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## Studies on genetic variability parameters in sesame (*Sesamum indicum* L.)

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**Abstract**

Thirty sesame genotypes (25 advanced lines and 5 released varieties) were evaluated during kharif 2018 for genetic variability and other related parameters in respect of ten quantitative characters. Analysis of variance revealed significant differences among genotypes for all the ten characters studied. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the number of capsules per plant while it was moderate for days to 50% flowering, plant height to first capsule, number of branches per plant. On the other hand, height of the main stem, capsule length, 1000 seed weight, days to maturity, oil content and seed yield per plant showed low genotypic and phenotypic coefficient of variation. High heritability and genetic advance as per cent mean was observed for days to 50 per cent flowering, number of branches per plant and plant height to first capsule where as high heritability with moderate genetic advance as per cent over mean was observed for height of the mainstem. Low heritability and genetic advance as per cent over mean observed capsule length, 1000 seed weight, days to maturity, oil content, and seed yield per plant.

**Keywords:** Sesame, Genetic variability Genetic advance as per cent of mean, Heritability

**Introduction**

Sesame ( $2n=26$ ) is a member of the Pedaliaceae family and is one of the most ancient oil seed crops. Sesame is cultivated in tropical, subtropical, and southern temperate regions of the world, but mainly in Asia, Africa, and South America (Anilakumar *et al.*, 2010)<sup>[2]</sup>. Sesame is mainly cultivated for its seeds. Sesame seeds are very nutritious with almost 50% oil and up to 25% protein content. Its worldwide production ranks fifth among annual oil crops and eighth among all consumable oil crops (Wongyai, 2007)<sup>[23]</sup>. Over 80% sesame producing areas are in the developing countries. Myanmar leads in sesame production with 890,000 tons, followed by India (636,000 tons), China (588,000 tons), Sudan (562,000 tons), and Tanzania (420,000 tons) (FAOSTAT, 2014)<sup>[7]</sup>. The species deserves its reputation as “queen of the oil seeds” because of its oil’s resistance to oxidative deterioration and a high, unsaturated fatty acid content of nearly 85%. In addition, polyunsaturated fatty acids constitute more than half of the unsaturated fatty acid fraction in seeds. The excellent stability of sesame oil is attributed to the presence of antioxidant lignans such as sesamin, sesamol, and sesaminol. The health benefits of these compounds, including antioxidant, antiaging, antihypertensive, anticancer, cholesterol lowering, and antimutagenic properties are reported by several authors (Anilakumar *et al.*, 2010)<sup>[2]</sup>.

Variation is a prerequisite to start a breeding programme in any crop. This variation can be exploited for the development of new varieties/ lines which have commercial value or may be used as the parents in the breeding programmes. Thus, measuring the genetic variation is crucial for selective breeding, rapid domestication and/or conservation in populations or species. The sesame breeding programme in our University (Acharya N.G. Ranga Agricultural University) has come up with black seeded sesame varieties with better quality, higher yield and better pod dehiscence traits and advanced breeding lines for the future release. Keeping this in view, the present investigation was planned to study the genetic variability parameters in sesame material developed at Agricultural Research Station, Yelamanchili, Visakhapatnam district of Andhra Pradesh for yield and yield traits.

## Material and Methods

The present investigation was carried out during *kharif* 2018 at Agricultural Research Station, Yelamanchili, Visakhapatnam District, Andhra Pradesh, which is located at 17° North latitude and 82° East longitude. with 30 (25 advanced lines and 5 released varieties) sesame genotypes. These genotypes were evaluated in a Randomized Block Design with three replications. Each plot consisted of three rows of 4.5 meters length with row and plant spacing of 30 and 15 cm, respectively. Standard cultural practices were adopted from sowing till harvest for better crop growth. The observations were recorded on ten randomly selected plants for eight quantitative characters *viz.*, height of the mainstem, number of branches per plant, number of capsules per plant, plant height to first capsule, capsule length, 1000 seed weight, oil content and seed yield per plant. The data on days to 50% flowering, and days to maturity were recorded on plot basis. The data was subjected to statistical analysis to estimate analysis of variance and genotypic and phenotypic coefficients of variation, heritability and genetic advance as per the formulae suggested by Chandra Mohan *et al.*, (2014)<sup>[5]</sup>, Patil *et al.*, (2018)<sup>[14]</sup> and Gagadhara *et al.* (2012), Gidey *et al.* (2012)<sup>[9]</sup>, Tripathy *et al.* (2013)<sup>[21]</sup>, Tirumala Rao *et al.* (2014)<sup>[4]</sup> respectively.

