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RESEARCH PAPER

Assessment of genetic variability for yield and yield attributes in sesame (*Sesamum indicum* L.)

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Abstract: Sesame (*Sesamum indicum* L.) is an ancient oil seed crop valued for its high quality edible oil, nutritional profile and resistance to oxidation. The present study was carried out during *kharif* 2024 at AICRP on Sesame and Niger, MARS, UAS, Dharwad, to assess genetic variability for yield and its attributes. Forty three advanced mutant lines along with six check varieties were evaluated under a randomized complete block design. Observations were recorded on twelve yield and its contributing characters. Analysis of variance revealed highly significant differences among genotypes for all traits, confirming sufficient variability for selection. Genotypic and phenotypic coefficient of variation were highest for seed yield per plant, while moderate values were observed for number of primary branches, number of capsules per plant, number of capsules on the main stem and number of seeds per capsule. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plant, number of primary branches, capsules on the main stem, capsules per plant and seeds per capsule, indicating that considerable genetic improvement can be achieved through simple selection.

Key words: Genetic variability, Genetic advance as per cent of mean, Heritability, Sesame

Introduction

Sesame (*Sesamum indicum* L.) is an ancient oil seed crop, considered as one of the earliest domesticated crop plants (Ashri and Singh 2006). It is often referred to as the 'Queen of oil seeds' and has been cultivated for centuries, particularly in Asia and Africa, owing to its high content of edible oil and protein (Anilakumar *et al*., 2010). In India sesame is grown in 15.2 million hactres with production of 8.02 million tons and productivity 530 kg per hectare (Anon, 2025). Its oil is well known for its high antioxidant content and contains several important fatty acids such as oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%) (Tripathi *et al*., 2013). Its seeds are equally important, containing 40-62% oil, 15-25% protein, 13.4-25.0% carbohydrates and about 9.8% digestible fiber (Dravie *et al.,*2020). Apart from its direct consumption, sesame has diverse applications, its seed and oil are used in cooking, preparation of sweets, as salad oil and in food industries like baking and candy making *etc.* It is also a major component in the production of cosmetics, soaps, perfumes, pharmaceutical products and insecticides (Tesfaye *et al.,*2022). Despite such immense nutritional, economic and cultural significance, sesame has received limited research attention compared to other major oilseed crops (Ukaan & Ogbonna, 2012). Yield improvement is challenging because yield is a complex character which is controlled by multiple genes and is influenced by environment to a greater extent (Hukumchand and Parameshwarappa, 2020).Therefore, emphasis should be given to traits which are less affected by environment. Continuous efforts in varietal improvement require a thorough understanding of the genetic mechanisms governing yield and yield contributing traits (Wattoo *et al*., 2009). Sesame is considered a breeder's dream crop because of its wide variability. The presence of such variability is crucial for genetic studies and plays a key role in crop improvement and selection (Mohanty *et al*., 2020) and it is necessary to study variability in respect of quantitative characters with reference to genetic parameters such as genotypic and phenotypic variances, heritability and genetic advance (Patidar *et al*., 2020) and further the efficiency of selection relies heavily on the assessment of genetic variability expressed through phenotypic characters (Umate, 2020). High estimates of heritability coupled with high genetic advance exoressed as percentage of mean are key factors determing effective trait selection during breeding programs (Johnson *et al*.1955). In this context, the present study was designed to estimate the extent of variation in yield and its associated traits in sesame, with the aim of generating useful insights to guide the formulation of effective breeding strategies.

Material and methods

The present study was carried out using 43 advanced mutant lines along with six checks (DS-5,TKG-22,DSM-17-1-1,DS-51, DS-61, and DSS-9) during *kharif* 2024 at the AICRP on Sesame and Niger, Main Agricultural Research Station, UAS, Dharwad. The experiment was laid out in a randomized complete block design with two replications. Each genotype was sown in two rows with ap lot size of 3.0 m×0.6 min spacing of 30 cm × 7.5 cm. The recommended package of practices was adopted to raise the crop. Observations were recorded on days to 50 per cent flowering, days to maturity, number of primary branches per plant, plant height (cm), height to first capsule (cm), number of capsules on the main stem, number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g) and seed yield per plant (g), based on five randomly selected plants. The data recorded were analysed using R Studio (version 4.5.1). Genotypic and phenotypic coefficient of variation were computed using the method suggested by

