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Variability studies for yield, yield attributes and oil content in sesame (*Sesamum indicum* l.) Germplasm

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ABSTRACT

The present study was undertaken to assess the magnitude of genetic variability, heritability and genetic advance for seed yield and its associated traits in 56 sesame genotypes during *rabi,* 2024-25 at Agricultural College Farm, Bapatla, Andhra Pradesh. The analysis of variance revealed significant differences among the genotypes for all characters studied, suggesting the presence of considerable genetic variation. High heritability coupled with high genetic advance as percent of mean was observed for plant height(cm), number of primary branches per plant, number of capsules per plant, basal length of the stem to the first capsule bearing(cm), 1000 seed weight(g), harvest index(%) and seed yield per plot(g) indicating the predominance of additive gene action in governing the inheritance of the above traits which may be exploited through simple selection in future sesame breeding programmes.

Keywords: *GCV, Genetic Advance, Heritability, PCV and Sesame*

Sesame (*Sesamum indicum* L.) is one of the most ancient important oil seed crops belonging to the family Pedaliaceae. It is recognised as "Queen of oilseed crops" due to its great nutritional quality and quantity of oil (40-63%). Lignans present in the sesame seeds have strong antioxidant activity and its oil have significant pharmacological benefits and health benefits. Despite its importance, the productivity of sesame remains low due to poor management practices, unavailability of suitable cultivars to diverse agroclimatic conditions resulting in low yields. Hence, development of high yielding cultivars is the major objective in sesame breeding (Begna *et al*., 2022). For the success of any breeding programme, understanding the nature and magnitude of genetic variability, heritability and genetic advance is critical. High heritability along with high genetic advance suggests the prevalence of additive gene action, which can be exploited through simple selection. Hence, the present study aims to estimate these parameters in a set of diverse sesame genotypes.

MATERIAL AND METHODS

The present investigation was carried out using 56 sesame genotypes including two checks and were evaluated in alpha lattice design for twelve yield, yield attributes and oil content at Agricultural College Farm, Bapatla, Andhra Pradesh during *rabi*, 2024-25. Each genotype was grown in two rows of 4.0m length with a spacing of 30cm between rows and 10cm between plants, within the row. The data was recorded on five competitive plants from each replication on plant height (cm), number of primary branches per plant, number of capsules per plant, capsule length (cm), capsule width (cm), basal length of the stem to the first capsule bearing (cm), 1000 seed weight (g), harvest index (%) and oil content (%). Data for the traits viz., Days to 50% flowering, days to maturity and seed yield per plot (g) was recorded on plot basis. Analysis of variance was worked out by the method suggested by Panse and Sukhtame (1967) and the genotypic and phenotypic coefficient of variations were estimated by the method suggested by Burton and Devane (1953). The data was analysed by using R software. The GCV and PCV are classified as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by using the formula given by Johnson *et al.* (1955) and are classified as low (<30%), moderate (30-60%) and high (>60%). The range of genetic advance as per cent of mean was

Table 1. Analysis of variance for twelve yield, yield attributes and oil content in sesame (*Sesamum indicum*. L)

S.No.	Source of variation	d.f.	DFF	DM	PH (cm)	NPB	NCP	CL (cm)	CW (cm)	BSFCB (cm)	TSW (g)	HI (%)	OC (%)	SYP (g)
	Mean sum of squares													
1	**Replication**	1	0.143	35.438	15.825	0.438	1.424	0	0	9.782	0.002	11.895	7.252	966.437
2	**Treatments**	55	21.062**	44.496**	223.834**	1.135**	973.216**	0.026**	0.005**	85.749**	0.316**	37.942**	39.885**	4088.080**
3	**Blocks (b)**	6	6.002	4.937	35.508	0.154	31.262	0.007	0.001	23.645	0.002	5.317	2.672	272.562
4	**Error**	49	3.0580	12.172	17.187	0.172	26.752	0.006	0.001	17.434	0.003	5.098	3.446	350.483
5	**Total**	111	30.265	97.043	292.354	1.899	1032.654	0.039	0.007	136.610	0.323	60.252	53.255	5678.291

*Significance at 5% level, ** Significance at 1% level

DFF- Days to 50 % flowering, **DM**- Days to maturity, **PH** (cm)- Plant height, **NPB**- Number of primary branches per plant, **NCP**- Number of capsules per plant, **CL**(cm) - Capsule length, **CW** (cm)- Capsule width, **BSFCB** (cm)- Basal length of the stem to the first capsule bearing, **TSW**(g) – 1000 seed weight, **HI**(%) - Harvest index, **OC**(%) - Oil content, **SYP** (g) -Seed yield per plot.

