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Unveiling the genetic variability, character association for yield and yield contributing traits in sesame (*Sesamum indicum* L.)

D Padmaja, N Balram, Rajini Bisen and Anand Kumar Vishwa Karma

D Padmaja
AICRP on Forage Crops unit, ARI, Rajendranagar, Professor Jayashankar Telangana Agricultural University, Telangana, India

N Balram
SRTC, Rajendranagar, Professor Jayashankar Telangana Agricultural University, Telangana, India

Rajini Bisen
Jawharlal Nehru Krishi Vishwa Vidyalay, Jabalpur, All India Coordinated Research Project on Sesame and Niger, Madhya Pradesh, India

Anand Kumar Vishwa Karma
Jawharlal Nehru Krishi Vishwa Vidyalay, Jabalpur, All India Coordinated Research Project on Sesame and Niger, Madhya Pradesh, India

Corresponding Author:
D Padmaja
AICRP on Forage Crops unit, ARI, Rajendranagar, Professor Jayashankar Telangana Agricultural University, Telangana, India

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Abstract

Sesame is an important oilseed crop used in food industries, cosmetics, and pharmaceuticals. Sesame grown in India over an area of 15.31 lakh hectares with production of 8.47 lakh tonnes and productivity of 553 kg ha^{-1}. In Telangana contributed significantly, producing 0.10 lakh tonnes with a productivity of 740 kg ha^{-1} from 0.14 lakh hectares (Indiastat, 2024). The objective of this study was to estimate the extent of genetic variability in genotypes of sesame during summer 2024. Fourteen genotypes were evaluated at Regional Agricultural Research Station, Polasa Jagtial. The experiment was laid out in a randomized block design with three replications. The highest phenotypic, genotypic coefficient of variation, heritability, and genetic advance as a percentage of the mean was observed for the number of capsules per plant. It indicates selection for this trait was effective for higher yield. It was influenced by additive gene action, which can be improved through a simple selection method. Similarly, the number of capsules per plant showed a positive significant correlation with seed yield per plant. Days to 50% flowering exhibited a positive significant correlation with days to maturity. Therefore, number of capsules per plant was the most contributing character to seed yield.

Keywords: Genetic variability, broad sense heritability, genetic advance as percent of mean, correlation and sesame (*Sesamum indicum* L.)

Introduction

Sesame (*Sesamum indicum* L.) (2n = 26), also known as Til or Gingelly, it is one of the most important oilseed crop of tropical and temperate regions. It is commonly known as “Queen of oilseeds”. Because of its excellent nutritional content and resistance to oxidation and rancidity, it is a major industrial food crop (Swapna *et al.* 2024) [32]

Sesame occupies an area of 21,000 ha with production and productivity of 15,000 tonnes and 714 kgha-1 respectively in Telangana [1]. It is grown as summer crop in Northern Telangana districts viz., Adilabad, Jagtial, Karimnagar and Nizamabad. However, the development of improved plant cultivars and increasing the production is restricted mainly due to narrow genetic pool, which results in limited possibility to restructure the sesame crop. Despite the economic importance for food, oil and medicine, the yield potential of sesame is not spectacular due to its cultivation in sub-marginal lands and non availability of superior high yielding varieties due to lack of an appropriate breeding program (Manjeet *et al.* 2020 and Pandey *et al.* 2015) [15, 21]. Effective breeding programs depend on the amount of variability existing in the genetic stocks of the crop so that, it can be exploited for crop improvement by geneticist and crop breeders. Genetic variation is the inherent variation which remains unchanged by the environmental factors and this type of variation is more useful to a breeder for exploitation by selection or hybridization (Manjeet *et al.* 2020 and Bagheri *et al.*, 2017) [15, 3]. Progress in any crop improvement project depends not only on the magnitude of genetic variability but also on the heritability and genetic advance under selection (Dutta *et al.* 2013) [8]. Heritability estimates the magnitude of variation present in a particular trait which is transmissible from the parent to the offspring which helps plant breeders for the selection of elite genotypes from diverse genetic populations (Patidar *et al.*, 2018) [22]. Since heritability is also influenced by environment, the information on heritability alone may not help in selecting characters on the basis of their phenotype (Nahak *et al.*, 2018) [18].

Therefore, the genetic advance is also considered important because high value of genetic advance is indicative of additive gene action which is the only genetic variance which response to the selection and it also provides information about the expected gain in a character from one cycle of selection (Dutta *et al.* 2013) [8]. Keeping in view of the above facts, the present study was carried out with the objective to assess genetic variability, heritability, genetic advance and character association among the seven morphological characters of sesame.

