



Indian Journal of Agriculture and Allied Sciences

A Refereed Research Journal

ISSN 2395-1109

e-ISSN 2455-9709

Volume: 2, No.: 4, Year: 2016

www.mrfsw.org

Received: 01.10.2016, Accepted: 24.10.2016

NATURE AND GENE ACTION FOR SEED YIELD AND OIL QUALITY TRAITS IN SESAME (*Sesamum indicum* L.)

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Abstract: Genetic analysis for seed yield and their attributing traits in sesame (*Sesamum indicum* L.) were analysed genetically in parents and 45 F_1 crosses (excluding reciprocals) to generate information on nature and magnitude of gene effects for seed yield and oil quality traits. Both additive (D) and dominance (H_1) components of genetic variation plays an important role in the inheritance of characters under study. The estimates of additive and dominance component revealed the predominance of additive component for days to 50 % flowering, days to maturity, plant height and number of branches plant⁻¹ whereas predominance of dominance components for number of capsules plant⁻¹, number of seeds capsule⁻¹ and seed yield plant⁻¹. The parents viz., JCSC-8, NIC-16207, IC-14329 and Swetha Til with maximum additive genetic variation may be utilised in hybridization programme of sesame for improvement of seed yield and oil quality traits.

Keywords: Additive and dominance components, yield and oil quality contributing traits.

Introduction: Progress in the genetic improvement of yield in any crop depends upon the genetic information available on inheritance of yield and other important related traits. Therefore knowledge of magnitude and type of genetic variance has a great importance for sesame breeder dealing with simultaneous improvement of oil quality and seed yield. The proper method developed for the crop improvement depends on assessment of the genetic and environmental components of variation. In most of the mating designs, it is assumed that non allelic interactions are absent where as estimates of additive and dominance components are biased to a greater extent in presence of non allelic interactions^[1]. The appropriate analysis of triple test cross and simplified triple test cross yields information on epistasis as well as additive and dominance components. Hence, an attempt was made in this study to estimate the epistasis, additive and dominance type of genetic components.

Materials and Methods

For the present study eighteen sesame genotypes involving three testers viz., AKT-64, Phule Til-1, JLT-7 and fifteen genotype (male

lines) viz., T-13, Tarun, Shekhar, RT-46, Hima, Swetha Til, GT-1, TKG-21, SI-7-2, SI-11, JCSC-8, SP-1162-B, NIC-16207, NIC-16205, IC-14329 were crossed in line x tester mating design during *kharif* 2010-11. The resulting 45 hybrids along with their parents were raised during *kharif* 2011-12 at Head, Department of Botany, Dr. Panjabrao Deshmukh Krushi Vidyapeeth, Akola in a Randomized Block Design with three replications. One row of fifteen plants of each genotype was sown at the spacing of 45 cm between rows and 15 cm between plants. Normal recommended cultural practices and plant protection measures were followed. Five competitive plats were randomly selected for recording biometrical measurements on days to 50% flowering, days to maturity, plant height (cm), number of branches plant⁻¹, number of capsules plant⁻¹, number of seeds capsules⁻¹, seed yield plant⁻¹ (g), 1000 seed weight (g), oil content (%) and fatty acid profile (%). The statistical and biometrical analysis was performed as per the methodology suggested^[2] for simplified triple test cross analysis.

Results and Discussion

The analysis of variance for sums ($\bar{L1i} + \bar{L2i}$) and differences ($\bar{L1i} - \bar{L2i}$) and estimates of additive (D) and dominance (H_1) components are presented (Table 1). The mean squares due to sums ($\bar{L1i} + \bar{L2i}$) were significant for days to 50 % flowering, days to maturity, plant height, number of branches plant⁻¹ and number of seeds capsule⁻¹. The mean squares due to differences ($\bar{L1i} - \bar{L2i}$) were significant for all the character except 1000 seed weight, oleic acid content and linoleic acid content. The additive (D) and dominance (H_1) components were estimated for different characters under epistatic model presented (Table

1). The estimates of additive (D) and dominance (H_1) indicated that the predominance of additive component for days to 50 % flowering, days to maturity, plant height and number of branches plant⁻¹ where as predominance of dominance component for number of capsules plant⁻¹, number of seeds capsule⁻¹ and seed yield plant⁻¹. Over dominance was observed for number of seeds capsule⁻¹ and seed yield plant⁻¹. Same was reported in mustard^[3], linseed^[4] and cotton^[5]. Therefore, the parents with high additive genetic variation may be utilized in sesame breeding programme.

Table 1 : Analysis of variance for the sums, differences and components of genetic variation for different characters.

