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Short Communication

Inheritance of branching and important biometrical traits in sesame (S*esamum indicum L)*

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Sesame (*Sesamum indicum* L.), is an important source of edible oil and is also widely used as a spice because of its ease of extraction and its great stability. India ranks second in production of sesame (7.3 lakh tons) next to China, with an area of 2.18 m. ha and productivity of 335 kg per ha [1]. Though the progress achieved is quite high in terms of area and production, the productivity is the lowest when compared to the world average. There is an inherent lacuna in sesame, as there will be yield loss due to poor population. The branched varieties need more space per plant and hence maintenance of population is very difficult in the commercial planting. This also poses serious problem in the countries where mechanical harvesting is restored. To overcome this situation, identification of mono stem or shy branching type of sesame suited to high - density planting is an important strategy, which will benefit the farming community by increased net return. The basic requirement in adopting a suitable breeding method is a sound understanding of the genetic behavior. Therefore, success in development of genotypes with desired characters depend on the knowledge of genetic makeup of the characters and their behavior in different genetic backgrounds. Hence, the present study was aimed at to study the inheritance and nature of gene action underlying the inheritance of branching and other biometric traits.

A generation mean experiment was designed using three branched, Paiyur 1, TMV 4, TMV 5, and two unbranched, KS 990812 and Cordebergea genotypes of sesame. Five combinations *viz.,* Paiyur 1 x Cordebergea, TMV 4 x Cordebergea, TMV5 x Cordebergea, TMV 4 x KS 990812 and TMV 5 x KS 990812, were produced during *rabi* 2004-2005. F_1 plants were randomly chosen to produce F_2, BC_1 and BC_2 generations. Thus besides P_1 and P_2, seeds of four generations *viz*., F_1, F_2, BC_1 and BC_2 were generated in each cross and were raised during summer 2005 at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. The parents and F_1s were planted in five rows of 5 m length. The BC_1 and BC_2 were planted in 5 rows of 6m length, while the F_2 of each crosses were raised in 10 rows of 6m length. The inter and intra row spacing was maintained at 30 x 30 cm. Seventy five plants each from parents and F_1 s , 100 plants from BC_1 and BC_2 generations and 300 plants from F_2 populations were randomly selected. Observations on ten biometrical characters including number of branches per plant were recorded for all these selected individuals. The data were subjected to generation mean analysis as suggested by Hayman [2]. The adequacy of the data for a simple additive-dominance model in a generation was first tested utilizing A, B and C scaling tests of Mather and Jinks [3]. The results obtained from the scaling tests were further confirmed by Joint scaling test as proposed by Cavalli [4].

Inheritance studies

Parents (P_1 and P_2), F_1, F_2, B_1 (BC_1) and B_2 (BC_2) generations of the five cross combinations were used to study the mode of inheritance of branching. The individuals were grouped as branched (> 2 branches) and monostem / shy branching plants (0 to 2 branches) based on number of branches per plant. The goodness of fit to Mendelian segregation of branched and monostem / shy branched classes in the segregating population were tested by Chi- Square (χ^2) test.

The mean performance for number of primary branches differs between generations and within the crosses in all combinations. The minimum number of branches was noticed in the parents Cordebergea and KS 990812, while, it was intermediate between those of the parents in F_1. In F_2 populations, the minimum number of branches was recorded in cross Paiyur1 x Cordebergea.

Gene effects

The simple additive-dominance model was not adequate to explain the inheritance of all the characters studied in all the cross combinations which showed the complexity of the characters and hence the analysis was extended to a digenic interaction (Table 1). The cross TMV5 x Cordebergea, showed adequacy for simple additive-dominance model for all the characters studied except for plant height, number of primary branches, capsule length and number of seeds per capsule. Hence this cross can be improved further through pedigree breeding for the above traits.