Materials and methods

The experiment was conducted in Randomised Block Design (RBD) with two replications at the Regional Agricultural Research Station in Polasa, Jagtial, during the summer, 2022. Each genotype was sown in eight rows of three meteres length, with inter-row spacing of 30 cm and intra row spacing of 15 cm. Sowing was done by dibbling the seed at 2-3 cm depth. All the standard package of practices were followed during crop growth period except spraying of insecticides. The experimental material used in the present investigation comprised of 14 advanced breeding lines of sesame including three checks i.e., two national checks (TKG 22 and GT 10), zonal check (Pragathi) and one local check (Swetha Til). The data were recorded on yield and yield attributing characters viz., days to 50% flowering (days), days to maturity (days), plant height (cm), number of branches per plant, number of capsules per plant, 1000 seed weight (g), seed yield (kg/ha) from five randomly selected plants in each replication and the collected mean data was subjected to Statistical analysis was performed as per the standard methods. Analysis of variance was used to assess genotypic variability following Federer (1956), with significance tested using F-values (Fisher and Yates, 1963) [9]. GCV and PCV were calculated as per Burton and de Vane (1953) [5], heritability (broad sense) as per Allard (1960) [1] and genetic advance and GAM according to Johnson *et al.* (1955) [12]. The GCV and PCV estimates were taken as low, medium and high as per the classification of Singh and Chaudhary, (1977) [30] while the heritability and genetic advance as percent of mean estimates were taken as low, medium and high as per the classification of Johnson *et al.*, (1955) [12]. The calculations were performed through computer generated programme WINDOSTAT, a statistical package at Computer Centre, PJTAU, Rajendranagar, Hyderabad, Telangana, India.

Results and Discussion

The presence of sufficient variability indicated that the materials of sesame under study were good enough for further study. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the characters studied, which reflected the role of the environment in the expression of the observed traits. Similar results were also reported by Revathi *et al.* (2012) [26], Wide variability was observed for seed yield (813-1045 Kg/ha) and other characters also. PCV showed higher values than GCV suggesting less impact of environmental factors on the studied traits. Genotypic and phenotypic coefficients of variation were observed as low for Days to 50% flowering and days to maturity which were similar to the findings of Saxena and Bisen (2017) [27] and Divya *et al.* (2018) [7]. Variation in days to maturity is essential in selection of early and late duration varieties which is important for further improvement.

Table 1: Genetic variability parameters for yield and yield attributing traits in sesame

	General Mean	Range	Vg	Vp	GCV	PCV	h^2 (Broad Sense)	Genetic Advancement 5%	Gen. Adv as % of Mean 5%
Days to 50% flowering	48.05	45-50	1.36	2.14	2.43	3.04	63.90	1.92	4.00
Days to Maturity	90.26	89-93	1.92	2.84	1.54	1.87	67.70	2.35	2.60
Plant Height	96.77	68.7-115.9	131.52	229.29	11.85	15.65	57.40	17.89	18.49
Number of Productive Branches plant	3.76	1.7-4.7	0.69	1.05	22.09	27.26	65.70	1.39	36.88
Number of Capsules plant	81.21	60.7-104	177.09	251.09	16.39	19.51	70.50	23.02	28.35
1000 seed weight	3.39	2.6-3.92	0.11	0.11	9.65	9.84	96.20	0.66	19.50
Seed Yield (kg/ha)	925.19	813-1045	2699.85	9758.02	5.62	10.68	27.70	56.30	6.09

Plant height and number of productive branches per plant showed a moderate extent of variation for both phenotypic and genotypic coefficients, which was on par with the results observed by Gayathri *et al.*, (2025) [24] Thouseem *et al.* (2022) [33] and Vamshi *et al.* (2021) [34] for plant height and Ashfaq *et al.* (2025) [2] reported for number of capsules per plant. Low PCV and GCV values were recorded for days to 50% flowering, days to maturity, test weight and seed yield which were in agreement with the results reported by Padmaja *et al.* (2022) [20] for 1000 seed weight, Gayathri *et al.* (2025) [24] for days to maturity and days to 50% flowering and test weight. Pavani *et al.* (2020) [23] reported for seed yield. Number of branches per plant recorded high PCV and GCV, which was on par with the findings reported by Swapna *et al.* (2024) [32]. The traits number of branches per plant recorded both high PCV and GCV. Similar observations were recorded by Divya *et al.* (2018) [7] and Swapna *et al.* (2024) [32]

