

Genetic variability, heritability and genetic advance for yield and its components in sesame (*Sesamum indicum* L.)

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SUMMARY

The present investigation was carried out with thirty one sesame (*Sesamum indicum* L.) genotypes during summer 2011 at Onattukara Regional Agricultural Research Station , Kerala Agricultural University, Kayamkulam. Variability parameters were estimated for yield and yield components. High heritability and high genetic advance as per cent of mean was recorded for the characters viz., plant height, number of branches, number of capsules per plant , oil content and yield. except days to 50% flowering and 1000 seed weight.

Key Words : Sesame, Genetic advance, Heritability, Yield

How to cite this article : Bindu, M.R., Sushamakumari, P., Indira, M., Vilasini, T.N., Seeja, S. and Achamma Yohannan, Ansu (2014). Genetic variability, heritability and genetic advance for yield and its components in sesame (*Sesamum indicum* L.). *Internat. J. Plant Sci.*, **9** (1): 167-169.

Article chronicle : Received : 12.06.2013; Revised : 05.11.2013; Accepted : 13.11.2013

Sesame (*Sesamum indicum* L.) is an annual plant that belongs to the family Pedaliaceae . It is an ancient oil yielding crop of India and known as “Queen of Oilseeds” due to high cooking quality and medicinal value of its oil. It is cultivated in the world mainly for its high quality edible oil. Sesame seed contains over 50 per cent oil and a balanced fatty acid composition with more or less equal percentages of oleic and linoleic acid. Sesame oil has good shelf life because of the presence of endogenous antioxidants, sesamol and sesaminol together with tocopherols (Baydar *et al.*, 1999), while its protein is used for industrial purposes (Ashri, 1998). India is the largest producer of sesame covering 42 per cent of world sesame area and 27 per cent of the production.

Sesame can grow well in many ecological regions of tropical and subtropical climate, and also grows in most kind of soils. However, it thrives best on well-drained soil with a moderate fertility and a pH between 5.5 and 7.0. Sesame is highly drought tolerant, and it can adapt and produce seed well under fairly high temperatures but is sensitive to wet condition and has a very low salt tolerance (Carlsson *et al.*, 2008).

However, in spite of its importance sesame has been mentioned as an “orphan crop” as it is not mandated to any of the CGIAR institutes which could be one of the reasons for lack of research in this crop. Hence, the first and foremost need in sesame research is identification and characterisation of sesame genotypes by using morphological and molecular markers. The presence of variability in a crop is important for genetic studies and consequently used for improvement and selection. Selection of superior genotypes will be possible only sufficient variability is present in the gene pool .The co-efficient of variation expressed in phenotypic and genotypic levels are used to compare the variability observed among different characters. . It is essential to partition the overall variability into heritable and non- heritable components with the help of genotypic co-efficient of variation, heritability and genetic advance. The present study was undertaken to estimate

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the variability, heritability and genetic advance for yield and yield contributing characters and to find out and establish suitable selection criteria for high yield.

MATERIAL AND METHODS

Thirty sesame genotypes received from All India Coordinated Research Project (Sesame), Jabalpur along with check variety Thilak were used in this experiment to study the genetic components of variability among the genotypes. Experiment was laid out in the field of Onattukara Regional Agricultural Research Station, Kayaamkulam under a triplicated Randomized Complete Block Design (RCBD) during 2011 summer. The plot size of 3x3.6m and a row to row distance of 30 cm and plant to plant distance of 10 cm

were maintained. Normal cultural practices were followed. Data on various characters were recorded and analysed.

RESULTS AND DISCUSSION

Genetic diversity of crops plays an important role in sustainable development and food security as it allows the cultivation of crops in the presence of various biotic and abiotic stresses. It is also important for selection of parents that can be used in plant breeding programs. Information on genetic diversity is important when working to improve crop varieties. Genetic diversity is studied by using various methods such as morphological, biochemical and molecular markers. Morphology has been a primary tool to estimate genetic differences among sesame genotypes. Several studies based

