture. The study material comprises of forty sesame genotypes presented in Table 1. To collect the quantitative data information, five plants were randomly selected from each genotype. The following characters *viz.*, Days to fifty percent flowering (DFF), Plant height (PH) (cm), number of primary branches per plant (NPB), number of capsules per plant (NCP), days to maturity (DM), number of seeds per capsule (NSC), capsule length (CL) (cm), 1000 seed weight (TSW) (g) and Seed yield per plant (SYP) (g) were measured.

**Table 1:** Materials used in the experiment

Sl.No	Genotype	Sl.No	Genotype	Sl.No	Genotype	Sl.No	Genotype
1	TMV 3	11	EC351890	21	IC500851	31	EC346449
2	TMV 4	12	IC43078	22	EC358020	32	IC204090
3	TMV6	13	IC130065	23	IC208501	33	TMV7
4	Darab	14	IC306052	24	IC43195	34	BD42
5	IC127293	15	IC132499	25	IC42459	35	KMR17
6	SVPR 1	16	IC110245	26	EC346393	36	NIC16227
7	VRI 1	17	EC346980	27	IC500678	37	Swetha
8	IC131518	18	IC204524	28	ICI31997	38	Rajeswari
9	CO 1	19	IC510990	29	IC132255	39	Ettupattai ellu
10	IC132549	20	IC203935	30	IC132578	40	IC205634

The experiment was taken in completely Randomized Block Design with three replications. Planting was done with a spacing of 30 cm x 15 cm., with the recommended crop management practices. Statistical analysis was performed using STAR package of IRRI, version 2.0.1, and R package for constructing dendrogram. The analysis of variances, mean performance and genetic variability parameters were estimated. By using ANOVA, the test of significance was determined between genotypes for the characters under study. According to the method suggested by Burton (1968) and Hanson *et al.*, (1956)

the Genotypic coefficient of variation, (GCV), phenotypic coefficient of variation (PCV) and heritability  $h^2$  (broad sense) was measured.

### Results and Discussion

The analysis of variance Table 2 revealed, the mean sum of squares due to genotypes were highly significant for the all traits of this study at the probability level of 1 and 5% respectively. This demonstrates the potential of free genetic variability exist in the materials taken for the study as reported by Tripathi *et al.*, (2013).

**Table 2 :** Analysis of variance

Sources of variation	Df	DFF	PH	DM	NPB	NCP	NSC	CL	TSW	SYP
Replication	2	4.85	7.85	10.22	2.71	1.77	35.23	0.14	3.39	1.35
Treatment	39	19.29**	263.84**	15.88**	3.47*	81.90**	213.93**	44.16**	0.70**	4.48**
Error	78	0.64	0.81	4.23	3.72	0.94	41.71	1.45	0.10	0.41

### Mean performance

Mean performance is a key tool in the assessment of variability. It helps the plant breeders to select and improve genotypes with desirable traits. It provides a central measure of how traits perform within and across environments, guide in selection process and contribute to the development of stable, high-performing cultivars. Table 3 represents the mean, range that is the maximum and minimum values of the traits included in the study. Days to fifty percent flowering had a flowering duration of 49.33 to 35 days, which shows the genotypes falls in less than 40 days can be chosen as early maturing genotypes. Early maturing genotypes are suitable for harvest in summer season. The plant height varied from 103.67 to 56.83 cm. Days to maturity is crucial character to categorize the crop as early and late. This value ranges from

114.67 to 75 days. In this study the crop maturation period varied from early to late maturing types. Another crucial trait in sesame is number of primary branches per plant. This is the one which bears a greater number of capsules in the plant, the primary branches have direct correlation with seed yield per plant. The maximum value of number of primary branches per plant was recorded to be 7.33 and the minimum value is 3.33. The results of the said characteristics mean values were also discussed Similarly by Umamaheswari *et al.*, (2019) for days to fifty percent flowering, plant height and number of primary branches. The traits number of capsules per plant recorded highest mean of (76), number of seeds per capsules (68.67), capsule length (3.13cm), thousand seed weight (3.37 g) and single plant yield with (11.56 g).

**Table 3 :** Mean performance

Sl. No	Traits	Maximum	Minimum	Mean	Standard deviation
1	DFP	49.33	35	41.01	4.52
2	PH	103.67	56.83	79.33	9.01
3	DM	114.67	75	95.47	3.12
4	NPB	7.33	3.33	4.92	1.11
5	NCP	76.00	22.33	43.92	11.01
6	NSC	68.67	68.67	53.23	6.29
7	CL	3.13	1.47	2.44	1.50
8	TSW	3.37	1.48	2.29	1.46
9	SYP	15.56	6.40	7.60	2.34

DFP: Days to fifty percent flowering; PH: Plant height; DM: days to maturity; NPB: number of primary branches; NCP: number of capsules per plant; NSC: number of seeds per capsule; Capsule length: CL; TSW: Thousand seed weight; SYP: Seed yield per plant

