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GENETIC ANALYSIS OF SEED YIELD AND ITS COMPONENT TRAITS IN SESAME (*Sesamum indicum* L.)

R.G. Zala^{1*}, D.R. Mehta², L.J. Raval² and J.M. Khaniya³

¹Potato Research Station, S.D. Agricultural University, Deesa - 385 535, Gujarat, India.

²Department of Genetics and Plant Breeding, Junagadh Agricultural University, Junagadh - 362 001, Gujarat, India.

³Department of Biotechnology, Junagadh Agricultural University, Junagadh - 362 001, Gujarat, India.

*Corresponding author E-mail : argzala@gmail.com

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ABSTRACT

An investigation was conducted with nine diverse parents to develop thirty-six F_1 's and F_2 's by using half-diallel mating design to understand the nature and magnitude of gene action in F_1 's and F_2 's involved in the inheritance of seed yield and its components. Estimation of components of variation revealed that both additive (D) as well as dominance (H_1 and H_2) gene effects were involved in the inheritance of most of the traits studied with preponderance of non-additive gene action for most of the traits. Average degree of dominance was found in the range of complete dominance to over dominance for all the characters in both generations. Asymmetrical distribution of positive and negative genes in the parental lines was observed in both the generations for most of the characters. An unequal frequency of dominant and recessive genes in the parents indicated that in F_1 generation, more number of recessive genes was found in all the traits. Similarly, in F_2 generation, proportion of recessive genes were found in most of the traits. Heritability (ns) estimates was low for number of capsule per plant; moderate for length of capsule and high for days to 50 per cent flowering, plant height, number of primary branches per plant, number of seeds per capsule, days to maturity, seed yield per plant, 1000-seed weight, oil content and harvest index in F_1 generation. In F_2 generation, most of the traits showed low heritability.

Key words : Additive gene action, Dominance gene action, Diallel analysis, Sesame.

Introduction

Sesame (*Sesamum indicum* L.) is one of the oldest cultivated oilseed crops in Asia, and it holds significant importance in the agricultural and economic landscape, particularly in tropical and subtropical regions. It belongs to the family Pedaliaceae and the order Tubiflorae, sesame has a chromosome number of $2n = 2x = 26$. Sesamum is commonly referred to as "Til", "Ellu", "Sim-sim" and "Nuvvulu" across different parts of India and is famously known as the "Queen of Oilseeds" due to the superior quality of oil and meal it produces (Sikarwar *et al.*, 2021). Its oil is highly valued for its stability, owing to the presence of natural antioxidants like sesamol, which offers resistance to oxidative rancidity. Originating from Africa and India, sesame remains a vital crop in tropical and subtropical regions across Asia and Africa, where it thrives under marginal conditions where other crops may

fail.

To formulate a more pragmatic breeding programme, knowledge about the nature and mode of inheritance of quantitative characters are of prime importance. The diallel cross technique has long been used for obtaining information regarding type of gene action involved in the inheritance of different quantitative characters. The present investigation was carried out with the objective to understand the nature and magnitude of gene action in F_1 's and F_2 's involved in the inheritance of seed yield and its component traits in sesame.

Material and Methods

The initial experimental materials comprised of nine parental genotypes viz., G.Til-4, U-76-10, AT-345, AT-375, AT-382, AT-338, IC-96127, IC-204169 and G.Til-10. A total of 36 crosses were made in half-diallel mating

design (excluding reciprocal) during *Summer* 2021 and their F_2 generation was made during *Kharif* 2021. The final evaluation trial comprised of nine parents along with 36 F_1 's, 36 F_2 's and one standard check (G.Til-6) was carried out during *Summer* 2022 at the Sagdividi Farm, Department of Seed Science and Technology, College of Agriculture, Junagadh Agricultural University, Junagadh. The parents and F_1 's were grown in single row and F_2 's with four rows plot with a spacing 30×10 cm. The trial was conducted in Randomized Block Design (RBD) with three replications. Observations were recorded on five competitive plants excluding border ones and was selected randomly from single row plot of each parents and F_1 's as well as 20 competitive plants of F_2 's were selected in each replication for seed yield per plant and its components *viz.*, days to 50 per cent flowering, plant height, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, length of capsule, days to maturity, 1000-seed weight, oil content and harvest index. The genetic components of variation was worked out from the 9×9 half-diallel cross data of F_1 's and F_2 's, as suggested by Hayman (1954) as well as Jinks (1954) and as described in details by Mather and Jinks (1982) and Singh and Chaudhary (1985).