Table 2. Estimation of genetic parameters for yield and yield component traits in sesame (*Sesamum indicum* L.)

Character	Mean	Standard error	Range		Coefficient of variation		h^2 (broad sense) (%)	Genetic advance	Genetic advance as % of mean
			Minimum	Maximum	Phenotypic (%)	Genotypic (%)			
Days to 50% flowering	41.8	1.23	35	47.5	8.3	7.17	74.64	5.34	12.76
Days to maturity	82.9	2.46	69	101.5	6.41	4.84	57.04	6.25	7.54
Plant height (cm)	87.6	2.93	68.9	116.1	12.52	11.59	85.73	19.38	22.11
Primary branches/plant	3.2	0.25	1.8	5.7	24.51	21.85	79.46	1.3	40.12
Capsules/plant	63.8	3.65	30	131.2	35.01	34.06	94.64	43.59	68.26
Capsule length (cm)	2.9	0.05	2.6	3.1	4.3	3.45	64.34	0.16	5.71
Capsule width (cm)	0.7	0.01	0.7	0.9	7.04	6.22	78.22	0.08	11.34
Basal length of stem to 1st capsule bearing (cm)	28.8	2.95	18	50.3	24.87	20.24	66.2	9.79	33.92
1000 seed weight (g)	2.7	0.04	1.51	3.76	14.45	14.29	97.82	0.8	29.12
Harvest index (%)	24.6	1.59	15.49	35.88	18.83	16.45	76.31	7.29	29.6
Oil content (%)	46.2	1.31	36	54.5	10.05	9.22	84.09	8.06	17.42
Seed yield/ plot (g)	169	13.23	94.5	274.5	27.81	25.52	84.21	81.72	48.25

classified as low (<10%), moderate (10-20%) and high (>20%) as suggested by Johnson *et al*. (1955).

RESULTS AND DISCUSSION

The analysis of variance for 12 characters revealed significant differences among the genotypes for all the characters studied, indicating the existence of ample variability among the genotypes (Table 1). The estimates of variability, heritability and genetic advance as per cent of mean were detailed in the (Table 2 and Figure 1).

Low GCV and PCV (<10%) values were recorded for the traits, days to 50% flowering, days to maturity, capsule length (cm), capsule width(cm) and Only low GCV for oil content (%) indicating less variability for these characters among the genotypes. Contrasting results were reported for these characters by Gautam *et al.* (2023), Gedifew (2023), Rahna *et al.* (2023), Patel *et al*. (2024). Moderate GCV and PCV (10-20%) values were recorded for the traits pant height, 1000 seed weight (g) and harvest index(%). These results were in agreement with the earlier reports of Menzir (2012), Gautam *et al.* (2023) and Rahna *et al.* (2023).

High PCV and GCV (>20%) values were recorded for most of the important yield contributing traits *viz.,* seed yield per plot, number of primary branches per plant, number of capsules per plant and basal length of the stem to the first capsule bearing, indicated that large amount of variation was present among the genotypes for these characters. suggesting considerable scope for selection. These results were in agreement with Zahran *et al.* (2020), Rahna *et al.* (2023) and Patel *et al.* (2024). High heritability coupled with high genetic advance as per cent of mean was reported for plant height (cm), number of primary branches per plant, number of capsules per plant, basal length of the stem to the first capsule bearing, 1000 seed weight(g), harvest index (%), seed yield per plot(g) indicating preponderance of additive gene action and simple phenotypic selection of these traits would be effective for overall yield improvement (Table 2 and Fig 1). Similar findings were earlier reported by Gogoi and sarma (2019), Pavani *et al*. (2020), Mohanty *et al*. (2020), Roy *et al.* (2022), Sundari *et al*. (2022), Khuntia *et al.* (2024), Patel *et al*. (2024), for different characters.

