

Unveiling the sesame germplasm- A study of genetic variability for yield (*Sesamum indicum*. L)

Abstract

Ninety-six sesame genotypes were evaluated in a Randomized Block Design (RBD) at ICAR-IIOR, Narkhoda farm, to determine the genetic variability, heritability and genetic advance for nine traits. Analysis of variance showed that significant variation was present in the genotypes studied. The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits. High GCV and PCV levels were recorded for seed yield per plant, number of capsules per plant and plant height. Heritability was high for seed yield per plant, 1000 seed weight, number of seeds per capsule, number of capsules per plant, plant height, days to maturity and oil content. GA (% mean) was high for all the traits except days to 50 % flowering, days to maturity. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plant, 1000 seed weight, number of seeds per capsule, number of capsules per plant, plant height and oil content.

Keywords: Sesame, genetic parameters, heritability, genetic advance

1. Introduction

Sesame (*Sesamum indicum* L.), an ancient and significant oilseed crop, belongs to the Pedaliaceae family. The name, sesame, derives from the Arabic word "simsim". It is commonly known by the names Sesamum, Til, Gingelly, Simsim, benniseed, Gergelim etc. In India, 2023-24 sesame is being grown over an area of 10.39 lakh hectares with the production of 8.11 lakh tonnes. Sesame is regarded as the "Queen of Oilseeds" because of its exceptional keeping quality, which is attributed to its high resistance to oxidation and rancidity [1]. Seeds and its oil are being utilized as important food ingredients. Sesame seeds contain 57 to 63% oil and 25% protein [2]. Sesame seed oil boasts a long shelf life due to the presence of lignans (Sesamin, Sesamol, Sesamolol) which have notable antioxidant properties that resist oxidation [3]. Additionally, the oil is rich in oleic and linoleic acids [4]. Several authors [5] have reported the health benefits of these compounds, which include antioxidant, anti-aging, antihypertensive, anticancer, cholesterol-lowering, and antimutagenic properties.

The presence of variation is vital for the success of any crop improvement program. Understanding genetic parameters such as variability, heritability, and genetic advance is essential for enhancing crop breeding efforts. Genetic variation among traits is critical for identifying desirable genotypes and establishing a strong genetic foundation for selective breeding. Studies on heritability, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance provide valuable insights into the traits under investigation. This knowledge aids in understanding gene action and determining the most suitable breeding methods to employ. With these considerations in mind, the present experiment was conducted to evaluate genetic variability in sesame genotypes.

2. Materials and methods

The present study was conducted at ICAR- Indian Institute of Oilseeds Research, Narkhoda farm, Hyderabad during early summer, 2024. The experiment was laid out with ninety-six sesame genotypes in a Randomized Block Design (RBD) with three replications. Recommended agronomic practices were followed during crop growth period. The genotypes were evaluated for the following traits: days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, seed yield per plant, oil content.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme [6]. The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane [7]. 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) and was estimated on genotype mean basis as described by Allard [8] and Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson et al. [9].

Table 1. Analysis of variance for yield components in ninety six genotypes of sesame

Source of Variation	df	Mean sum of squares								
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Number of seeds per capsule	1000 seed weight	Seed yield per plant (g)	Oil content (%)
Replications	2	2.44	2.52	0.00	1.38	8.69	0.014	0.12	0.00	2.42
Genotypes	95	6.16**	76.52**	534.03**	1.90**	1016.70**	227.25**	0.59**	18.82**	108.74**
Error	190	1.08	1.25	1.66	0.652	3.95	2.126	0.04	1.30	1.14
Total	287	2.77	26.18	177.87	1.07	339.21	76.63	0.22	7.09	36.76

*-Significance at 5% level of probability

** -Significance at 1% level of probability

3. Results and Discussions

The analysis of variance showed significant differences among the genotypes for all the traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, seed yield per plant and oil content indicating the presence of considerable genetic variability among the experimental material under study (Table 1).

The value of Genotypic Coefficient of variation (GCV) ranged from 3.39 for days to 50 % flowering to 44.12 for seed yield per plant. High GCV was observed for seed yield per plant (44.12), number of capsules per plant (40.26), plant height (23.54). Thouseem *et al.* [10], Srikanth and Ghodke [11] also reported higher estimates of GCV for seed yield per plant and number of seeds per capsule and for plant height by Roy *et al.* [12], Umateet *et al.* [13]. Traits like number of branches per plant (18.95), number of seeds per capsule (16.84), 1000 seed weight (14.20), oil content (14.87) showed moderate genotypic coefficient of variation. Vamshi *et al.* [14] reported moderate GCV for number of branches per plant and oil content, Thouseem *et al.* [10] reported moderate GCV for number of seeds per capsule and 1000 seed weight. The existence of moderate variability suggests that selection for these traits is potential to some extent for the enhancement. Low genotypic coefficient of variation was observed for days to 50% flowering (3.39) and days to maturity (5.64). Padmaja *et al.* [15], Khuntia *et al.* [16] also reported low GCV for days to 50 % flowering and days to maturity.