Results and Discussion

The estimates of genetic parameters and their ratios for yield and its components are presented in Table 1. The estimates of 'D' which measures variance due to additive genetic effect as well as H_1 and H_2 , which measures the variance due to non-additive effects were significant for all the characters in both F_1 and F_2 generations except for length of capsule, oil content and harvest index in both the generations for 'D' and days to 50 per cent flowering and number of seeds per capsule for 'D' in F_2 generation, while seed yield per plant in F_1 generation. The above findings indicated that both additive and dominance components were important in the inheritance of these traits. However, additive component was lower in magnitude than dominance component for all the characters in both the generations, which revealed pre-dominance of dominance. Similar findings were reported by Fahmy *et al.* (2015), Sapara *et al.* (2019), Gami *et al.* (2020) and Rathod *et al.* (2021) in sesame.

The overall dominance effect (h^2) over all loci in heterozygous phase for all crosses in F_1 generation was found significant for all the characters except oil content, while in F_2 generation, plant height, number of primary branches per plant, number of seeds per capsule, length of capsule, seed yield per plant and harvest index was found significant for h^2 . This indicated that there is an

involvement of dominant gene in the expression of the traits in F_1 and F_2 generation, while non-significant traits in both generations indicated recessive genes were more prevailed in the traits inheritance. Significant h^2 values were also reported by Reddy *et al.* (2015), Tripathy *et al.* (2016) and Abd El-Kader *et al.* (2017) for seed yield and its components traits in sesame. The positive value of 'F' in F_1 generation was reported for days to maturity which indicated more proportion of dominant alleles among the parents, while the days to 50 per cent flowering, plant height, number of primary branches per plant, number of capsule per plant, number of seeds per capsule, seed yield per plant, 1000-seed weight, oil content and harvest index reported negative 'F' values indicated, more proportion of recessive alleles among the parents. Likewise, in F_2 generation, positive values were observed for days to 50 per cent flowering, number of primary branches per plant and 1000-seed weight which indicated presence of dominant alleles, while negative values were exhibited by plant height, number of capsule per plant, number of seeds per capsule, seed yield per plant, oil content and harvest index which indicated presence of recessive alleles among the parents. The positive as well as negative values were observed for an estimate 'F' in F_1 and F_2 generations for the traits under studied. The positive value of F component was earlier reported by Abd El-Kader *et al.* (2017). However, Swain *et al.* (2001) reported negative value of 'F' for number of capsule per plant and Suganthi (2018) for days to 50 percent flowering and number of capsules per plant.

The non-significant estimate of 'E' reported for days to 50 per cent flowering, number of capsules per plant, length of capsule, days to maturity, seed yield per plant and 1000-seed weight, while, it was significant for plant height, number of primary branches per plant, number of seeds per capsule, oil content and harvest index in F_1 generation. Likewise, in F_2 generation, non-significant estimate of 'E' were observed for days to 50 per cent flowering, number of primary branches per plant, length of capsule, days to maturity, seed yield per plant and 1000-seed weight, whereas traits *viz.*, plant height, number of capsules per plant, number of seeds per capsule, oil content and harvest index showed significant environment 'E' component in F_2 generation. Significance of environmental 'E' component revealed environment play a pivotal role in the expression of this traits and *vice versa*. The non-significant estimate of 'E' was earlier observed by Sakhiya (2013) and Abd El-Kader *et al.* (2017).

The average degree of dominance $(H/D)^{1/2}$ in F_1 and F_2 generations, indicated over dominance type of gene

Table 1 : Estimation of genetic components of variance with their standard errors and ratios for eleven characters in sesame.