## Results and Discussion

The analysis of variance showed significant differences among the genotypes for all the traits *viz.*, days to 50 % flowering, Height of the main stem, number of branches per plant, number of capsules per plant, plant height to the first

capsule, capsule length (cm), 1000- seed weight (g), oil content (%), days to maturity and seed yield per plant (g) indicating the presence of considerable genetic variability among the experimental material under study (Table 1). Presence of adequate variability and critical analysis of genetic variability are needed for initiating any crop improvement programme and for adopting appropriate selection techniques. Greater variability in the initial breeding material ensures better chances of producing a desired genotype.

The genotypic and phenotypic coefficients of variation, heritability and genetic advance and genetic advance as per cent of mean were estimated and the results are furnished in Table 2.

**Table 1:** Analysis of variance for yield and yield components in sesame (*Sesamum indicum* L.).

Source of Variation	Replications	Treatments	Error
Degrees of freedom	2	29	58
Days to 50% flowering	0.41	54.4 **	1.27
Height of the main stem (cm)	4.18	417.6**	7.92
No. of branches/ plant	0.03	1.65**	0.24
No. of capsules/ plant	17.90	2204.6**	42.23
Plant height to the first capsule (cm)	0.233	425.7**	19.23
Capsule length (cm)	0.004	0.049*	0.027
1000 seed weight	0.0001	0.0199*	0.010
Days to maturity	15.6	26.3**	11.5
Oil content (%)	55.6	12.12*	6.65
Seed yield/ plant (gm)	0.22	0.28*	0.14

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

**Table 2:** Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed yield and yield components in Sesame (*Sesamum indicum* L.).

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5%)
			Min.	Max.	PCV (%)	GCV (%)		
1.	Days to 50% flowering	39.92	34.33	49.00	10.92	10.54	93.3	20.99
2.	Height of the main stem (cm)	144.84	120.80	167.40	8.29	8.06	94.5	16.15
3.	No. of branches/ plant	5.10	4.00	6.00	16.55	13.48	66.3	22.61
4.	No. of capsules/ plant	113.92	65.00	152.66	24.24	23.56	94.5	47.18
5.	Plant height to the first capsule (cm)	90.26	59.33	121.33	13.78	12.89	87.6	24.86
6.	Capsule length (cm)	2.31	2.06	2.64	8.07	3.71	21.2	3.53
7.	1000 seed weight	3.02	2.86	3.15	3.90	1.81	21.7	1.74
8.	Days to maturity	84.03	76.00	89.00	4.83	2.63	29.8	2.96
9.	Oil content (%)	44.30	41.21	47.10	6.57	3.04	21.5	2.91
10.	Seed yield/ plant (gm)	5.42	4.70	6.24	8.06	4.07	25.5	4.23

Min.: Minimum Max.: Maximum

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

### Days to 50 per cent flowering

This character exhibited a range from 34 to 49 days with a general mean of 39.2 days. Among all the genotypes, MLTS-2 was the earliest (34 days), while YLM-163 (49 days) was the long duration genotype. Moderate genotypic and phenotypic coefficients of variation were recorded for days to 50 per cent flowering *i.e.*, 10.54% and 16.92%, respectively. Higher PCV values indicated that variation in the lines is not only due to genotypes but also by the influence of environment. Hence, simple selection for this trait in these genotypes will be misleading and not recommended. Similar results were found by Chandra Mohan *et al.*, (2014)<sup>[5]</sup> and Patil *et al.*, (2018)<sup>[14]</sup>. The heritability observed for the trait was high (93.3%) with low genetic advance as per cent of mean (20.99%) indicating the predominance of additive and non-additive gene actions in the expression of the trait. Simple selection would not be effective for the improvement

of this trait. These results were confirmed by Gagadhara *et al.* (2012), Gidey *et al.* (2012)<sup>[9]</sup>, Tripathy *et al.* (2013)<sup>[21]</sup>, Tirumala Rao *et al.* (2014)<sup>[4]</sup>.

