

"EXPLORING GENETIC VARIABILITY IN SESAME (*SESAMUM INDICUM* L.) GENOTYPES FOR BREEDING AND IMPROVEMENT"

ABSTRACT:

The study was conducted in the summer of 2020 at RARS, Polasa, Jagtial, to evaluate genetic variability among 68 sesame (*Sesamum indicum* L.) genotypes. Analysis of variance revealed significant differences among the genotypes for all traits studied. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the number of branches per plant, number of capsules per plant, and seed yield per plant. Traits such as days to 50% flowering, days to maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, seed yield per plant, and 1000-seed weight exhibited high heritability along with high genetic advance (GAM), suggesting these traits are primarily controlled by additive gene effects. Therefore, phenotypic selection for these traits could be effective for future breeding programs.

Keywords - Genetic variability, Heritability, Genetic advance, *Sesamum indicum*

1. INTRODUCTION:

Sesame (*Sesamum indicum* L.) ($2n = 26$), commonly known as Til or Gingelly, is a vital oilseed crop in both tropical and temperate regions. Often referred to as the "Queen of Oilseeds" due to its resistance to oxidation and rancidity, sesame also plays a key role as an industrial food crop due to its high nutritional value. Sesame seeds contain 40-63% oil, rich in oleic and linoleic acids. Globally, sesame is cultivated over 8.8 million hectares, with an annual production of around 2.8 million tonnes and an average productivity of 382 kg/ha. India is the leading producer, accounting for 25.8% of global production from 29.8% of the area, and is also the highest exporter, contributing 40% to global exports. In India, sesame is grown across 1.58 million hectares, with a production of 1.74 lakh tonnes and a productivity of 478 kg/ha. In Telangana, sesame is grown over 21,000 hectares, yielding 15,000 tonnes with a productivity of 714 kg/ha. It is primarily cultivated as a summer crop in districts of northern Telangana, such as Adilabad, Jagtial, Karimnagar, and Nizamabad.

A diverse germplasm is essential in plant breeding programs, as it offers a pool of desirable traits for selection. However, evaluating and maintaining a large number of germplasm lines can be challenging. The concept of creating novel variation from a large gene pool was successfully established by Ellis et al. (1998). Genetic improvement of crops depends on understanding key genetic parameters, such as phenotypic and genotypic variances, phenotypic and genotypic coefficients of variation (PCV and GCV), broad-sense heritability, and genetic gain, which inform breeding methods for crop enhancement. Evaluating germplasm diversity is crucial for plant breeding programs aimed at improving crop traits.

The success of plant breeding hinges on the extent of genetic variability in the crop. Analyzing and estimating genetic variability in germplasm is a prerequisite for initiating crop improvement programs and adopting suitable selection methods to develop high-yielding genotypes. Heritability reflects the transmissibility of traits to future generations, helping breeders determine whether observed variability is heritable. Knowledge of heritability is essential for selecting traits to improve yield. Genetic advance measures the difference between the mean genotypic values of selected populations and their original populations, providing insight into the potential genetic gain from selection. Heritability estimates, when combined with genetic advance, offer a more reliable prediction of genetic gain under selection than heritability alone. In light of these considerations, this study was conducted to assess genetic variability, heritability, and genetic advance for several quantitative traits in 68 sesame accessions.

2. MATERIAL AND METHODS

2.1 Description of Experimental Site

The experiment was carried out at Regional Agricultural Research Station, Polasa, Jagtial, during *summer 2020*. The research station is situated in Northern Telangana Zone, India at 18° 48' N latitude, 78° 56' E longitude and 281m altitude of mean sea level.

2.2 Experimental Material and Design

The experimental material used in the present investigation comprised of 68 genotypes of sesame. These 68 genotypes include one National Checks (TKG 22) and 2 Local checks (YLM 11, YLM 66, YLM 17). The experiment was laid out in Randomized Block Design (RBD) with three replications. Each genotype was sown in three rows of two metres length with inter-row

spacing of 30 cm and intra row spacing of 10 cm. Sowing was done by dibbling the seed at 2-3 cm depth. All the standard package of practices were followed during the crop growth period.

2.3 Data collection

The data was recorded on yield and yield attributing characters from five randomly selected plants in each replication. Data were recorded for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, seed yield per plant, 1000 seed weight.

2.4 Data Analysis

of variance was computed for replicated data (RBD) as per the standard statistical procedure (Panse and Sukhatme, 1985). The significance was tested by referring to the values of “F” table (Fisher and Yates, 1963). The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane (1953). Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) was computed as described by Allard (1960). Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the populations was estimated according to the method illustrated by Johnson *et al.* (1955).