High heritability with moderate genetic advance as percent of mean was observed for Days to 50% flowering, capsule width (cm) and oil content (%) indicated existence of both additive and non-additive gene action and simple selection will not be rewarding for improvement of these traits. Similar findings were earlier reported by Kiruthika *et al.* (2018), Gautam *et al.* (2023), Mahla *et al*. (2024), and Patel *et al*. (2024) for different traits.

CONCLUSION

High PCV and GCV was recorded from the present study for most of the yield contributing traits viz., seed yield per plot, number of primary branches per plant, number of capsules per plant and basal length of the stem to the first capsule bearing indicating ample variation among the genotypes included. High heritability coupled with high genetic advance as percent of mean was recorded for yield traits viz., plant height (cm), number of primary branches per plant, number of capsules per plant, 1000 seed weight(g), harvest index (%) and seed yield per plot(g) indicating that these traits are under the control of additive gene action and simple direct phenotypic selection of these traits may be effective for overall yield improvement in sesame. The germplasm can be used for improvement of above mentioned characters and effectively used in future crop improvement programmes depending on the objective.

LITERATURE CITED

Begna T, Gichile H and Yali W 2022. Genetic diversity and its impact in enhancement of crop plants. *Global Journal of Agricultural Research*. 10 (2): 13-25.

Burton G W and Devane E M 1953. Estimating heritability in tall fescue (*Festuca arundinaceous*) from replicated clonal material. *Agronomy Journal*. 51: 515-518.

Gautam S, Mishra S P, Gautam S, Rao S and Dwivedi P 2023. Morphological and biochemical character studies in sesame (*Sesamum indicum* L.) varieties. *The Pharma Innovation Journal.* 12 (10): 1–3.

Gedifew S 2023. Genetic variability in sesame (*Sesamum indicum* L.) for yield and yield related traits. *Harran Journal of Agricultural and Food Sciences.* 27 (2): 153-165.

Gogoi L R and Sarma R N 2019. Variability and path coefficient analysis in sesame (*Sesamum*