Source of variance	d. f.	Means square									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant ⁻¹	Number of capsules plant ⁻¹	Number of seeds capsule ⁻¹	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Linoleic acid content (%)	Oleic acid content (%)
Sums ($\bar{L1i} + \bar{L2i}$)	14	19.30**	87.93**	1015.85**	0.03**	50.11	65.37**	2.34	0.16	4.78	15.02
Error	28	1.12	2.85	3.51	0.04	27.15	14.24	1.16	0.08	9.67	10.65
Differences ($\bar{L1i} - \bar{L2i}$)	14	4.56**	22.93**	415.77**	0.25**	158.26**	110.03**	4.29**	0.08	15.33	2.93
Error	28	1.30	7.24	3.83	0.04	26.84	18.15	1.44	0.08	10.10	5.67
Components of genetic variation											
D		12.12	56.72	674.90	0.19	15.31	34.08	0.79	--	--	--
H₁		2.17	10.46	274.63	0.14	87.62	61.25	1.90	--	--	--
H₂		0.42	0.43	0.64	0.86	2.39	1.34	1.56	--	--	--

* Significant at 5% and ** Significant at 1%

The estimates of individual line contribution to the additive and dominance components were presented (Table 2 and Table 3). Maximum additive variation was recorded by Hima, Swetha Til, NIC-16207, JCSC-8, IC-14329, TKG-21 and RT-46 for the characters days to 50% flowering, days to maturity, plant height, number of branches plant⁻¹, number of capsules plant⁻¹, seed yield plant⁻¹, oil content, oleic acid content and linoleic acid content, respectively. Maximum dominance for the plant height, number of capsule plant⁻¹ and number of seeds capsule⁻¹ was recorded by NIC-16207.

Swetha Til recorded maximum dominance variation for days to 50 % flowering and oleic acid content. SP-1162-B recorded maximum dominance variation for days to maturity, seed yield plant⁻¹ and oil content. For 1000 seed weight, maximum dominance variation was recorded by SI-7-2. For linoleic acid content maximum dominance variation was recorded by SI-11. JCSC-8 recorded maximum dominance for number of branches plant⁻¹. The parents JCSC-8, NIC-16207, IC-14329, Swetha Til with additive genetic variation may be used in sesame breeding programme.

Table 2 : Individual line (Pi) contribution to the additive component ($\bar{L1i} + \bar{L2i}$) for different characters.

S. N.	Male lines	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant ⁻¹	Number of capsules plant ⁻¹	Number of seeds capsule ⁻¹	Seed yield plant ⁻¹ (g)	1000 Seed weigh t(g)	Oil content (%)	Oleic acid content (%)	Linoleic acid content (%)
1	SI-7-2	80.00	201.67	267.13	6.63	75.07	85.00	14.67	4.84	100.63	93.56	78.94
2	SI-11	78.33	199.33	264.53	6.57	82.07	84.67	13.03	4.17	101.97	93.05	79.54
3	JCSC-8	82.00	204.67	303.73	7.50	96.47	99.67	12.70	4.17	101.28	80.59	82.01
4	SP-1162-B	77.33	199.33	250.80	6.57	87.53	80.67	15.43	4.84	100.62	91.21	81.46
5	NIC-16207	80.00	202.00	306.27	7.67	95.80	79.00	15.37	4.51	102.12	91.33	80.37
6	NIC-16205	81.00	208.33	291.33	7.17	90.93	96.67	14.67	4.67	101.52	90.42	82.51
7	IC-14329	79.67	210.00	283.33	6.97	90.53	88.67	15.47	4.01	101.79	90.50	82.55
8	T-13	79.33	207.33	258.47	6.93	81.13	87.00	14.10	4.51	100.25	90.63	82.67
9	Tarun	77.67	205.67	261.87	7.07	91.13	91.00	14.77	4.17	100.65	89.85	81.54
10	Shekhar	77.33	203.33	262.33	6.87	90.00	92.33	13.73	4.34	99.84	90.19	81.73
11	RT-46	77.00	204.00	273.27	6.90	92.93	99.00	14.87	4.84	100.44	88.73	84.61
12	Hima	88.33	223.00	325.13	7.53	85.20	80.00	12.10	5.17	101.64	88.61	84.22
13	Swetha Til	86.67	225.33	338.87	7.10	92.43	94.00	13.60	4.67	101.07	91.74	80.81
14	GT-1	74.67	205.00	271.67	5.90	91.60	91.33	15.00	4.34	101.05	91.26	81.83
15	TKG-21	79.00	203.33	298.00	6.43	89.13	87.33	11.53	4.67	96.05	94.46	78.11

Simplified triple test crosses yields comparatively unbiased estimates of degree of dominance in presence of epistasis^[6]. The choice

of appropriate tester for simplified triple test cross is therefore crucial.