3. RESULTS AND DISCUSSIONS

All the sesame genotypes included in this study exhibited significant differences in their mean performance for the traits evaluated (Table 1), suggesting the presence of substantial variability across the genotypes for most of the traits. This variability is crucial for plant breeding programs as it provides the opportunity to select genotypes with desirable traits for further improvement. Understanding the genetic variability in a crop species is fundamental to the success of any breeding effort, as it directly influences the potential for selecting superior genotypes. The coefficient of variation, a key indicator of variability, revealed that the Phenotypic Coefficient of Variation (PCV) was higher than the Genotypic Coefficient of Variation (GCV) for all the traits under study, though the differences between them were narrow. This suggests that environmental influences had minimal impact on the variability of the traits, and a greater proportion of the observed variability can be attributed to genetic factors. Traits

such as **seed yield per plant** and **number of capsules per plant** exhibited high PCV and GCV values, indicating substantial genetic variation and providing greater potential for selection and improvement in these traits through breeding. The heritability estimates, when considered alongside the genetic advance as a percentage of the mean, provide a more reliable prediction of potential genetic gain under selection than heritability alone. As highlighted by Hamouda et al. (2016), the combination of heritability and genetic advance is crucial for effective crop improvement, as it helps identify traits that are likely to respond positively to selection. High values for both heritability and genetic advance, particularly for traits like **seed yield per plant** and **number of capsules per plant**, suggest that these traits are predominantly governed by additive genetic effects and can be efficiently improved through selection.

The detailed phenotypic and genotypic coefficients of variation, heritability estimates, and genetic advance as a percentage of the mean for the yield and yield-attributing traits are summarized in Table 2, with graphical representations of the PCV and GCV (Fig. 1) and the heritability and genetic advance as percentage of the mean (Fig. 2). These results underscore the potential for genetic improvement of sesame, particularly for traits that exhibit high genetic variability and strong heritable components.

3.1 Studies on PCV, GCV, Heritability and Genetic Advance for yield and yield contributing characters

The study evaluated various quantitative traits in 68 sesame genotypes, and the results are summarized as follows:

1. Days to 50% Flowering: The number of days to 50% flowering ranged from 40.00 (JCS 3985) to 59.00 days (JCS 3593), with a mean of 50.03 days. JCS 3985 was the earliest flowering genotype, while JCS 3593 exhibited the latest flowering. Both genotypic and phenotypic coefficients of variation (GCV and PCV) were moderate at 9.11% and 9.31%, respectively. This trait exhibited high heritability (95.80%) and a moderate genetic advance (18.37%), suggesting it is influenced by additive gene action.
2. Maturity Duration: Maturity duration ranged from 83.00 days (YLM-17) to 98.00 days (JCS 3593, JCS 3762), with an average of 90.84 days. YLM-17 was early maturing, while JCS 3593 and JCS 3762 were late-maturing. Both GCV and PCV for this trait were

low at 3.85% and 3.97%, respectively, indicating less variability. Maturity duration showed high heritability (94.00%) but low genetic advance (7.70%), implying it is primarily governed by additive gene effects and can be improved through simple selection.

3. **Plant Height:** Plant height varied from 70.50 cm (FFAT-147) to 112.00 cm (JCS 3997), with an overall mean of 89.24 cm. FFAT-147 was the shortest, and JCS 3997 was the tallest. The GCV (10.74%) and PCV (13.38%) were moderate. The trait exhibited moderate heritability (64.50%) and a moderate genetic advance (17.76%), suggesting non-additive gene action, where selection may be less effective for further improvement.
4. **Number of Branches per Plant:** The number of branches ranged from 2.0 (JCS 3899) to 5.00 (Swetha Til), with a mean of 2.86 branches. JCS 3599, JCS 3287, JCS 3265, and JCS 2611 had high branching. Both GCV and PCV were high at 23.53% and 24.09%, respectively. High heritability (95.40%) and a high genetic advance (47.35%) indicate that this trait is under additive genetic control and selection can be effectively used for improvement.
5. **Number of Capsules per Plant:** This trait ranged from 14.00 (FFAT-140) to 62.00 (JCS 2611), with a mean of 39.94 capsules. FFAT-140 and FFAT-146 produced fewer capsules, while JCS 2611 produced the most. GCV and PCV were high at 33.04% and 34.22%, respectively. The trait exhibited high heritability (93.20%) and a high genetic advance (65.73%), suggesting the potential for significant improvement through selection.
6. **Capsule Length:** Capsule length ranged from 1.95 cm (JCS 3899) to 2.5 cm (JCS 2454), with an average of 2.25 cm. The GCV (4.22%) and PCV (6.38%) were low, indicating limited variability. The trait showed moderate heritability (43.80%) and low genetic advance (5.75%), suggesting it is controlled by non-additive gene action and selection for this trait is not likely to be effective.
7. **Capsule Width:** Capsule width varied from 0.43 cm (JCS 3999) to 0.61 cm (TKG 22), with a mean of 0.53 cm. The GCV (7.51%) and PCV (8.17%) were low. High heritability (84.50%) and moderate genetic advance (14.23%) suggest that this trait is also controlled by non-additive gene action, making selection less effective.