The Phenotypic Coefficient of Variation (PCV) was found high for seed yield per plant (48.82), number of capsules per plant (40.49), number of branches per plant (30.35) and plant height (23.65). Moderate PCV was observed for number of seeds per capsule (17.07), 1000 seed weight (15.67), oil content (15.10). Low PCV was observed for days to 50 % flowering (4.34), days to maturity (5.78). The PCV estimates were higher than the GCV for all traits studied, suggesting that environmental factors significantly influence trait expression. This indicates that selection based on these traits could be effective, as their phenotypic expression reliably reflects their genetic potential. According to Padmaja *et al.* [15] days to 50 % flowering, days to maturity showed low genotypic and phenotypic coefficient of variation. (Fig. 1).

The minor differences between genotypic and phenotypic coefficients of variation in this investigation is due to the minimal environmental impact, suggesting that the phenotype closely resembles the genotype.

High heritability was obtained for plant height (99.10), number of capsules per plant (98.80), number of seeds per capsule(97.20), oil content (96.90), days to maturity (95.20), 1000 seed weight (82.10), seed yield per plant (81.70). Similar results are also reported by Durodola *et al.* [17]. Moderate heritability is observed for days to 50 % flowering (60.90), reported by Vanishree *et al.* [18]. Low heritability was observed for number of branches per plant (39.00).

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Table 2. Genetic parameters for yield components in ninety nine genotypes of sesame

S.No.	Trait	Range		Mean \pm SEM	Variance		Coefficient of Variation		h^2 (%)	GAM (%) at 5 %
		Min	Max		Genotypic	Phenotypic	GCV (%)	PCV (%)		
1	Day to 50% flowering	35.00	41.00	38.34 \pm 0.59	1.69	2.78	3.39	4.34	60.90	5.45
2	Day to maturity	80.00	98.00	88.69 \pm 0.64	25.08	26.35	5.64	5.78	95.20	11.35
3	Plant height (cm)	36.23	108.8	56.57 \pm 0.74	177.45	179.12	23.54	23.65	99.10	48.28
4	Number of branches per plant	2.00	6.00	3.40 \pm 0.46	0.41	1.06	18.95	30.35	39.00	24.39
5	Number of capsules per plant	10.00	99.00	45.63 \pm 1.14	337.58	341.53	40.26	40.49	98.80	82.46
6	Number of seeds per capsule	34.00	70.00	51.43 \pm 0.83	75.04	77.16	16.84	17.07	97.20	34.21
7	1000 seed weight (g)	1.72	3.92	3.01 \pm 0.11	0.18	0.22	14.20	15.67	82.10	26.52
8	Seed yield per plant (g)	2.42	14.44	5.47 \pm 0.65	5.83	7.14	44.12	48.82	81.70	82.16
9	Oil content (%)	25.53	51.87	40.73 \pm 0.61	26.54	27.89	12.64	12.96	96.90	30.16