Table 1 : Performance of sesame genotypes

Sr. No.	Variety	DFP	Plant Ht. (cm)	DM	No. of branches	No. of capsules/ plant	1000 seed wt. (g)	Oil (%)	Yield (kg ha ⁻¹)
1.	PKDS-100	34	75.6	80	4.6	85.0	3.4	47.75	332
2.	PKDS-101	32	96	76	5.6	81.3	3.3	50.80	430
3.	OSC-440	34	104	76	2.6	43.3	3.4	51.11	253
4.	TKG-22	29	92.6	70	3.6	52.6	3.3	49.14	430
5.	LT-8	30	102	68	4.0	64	3.2	50.45	904
6.	JLS-110-12	33	102.6	78	5.0	89.6	2.6	37.65	1011
7.	MT-12-07	32	102	74	7.3	98.6	3.2	48.80	1013
8.	RT-357	29	116.3	72	33	53	3.9	47.99	316
9.	RT-358	25	131.6	74	6.0	61.3	3.3	52.11	658
10.	RT-54	32	97.6	71	4.6	62.6	2.8	38.13	724
11.	RT-359	30	105.6	68	7.0	90.3	3.0	58.47	1053
12.	SSD-3	34	146	74	3.3	67.3	3.0	53.23	750
13.	OSC-32-09	31	101	69	5.3	55.3	3.0	48.38	425
14.	SSD-4	34	124.3	76	3.6	46.3	3.1	51.18	645
15.	VS-OT-034	34	121.3	72	5.0	63.3	2.8	49.55	486
16.	CST-2001-9	29	85.0	68	5.0	36.6	3.0	53.75	693
17.	OSC-366-1	32	111.6	74	4.3	58.3	3.1	52.47	891
18.	YLM-98	35	126.6	72	5.3	123.3	3.1	50.37	333
19.	TKG-307	31	92.3	70	5.3	73.0	3.0	52.17	421
20.	AT-159	32	66	69	4.6	32.6	3.1	52.54	408
21.	AT-191	33	99.3	67	6.6	89.6	3.2	50.37	671
22.	AT-179	30	100.6	67	3.6	92.3	3.3	52.17	237
23.	AT-175	31	95.0	74	3.3	56.0	3.2	52.547	50
24.	AT-183	29	79.3	69	3.0	103.6	3.2	4.18	737
25.	AT-186	29	108.6	70	3.3	2.8	3.0	500	500
26.	SSD-5	33	129.3	70	5.6	100.3	2.8	52.60	316
27.	SSD-6	33	132.0	74	5.6	74.0	3.2	52.06	562
28.	YLM-86	30	114.3	72	7.0	37.3	3.1	51.75	237
29.	PKDS-102	33	106.3	74	5.0	113.0	2.7	52.35	495
30.	PKDS-703	29	103.6	68	7.3	63.6	3.1	51.65	198
31.	Thilak	34	130.6	78	6.6	220.3	3.3	50.28	605
	CD	3.18	6.32	3.66	0.66	4.62	0.34	2.35	59.59
	CV	6.1	3.62	3.11	8.0	3.67	6.38	2.85	8.5

Table 2 : Genetic variability components of sesame genotypes

Characters	Mean	PV	GV	PCV	GCV	Heritability	GA %
Days to 50% flowering	31.68	7.527	3.727	8.66	6.09	49.5	8.83
Plant height	106.84	323.51	308.52	16.83	16.44	95.36	33.07
No. of branches	5.0	1.893	1.733	27.5	26.32	91.54	51.89
No. of capsules	77.04	1308.45	1300.44	46.95	46.80	99.39	96.13
1000 seed weight	3.13	0.083	0.043	9.2	6.6	51.8	9.82
Days to maturity	71.87	16.48	11.46	5.64	4.71	69.54	8.08
Oil	50.32	17.05	14.98	8.2	7.69	87.66	16.90
Yield/ha	0.428	0.037	0.036	44.94	44.33	97.29	90.20

on morphological markers have found a high genetic diversity in sesame populations (Arriel *et al.*, 2007). In the present study also, the thirty one genotypes exhibited distinct differences in all the eight characters studied (Table 1). RT-358 recorded the maximum height (131.6 cm) followed by Thilak (130.6 cm). Minimum days for maturity was taken by AT-191 and AT-179 (67 days) and maximum number of days for maturity was taken by PKDS-100 (80 days). Maximum number of branches were produced by MT-12-07 and PKDS-703 (7.3 per plant) and highest number of capsule per plant was produced by the check variety Thilak (220.3 per plant). RT-357 recorded the highest 1000 grain weight (3.9 g) and RT-359 recorded the highest oil content (58.47%). Highest per hectare yield was recorded by MT-12-07 followed by Nirmala (1013 kg and 1011 kg, respectively).

The basic key to bring out the genetic gain to a crop is to utilize the available or created genetic variability. It is difficult to judge about what proportion of variability is heritable and what proportion is non-heritable *i.e.* environmental. So, it becomes necessary to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters such as genetic co-efficient of variation, heritability and genetic advance (Nath and Alam, 2002).

High level of variability was observed in all the genotypes for both PCV and GCV in number of branches per plant, number of capsules per plant and seed yield per plant (Table 2). The results are in confirmation with Parameshwarappa *et al.* (2009), Chowdhury *et al.* (2010) and Rao (2011) in sesame. High heritability and high genetic advance as per cent of mean was recorded for all the characters except days to 50% flowering and 1000 seed weight. Similar findings were reported by Parameshwarappa *et al.* (2009) and Chowdhury *et al.* (2010). The result indicated the lesser influence of environment in expression of characters and prevalence of additive gene action in their inheritance, hence, it is amenable for simple selection for crop improvement. Thousand seed weight recorded moderate heritability with low genetic advance as per cent of mean. This result is in conformity with the findings of Sarwar and Haq (2005) indicating that these characters were controlled by non-

additive gene action. The result revealed that height of the plant, number of branches per plant, number of capsules per plant and oil content are controlled by additive genes and simple selection can increase the yield.

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