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## Genetic variability, heritability and genetic advance studies in sesame (*Sesamum indicum* L.)

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### Abstract

The current study was conducted on 30 genotypes, including one local check, at the AICRP Experimental Farm on Safflower at Vasantnao Naik Marathwada Krishi Vidyapeeth, Parbhani (Maharashtra) during the summer of 2022–2023. Three replications of a randomized block design were used to conduct the current experiment. There were notable differences for every character, according to the analysis of variance. The degree of variability in the experiment material was also shown by the genotypic and phenotypic coefficient of variation (GCV and PCV). For the majority of the traits in the current analysis, a large range of variability was noted. Characteristics such as plant height, number of seeds per capsule, seed output per plant, days to 50% flowering, number of capsules per plant, and 1000 seed weight had a larger mean variance range. For each plant, a substantial genetic progress (20.55%) along with high heritability (80.02%) was seen in the seed yield. For the traits of plant height, number of branches per plant, number of capsules per plant, and seed output, the percent mean of all the genotypes under investigation has demonstrated high heritability along with high genetic advance.

**Keywords:** Variability, heritability, genetic advance, GCV, PCV

### Introduction

From roughly 40° N latitude, one of the most significant oil seed crops in mild, temperate, and tropical countries is sesame (*Sesamum indicum* L.). Although cross-pollination can range from 5 to over 50%, it typically self-pollinates (Pathirana, 1994) [11]. It is a member of the Tubiflorae (Pedaliaceae) order of family. One of the most popular nicknames for it is "queen of oil crop." It is grown in more than 50 countries across the globe. Despite the crop's African origins, India is thought to be the primary hub of genetic variation (Maiti *et al.*, 2012) [8]. Common names for sesame include gingelly, til, and tila. Because to its high oil content (38%–54%), protein (18%–25%), calcium, phosphorus, oxalic acid, and superior seed oil characteristics, sesame is known as the "Queen of oilseeds". Because lignans (sesamin, sesaminol, and sesaminolol) have a remarkable antioxidant effect and can withstand oxidation, sesame seed oil has a long shelf life. Sesame is the fifth-most popular spice and edible oil. It is also utilized in pharmaceutical and skin care products and acts as a synergistic pesticide. Cattle are given residual oil extraction residues as a source of crude protein. You can eat the grains as sweetmeats, fried, or sweetened. High-quality edible oil or an oily paste (tahini) are made from crushed seeds. The expression of yield, a complicated character, is dependent on the influence of yield-attributing features. Therefore, breeders will greatly benefit from a thorough assessment of the amount of genetic variation available for the yield qualities. Any crop improvement program's ability to succeed mostly relies on the kind and magnitude of crop variability.

### Materials and Methods

In the summer of 2022-2023, the experiment was carried out on the AICRP experimental farm on safflower in Vasantnao Naik Marathwada Krishi Vidyapeeth, Parbhani (Maharashtra). Thirty sesame germplasm collections made up the study's material. Three replications of the experimental material were assessed using Randomized Block Design (RBD). For the purpose of documenting observations, five plants were randomly chosen from each genotype in each replication. The average value of every characteristic was calculated using the measurements made on certain plants. The following characteristics were noted: days to fifty percent of the plants flowered, plant height (cm), number of branches per plant, number of capsules per plant, length of capsules (cm), number of seeds per capsule, 1000 seed weight (g), days till maturity, and number of seeds produced per plant (g).

Following Panse and Sukhatme's typical protocol, an ANOVA was computed to determine the significance of differences between the treatments for each trait (1985). By dividing the total value of the observations by the number of observations, the mean values of all the treatments for the different genotype attributes were calculated. The genotypic and phenotypic variance was computed using the mean square from the variance table (Burton, 1952) [1]. Burton's (1952) [1] approach was utilized to assess the genotypic and phenotypic coefficient of variation, or PCV and GCV. In a broad sense, heritability is the ratio of genotypic variance to the total amount of observable variance within a population. In its broadest sense, heritability ( $h^2$ ) was computed using the formula provided by Johnson *et al.* (1955) [6]. The genetic progress for every character at 5% selection intensity was computed using the Johnson *et al.* (1955) [6] formula.