### Variability parameters

The phenotypic coefficient of variation of this experiment recorded higher values than Genotypic Coefficient of variation for the traits such as days to fifty percent flowering, plant height, capsule length, thousand seed weight and seed yield, Table 4. They were found to be moderate according to the classification of Burton (1968) where less than 10% (Low), 10–20% (Moderate) and more than 20% (High). The other characters *viz.*, days to maturity, number of primary branches, number of capsules per plant registered low PCV value and higher GCV value whereas the trait number of seeds per capsule seems to be low for PCV value. This demonstrate that the variation arises because of interaction between genotype and phenotype, where phenotype is combination of both genotype and environment. Similar findings were also observed by Patil and Loksha (2018). The GCV value are found to be higher

for all the characters studied except number of seeds per capsule, capsule length both recorded moderate value and thousand seed weight recorded low GCV value. This clearly indicated whenever higher GCV value are recorded showing the less environment variation. In such cases, selection of this characters are highly rewarding in the breeding program. Heritability is an important genetic parameter, which determines the effectiveness of selection Divya (2018). Based on the heritability, traits are categorized as  $h^2 < 30\%$  low, 30-60% is moderate and  $>60\%$  as high heritable Yeshiwas *et al.* (2017). High heritability was observed for the characters days to fifty percent flowering, plant height, days to maturity, seed yield per plant, number of capsules per plant and Seed yield per plant as reported by Kalaiyarasi *et al.* (2019) and Patel *et al.* (2023). The high heritability of these traits implies that they are less influenced by environmental factors and exhibit greater consistency across various growing

environment. Consequently, breeders can achieve more predictable outcomes when targeting these traits for crop enhancement. Moderate heritability was recorded for the character number of primary branches, number of seeds per capsule as mentioned by Anbanandan, (2018) and low heritability was registered for thousand

seed weight as similar results to Pavani *et al.*, (2020) indicating a significant influence of environmental factors on this trait. This suggests that thousand seed weight in sesame is largely affected by quantitative traits.

**Table 4 :** Genetic Parameters

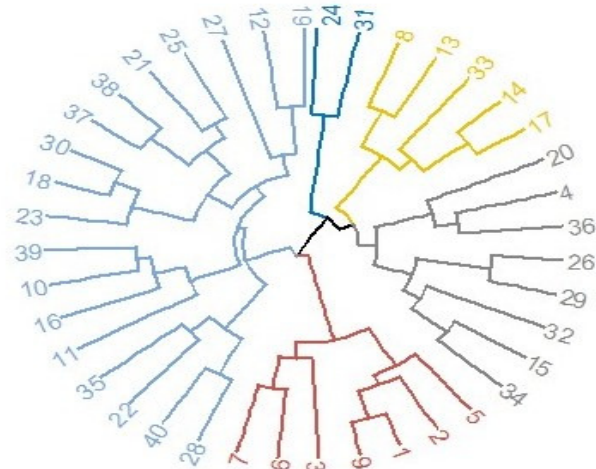
Sl.No	Traits	Coefficient of variation		h <sup>2</sup> Heritability
		GCV	PCV	
1	DFP	24.78	28.9	73.4
2	PH	24.31	28.53	72.63
3	DM	25.78	22.06	73.4
4	NPB	31.25	21.39	45.83
5	NCP	30.57	24.20	64.71
6	NSC	14.24	5.94	41.00
7	CL	7.21	13.21	35.68
8	TSW	6.95	12.41	23.50
9	SYP	45.58	53.72	72.01

GCV- Genotype Coefficient of variation; PCV- Phenotype Coefficient of variation

### Cluster analysis

Cluster analysis is a critical tool in studying the genetic diversity of sesame genotypes. The use of clustering reveals how closely or distantly the genotypes taken for investigation are related and which will aid in selecting parents for breeding program. Several cluster analysis studies were performed in sesame crop and dendrogram was constructed. Priyadarshini *et al.* (2018) obtained five clusters for salinity stress in ten genotypes. Teklu *et al.*, (2021) studied the phenotypic and genotypic diversity in 100 diverse germplasm of Ethiopian sesame varieties which were grouped into two major clusters. In the present study the genetic diversity was assessed by constructing a dendrogram using Euclidean distance and complete linkage method (Figure 1) using R package. The forty genotypes were grouped into five clusters (Table 4) based on a cophenetic correlation coefficient of 0.692, which indicates the reliability of the dendrogram in representing the true data structure of this study. Cluster I grouped with seven genotypes, Cluster II with eight, Cluster III has five, Cluster IV contains eighteen and Cluster V comprises two genotypes respectively. The dendrogram provides a clear picture of the variability and similarity among the genotypes. Genotypes that fall within the same cluster show less variability, while those across different clusters exhibit greater diversity. Breeders are naturally interested in selecting genotypes from different clusters rather than within the same cluster to maximize the diversity. For initiating a hybridization program, diverse parents can be selected from different clusters such as cluster 1, II, III, IV and the genotypes which

falls in single cluster will not show much variation and they are more similar for most of the characters. Similar pattern of study was also reported by Baraki.F. *et al.*, (2020) in which 25 sesame genotypes were grouped into four clusters based on yield and yield related traits.



**Fig. 1 :** Dendrogram - Agglomerative cluster method  
**Table 5:** Cluster and Members

Sl.No	Members
1	TMV3, TMV4, TMV6, IC127293, SVPR1, VRI 1, CO 1
2	Darab, IC132499, IC203935, EC346393, IC132255, IC204090, BD42-42, NIC16227
3	IC131518, IC130065, IC306052, EC346980, TMV7
4	IC132549, EC351890, IC43078, IC110245, IC204524, IC510990, IC500851, EC358020, IC208501, IC42459, IC500678, IC131997, IC132578, KMR 17, SWETHA, Rajeswari, Ettupattai ellu, IC205634
5	IC43195, EC346449

## Conclusion

This study highlights the significance on dissecting the variable components of variances such as GCV, PCV and heritability of key traits among forty sesame genotypes. This reinforces the potential for improving crop productivity through targeted breeding programs. The high heritability of traits such as seed yield, plant height, and days to fifty percent flowering suggests that these traits can be effectively selected to enhance crop performance. The cluster analysis further identified distinct five groups of forty genotypes with diverse genetic backgrounds, offering valuable insights for the selection of parents for hybridization. These findings underscore the importance of continued research and breeding efforts to develop high-yielding, resilient sesame cultivars suited to a varied agro-ecological conditions.

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