### Height of the main stem

Plant height exhibited wide variability ranging from 120.8 cm to 167.4cm with a general mean of 144.8 cm. The genotype, TKG-22, was the shortest while, the genotype, GOURI, was the tallest. The genotypic and phenotypic coefficients of variation estimates observed for the trait were low *i.e.*, 8.06% and 8.29%, respectively. The difference between GCV and PCV values was very low indicating a little role of environment component in the variation. These results are in line with that of Bharathi *et al.* (2014)<sup>[4]</sup>, Chandra Mohan (2014)<sup>[5]</sup> and Abate and Mekbib (2015)<sup>[1]</sup>. High heritability (94.5%) coupled with moderate genetic advance as per cent of mean (16.15%) was recorded indicating the existence of both

additive and non additive gene actions in the expression of the trait. Hence simple selection will not be rewarding in improving this trait. These results were confirmed by Vanishree *et al.* (2013) [22], Chandra Mohan *et al.* (2014) [5] and Tirumala Rao *et al.* (2014) [4].

#### Number of branches per plant

The mean value of genotypes for this trait was 5.1 with a range of 4 to 6. The genotype, YLM-17, had lower number of branches per plant (4) and the lines, MLTS-1, MLTS-4, TKG-22, YLM-153, YLM-156, YLM-66 and YLM-11, showed higher number of branches per plant (6). Genotypic and phenotypic coefficients of variation were moderate *i.e.*, 13.48% and 16.55%, respectively. Higher PCV than GCV revealed that the variation is being influenced by environment and therefore simple selection will be misleading. Similar results were also reported by Gangadhararao *et al.* (2012) [8], Hika *et al.* (2015) [10] and Patil *et al.* (2018) [14]. Higher heritability (66.3) and higher genetic advance as per cent of mean (22.61) were noted for this character which may be due to the predominance of additive gene action and the desired results may be obtained by simple selection. Similar results were reported by Ismaila and Usman (2012) [11] and Mustafa *et al.* (2015) [13].

#### Number of capsules per plant

Among the lines, the trait, number of capsules per plant, was found to be the lowest in GOURI (65.0) and the highest was observed in MLTS-2 (152.0) with a general mean of 113.9 capsules per plant. High genotypic and phenotypic coefficients of variation were observed *i.e.*, 23.56 % and 24.24 %, respectively. Low difference between GCV and PCV values indicated the little role of environmental component in the observed variation. The results are in conformity with the findings of Revathi *et al.* (2012) [15], Thirumala Rao *et al.* (2013) [4] and Vanishree *et al.* (2013) [22]. High heritability (94.5%) and high genetic advance as per cent of mean (47.18 %) were recorded for this trait indicating the predominance of additive gene effect which is easily fixable and can be taken as unit character for effective selection. The results are in conformity with the findings of Siva Prasad *et al.* (2013) [17], Ismaila and Usman (2012) [11] and Mustafa *et al.* (2015) [13].

#### Plant height to the first capsule

Among the 30 lines, the trait, plant height to the first capsule, was found to be the lowest in the line, YLM-163 (59.3cm) and was the highest in the lines, MLTS-3 (121.3cm) with a general mean of 90.26cm. Genotypic and phenotypic coefficients of variation observed for this trait were moderate *i.e.*, 12.89 % and 13.78 %, respectively, indicating the presence of moderate variation for plant height to first capsule among the lines studied. The results are in accordance with Bedawy *et al.* (2018) [3]. High heritability (87.6%) and high genetic advance as per cent of mean (24.86 %) were noted for this trait which may be due to the predominance of additive gene action and the desired results may be obtained through the simple selection. The results are in accordance with Patil *et al.* (2018) [14] and Bedawy *et al.* (2018) [3].

#### Capsule length (cm)

The trait, capsule length, was found to be the lowest in the line, MLTS-3 (2.06cm) and was the highest in the line, YLM-155 (2.64cm) with a general mean of 2.31cm. Genotypic and phenotypic coefficients of variation observed for this trait

were low *i.e.*, 3.71% and 8.07%, respectively. Higher PCV values than GCV indicated that the variation is not only due to the genotype component but also due to the influence of environment. This clearly indicated that simple selection will be misleading for the improvement of this trait. These results are in harmony with that of Shekhawat *et al.* (2013) [16], Thirumala Rao *et al.* (2013) [4], Tripathi *et al.* (2013) [21] and Bharathi *et al.* (2014) [4]. Low heritability (87.6%) and high genetic advance as per cent of mean (24.86 %) were noted for this trait which may be due to the predominance of non additive gene actions hence the simple selection is ineffective. These results are in harmony with Mustafa *et al.* (2015) [13].