## Results and Discussion

The goal of the current study was to quantify genetic diversity, character associations, and the direct and indirect effects of these factors on the number of seeds produced per plant. The type and degree of genetic variability for the traits found in the experimental material determine the prerequisites in farming for any crop development program. The degree to which improvement was possible through phenotypic selection was indicated by the genetic variability of a character found in the experimental material. To determine the degree of variation for different characters, a general analysis of variance was performed for each character. For every character under study, the genotype variations were highly significant (Table 1), suggesting that there is sufficient variability among the genotypes for all the traits being studied and suggesting that future generations may be able to improve yield through recombination and selection. Numerous factors were examined for the variable under investigation, including heritability (broad sense), genetic advance, genotypic variance ( $\sigma_g^2$ ), phenotypic variance ( $\sigma_p^2$ ), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV). Table 2 presents the findings. Together, estimates of genetic advancement and heritability provide insight into the role that genes play in the manifestation of different polygenic traits and offer a solid standard for selection programs. Figures 1 and 2, respectively, provide the graphical representations of GCV, PCV, heritability, and genetic advance.

Characteristics such as plant height, number of seeds per capsule, seed yield per plant, days to 50% flowering, number of capsules per plant, and 1000 seed weight had a larger mean variance range. The features plant height (71.80-105.90 cm), number of seeds per capsule (52.26-70.33), number of capsules per plant (24.56-44.63), and days to 50% flowering (32.00-41.66 days) had a wider range of variability based on mean values. Numerous researchers have documented wide variations for various yield-contributing features in sesame, including Kumhar *et al.* (2008) [7], Jadhav and Mohrir (2013) [5], Revathi *et al.* (2012) [13], and Ismaila and Usman (2014) [4]. Sivasubramanian and Menon (1973) [16] suggested the

classification of GCV and PCV as low for 0-10%, moderate for 10-20% and 20% and above for high. In present investigation phenotypic coefficient variation was greater than genotypic coefficient variation for all the traits studied and there was a little difference between the values of GCV and PCV. Similar results were obtained by Manjeet *et al.* (2020) [9] and Saxena, K. & Bisen, R. (2016) [14]. Moderate PCV and GCV values were recorded for the traits *viz.*, plant height (11.97%, 11.39%), number of branches per plant (17.47%, 16.53%), number of capsules per plant (13.98%, 12.63%) and seed yield per plant (12.46%, 11.15%). Low PCV and GCV values were recorded for the days to 50 percent flowering (7.20%, 6.69%), days to maturity (4.35%, 4.13%) and capsule length (8.66%, 2.12%). Moderate PCV with low GCV was observed for 1000 seed weight (12.29%, 9.53%) and number of seeds per capsule (11.0%, 8.54%). Similar results were obtained by Pavani *et al.* (2020) [12] for days to maturity, capsule length were low and for number of branches per plant were moderate. Umamaheswari *et al.* (2019) [20] reported similar results for number of capsules per plant as moderate PCV and GCV. Similar results of moderate PCV and GCV for plant height and low PCV and GCV for days to 50 percent flowering were reported by Thiyagu K. *et al.* (2023) [18]. Moderate PCV and GCV for seed yield per plant was also observed by Ismail, M.B. and Mohamed, N.E. (2018) [3]. Heritability estimates were grouped by Johnson *et al.*, (1955) [6] as low for below 30%, moderate for 30-60% and above 60% as high. Genetic advance as percent of mean was grouped by Johnson *et al.*, (1955) [6] as high for 20% and above moderate for 11-20% and below 10% as low. In present study, heritability ranged from 06.00% to 90.49%, while genetic advance as percent mean ranged from 1.07% to 32.22% was observed. All the genotypes under study have shown high heritability coupled with high genetic advance as percent mean for characters *viz.*, number of branches per plant, plant height, number of capsules per plant and seed yield. High heritability along with moderate genetic advance was shown by days to 50 percent flowering, number of seeds per capsule and 1000 seed weight. High heritability with low genetic advance for days to maturity. Low heritability with low genetic advance for capsule length. Heritability (BS) was found higher for plant height, number of branches per plant, number of capsules per plant, 1000 seed weight and seed yield per plant which is in accordance with the findings of Manjeet *et al.* (2020) [9]. Similar results were obtained by Umamaheswari *et al.* (2019) [20] for days to 50 percent flowering, plant height, number of branches per plant, number of capsules per plant and seed yield per plant. High heritability with moderate genetic advance for number of seed per capsule were obtained by Tushar *et al.* (2020) [19]. High heritability with high genetic advance percent mean for number of branches per plant, number of capsules per plant and seed yield per plant are in accordance with the findings of Sirisha, ABM *et al.* (2020) [12]. High heritability with low genetic advance for days to maturity is in accordance to Chandramohan *et al.* (2014) [2] and Tirumala Rao *et al.* (2013) [21].