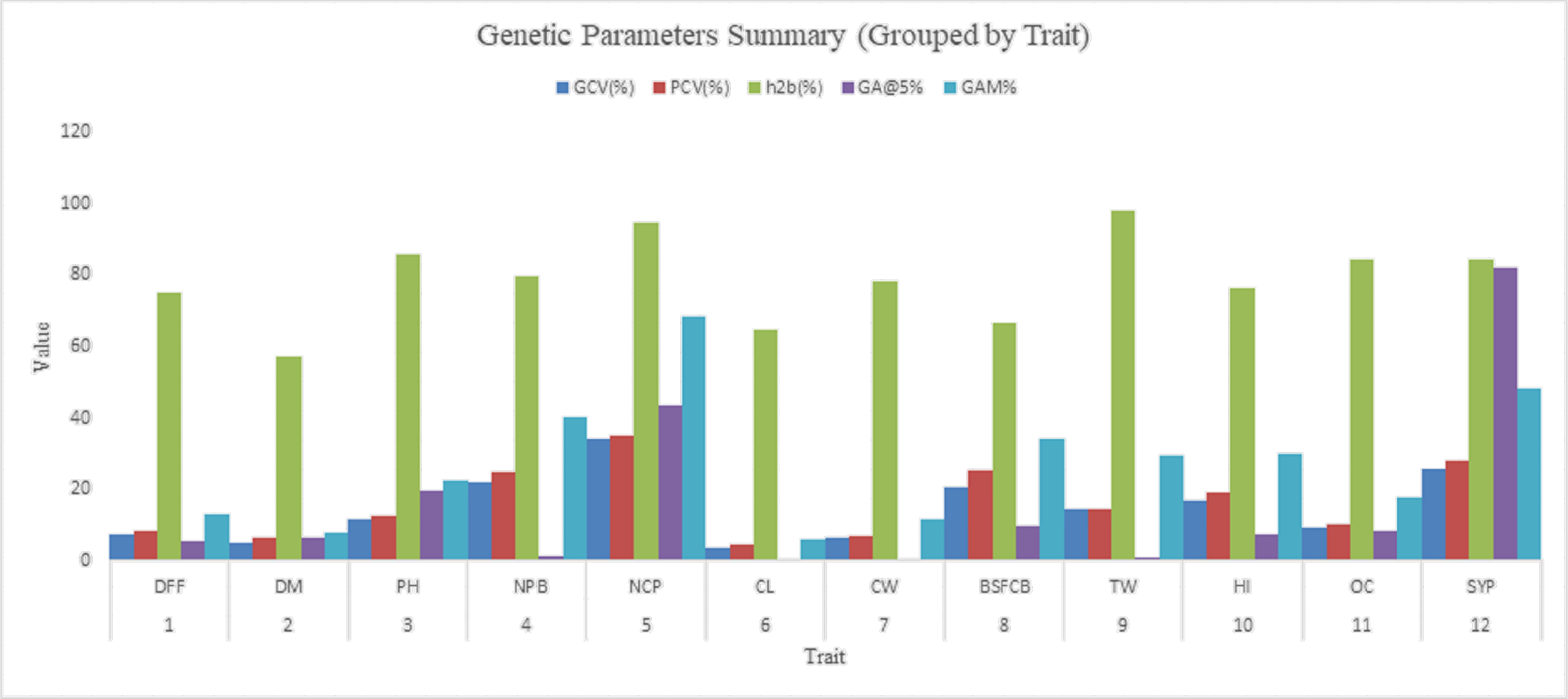

Fig. 1. Pattern of genetic parameters for 12 traits in 56 genotypes of sesame (*Sesamum indicum* L.)

indicum L.). *International Journal of Current Microbiology and Applied Sci*ences 8 (7): 229-237.

Johnson H W, Robinson H F and Comstock R E 1955. Estimates of genetic and environmental variability in soybeans . *Agronomy Journal*. 47 (7): 314-318.

Khuntia J B, Dash A P, Kar R K, Lenka B, Pradhan H, Samal A, Pattanayak S, Mishra S, Pani B and Satapathy S 2024. Unveiling genetic variability and character associations in sesame. *Biochemical and Cellular Archives*. 24 (1): 1135-1142.

Kiruthika S, Narayanan S L, Parameswari C, Mini M L and Arunachalam P 2018. Genetic variability studies for yield and yield components in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*. 9 (4): 1529-1537.

Mahla N U, Jagtap P K and Patel H R 2024. Genetic variability and association among yield and yield related traits of sesame (*Sesamum indicum* L.) genotype. *International Journal of Plant and Soil Science.* 36 (2): 197-206.

Menzir A 2012. Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. *Nature and Science*. 10 (10): 117-126.

Mohanty T A, Singh U K, Singh S K, Kushwaha N and Singh D 2020. Study of genetic variability, heritability and genetic advance in sesame (*Sesamum indicum* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences*. 9 (2): 347-356.

Panse and Sukhatme P V 1967. Statistical *Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi. 103-108.

Patel N B, Acharya R R, Patel D A, Parmar H, Macwana S M and Patel N J 2024. Variability and character association for seed yield and yield contributing traits in sesame (*Sesamum indicum* L.). *International Journal of Advanced Biochemistry Research.* 8 (12): 1081-1086.

Pavani K, Ahamed M, Ramana J V and Sirisha A B M 2020. Morphological characterization of sesame (*Sesamum indicum* L.) genotypes using DUS descriptors. *Journal of Plant Development Sciences*. 12(6): 349-354.

Rahna K, Kalaiyarasi R, Umadevi M, Senthil A and Sudha M 2023. Genetic variability and diversity analysis in sesame (*Sesamum indicum* L.) germplasm. *Electronic Journal of Plant Breeding*.14 (3): 1055-1062.

Roy B, Pal A K and Basu A K 2022. The estimation of genetic variability and genetic divergence of some advance lines of sesame based on morphological traits. *Plant Science Today.* 9 (2): 281-287.

Sivasubramanian M M and Madhavamenon P M 1973. Inheritance of short stature in rice. *Madras Agricultural Journal*. 60: 1129-1133.

Sundari K S, Vasline Y A and Saravanan K 2022. Selection of traits for seed yield improvement through variability parameters in sesame (*Sesamum indicum* L.) genotypes. *Journal of Applied and Natural Science.* 14 (3): 329-834.

Zahran H A, Abd-Elsaber A and Tawfeuk H Z 2020. Genetic diversity, chemical composition and oil characteristics of six sesame genotypes. *Oilseeds & Fats Crops and Lipids.* 27: 39.

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