



## **Genetic Variability Studies for Yield and Its Attributing Traits in Dark Brown Sesame (*Sesamum indicum* L.)**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

The present experiment was carried out during *Kharif*, 2019 at Jawaharlal Nehru krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India. A total of 500 accessions were evaluated and observations were recorded on twelve traits *viz.*, days to flower initiation, days to fifty percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g), seed yield per plant (g) and oil content (%). REML analysis revealed significant differences among the 500 accessions for all the traits. It indicates an adequate amount of genetic variability present among the accessions for yield and yield attributing traits. Phenotypic coefficients variation values were higher than Genotypic coefficients variation values under the study. High heritability was recorded for all the traits under experiment. Genetic advance as percentage of mean recorded low for traits days to flower initiation, days to 50% flowering, days to maturity. Medium for traits oil content (%), plant height, number of seeds per capsule, whereas traits capsule length, number of capsule per plant, thousand seed weight, number of primary branches per plant, seed yield per plant, number of secondary branches per plant recorded in high magnitudes. This result indicates preponderance of additive gene effect, which will help to make selection in early segregating generation.

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## 1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oil seed crop and one of the ancient oil seed crops, belonging to Pedaliaceae family. It is considered as the “Queen of oilseeds” as the seeds are major source of various micro elements Iron (Fe), Magnesium (Mg), Copper (Cu) and some important vitamins (B1, E). It is cultivated in most of the parts of the world and majorly in Asia, Africa and South America [1]. In sesame seeds calcium content is three times higher than milk [2]. Iron deficiency causes anaemia, which has been proven to have severe effects in children than in adults, resulting in fatigue, weakness, and irritability, as well as impaired mental development and disease susceptibility. [3]. Sesame oil has high amount of fatty acid content and high levels of fat and protein. Mostly, sesame is consumed in the form of oil and meal which is increasing in India and globally mainly due to changing consumption patterns and increasing health awareness and its consumption estimated was USD 6.67 billion in 2019, and may reach USD 7.56 billion by 2027, with a CAGR (compound annual growth rate) of 1.5% [4].

Existence of variation is a prerequisite for any crop improvement programme to succeed in any crop [5] and the ability to identify this genetic variation and exploiting it is of immense value for planning efficient breeding programme to improve the yielding potential of genotypes. Knowledge on genetic parameters like variability, heritability and genetic advance are the pre requisites to improve any crop breeding programme. The success of any crop improvement programmes mostly depend on the existence of genetic variability in the accessions evaluated. Genetic variation among characters is important for selecting desirable genotypes and provides strong genetic base for selective breeding. Studies on heritability, GCV, PCV, genetic advance can help us to get clear information of the traits under study and know the gene action and breeding methods to be employed. Keeping this in view, the present experiment was conducted to evaluate genetic variability in dark brown sesame accessions.

## 2. MATERIALS AND METHODS

In this experiment 500 accessions along with four checks (TKG-21, TKG-22, JTS-8, GT-10) were

evaluated in un-replicated Augmented Design during *Kharif*, 2019. Spacing between row to row and plant to plant was kept 30 cm and 10 cm. These accessions were procured from Project Coordinating Unit, AICRP on Sesame & Niger, JNKVV Campus, Jabalpur, Madhya Pradesh, India. In order to record the observations, five randomly chosen competitive plants were selected from each genotype. Observations were recorded on twelve traits viz., days to flower initiation, days to fifty percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g), seed yield per plant (g) and oil content (%). Genetic parameters were evaluated using standard statistical procedures given below.

### 2.1 Coefficients of Variation

Phenotypic and Genotypic coefficients of variation (PCV and GCV) were computed according to Burton [6].

Phenotypic coefficient of variation (PCV) = Phenotypic variance ( $\sigma_p$ ) / General mean ( $\bar{X}$ ) x 100

Genotypic Coefficient of Variation (GCV) = Genotypic variance ( $\sigma_g$ ) / General mean ( $\bar{X}$ ) x 100

GCV and PCV were categorized into Low = Less than 10%; Moderate = 10-20%; High = More than 20%.

### 2.2 Heritability

Heritability in broad sense was estimated by the following formula given by Hanson [7]

$$h^2 (bs) \% = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson et al [8].

#### 2.2.1 Genetic advance as percentage of mean

Genetic advance as percentage of mean was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as < 10 per cent as low, 10-20 per cent as moderate, >20 per cent as high.