The additive, dominance gene effects and epistatic interactions were important for the trait, number of branches per plant. The positive and significant additive gene effect was recorded for branches in the crosses Paiyur 1 x Cordebergea and TMV 4 x Cordebergea. The dominance gene action was positive and significant in all the crosses except TMV 5 x Cordebergea for this trait. Hence these crosses can be utilized to exploit the heterosis for this trait. Both additive and dominance gene action was found to be present in the crosses Paiyur 1 x Cordebergea and TMV 4 x Cordebergea for branches. Among non allelic interactions, additive x additive gene action was observed in all the crosses except TMV 5 x Cordebergea. As the estimates of 'h' and 'l' were significant and in the same direction, there was complementary epistasis for number of branches per plant in TMV 5 x Cordebergea and the remaining four crosses showed duplicate epistasis for this trait. Additive gene action by Das and Gupta [5] and duplicate epistasis by Deenamani [6] was reported for number of branches per plant. Therefore, it is suggested that the trait number of branches per plant can be improved by simple selection programme, since the transgressive segregants available in this cross may get stabilized in the early generations by simple pedigree breeding procedures.

In the crosses showing non-allelic interactions as revealed by the significance of the scale, the additive [d] component was significantly positive for days to flowering, days to maturity, plant height, 100-seed weight and seed yield in Paiyur 1 x Cordebergea; number of capsules and seed yield for TMV 4 x Cordebergea and number of seeds and seed yield in the cross TMV 5 x Cordebergea, indicating the presence of additive gene action. Variances available in the above crosses for the characters mentioned will be useful in pedigree breeding for selection of superior segregants. Additive genetic variance was reported by Devasena *et al*. [7] for days to 50 per cent flowering and seed yield. The dominance component [h] was positive and

Table 2. Chi square test for goodness of fit with standard ratios in the segregating generations for monostem/shy branching

Combinations	Generations	Ratio to which segregation fits		χ^2 value	Remarks
		Expected	observed		
Paiur1 x Cordebergea	F_2	-	3:1	0.03	Non significant
	BC_1	2:0	-	-	-
	BC_2	1:1	1:1	3.52	Non significant
TMV4 x Cordebergea	F_2	-	9:7	0.22	Non significant
	BC_1	4:0	-	-	-
	BC_2	1:1	-	-	-
TMV5 x Cordebergea	F_2	-	9:7	1.03	Non significant
	BC_1	4:0	4:0	0.00	Non significant
	BC_2	1:1	1:1	1.78	Non significant
TMV 4 x KS990812	F_2	-	9:7	3.18	Non significant
	BC_1	4:0	-	-	-
	BC_2	1:1	-	-	-
TMV 5 x KS990812	F_2	-	3:1	0.21	Non significant
	BC_1	2:0	-	-	-
	BC_2	1:1	1:1	1.12	Non significant

significant for days to first flowering, days to maturity, plant height, capsule number and seed yield in TMV 4 x KS 990812; all the characters except capsule length, number of seeds per capsule, seed yield and oil content in TMV 4 x Cordebergea; all the other traits except days to first flowering, capsule length and oil content in Paiyur 1 x Cordebergea; plant height, capsule number, capsule length, hundred seed weight and seed yield in TMV 5 x KS 990812; plant height in TMV 5 x Cordebergea; indicating the presence of dominance gene action for the above mentioned characters in the respective crosses. Dominance gene action was reported by Saravanan and Nadarajan [8] for number of capsules, number of seeds per capsule and seed yield per plant.