Genetic Components	Days to 50% flowering		Plant height (cm)		No. of primary branches per plant		No. of capsules per plant		No. of seeds per capsule		Length of capsule (cm)	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	5.878** ± 2.070	5.678 ± 3.858	27.731* ± 13.348	26.953* ± 11.883	0.532** ± 0.063	0.559** ± 0.039	25.904** ± 6.789	20.059** ± 8.097	11.860* ± 5.938	8.749 ± 6.412	0.033 ± 0.025	0.030 ± 0.022
H₁	20.678* ± 4.569	132.645** ± 34.057	176.304** ± 29.461	473.211** ± 104.913	0.740** ± 0.148	2.251** ± 0.342	115.097** ± 14.984	371.765** ± 71.489	96.940** ± 13.106	178.621* ± 56.612	0.416** ± 0.054	0.780** ± 0.196
H₂	17.001* ± 3.927	125.069** ± 29.276	131.764** ± 25.326	380.169** ± 90.188	0.656** ± 0.140	2.063** ± 0.294	90.585** ± 12.881	372.063** ± 61.455	79.407** ± 11.267	166.868* ± 48.666	0.372** ± 0.047	0.732** ± 0.169
h²	29.669* ± 2.631	-0.784 ± 19.613	251.915** ± 16.966	381.251** ± 60.41	1.063** ± 0.120	0.494** ± 0.197	169.511** ± 8.629	2.997 ± 41.169	157.174** ± 7.548	226.593* ± 32.602	0.630** ± 0.031	0.497** ± 0.113
F	-5.511 ± 4.829	6.932 ± 17.998	-70.974 ± 31.138	-9.99 ± 55.443	-0.278 ± 0.081	0.326 ± 0.181	-47.071 ± 15.837	-13.611 ± 37.779	-23.759 ± 13.852	-26.628 ± 29.917	-0.095 ± 0.057	-0.074 ± 0.104
E	0.956 ± 0.654	1.156 ± 1.220	8.568* ± 4.221	9.346* ± 3.758	0.049* ± 0.020	0.022 ± 0.012	2.669 ± 2.147	8.513* ± 2.561	4.801* ± 1.878	7.912* ± 2.028	0.010 ± 0.008	0.014 ± 0.007
(H₁/D)^{1/2}	1.876	2.417	2.521	2.095	1.180	1.003	2.108	2.152	2.859	2.259	3.541	2.550
(H₂/4H₁)	0.206	0.236	0.187	0.201	0.222	0.229	0.197	0.250	0.205	0.234	0.224	0.235
K_D/K_R	0.600	1.676	0.327	0.837	0.637	1.819	0.398	0.728	0.481	0.195	0.423	0.346
h²/H₂	1.745	-0.006	1.912	1.003	1.619	0.240	1.871	0.008	1.979	1.358	1.695	0.679
Heritability (ns)	0.591	0.089	0.633	0.384	0.677	0.281	0.658	0.141	0.519	0.322	0.455	0.280
t²	9.991**	2.722	16.282**	4.113	2.900	0.498	16.111**	3.372	19.230**	9.575**	13.205**	4.721**

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

Table 1 continued...

Genetic Components	Days to maturity		Seed yield per plant (g)		1000 seed weight (g)		Oil content (%)		Harvest index (%)	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	23.454** ± 5.285	23.156* ± 6.666	1.135 ± 0.944	1.154* ± 0.551	0.055* ± 0.026	0.055** ± 0.013	0.159 ± 0.591	0.210 ± 0.387	2.496 ± 4.760	1.999 ± 3.191
H₁	49.560** ± 12.328	373.231** ± 58.851	10.746** ± 2.085	24.276** ± 2.572	0.374** ± 0.058	0.527** ± 0.112	5.735** ± 1.305	9.649* ± 3.418	81.273** ± 10.507	112.582** ± 28.176

Table 1 continued...

Table 1 continued...

H_2	33.684* 11.664	282.446** 50.590	7.217** 1.792	22.288** 4.866	0.308** 0.050	0.470** 0.097	4.711** 1.122	8.410* 2.938	48.769** 9.032	117.961** 24.221
h^2	45.388** 10.027	1.368 ± 33.890	20.475** 1.200	16.357** 4.183	0.151** 0.033	-0.002± 0.065	1.340 ± 0.752	1.670± 1.968	60.031** 6.051	135.448** 16.226
F	1.028± 6.717	-8.453 ± 31.100	-3.889± 2.203	-1.542± 2.802	-0.090± 0.061	0.031± 0.059	-2.871± 1.379	-3.650± 1.806	-3.080± 11.105	-16.885± 14.890
E	2.101± 1.671	2.400 ± 2.108	0.212 ± 0.299	0.193± 0.174	0.009± 0.008	0.009± 0.004	0.646*± 0.187	0.595*± 0.122	5.126*± 1.505	5.622*± 1.009
$(H_1/D)^{1/2}$	1.454	2.007	3.077	2.294	2.603	1.549	6.003	3.389	5.707	3.752
$(H_1/4H_1)$	0.170	0.189	0.168	0.230	0.205	0.223	0.205	0.218	0.150	0.262
K_D/K_R	1.031	0.833	0.285	0.549	0.525	1.450	-0.201	-0.439	0.805	-0.059
h^2/H_2	1.347	0.005	2.837	0.734	0.490	-0.005	0.284	0.199	1.231	1.148
Heritability (ns)	0.645	0.456	0.680	0.289	0.551	0.241	0.526	0.486	0.524	0.161
t^2	5.653**	2.981	11.427**	23.087**	0.629	0.211	71.862**	22.827**	10.629**	15.405**

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

action for all the traits viz., days to 50 per cent flowering, plant height, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, length of capsule, days to maturity, seed yield per plant, 1000-seed weight, oil content and harvest index except number of primary branches per plant in F_2 generation which show complete dominance. Over dominance for seed yield and important yield components was reported earlier by Abd El-Kader *et al.* (2017), Suganthi (2018) and Sapara *et al.* (2019) in sesame.