Table1. Analysis of variance for twelve characters in sesame genotypes

Sources of variation	Mean sum of squares		
	Treatments (df=48)	Replications (df=1)	Error (df=48)
Days to 50 percent flowering	7.68**	0.04	1.17
Days to maturity	56.74**	0.50	1.31
Number of primary branches	0.33**	0.01	0.04
Plant height (cm)	34.51**	27.68	7.08
Height to first capsule (cm)	34.29**	16.99	8.86
Number of capsules on main stem	12.34**	0.30	2.98
Number of capsules per plant	53.57**	2.55	10.27
Number of seeds per capsule	86.70**	35.04	9.54
Capsule length (cm)	0.03**	0.01	0.001
1000 seed weight (g)	0.06**	0.02	0.01
Oilcontent (%)	11.54**	2.13	2.41
Seed yield per plant(g)	0.88**	1.19	0.38

*-Significant at 5% probability level **-Significant at 5% and 1% probability level

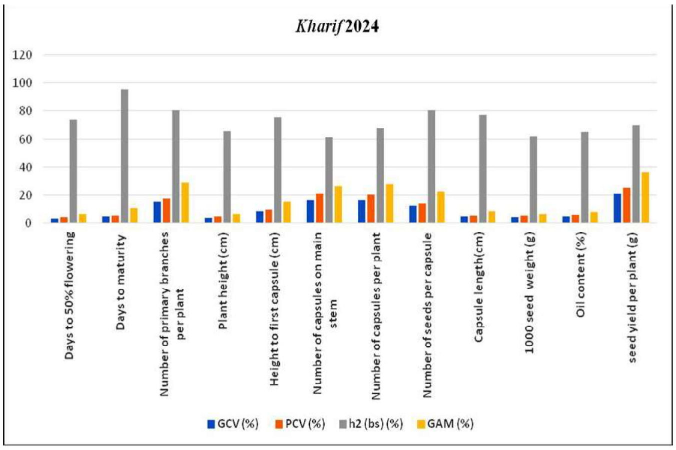

Fig1. Genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean for twelve traits during *kharif* 2024

Burton and Devane (1953). Heritability in the broad sense was estimated following Hanson *et al.* (1956), while genetic advance as a percent of mean was calculated using the method proposed by Johnson *et al.* (1955).

Results and discussion

The Analysis of variance revealed highly significant differences among the genotypes for the traits *viz*., days to 50 percent flowering, days to maturity, number of primary branches per plant, plant height (cm), height to first capsule (cm), number of capsules on main stem, number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g) and seed yield per plant (g) (Table 1). It suggested the presence of substantial amount of variability in these genotypes. This variability offers a strong basis for effective selection and provides scope for identifying suitable breeding strategies aimed at yield improvement and trait enhancement in sesame. Similar results were reported in earlier studies by Swapna *et al.* (2024), Zeinalzadeh *et al.* (2024), Bhattacharya *et al.* (2025) and Lakho *et al.* (2025).

The mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean for yield and its attributes were worked out and presented in Table 2 and Fig.1. The observed range was broad for all the twelve quantitative characters. Similar observations have been made in earlier research conducted by Ranjithkumar *et al.* (2022), Mitkari *et al.* (2023), Khuntia *et al.* (2024) and Lakho *et al.* (2025). PCV was greater than GCV for all the studied characters and difference between them was minimum.Thus, it indicated the less influence of environment on expression of these characters, which is enabled efficient selection of these characters. These results corroborate earlier findings by Patil and Lokesha (2018), Pavani *et al.* (2020), Patel *et al.* (2023), Khuntia *et al.* (2024) and Bhattacharya *et al.* (2025).

Among the studied traits both GCV and PCV were high for seed yield per plant. This highlighted that seed yield possessed a strong genetic component and considerable variability, suggesting that direct selection for this trait would be effective, which is in close agreement with the earlier reports of Ranjithkumar *et al.*(2022), Parihar *et al.*(2022), Sala *et al.*(2023), Patel *et al.*(2023) and Khuntia *et al.*(2024). Moderate GCV and PCV were observed for traits *viz*., number of primary branches, capsules on mainstem, number of capsules and seeds

Table 2. Genetic variability parameters for yield and yield related characters in sesame genotypes