Both additive and dominance gene action was found to be present in the crosses Paiyur 1 x Cordebergea for days to maturity, plant height and hundred seed weight and number of capsules per plant and seed yield per plant. This type of gene action makes it necessary for resorting to special techniques like intermating segregants or recurrent selection to harness the different kinds of gene effects. The additive x additive gene action was the only fixable epistatic component of genetic interaction observed in the crosses, TMV 4 x KS 990812 for days to first flowering, days to maturity, plant height and seed yield; Paiyur 1 x Cordebergea for all the characters studied except capsule length and oil content; TMV 4 x Cordebergea for all the other traits except capsule length, number of seeds per capsule and oil content, TMV 5 x KS 990812 for plant height, number of capsules, capsule length and seed yield; TMV 5 x Cordebergea for plant height; In all these crosses additivity was recorded which could be harnessed by adopting suitable breeding methods like simple pedigree selection for the improvement of the respective characters. The prevalence of additive x additive epistasis was earlier reported by Dharmalingam, [9] for number of capsules on main stem, length of capsule, 100-seed weight and seed yield per plant in most of the crosses.

The opposite signs of [h] and [l] components was revealed by the crosses TMV 4 x KS 990812 for seven characters, TMV 5 x KS 990812 for seven traits, and Paiyur1 x Cordebergea for eight characters in each, TMV 4 x Cordebergea for nine characters and TMV 5 x Cordebergea for two characters indicating the predominance of duplicate epistasis for the above crosses in respect of their economic traits. However, the complementary epistasis was evident for days to first flowering and days to maturity in TMV 5 x KS 990812, number of seeds per capsule in TMV5 x Cordebergea as noticed from the same sings of [h] and [l] components. In general duplicate epistasis was found to be predominant when compared to complementary epistasis. Therefore in order to exploit the presence of interaction effects mainly dominance x dominance and duplicate x dominance type, delayed selection and intermating of segregants followed by recurrent selection will be helpful for improvement. Additive as well as additive x additive interaction effects along with duplicate epistatis was observed in the crosses Paiyur 1 x Cordebergea for days to first flowering, days to maturity, plant height, number of primary branches, hundred seed weight and seed yield and TMV 4 x Cordebergea for number of primary branches number of capsules and seed yield. Rapid improvement by simple selection programme is possible, since the transgressive segregants available in this cross may get stabilized in the early generations by simple pedigree breeding procedures.

In two crosses *viz*., TMV 5 x KS990812, and Paiyur 1 x Cordebergea a monogenic inheritance of 3:1 with simple dominance recessive relationship was noticed for branching and monostem / shy branching character respectively (Table 2). Baydar and Turgut [10] also reported 3: 1 segregation ratio for branching and non-branching types respectively. The segregation of F_2 progenies for the remaining three crosses was non - mendalian. In three crosses *viz*., TMV 4 x KS 990812, TMV 4 x Cordebergea and TMV 5 x Cordebergea the segregation was in 9:7 ratio for branching and monostem / shy branching characters respectively. This indicated the presence of complementary gene action.

The segregation for BC_1 progenies was expected to be in the ratio of 2:0 and 4:0 for branching and monostem / shy branching characters for monogenic and digenic F_2 ratios respectively. This ratio was fitted well with only one cross TMV 5 x Cordebergea with the F2 ratio of 9:7. In general the ratio observed for BC_1 progenies was 3:1 in most of the crosses. This variation may be due to the effect of modifier genes.

In case of test cross progenies the segregation ratios differed according to the observed epistatic ratios. When the F_2 ratios observed were in the ratio of 9:7 indicating complementary gene action, the test cross ratio expected was 1:1 for branching and monostem / shy branching characters respectively. The segregants in the test cross progenies fitted well with the expected ratio of 1:1 in the crosses TMV 5 x KS 990812, and Paiyur 1 x Cordebergea which was expected to a 3:1 monogenic ratio. Among the three crosses which expressed 9:7 ratio in F_2, only one test cross progeny

Table 1. Components of generation mean with 3 and 6 parameter models for different characters in sesame