**Table 1:** Analysis of variance (ANOVA) for nine characters in sesame

Sr. No.	Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height	Capsule length	1000 Seed weight	No. of Branches	No. of seeds/Capsules	No. of capsules/plant	Seed yield/plant
1	Replication	2	0.667	3.991	4.013	0.005	0.007	0.006	2.056	0.763	0.036
2	Genotypes	29	12.237**	25.838**	221.724**	0.044	0.272**	0.878**	67.187**	43.161**	1.793**
3	Error	29	0.745	4.230	4.686	0.004	0.007	0.010	2.437	0.826	0.042

\*\* Significant at 1% level of probability or level of significance

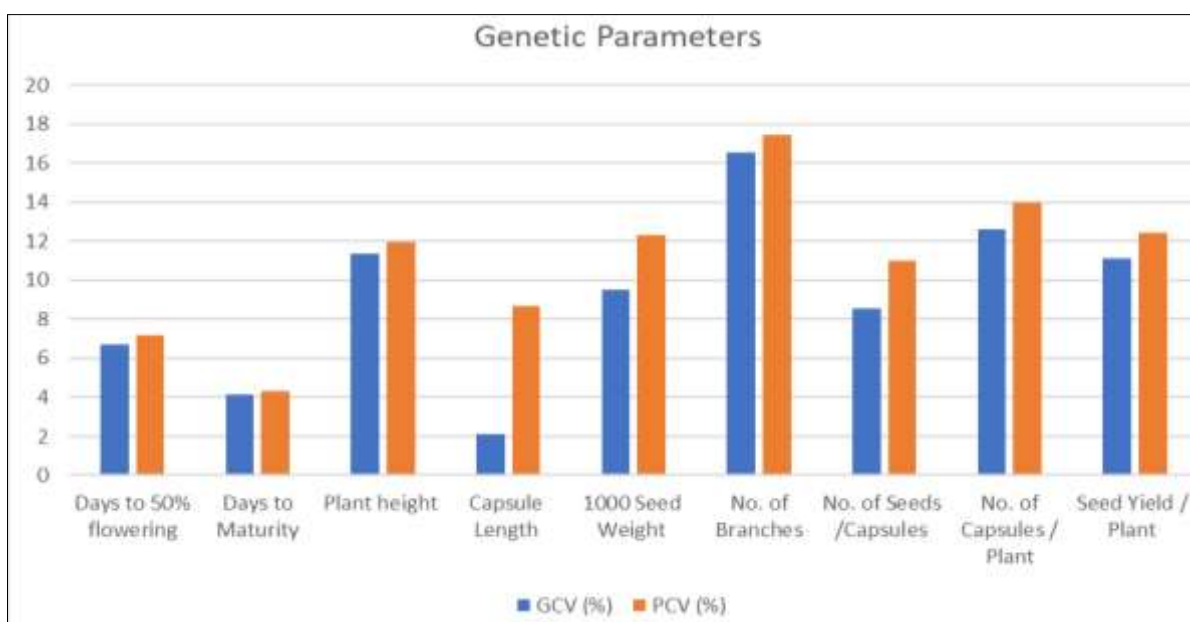
**Table 2:** Estimates of variability parameters for nine characters in sesame