#### 1000 seed weight (g)

The mean values for this trait ranged from (2.87 g) to (3.15 g) with a general mean of 3.02g. The genotype, YLM-161, recorded the highest value for this trait and was superior to all the other genotypes, whereas, YLM-151 recorded the lowest values. This trait also exhibited low genotypic and phenotypic coefficients of variation *i.e.*, 1.81% and 3.90 %, respectively. Similar results were also reported by Sudhakar *et al.* (2007) [18] and Tirumala Rao *et al.* (2014) [4]. Low heritability (21.7%) with low genetic advance as per cent of mean (1.74%) was reported indicating the preponderance of non-additive gene action in controlling the trait. Hence, direct selection would be ineffective for the improvement of this trait and further improvement would be possible through heterosis breeding. Chandra Mohan *et al.* (2014) [5] and Mustafa *et al.* (2015) [13] also reported similar type of variability parameters for 1000 seed weight in sesame.

#### Days to maturity

The average number of days taken for maturity varied from 76 days (YLM-153) to 89 days (MLTS-5) with a general mean of 84.30 days. The highest number of days to maturity was found in the line, MLTS-5 and the lowest was found in the line, YLM-153. This trait exhibited low values for genotypic and phenotypic coefficients of variation *i.e.*, 3.04 % and 6.57 %, respectively. Similar results were reported by Tripathi *et al.* (2013) [21], Vanishree *et al.* (2011) [22], Thirumala Rao *et al.* (2014) [4], Bharathi *et al.* (2014) [4] and Hika *et al.* (2015) [10]. Low heritability (29.8%) and low genetic advance as per cent of mean (2.96 %) were observed for this trait which indicated the presence of non additive gene action and ineffectiveness of simple selection for the improvement of this trait. This is in accordance with the results reported by Mustafa *et al.* (2015) [13] and Chandra Mohan *et al.* (2014) [5].

#### Oil content (%)

The mean values for this trait ranged from (41.22) to (47.10) with a general mean of 44.3%. The genotype, MLTS-1, recorded the highest (47.10) and was superior to all the other genotypes, whereas YLM-149 recorded the lowest (41.21) values for this trait. Low genotypic and phenotypic coefficients of variation were observed for this trait *i.e.*, 3.04 % and 6.57 %, respectively. Higher PCV values over GCV revealed that variation is being influenced by the environment. The results were in accordance with Abate (2015) [1] and Kanak Saxena *et al.* (2016) [12]. Low heritability (21.5 %) and low genetic advance as per cent of mean (2.91%) were noted which is due to the predominance of non additive gene actions hence that selection for this character would be ineffective. Similar results were also reported by Chandra Mohan *et al.* (2014) [5] and Mustafa *et al.* (2015) [13].

**Seed yield per plant (g)**

Seed yield per plant ranged from 4.70g to 6.24g with a general mean of 5.41g. The highest seed yield was observed in the lines, MLTS-1 and the lowest was found in the lines, YLM-158. Genotypic and phenotypic coefficients of variation observed for this trait were low *i.e.*, 3.71 and 8.07, respectively. High difference between GCV and PCV values indicated that there is a influence of environment on the expression and simple selection will be misleading. These results were confirmed by Chandra Mohan *et al.* (2014)<sup>[5]</sup>, Tirumala Rao *et al.* (2014)<sup>[4]</sup> and Bedawy *et al.* (2018)<sup>[3]</sup>. Low heritability (25.5%) coupled with low genetic advance as per cent of mean (4.23 %) was noted for this trait indicating the predominance of non-additive gene action in the expression of this trait. Similar results were also found by Mustafa *et al.* (2015)<sup>[13]</sup>, Chandra Mohan *et al.* (2014)<sup>[5]</sup>.

Thus, the present study indicated the use of direct selection for the improvement of the trait, number of capsules per plant while, the traits, plant height to the first capsule and number of branches per plant recorded high heritability and genetic advance but the variability in the form of PCV and GCV were low indicating the cautious application of simple breeding for direct selection and application of other breeding methods like heterosis breeding for the improvement of remaining traits.

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