### 3. RESULTS AND DISCUSSION

In present experiment, 500 sesame accessions were evaluated to assess their genetic potential. The REML analysis revealed that significant differences are present among the sesame genotypes (Table 1) for all the traits under study indicating high magnitude of variability in the genotypes. Mean, range, heritability, GCV, PCV and genetic advance as percent of mean are presented in Table 2.

Days to flower initiation ranged from 35.77 to 38.76 with a mean of 37.18 days. Days to 50% flowering exhibited a mean value 41.51 days and varied from 38.36 to 45.87 days. Days to maturity showed mean value of 93.78 and varied from 84.58 to 97.92 days. Plant height was observed in a range from 94.20 cm to 136.80 cm with mean of 114.74 cm. Number of primary branches for plant varied from 2.27 to 5.40 with mean of 3.51. Number of secondary branches for plant ranged from 0.20 to 2.77 with an average value of 1.18. Number of capsules per plant varied from 36.40 to 67.66 with mean value of 49.34. Capsule length was observed within a range from 1.58 cm to 3.22 cm with an average value 2.34 cm. Number of seeds per capsule exhibited mean value 59.84 and varied from 43.74 to 73.56. One thousand seed weight 1000-seed weight ranged from 2.19 g to 3.92 g with mean value of 3.01 g. Oil content varied between 30.84 and 49.13 with average value of 42.33 and seed yield per plant ranged from 5.12 g to 11.84 g with an average value of 7.49 g.

All traits under this experiment revealed that PCV values were higher than GCV representing the effect of environment on expression of traits [9]. High genotypic and phenotypic coefficients of variation were observed for the trait secondary branches (52.12% and 56.87%) followed by seed yield per plant (20.76 % and 22.2%). Similar results have been observed by Patil and Lokesha [10], Kalaiyarasi et al.[11], Aye and Htwe [12] and Singh et al. [13].

Moderate genotypic and phenotypic coefficient variations were observed for number of primary branches per plant (18.76% and 19.99%),

number of capsules per plant (17.12% and 19.41 %), 1000-seed weight (16.77% and 17.16%), number of seeds per capsule (10.06 % and 10.34%) and capsule length (11.61% and 11.64%). Similar results have been observed by Gangadhara et al. [14] for number of seeds per capsule and capsule length; Patil and lokesha [10] for number of branches per plant and number of seeds per capsule.

Whereas low genotypic and phenotypic coefficient of variation were recorded for days to maturity (2.62% and 2.67%), days to flower initiation (2.25% and 2.56%), days to fifty percent flowering (3.44% and 3.62%), oil content (8.36% and 8.81%) and plant height (9.34% and 9.69%). Similar results were obtained by Gangadhara et al. [14] for days to 50% flowering, days to maturity and oil content ; Parameshwarappa et al.[15] for days to maturity and days to 50% flowering.

High heritability was recorded for traits such as capsule length (99.61%), 1000-seed weight (95.58%), number of seeds per capsule (94.65%), days to maturity (96.25%), oil content (90.02%), days to fifty percent flowering (90.41%), number of primary branches (88.04%), number of secondary branches (83.99%), plant height (92.80%), seed yield per plant (87.45 %), number of capsules per plant (77.82%) and days to flower initiation (76.95%) indicated that the significance of genetic components in their expression and low influence of environmental component [16]. Similar results were given by Kadvani et al. [17] for 1000-seed weight, oil content, days to flowering, capsule length, number of capsule per plant, days to maturity, seed yield per plant; Kiruthika et al. [18] for days to fifty percent flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of capsules per plant, number of seeds per capsule, capsule length, 1000-seed weight, oil content; Divya et al. [19] for days to maturity, days to fifty percent flowering, plant height, seed yield per plant, number of branches per plant and number of capsules per plant.