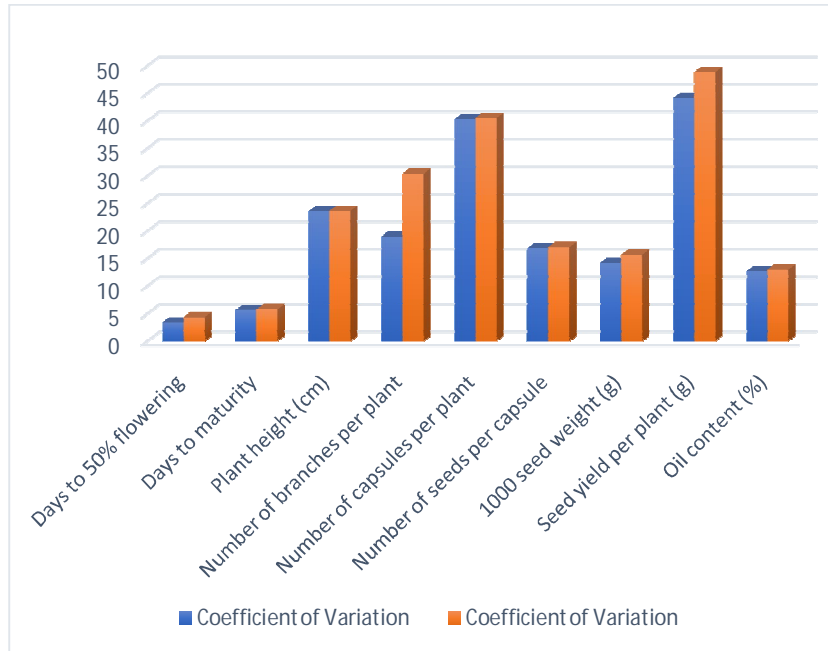


Fig 1. Genotypic and phenotypic coefficients of variation for yield components in sesame genotypes

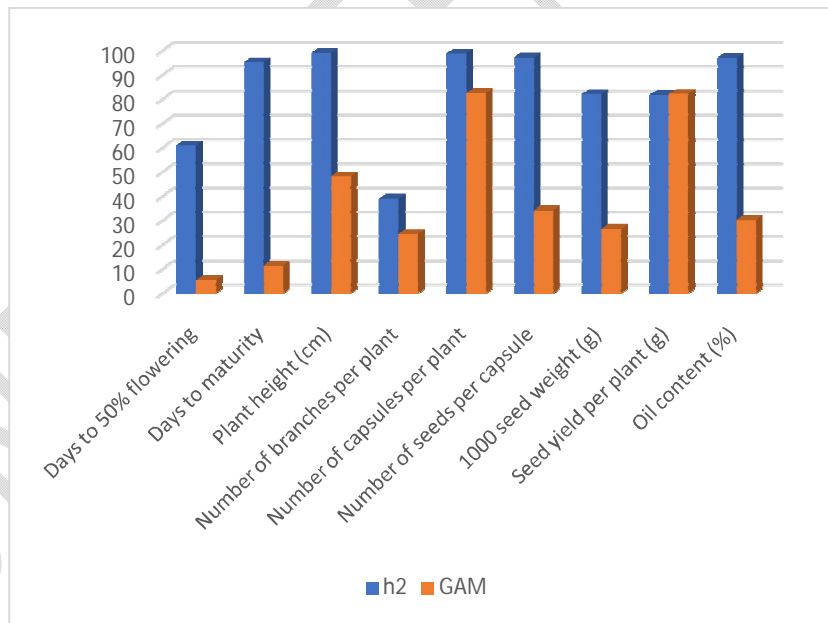


Fig 2. Heritability and genetic advance as per cent of mean for yield components in sesame genotypes

The highest estimate of genetic advance as percent of mean was recorded for number of capsules per plant (82.46), followed by seed yield per plant (82.16), plant height (48.28), number of seeds per capsule (34.21), oil content (30.16), 1000 seed weight (26.52), number of branches per plant (24.39). Moderate genetic advance was recorded for days to maturity (11.35). Low genetic advance was observed for days to 50 % flowering (5.45) (Fig. 2). Takele and Abera [19], Zeinalzadeh[20] also reported low genetic advance for days to 50 % flowering. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plant, 1000 seed weight, number of capsules per plant, number of seeds per capsule, oil content and plant height showed that these traits were controlled by additive genetic influences. Similar results are also reported by Sasipriya *et al.* [21], Kumar *et al.* [22], Thouseem *et al.* [10], Srikanth and Ghodke [11], Khuntia *et al.* [16], Durodola *et al.* [17]. Vamshi *et al.* [14] found high heritability with high genetic advance on oil content. High heritability with moderate genetic advance was recorded for days to maturity indicates the limited feasibility for further improvement due to the existence of both additive and non additive genetic influences (Hedge *et al.* [24]).

Analysis of heritability, genetic advance and genotypic coefficient of variation suggests the notability of seed yield per plant, number of capsules per plant and 1000 seed weight in the selection of genotypes with high yield potential Mustafa *et al.* [23].

4. Conclusion

Greater genetic variability enhances the likelihood of selecting superior genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) on seed yield per plant, number of capsules per plant, number of branches per plant and plant height gives us an idea about the magnitude of variability present in these characters in a genetic population. High heritability along with high genetic advance as percent of mean in the traits, seed yield per plant, 1000 seed weight, number of capsules per plant, number of seeds per capsule, oil content and plant height indicated additive gene action predicting genetic gain under selection than heritability estimates alone. Therefore, plant breeding efforts should focus on manipulating existing genetic diversity in the desired direction through appropriate crop improvement programs to develop sesame with enhanced seed yield and oil content.

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