Characters	Mean	Range		Coefficient of variation		h^2_{bs}(%)	GA	GAM (%)
		Min	Max	GCV(%)	PCV(%)			
DFF	49.4	43.5	52.5	3.6	4.3	73.6	3.2	6.5
DM	98.6	91.5	107.0	5.3	5.5	95.5	10.6	10.7
NPB	2.5	1.7	3.6	15.7	17.5	80.6	0.7	29.0
PH(cm)	90.8	81.6	99.0	4.1	5.0	66.0	6.2	6.8
HFC (cm)	45.2	33.3	54.6	8.6	9.9	75.5	6.9	15.4
NCM	13.1	7.5	18.2	16.5	21.2	61.1	3.5	26.6
NCP	27.9	17.1	39.5	16.7	20.2	67.8	7.9	28.3
NSC	50.2	32.2	63.0	12.4	13.8	80.2	11.5	22.8
CL(cm)	2.2	1.9	2.8	4.9	5.6	77.1	0.2	8.9
TSW (g)	3.5	3.1	4.0	4.3	5.4	62.1	0.2	6.9
OC (%)	43.8	37.3	46.8	4.9	6.0	65.4	3.6	8.1
SYP(g)	3.7	2.4	5.4	21.2	25.4	69.9	1.0	36.6

DFF-Days to 50% flowering; DM-Days to maturity;NPB-Number of primary branches per plant;PH: Plant height (cm); HFC: Height to first capsule (cm); NCM- Number of capsules on main stem; NCP- Number of capsules per plant; NSC-Number of seed per capsule;CL-Capsule length (cm);TSW-1000 seed weight (g); OC-Oil content (%); SYP- Seed yield per plant (g).

percapsule.Comparable results were found by Hukumchand and Parameshwarappa (2020). In contrast, low GCV and PCV were recorded for days to 50 per cent flowering, days to maturity, plant height, height to first capsule, capsule length, 1000 seedweight and oil content. Mitkari *et al.*(2023) and Takele and Dhabessa (2024) found low GCV and PCV for days to 50 per cent flowering, days to maturity and capsule length in their study.

Heritability was high for all the studied traits, signifying that genetic factors largely govern their expression as reported by Parameshwarappa *et al.* (2010), Divya *et al* (2018) and Khuntia *et al.* (2024). High heritability coupled with high genetic advance as percent of mean was noticed for the characters such as number of primary branches, number of capsules on mainstem, number of capsules per plant and number of seeds per capsule and seed yield per plant.This combination suggested the predominance of additive geneaction, implying the effectiveness of direct selection based on phenotypic expression. Similar findings were documented by Jadhav and Mohrir (2012), Hukumchand and Parameshwarappa (2020), Patidar *et al.*(2020), Mitkari *et al.*(2023) and Khuntia *et al.* (2024). On the other hand, high heritability associated with moderate genetic advance as percent of mean was noticed for days to maturity and height to first capsule. It represents the involvement of both additive and non-additive gene action in the 8 expression of these traits. Reports by Khairnar and Monpara (2013), Teklu *et al.* (2014) and Pavani *et al.* (2020) are in agreement with this interpretation. High heritability coupled with low genetic advance as percent of mean was observed for days to 50 percent flowering, plant height (cm), capsule length (cm), 1000 seed weight and oil content. This suggested that, although the trait is largely heritable, the expected genetic progress through selection might be limited due to the low genetic advance. Parallel results were revealed by Kalaiyarasi *et al.* (2019), Hukumchand and Parameshwarappa (2020), Saravanan *et al.*(2020), Mitkari *et al.* (2023) and Khuntia *et al.* (2024).

Conclusion

The current study demonstrated the presence of substantial genetic variability among sesame genotypes for yield and its attributes. The minimum difference between phenotypic coefficient of variation and genotypic coefficient of variation for all the studied characters indicated less influence of environment and reflects stability of trait expression. High level of variability observed for seed yield per plant and moderate variability for number of primary branches, number of capsules on mainstem, number of capsules per plant and number of seeds per capsule, highlighted their potential for effective selection and improvement in sesame breeding programs. High heritability coupled with high genetic advance as per cent of mean for traits such as number of primary branches, number of capsules on mainstem, number of capsules per plant and number of seeds per capsule and seed yield per plant suggested the predominance of additive gene action, offering promising scope for genetic improvement through selection.These traits, therefore, emerge as reliable selection criteria.

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