Genetic advance as percentage of mean was observed to be the highest for number of secondary branches (98.39 %) followed by seed yield per plant (40.00 %), number of primary branches (36.26%), number of capsules per plant (31.11%), 1000 seed weight (33.78%), capsule length (23.88%) and number of seeds per capsule (20.15). Similar findings have been

**Table 1. Variance components due to genotypes ( $\sigma^2_g$ )**

Traits	$\sigma^2_g$	SE
Days to flower initiation	0.6970**	0.1920
Days to 50% flowering	2.0370**	0.3330
Days to maturity	6.0200**	0.5770
Plant height (cm)	109.0800**	21.9200
Number of primary branches per plant	0.4335**	0.0818
Number of secondary branches per plant	0.3838**	0.0903
Number of capsules per plant	71.4000**	26.9000
Capsule length	0.0741**	0.0049
Number of seeds per capsule	36.2100**	4.1500
1000 seed weight	0.2542**	0.0255
Seed yield per plant	2.4220**	0.4900
Oil content	12.525**	2.022

\*\*Significant at  $P \leq 0.05$ **Table 2. Genetic parameters of variability for yield and its attributing traits**

Traits	Grand mean	Range		Coefficient of variation		$h^2$ (bs) (%)	GA as % of mean
		MIN	MAX	GCV (%)	PCV (%)		
Days to flower initiation	37.18	35.77	38.76	2.25	2.56	76.95	4.06
Days to 50% flowering	41.51	38.36	45.87	3.44	3.62	90.41	6.73
Days to maturity	93.78	84.58	97.92	2.62	2.67	96.25	5.29
Plant height (cm)	114.74	94.20	136.80	9.34	9.69	92.80	18.53
Number of primary branches per plant	3.51	2.27	5.40	18.76	19.99	88.04	36.26
Number of secondary branches per plant	1.18	0.2	2.77	52.12	56.87	83.99	98.39
Number of capsules per plant	49.34	36.40	67.66	17.12	19.41	77.82	31.11
Capsule length	2.34	1.58	3.22	11.61	11.64	99.61	23.88
Number of seeds per capsule	59.84	43.74	73.56	10.06	10.34	94.65	20.15
1000 seed weight	3.01	2.19	3.92	16.77	17.16	95.58	33.78
Seed yield per plant	7.49	5.12	11.84	20.76	22.20	87.45	40.00
Oil content	42.33	30.84	49.13	8.36	8.81	90.02	16.34

recorded by Kehie et al. [20] for seed yield per plant; Saxena and Bisen [21] for number of seeds per capsule. Begum et al. [22] for seed yield, capsule number and 1000-seed weight; Bamrotiya et al. [23] for seed yield per plant, number of seeds per capsule, number of capsules for plant, capsule length, number of branches per plant. Moderate genetic advance as percentage of mean was observed for traits plant height (18.53%) and oil content (16.34%). Similar findings were recorded by Pavani et al. [24] and Sirisha et al. [25] for plant height. Days to flower initiation (4.06%), days to maturity (5.29%) and days to fifty percent flowering (6.73%) exhibited low genetic advance as percentage of mean. similar findings were recorded by Pavani et al. [24], Sirisha et al. [25] and Mohanty et al. [26] for days to maturity.

Heritability along with genetic advance gives a good idea regarding the effectiveness of selection for improving the traits. According to Noor et al. [27] high heritability alone is not an index of high genetic gain therefore it should be accompanied with high genetic advance.

High heritability coupled with genetic advance recorded for number of secondary branches per plant followed by 1000-seed weight, seed yield per plant, number of primary branches per plant, capsule length, Number of seeds per capsule, Number of capsules per plant. Similar findings were recorded by Reddy et al. [28] and Krishnaiah et al. [29]. High heritability coupled with moderate genetic advance as percentage of mean recorded for plant height and oil content, while traits days to maturity, days to 50% flowering and days to flower initiation observed as high heritability coupled with low genetic advance percent as mean. Similar finding were recorded by Hika et al. [30] for days to maturity and days to 50% flowering.

#### 4. CONCLUSION

In this present experiment, 500 accessions were evaluated for genetic variability studies. REML analysis exhibited highly significant differences among the accessions for the twelve traits under study which indicated that extensive genetic variation is present in the accessions. High heritability exhibited for all the traits. Phenological traits were recorded low magnitude of genetic advance as percentage of mean, plant height and oil content were recorded moderate amount and rest of the traits were recorded high in magnitude. Heritability along with genetic

advance gives a good idea regarding the effectiveness of selection for improving the traits. High heritability coupled with genetic advance recorded for number of secondary branches per plant. This experiment results revealed significant variations among the accessions. As a result, there is tremendous opportunity of utilizing these genotypes in different breeding programmes for improve the crop yield.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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