8. **Number of Seeds per Capsule:** The number of seeds ranged from 39.50 (FFAT-135) to 79.00 (GT 10), with an average of 56.76 seeds. Genotypes such as JCS 2454 (79 seeds) exhibited the highest seed count, while FFAT-135 had the lowest (39.50). The GCV (17.36%) and PCV (17.95%) were moderate. High heritability (93.50%) and a high genetic advance (34.58%) indicate additive genetic control, making this trait suitable for selection.
9. **Seed Yield per Plant:** Seed yield ranged from 2.85 g (JCS 4001) to 13.01 g (JCS 2454), with a mean of 6.89 g. JCS 4001 recorded the lowest yield, while JCS 2454 had the highest. The GCV (36.79%) and PCV (37.98%) were high, indicating substantial variability. High heritability (93.90%) and a high genetic advance (73.43%) suggest that this trait is highly heritable and can be effectively improved through selection.
10. **1000 Seed Weight:** The 1000 seed weight ranged from 1.90 g (JCS 4049) to 4.00 g (GT-10), with a mean of 3.07 g. The GCV (13.24%) and PCV (14.17%) were moderate. The trait exhibited high heritability (87.30%) and a high genetic advance (25.49%), indicating it is largely controlled by additive gene action, making selection for this trait effective.

The present study revealed significant genetic variability for key agronomic traits in sesame, with high heritability and genetic advance observed for traits such as **number of branches per plant**, **number of capsules per plant**, **number of seeds per capsule**, **seed yield per plant**, and **1000 seed weight**. These traits are primarily controlled by additive gene effects, making them suitable for direct selection in breeding programs. Traits with high heritability and genetic advance, such as **seed yield** and **number of branches**, offer excellent potential for improving productivity and yield in sesame. Conversely, traits like **capsule length** and **capsule width** exhibited lower genetic variability and may require alternative breeding strategies or multi-trait selection. Overall, the results of this study provide valuable insights for breeding high-yielding sesame varieties with improved agronomic traits, benefiting both commercial production and genetic resource conservation.

4. Conclusion

In summary, the study's findings highlight the importance of considering both heritability and genetic advance when selecting traits for improvement. Traits with high heritability and genetic advance, such as number of branches per plant, number of

capsules per plant, number of seeds per capsule, and seed yield, show the greatest potential for genetic improvement through selection. These traits should be prioritized in breeding efforts aimed at enhancing the productivity and performance of sesame.

Table 1. Analysis of Variance for yield and yield attributing traits in sesame at RARS, Polasa, Jagtial during *summer*, 2020.

S.No.	Character	Mean Sum of Squares		
		Replication	Genotype	Error
1.	Days to 50% Flowering	0.01	42.49 ***	0.91
2.	Days to Maturity	0.59	25.34 ***	0.79
3.	Plant Height (cm)	5.68	234.51 ***	50.69
4.	Number of Branches per Plant	0.34	0.93 ***	0.02
5.	Number of Capsules per Plant	0.04	361.24 ***	12.66
6.	Capsule length (cm)	0.16	0.03***	0.01
7.	Capsule width (cm)	0.01	0.007**	0.00
8.	Number of seeds per capsules	1.88	200.94 ***	6.71
9.	Seed yield per plant (g)	0.02	13.28***	0.42
10.	Test weight (g)	0.01	0.36 ***	0.02

*- Significance level at 5% level of probability (1.43)

** Significance level at 1% level of probability (1.65)

Table 2. Genetic parameters for yield and yield attributing traits in sesame at RARS, Polasa, Jagital during *summer*, 2020

