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Genetic analysis of yield and its contributing traits in sesame (*Sesamum indicum* L.)

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Abstract

The present experiment was conducted at Education and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli (MH.) during Rabi 2024-25. The experimental materials comprised of ten parents, their twenty one F₁'s made by using LxT mating design and one check viz., JLT 408. The research work was conducted in a Randomized Block Design with three replications. The experimental plots (3 x 0.9 m²) comprised 60 plants spaced 30 x 15 cm apart. Significant genetic variability was demonstrated across all characters through measures of heritability, genetic advance and coefficient of variation. The results of an experiment revealed that the phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters studied reflecting the prominent role of environmental factors in their expression. High heritability coupled with high genetic advance as percentage of mean was recorded for days to 50% flowering (90.92% and 26.20%), number of branches per plant (94.33% and 63.89%), number of capsules per plant (90.99% and 35.76%), seed yield per plant (g) (90.96% and 69.79%), oil content (%) (95.88% and 23.00%), protein content (%) (97.09% and 27.10%) and carbohydrate content (%) (95.29% and 24.61%).

Keywords: Sesame, genetic variability, heritability, genetic advance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

Introduction

Sesame (*Sesamum indicum* L.) is the oldest indigenous oilseed crop with longest history of cultivation in India. Sesame originated in Africa and spread to West Asia, India, China and Japan, turning those regions into secondary centers of diversity (Weiss, 1983) [16]. Its seed contains oil is used as base for ayurvedic preparations and is often called the 'Queen of oils'. Sesame seeds were one of the first crops processed for oil as well as one of the earliest condiments (De Carvalho *et al.*, 2001) [7]. Sesame is cultivated on 12.97 million hectares of land worldwide (FAOSTAT, 2024) [8]. Sesame is cultivated in eight Indian states: Rajasthan, Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, Gujarat, Maharashtra, Tamil Nadu and Orissa. In India, sesame is cultivated over an area of 15.23 lakh hectares with a productivity of 527 kg/ha and production of 8.02 lakh tonnes (Indiastat, 2023) [11]. India plays a major role in global oilseeds, contributing 29% to the total land area and 26% to overall production. In Maharashtra, for Kharif season the area under sesame crop is 3.85 thousand ha, production is 1.15 thousand tonnes and productivity is 227 kg/ha and for Rabi season area 1.32 thousand ha, production 0.92 thousand tonnes (Final advance estimates, Commissionerate of Agriculture, GoM 2023-24).

The success of any breeding program is fundamentally dependent on the amount of genetic variation available within the population. Since, the efficiency of a selection programme is mainly dependent on the magnitude of genetic variation and heritability of a trait. Greater genetic variability provides more opportunities for selecting desirable genotypes. Effective selection is possible only in populations exhibiting high heritability. Furthermore, an understanding of the inheritance pattern of various traits is essential for selecting an appropriate breeding method. In the absence of genetic variability, selection is unlikely to be effective.

Heritability is the extent to which genetic factors contribute to the transmission of traits from parents to offspring.

It plays an important role in determining the most effective selection methods for improving specific traits in a population and acts as a predictive tool in the genetic analysis of quantitative traits. However, heritability by itself is insufficient to estimate the degree of genetic gain achieved through selection. Therefore, assessing different selection methods in crop improvement is crucial to understand the relationship between genetic advance and heritability.

Materials and Methods

The present experiment was conducted at Education and Research Farm, College of Agriculture, Dapoli (MH.) during Rabi 2024-25. The experimental materials comprised of 7 lines, 3 testers, 21 F₁'s made by using LxT mating design and 1 check viz., JLT 408 was laid out in a Randomized Block Design with three replications. The crop was raised as per the recommended package of practices. Five plants were randomly selected and tagged from each row in every replication for recording observations and their mean values were used for statistical analysis. The data were analyzed statistically as described below:

Estimation of mean and range

Mean values of all characters were obtained by dividing the total sum by the corresponding number of observations.

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where,

$\bar{X}$ = Mean of character

n = Number of observations

While, the lowest and highest values for each character was taken as range.

Genotypic coefficient of variation (GCV)

The genotypic coefficient of variation was calculated according to Burton (1952) [6].

Phenotypic coefficient of variation (PCV)

The phenotypic coefficient of variation was obtained by dividing the square root of phenotypic variance by the population mean and multiplying by 100.

Heritability

Heritability was computed from the variance components. Heritability was computed following the method described by Hanson *et al.* (1952) [10].

$$h^2(bs) = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_E^2}$$

Where,

σ_A^2 = Additive genetic variance

σ_D^2 = Dominance genetic variance

σ_E^2 = Environmental variance

Genetic advance

Genetic advance expressed as percentage of mean = $\frac{h_b \times K \times \sigma_p}{\bar{X}}$