Characters	Range	Genotypic variance ( $\sigma^2_g$ )	Phenotypic variance ( $\sigma^2_p$ )	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic advance	Genetic advance as % of Mean
Days to 50% flowering	32.00-41.66	5.81	6.72	6.69	7.20	86.45	4.61	12.82
Days to Maturity	78.33-92.00	12.48	13.79	4.13	4.35	90.40	6.92	8.11
Plant height	71.80-105.90	107.09	118.39	11.39	11.97	90.40	20.2	22.31
Capsule Length	2.50-3.30	0.003	0.06	2.12	8.66	06.00	0.03	1.07
1000 Seed Weight	2.92-4.20	0.11	0.18	9.53	12.29	60.08	0.53	15.20
No. of Branches	2.63-5.10	0.42	0.47	16.53	17.47	89.50	1.26	32.20
No. of Seeds /Capsules	52.26-70.33	27.55	45.67	8.54	11.00	60.30	8.39	13.67
No. of Capsules / Plant	24.56-44.63	20.06	24.60	12.63	13.98	81.50	8.33	23.50
Seed Yield / Plant	6.13-9.86	0.82	1.03	11.15	12.46	80.00	1.67	20.50

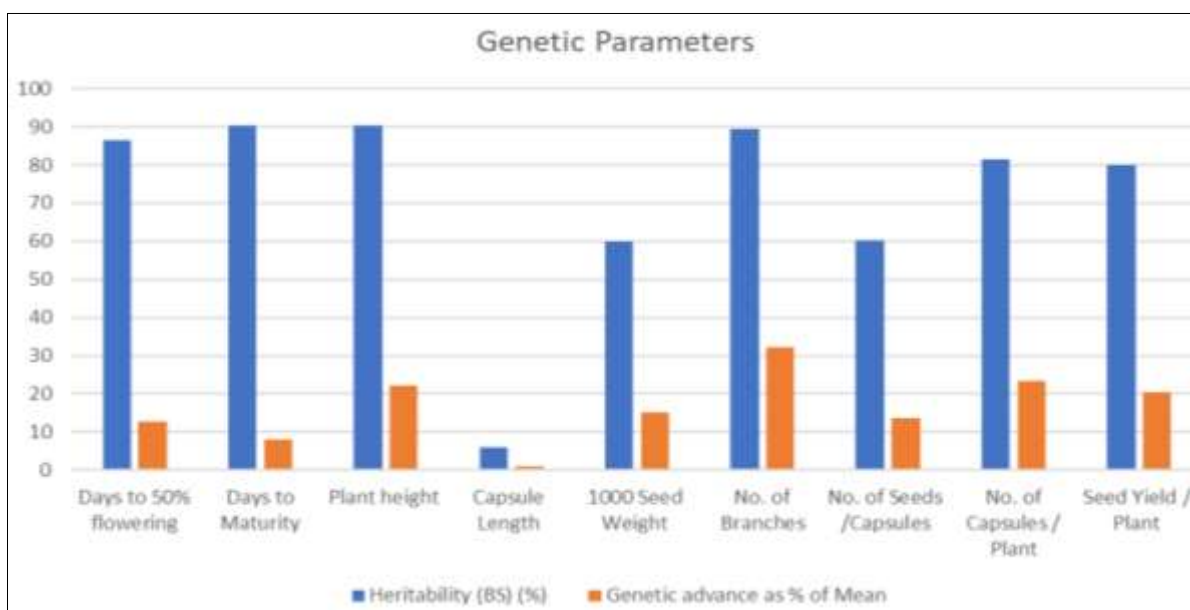
GCV = Genotypic coefficient of variation

BS = Broad sense

PCV = Phenotypic coefficient of variation



**Fig1:** Genotypic and Phenotypic coefficient of variation for nine characters in sesame



**Fig 2:** Heritability and Genetic advance as percent of mean for nine characters in sesame

**Conclusion**

There were notable differences for every character, according to the analysis of variance. There was a good degree of

variability in the experiment material, as evidenced by the magnitude of the genotypic and phenotypic coefficient of variation. Plant height, the number of branches on each plant,

the number of capsules on each plant, and the amount of seed produced by each plant have all shown reasonable estimates of PCV and GCV. On the other hand, low estimates of GCV and PCV were obtained for features like days to 50% flowering, days to maturity, and capsule length; low and moderate estimates of GCV and PCV were discovered for the traits 1000 seed weight and number of seeds per capsule. Plant height, number of branches per plant, number of capsules per plant, and seed yield per plant were found to have high heritability in conjunction with high genetic progress, which confirmed the supremacy of additive gene action in regulating these traits.

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