Crosses	A	B	C	χ^2	[m]	[d]	[h]	[i]	[j]	[l]
Days to first flowering										
TMV4xKS990812	1.19	11.36**	3.41	107.89**	46.42**	–0.65	6.88**	9.15**	–5.08*	–21.70**
TMV5xKS990812	–2.84*	5.64**	1.65	16.08**	45.46**	–0.33	–1.10	1.15	–4.24**	–3.95
Paiur1xCordebergea	1.97**	0.64	-6.22**	48.67**	43.59**	3.27**	2.23	8.83**	0.67	–11.45**
TMV4xCordebergea	1.48	7.77**	3.44	58.91**	49.84**	–0.50	6.78**	5.81**	–3.14**	–15.06**
TMV5xCordebergea	–1.50	–1.18	–1.90	1.35	44.21**	1.96	–7.34*	A	A	A
Days to maturity										
TMV4xKS990812	–0.34	19.57**	5.20	130.45**	92.34**	–2.65	11.30*	14.03*	–9.96**	–33.26**
TMV5xKS990812	–6.62*	11.57**	1.07	19.26**	90.39**	–1.63	–0.99	3.88	–9.09**	–8.83
Paiur1xCordebergea	9.14**	1.97	–11.83**	91.09**	87.06**	8.14**	9.49**	22.95**	3.58**	–34.06**
TMV4xCordebergea	3.87**	12.59	7.04**	74.66**	99.98**	–0.59	13.97**	9.42**	–4.36**	–25.89**
TMV5xCordebergea	–4.03	–4.36	–8.58*	5.92	88.07**	4.08	–11.58	A	A	A
Plant height										
TMV4xKS990812	9.91	31.63**	-23.25**	69.05**	85.35**	–0.23	79.66**	64.79**	–10.86**	–106.33**
TMV5xKS990812	–16.67**	39.74**	–24.47**	116.18**	89.51**	–11.29	58.79**	47.54**	–28.20**	–70.61**
Paiur1xCordebergea	–7.36	3.20	–48.62**	47.12**	72.67**	17.51**	49.92**	44.46**	–4.48	–40.30*
TMV4xCordebergea	23.82**	50.52**	–26.46*	182.32**	80.84**	4.18	122.07**	100.80**	–13.35**	–175.14**
TMV5xCordebergea	–32.09**	18.02*	–49.92**	46.96**	72.82**	–1.24	40.23**	35.85**	–25.05**	–21.78
No.of primary branches										
TMV4xKS990812	0.78	3.07**	–0.29	19.75**	3.56**	0.24	5.42**	4.15**	–1.15	–8.01**
TMV5xKS990812	–0.64	2.61**	–0.81	14.70**	3.97**	0.27	4.10**	2.77*	–1.62**	–4.74*
Paiur1xCordebergea	1.23*	0.82	–3.16**	47.69**	2.88**	2.05**	5.65**	5.22**	0.20	–7.27**
TMV4xCordebergea	2.29*	2.33**	–1.46	31.66**	3.62**	1.38**	8.08**	6.08**	–0.02	–10.70**
TMV5xCordebergea	–2.28**	0.89	–1.64	20.10**	3.31**	0.31	0.66	0.25	–1.59**	1.14
No.of capsules per plant										
TMV4xKS990812	–3.89	–3.84	–69.76**	20.95**	58.42**	15.75	114.74**	62.03	0.02	–54.31**
TMV5xKS990812	–21.08	52.85**	–20.08	33.07**	66.74**	–15.20*	34.37**	51.85*	–32.28**	–47.51
Paiur1xCordebergea	–14.99	12.46	–94.90**	89.54**	39.79**	11.54	105.91**	92.37**	–13.72	–89.83**
TMV4xCordebergea	102.88**	90.83**	28.96	132.60**	69.87**	22.93**	193.25**	164.76**	6.03	–358.47**
TMV5xCordebergea	–6.05	18.66	1.55	2.46	60.70**	10.54	22.94	A	A	A
Capsule length										
TMV4xKS990812	–0.10	–0.15	–0.10	2.02	2.71**	–0.11	0.09	A	A	A
TMV5xKS990812	0.19*	0.07	–0.13	9.41*	2.61**	–0.06	0.41*	0.39*	0.06	–0.64
Paiur1xCordebergea	0.16	0.08	0.06	2.55	2.63**	–0.19	0.07	A	A	A
TMV4xCordebergea	–2.67*	–0.51**	–0.51**	23.59**	2.45**	–0.05	–0.41*	–0.26	0.12	1.04**
TMV5xCordebergea	–0.35**	–0.72**	–0.50**	46.91**	2.61**	0.03	–0.43*	–0.57**	0.19*	1.65**
No.of seeds per capsule										
TMV4xKS990812	–6.83	–2.89	–4.31	3.27	52.72**	–7.18**	2.14	A	A	A
TMV5xKS990812	8.68**	–6.88	–6.40	23.17**	48.15**	1.91	8.99	8.20	7.78**	–10.00
Paiur1xCordebergea	9.58*	13.49**	1.88	22.09	46.69**	–4.80*	17.82**	21.19**	–1.96	–44.26**
TMV4xCordebergea	–6.69	–12.03*	–16.94**	13.05**	42.87**	–0.30	–3.13	–1.78	2.67	20.51
TMV5xCordebergea	5.95	–16.02**	–16.65**	21.65**	45.88**	7.35*	12.45	6.58	10.98**	3.48

