(1998). The inter- and intra- cluster distance amongst the cluster revealed the lowest intra-cluster distance of cluster V, whereas maximum intra-cluster distance was observed in cluster VII. Maximum inter-cluster distance was observed between cluster I and IV followed by between IV and VII indicating that the genotypes included in these clusters are genetically more divergent. The average cluster means for six traits (Table 3) indicated that the genotypes indicated in cluster I were of early flowering and maturity type with average height whereas, genotypes included in cluster VII are of late maturity duration. Genotypes in cluster VI had highest mean seed yield/plot followed by the only one genotype of cluster IV with maximum number of productive capsules/plant. Based on the present findings, it can be concluded that the genotypes grouped in clusters, I, IV and VII hold good promises diverse parents to get desirable segregants for developing high yielding short duration varieties of sesame with moderate plant height.

Table 3. Cluster mean and per cent contribution of six characters of divergence in sesame

Clusters	Plant height	Days to 50% flowering	Days to maturity	No. of productive capsules/ plant	1000-seed weight (g)	Seed yield/ plot (g)
I	111.21	34.79	75.92	34.79	2.78	45.04
II	137.11	35.1	82.11	41.50	2.66	166.67
III	116.87	37.60	77.30	34.53	2.54	159.67
IV	152.00	40.67	83.33	62.00	2.50	178.33
V	126.44	36.00	82.07	36.13	0.280	108.64
VI	119.33	36.00	82.07	36.13	02.83	199.87
VII	108.33	43.50	88.00	35.00	0.249	039.00
VIII	128.00	40.67	83.50	42.50	02.84	110.61
Per cent contribution	0.29	05.60	03.38	00.97	61.354	028.41

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Genetic Studies in Sesame as a Pre-breeding Approach

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Sesame (*Sesamum indicum* L.) is an ancient and most important oil crop of India because it contains more than 50% high quality oil and known as "queen of oilseed crops". However, it has not contributed its best to the current bright oilseed scenario mainly due to its low yield level. So, there is an urgent need for bringing about genetic improvement in yield potential. The knowledge of genetic analysis helps in formulation of an efficient breeding programme, hence, the present study was undertaken to study the genetics of seed yield and yield attributes in sesame to generate pre-breeding information.

Seven genetically diverse genotypes of sesame *viz.*- T-4, MT-2, TRS-9, RT-274, RT-264, AT-09 and DSS-13 were crossed in all possible combinations excluding reciprocals. The parents along with their $21F_1$s were grown in a randomized block design with three replication during *Kharif*, 1998 at Crop Research Farm, Mauranipur. Each entry was sown in a single row of 5 m length having 30 x 15 cm crop geometry. A single non-experimental row was grown all around the experimental area to neutralize the border effect. Recommended agronomic practices were adopted. Data were recorded on five randomly selected plants in each row for seven metric traits (Table 1). Genetic components of variation were calculation for seed yield and its components following Hayman (1954).

The estimates of genetic components of variation

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Table 1. Estimates of genetic components for seed yield and yield attributes in sesame

Source	Plant height (cm)	Days to maturity	No. of primary branches/ plant	No. of capsules/ plant	Capsules on main stem	1000-seed weight (g)	Seed yield/ plant (g)
D	327.72**	16.69*	0.72**	87.63	9.87	0.16**	2.29
H_1	662.21**	85.33*	2.37**	868.54*	92.77	0.37**	81.33*
H_2	467.78**	59.07**	1.54**	789.53**	66.24**	0.28**	73.00**
h^2	751.78**	34.72**	0.58	1248.87**	40.00**	0.03	150.99*
F	269.91**	26.28	1.38*	123.83	12.45	0.17	-1.32
E	1.12	0.30	0.18*	5.02	2.53	0.00	0.59
$(H_1/D)^{1/2}$	1.42	2.26	1.81	3.15	3.07	1.54	5.96
$H_2/4H_1$	0.18	0.17	0.16	0.23	0.18	0.19	0.22
$(4DH1)^{1/2}{}_{+}F$ $(4DH1)^{1/2}{}_{-}F$	1.82	2.07	3.24	1.58	1.52	2.07	0.91
h^2/H_2	1.61	0.59	0.38	1.58	0.60	0.12	2.07
Heritability (NS)	45.23	21.69	29.71	10.28	9.84	43.40	2.63

*, ** Significant at P= 0.05 and P = 0.01 level, respectively.

presented in Table 1 revealed that D components (additive variation) was non-significant for number of capsules/ plant, number of capsules on main stem and seed yield/ plant. The H_1 components *i.e.* dominance variation was highly significant and larger in magnitude than D components for all the traits indicating the predominant role of dominance component in the inheritance of these traits. Similar reports were made by Murty and Hashim (1973), Dixit (1976) and Godawat and Gupta (1985) who found that relative contribution of dominant gene action was higher than additive gene action. The positive and significant value of h^2 for all the traits except primary branches/plant and 1000-seed weight indicated that dominance was in positive direction.

The estimates of $(H_1D)^{1/2}$ was greater than unity for all the characters suggesting the presence of over dominance. The highly significant H_2 values were smaller than H_1 and $H_2/4H_1$ ratio was less than 0.25, confirming the unequal allelic frequencies and asymmetrical distribution of positive and negative alleles among the parents and in F1. $(4DH_1)^{1/2} + F/(4DH_1)^{1/2}–F$ ratio which measures the proportion of dominant and recessive genes in parents was less than unity for seed yield/plant, greater than unity for the remaining traits, showing an excess of recessive genes for seed yield/plant which was further confirmed by the negative value of F for seed yield/ plant. Heritability in narrow sense was very low for seed yield/plant, whereas for the remaining traits it was moderate.

It is concluded that there is preponderance of dominance genetic variance for seed yield and yield components, hence, top priority should be given on the development of hybrids in sesame.

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