Trait	Range		Mean \pm SEM	Variance		Coefficient of Variation		h^2 (%)	GAM (%) at 5%
	Min	Max		Genotypic	Phenotypic	GCV (%)	PCV (%)		
Days to 50% flowering	40.50	59.00	50.03 \pm 0.67	20.79	21.70	9.11	9.31	95.80	18.37
Days to maturity	83.00	98.50	90.84 \pm 0.62	12.27	13.06	3.857	3.97	94.00	7.70
Plant height (cm)	70.50	112.50	89.24 \pm 5.03	91.91	142.60	10.742	13.38	64.50	17.76
Number of branches per plant	2.0	5.00	2.86 \pm 0.10	0.45	0.47	23.533	24.09	95.40	47.35
Number of capsules per plant	14.00	62.00	39.94 \pm 2.51	174.28	186.95	33.049	34.22	93.20	65.73
Capsule length (cm)	1.950	2.50	2.25 \pm 0.07	0.009	0.021	4.222	6.38	43.80	5.75
Capsule width (cm)	0.43	0.61	0.53 \pm 0.01	0.002	0.002	7.516	8.17	84.50	14.23
Number of seeds per capsule	39.50	79.10	56.76 \pm 1.83	97.11	103.82	17.361	9.18	93.50	34.58
Seed yield per plant (g)	2.85	13.00	6.89 \pm 0.45	6.43	6.85	36.797	37.98	93.90	73.43
1000 seed weight (g)	2.30	4.34	3.11 \pm 0.11	0.17	0.19	13.243	14.17	87.30	25.49

Fig 1. Genotypic and phenotypic coefficients of variation for yield and yield attributing traits in sesame genotypes

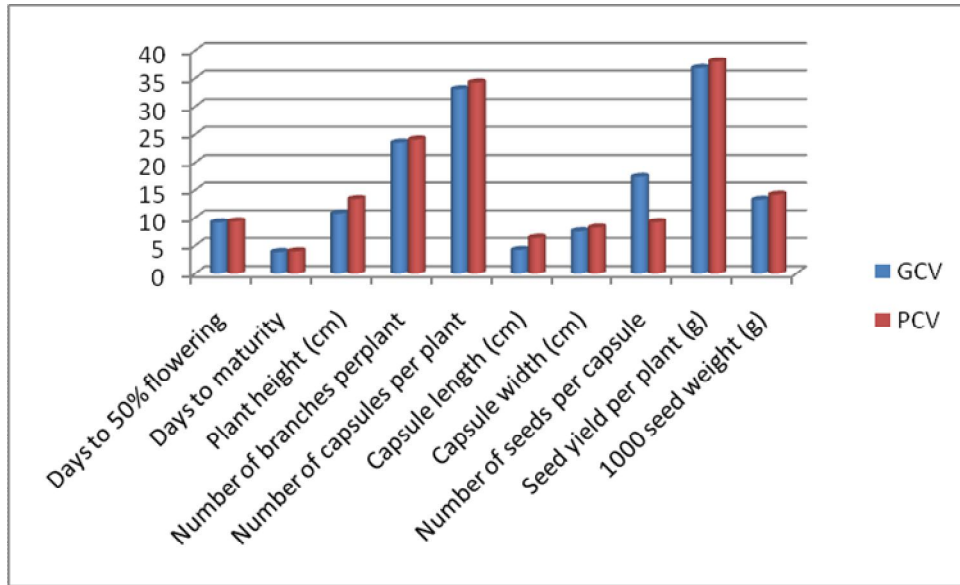
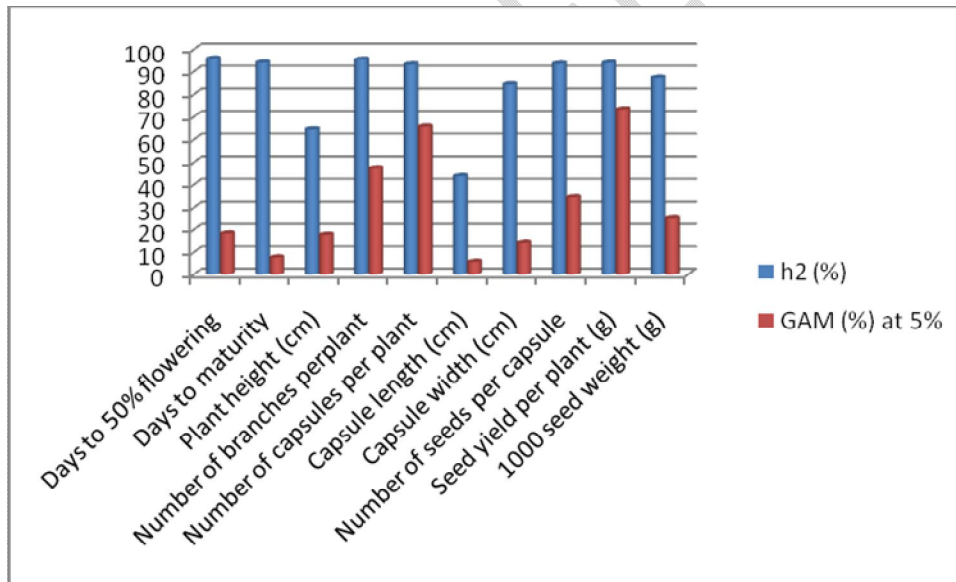


Fig 2. Heritability and Genetic advance as per cent of mean for yield and yield attributing traits in sesame genotypes



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