Where,

H_b = Heritability coefficient broad sense

K = The selection differential at 5% selection intensity and its value is 2.06

σ_p = Standard deviation of phenotypic values

$\bar{X}$ = Mean of character

Results and Discussion

Coefficient of Variation

The results pertaining genetic variability parameters viz., coefficient of variation at phenotypic level (PCV), coefficient of variation at genotypic level (GCV), broad sense heritability (h^2_{bs}) and genetic advance expressed as percentage of mean (GAM) for all the thirteen characters (Table 1). The coefficient of variation at genotypic level ranged from 4.64% to 35.52% for different characters under study. Highest genotypic coefficients of variation was observed for seed yield obtained per plant (g) (35.52%) trailed by number of branches per plant (31.94%), number of capsules obtained per plant (18.20%), protein content (%) (13.35%), days to 50% flowering (13.34%), carbohydrate content (%) (12.24%) and oil content (%) (11.40%) while coefficient of variation at phenotypic level (PCV) was ranged from 5.55% to 37.25% for various traits under investigation. Maximum coefficient of variation at phenotypic level (PCV) was observed for seed yield/plant (g) (37.25%) and was trailed by number of branches/plant (32.88%), number of capsules/plant (19.08%), days to 50% flowering (13.99%), protein content (%) (13.55%), carbohydrate content (%) (12.54%) and oil content (%) (11.64%). Among the traits studied seed yield per plant, number of branches per plant, number of capsules per plant, days to 50% flowering and protein content showed maximum GCV and PCV. The coefficient of variation at phenotypic level (PCV) was greater than the coefficient of variation at genotypic level (GCV) for all the characters studied. Similar results were also reported by Bhattacharjee *et al.* (2019) [4] and Sultana *et al.* (2019) [15].

Heritability (h^2)

The broad-sense heritability estimates ranged from 63.51% for (1000-seed weight) to 97.09% for (protein content) (Table 1). The estimates of heritability were high (>60%) across all traits. The estimates of heritability were high for protein content (97.09%), oil content (95.88%), carbohydrate content (95.29%), number of branches/plant (94.33%), number of capsules/plant (90.99%), seed yield/plant (g) (90.96%), days to 50% flowering (90.92%), no. of seeds/capsule (78.92%), plant height (cm) (78.29%), capsule width (cm) (72.04%), days to maturity (69.82%), capsule length (cm) (67.21%) and 1000-seed weight (g) (63.51%).

Genetic Advance

The genetic advance expressed as percentage of mean of mean varied from 7.98% in days to maturity to 69.79% in seed yield/plant. The highest genetic advance as percent of mean was recorded by the seed yield per plant (69.79%) followed by number of branches per plant (63.89%), number of capsules per plant (35.76%), protein content (27.10%), days to 50% flowering (26.20%), carbohydrate content (24.61%) and oil content (23.00%).

The present study revealed high heritability coupled with high genetic advance expressed as percentage of mean for

majority of the traits. Similar results were reported by Bhattacharjee *et al.* (2019) ^[4], Kalaiyarasi *et al.* (2019) ^[13],

Rhman *et al.* (2019) ^[1], Manisha Kumari *et al.* (2020) ^[14], Gautam *et al.* (2023) ^[9] and Bhattacharya *et al.* (2025) ^[5].

Table 1: Genetic parameters for yield and yield related traits in Sesame

Characters	Grand Mean	Range		GCV (%)	PCV (%)	h ² b (%)	Genetic advance	Genetic advance expressed as (%) of mean
		Min	Max					
Days to 50% flowering	37.71	30.00	47.67	13.34	13.99	90.92	9.88	26.20
Days to maturity	81.38	76.00	90.33	4.64	5.55	69.82	6.50	7.98
Plant height (cm)	101.54	80.00	117.33	7.20	8.13	78.29	13.32	13.12
Number of branches/plant	5.54	3.00	9.33	31.94	32.88	94.33	3.49	63.89
Number of capsules/plant	105.58	60.33	144.00	18.20	19.08	90.99	37.76	35.76
Number of seeds/capsule	64.09	51.00	72.00	8.46	9.52	78.92	9.92	15.48
Length of capsule (cm)	2.76	2.41	3.04	5.08	6.20	67.21	0.24	8.59
Width of capsule (cm)	0.65	0.51	0.72	6.35	7.48	72.04	0.07	11.10
1000-seed weight (g)	3.35	2.78	3.81	7.24	9.09	63.51	0.40	11.89
Seed yield/plant (g)	11.58	4.80	20.27	35.52	37.25	90.96	7.56	69.79
Oil content (%)	46.96	33.00	54.50	11.40	11.64	95.88	11.09	23.00
Protein content (%)	17.61	10.95	21.90	13.35	13.55	97.09	4.77	27.10
Carbohydrate content (%)	21.09	15.30	25.50	12.24	12.54	95.29	5.34	24.61

Conclusion

Maximum GCV and PCV were observed for seed yield per plant, number of branches per plant, number of capsules per plant, days to 50% flowering and protein content suggesting the presence of sufficient variability. All the yield related traits viz., protein content, oil content, carbohydrate content, number of branches per plant, number of capsules per plant, seed yield per plant, days to 50% flowering, number of seeds per capsule, plant height, capsule width, days to maturity, capsule length and 1000-seed weight recorded high heritability, suggesting high inheritance of these traits. Moreover, high genetic advance for these traits indicates substantial scope for genetic improvement through selection. The present investigation offers a basis for selection and improvement of yield related traits in crop breeding programs.

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