					100 seed weight					
TMV4xKS990812	–0.02	0.14	–0.03	4.31	0.30**	–0.05	0.16	A	A	A
TMV5xKS990812	–0.04*	0.04*	–0.05*	17.05**	0.29**	–0.01	0.06*	0.06*	–0.04**	-0.06
Paiur1xCordebergea	–0.008	–0.02	–0.11**	45.4**	0.27**	0.04**	0.09**	0.08**	0.007	-0.05
TMV4xCordebergea	–0.05*	0.08**	–0.05*	48.82**	0.29**	–0.03**	0.09**	0.08**	–0.07**	-0.10
TMV5xCordebergea	–0.05*	–0.01	–0.03	5.27	0.29**	0.01	–0.04	A	A	A
					Seed yield per plant					
TMV4xKS990812	–2.59	0.46	–9.64**	21.57**	5.75**	1.04	13.13**	7.50*	–1.52	–5.37
TMV5xKS990812	–3.14*	4.98**	–4.46*	28.52**	6.31**	–1.14	9.73**	6.29**	–4.06**	–8.13*
Paiur1xCordebergea	–3.45*	0.11	–12.98**	95.48**	3.43**	1.96*	10.95**	9.64**	–1.78	–6.29
TMV4xCordebergea	8.72**	9.27**	–3.07	65.54**	6.67**	2.54*	25.76**	21.07**	–0.28	–39.07**
TMV5xCordebergea	–1.25	0.62	–2.07	1.46	5.62**	2.25*	2.80	A	A	A
					Oil content					
TMV4xKS990812	–2.55**	0.48	–0.15	10.20*	40.16**	–0.83	–1.60	–1.93	–1.52**	3.99*
TMV5xKS990812	0.39	0.65	–0.24	2.33	39.88**	0.16	1.90	A	A	A
Paiur1xCordebergea	0.77	0.62	–0.05	3.55	39.86**	0.32	1.52	A	A	A
TMV4xCordebergea	–0.40	–0.36	0.24	1.25	40.19**	0.55	–1.03	A	A	A
TMV5xCordebergea	–0.10	0.58	0.37	0.80	40.40**	–0.17	1.23	A	A	A

*Significant at 5 % level; **Significant at 1 % level

TMV5 x Cordebergea fitted into the expected ratio of 1:1 and confirmed the complementary gene action in these crosses. The only cross TMV5 x Cordebergea which expressed the segregation ratio of 9:7 in F_2 for branching and monostem / shy branching respectively which was confirmed by both back cross (BC_1) and test cross (BC_2) ratios. This indicates the possibility of transferring the genes responsible for monostem / shy branching nature into the high yielding varieties. Generation mean analysis also exhibited the complementary gene action for this particular cross, which helps in effective execution of pedigree breeding.

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