In contrast, when both heritability and genetic advance are low, it suggests a strong environmental influence on the trait, and selection in such cases would likely be ineffective. Heritability values in the present investigation ranged from 27.7 % to 96.20%, while GAM (genetic advance as percent of mean) spanned from 2.6% to 36.88 %. Traits such as number of branches per plant and number of capsules per plant exhibited high heritability along with a high genetic advance as a percent of the mean. Similar findings for number of capsules per plant and number of branches per plant were reported by Divya *et al.* (2018) [7] and Gayathri *et al.* 2025 [24]. Results indicate that the trait was controlled by additive gene action and selection can be effective. Moderate heritability coupled with moderate genetic advance as percent of mean was observed for plant height. Similar findings reported by Rajitha *et al.* (2021) [25] and Nisha *et al.* (2024) [19].

High heritability along with moderate GAM was observed for 1000 seed weight. Similar results were obtained by Mitkari *et al.* (2023) [20] and Gayathri *et al.* 2025 [24]. It indicates that this trait was less influenced by environment and selection may be effective. High heritability coupled with low GAM was observed for days to 50% flowering and days to maturity which align with the findings observed by Gayatri *et al.* 2025 [24]. High heritability and low genetic advance as percent of mean of this trait indicates that this trait is governed by non additive gene effects play an important role in the expression of this trait. Therefore, the results indicated a little scope for further improvement through individual plant selection. Seed yield recorded low heritability coupled with low GAM. These results are similar with the findings of Padmaja *et al.*, 2022 [20].

Table 2: Correlation coefficient for yield and yield related traits in sesame

	Days to 50% flowering (days)	Days to Maturity (days)	Plant height (cm)	Producti Branches plant	Producti Capsules plant	1000 seed weight (g)	Seed Yield (kg/ha)
1. Days to 50% flowering (days)	1.000	0.666***	0.0542	0.2958	0.043	-0.284	0.482 **
2. Days to Maturity (days)		1.000	0.1747	0.1368	0.079	-0.482 **	0.268
3. Plant height (cm)			1.000	0.2897	0.210	-0.423) **	0.029
4. Productive Branches/plan				1.000	-0.142	-0.271	0.162
5. Productive Capsules/plan					1.000	-0.265	0.350 *
6. 1000 seed weight (g)						1.000	-0.273
7. Seed Yield (kg/ha)							1.000

The estimates of correlation coefficients between seed yield and other yield contributing traits were given in Table 2. Relative higher magnitude of correlation coefficients indicating a strong heritable association among various yield contributing characters. Therefore, selection based on the phenotype would be effective for yield improvement. Days to 50% flowering (0.482) and number of capsules per plant (0.350) had positive significant correlation with seed yield. Similar results reported by Ashfaq *et al.* (2025) [2] for days to 50% flowering and Rajitha (2025) [25] and Madhu *et al.*, 2023 [14] number of capsules per plant. This type of character association indicates the improvement in seed yield can be achieved by improving the characters like number of capsules per plant. Some characters viz., days to maturity (0.268), plant height (0.029), number of primary branches per plant (0.162) found to have positive and non-significant association with seed yield per plant. The results were similar to the findings of Bharathi *et al.* (2015) [4], Saxena and Bisen (2016) [28] for days to maturity, Madhu *et al.*, 2023 [14] for plant height and number of branches per plant. While one character viz., 1000 seed weight (-0.273) exhibited non significant negative correlation with seed yield per plant. These results were in confirmation with Iqbal *et al.* (2016) [11] Laghari *et al.* (2016) [13]. Days to maturity exhibited significant positive association with days to 50% flowering (0.666). These results are similar with the findings of Madhu *et al.*, 2023 [14]. 1000 seed weight was negative significant correlation with days to maturity (-0.423) and plant height (-0.423). These results are in agreement with the findings of Ashfaq *et al.* (2025) [2] and for plant height by Singh *et al.* (2018) [29].

Conclusion

The present experiment revealed substantial genetic variability in the studied sesame genotypes. Traits such as Number of Productive Branches and plant number of capsules, seed yield per plant exhibited substantial heritability coupled with considerable genetic advance as percent of mean, indicating the predominance of additive genetic effects and the potential for effective improvement through selection. These traits should be prioritized in breeding programmes aimed at yield enhancement improvement in sesame.

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Competing Interests

Authors have declared that no competing interests exist.

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