Table 3 : Individual line (Pi) contribution to the dominance component ($\overline{LH} - \overline{L2}$) for different characters.

Sr. No	Male lines	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant ⁻¹	Number of capsules plant ⁻¹	Number of seeds capsule ⁻¹	Seed yield plant ⁻¹ (g)	1000 Seed weight (g)	Oil content (%)	Oleic acid content (%)	Linoleic acid content (%)
1	SI-7-2	0.00	-1.00	3.40	0.23	0.13	-1.00	2.00	0.50	0.61	-1.72	1.52
2	SI-11	2.33	-0.67	-12.40	0.23	-17.27	-5.33	0.10	0.16	-0.07	-2.57	2.98
3	JCSC-8	0.00	-0.67	11.60	0.70	-1.67	-2.33	0.77	0.16	-1.14	-11.65	1.53
4	SP-1162-B	1.33	4.67	-6.67	-0.23	-7.80	2.00	2.10	0.17	3.58	-3.09	2.54
5	NIC-16207	-2.00	-2.67	22.13	0.73	10.47	5.67	1.97	0.17	0.40	-2.85	2.25
6	NIC-16205	1.00	-5.67	14.53	-0.37	-10.00	-13.33	-2.53	0.34	-0.26	-0.68	0.01
7	IC-14329	-0.33	-2.67	4.00	-0.17	10.40	13.33	1.66	0.00	-0.35	-3.04	2.81
8	T-13	-0.67	-2.67	-21.80	-0.20	-1.13	-3.67	0.37	0.17	-1.05	-0.49	0.03
9	Tarun	-0.33	-1.67	-20.80	0.13	-5.53	5.00	-0.57	-0.17	-1.01	1.39	-1.30
10	Shekhar	-0.67	-3.33	-16.07	-0.67	-12.00	-19.00	-1.13	0.00	-0.46	-0.13	0.13
11	RT-46	-3.00	-2.00	-8.47	0.10	-21.60	-0.33	-2.73	-0.16	-0.02	-1.25	1.25
12	Hima	-1.67	-10.33	-4.07	-0.53	-13.07	-2.67	-0.30	-0.16	0.04	-1.43	1.36
13	Swetha Til	3.33	-11.33	-36.87	-0.30	-20.90	-10.00	-1.93	-0.34	0.11	1.58	-1.07
14	GT-1	-2.67	-1.67	-20.60	0.23	4.13	-16.00	-1.80	0.00	0.65	0.70	-0.49
15	TKG-21	-0.33	-0.67	-26.93	0.03	1.67	-3.33	1.33	0.34	1.63	0.96	-0.05

In the present study, both additive (D) and dominance (H₁) components of genetic variation plays an important role in the inheritance of characters. The presence of additive gene action for the traits, days to 50 % flowering, days to maturity, plant height and number of branches plant⁻¹ implies that early generation selection may be useful for the improvement of these traits. However, for the traits, number of capsules plant⁻¹, number of seeds capsule⁻¹ and seed yield plant⁻¹ showing dominance components of variants, heterosis breeding may be useful for exploitation of hybrid vigour through hybrid varieties in sesame. The parents with maximum additive genetic variation will be useful for improvement of economic traits and may be utilized in hybridization programme.

References

1. Baker, R.J. (1978). Issues in diallel analysis, *Crop Science*, 18 : 533-536.

2. Jinks, J.L., Perkins, J.M. and Breese, E.L. (1969). A general method of detecting additive, dominance and epistasis variation for metrical traits II. Application to inbred lines. *Heredity*, 24 : 115-127.
3. Dond, K.R., Nair, B., Patil, S., Puttawar, M.R. and Katre, L.A. (2012). Genetic analysis of yield and yield contributing components in mustard (*Brassica juncea*). *J. Soils Crops*, 22: 192-196.
4. Prasad, B.H.V., Manapure, P.R., Kurhade, G.M. and Lende, A.R. (2014). Simplified triple test cross analysis in linseed. (*Linum usitatissimum* L.). *J. Soils Crops*, 24: 132-135.
5. Jayade, V.S., Patil, S.R., Peshattiwar, P.D. and Kalamkar, V.B. (2014). Simplified triple test cross analysis for yield, yield contributing and fibre traits in cotton (*Gossypium hirsutum* L.). *J. Soils Crops*, 24: 72-78.
6. Chahal, G.S. and Singh, T.H. (1974). Application of different mating designs to determine gene action in *Gossypium arborium* L. I. diallel versus Simplified triple test cross. *Crop improve*, 1 : 61-71.