The equal distribution of positive and negative genes in the parents was revealed from the estimate, $H_2/4H_1$ and helps the plant breeders in selecting a particular desirable trait without losing other traits of interest. In the present study, asymmetrical distribution of positive and negative genes in the parental lines was observed in both the generations for all the characters except days to 50 per cent flowering, number of capsules per plant, number of seeds per capsule, length of capsule and seed yield per plant, which showed symmetrical distribution of alleles among the parents in F_2 generation. Asymmetrical distribution of positive and negative genes in the parental lines was earlier observed by Sakhiya (2013) and Sedeck and Shafie (2013). Whereas, Swain *et al.* (2001) reported symmetrical distribution of alleles for capsules per plant and seed yield per plant in sesame.

The ratio of number of dominant to recessive alleles in the parents (K_D/K_R) indicated unequal frequency of dominant and recessive genes. In F_1 generation, more number of recessive genes was found in all the traits except for days to maturity. Similarly, in F_2 generation, proportion of recessive were found in most of the traits except for days to 50 per cent flowering, number of primary branches per plant and 1000-seed weight in which proportion of dominant genes were more. More proportion of recessive genes for the traits reported by Gami *et al.* (2020) in sesame.

Knowledge of number of gene groups responsible for a particular trait is important for the genetic progress through selection. In the present study, the value of h^2/H_2 was more than unity in F_1 generation for all the traits (except 1000-seed weight and oil content), whereas the value of h^2/H_2 was less than unity in F_2 generation for all the traits (except plant height, number of seeds per capsule and harvest index). This indicated more genes or group of genes were exhibited dominance and controlling the traits in

Table 2 : Comparative evaluation of results obtained from different statistical analysis for different characters in sesame.

S. no.	Characters	Variance				Degree of dominance (H_1/D) ^{1/2}			Heritability (Narrow sense)	
		D		H_1		F_1	F_2	F_1	F_2	F_2
		F_1	F_2	F_1	F_2					
		**	-	**	**	Over dominance	Over dominance	High	High	Low
1	Days to 50 per cent flowering	*	*	**	**	Over dominance	Over dominance	High	High	Moderate
2	Plant height (cm)	**	**	**	**	Over dominance	Complete dominance	High	High	Low
3	Number of primary branches per plant	**	**	**	**	Over dominance	Over dominance	Low	Low	Low
4	Number of capsules per plant	*	-	**	*	Over dominance	Over dominance	High	High	Low
5	Number of seeds per capsule	-	-	**	**	Over dominance	Over dominance	Moderate	Moderate	Low
6	Length of capsule (cm)	**	*	**	**	Over dominance	Over dominance	High	High	Moderate
7	Days to maturity	-	*	**	**	Over dominance	Over dominance	High	High	Low
8	Seed yield per plant (g)	*	**	**	**	Over dominance	Over dominance	High	High	Low
9	1000-seed weight (g)	-	*	**	**	Over dominance	Over dominance	High	High	Low
10	Oil content (%)	-	-	**	*	Over dominance	Over dominance	High	High	Moderate
11	Harvest index (%)	-	-	**	**	Over dominance	Over dominance	High	High	Low

*, ** Significant at 5% and 1% levels, respectively.

F_1 generation, while one group of genes responsible for dominance in F_2 generation. Suganthi (2018) reported that most of characters were under control of at least single group of genes. While, Tripathy *et al.* (2016) reported more number of gene group showing dominance controlling for seed yield per plant in sesame.

Narrow sense heritability (Table 2) in F_1 generation was low for number of capsule per plant; moderate for length of capsule and high for days to 50 per cent flowering, plant height, number of primary branches per plant, number of seeds per capsule, days to maturity, seed yield per plant, 1000-seed weight, oil content and harvest index. On the other hand, in F_2 generation, all the cross showed low heritability except plant height, days to maturity and oil content which showed moderate narrow sense heritability. Low heritability estimates indicated a major role of non-additive gene action in the inheritance of characters studied and hence there is a limited scope for genetic improvement through direct selection. Low heritability values were reported by Reddy *et al.* (2015) and Sapara *et al.* (2019). Whereas, Saravanan *et al.* (2000) reported high narrow sense heritability for days to 50 per cent flowering, days to maturity and oil content in sesame.

In the present investigation, the non-significance values of t^2 assured the fulfillment of assumptions underlying diallel analysis for number of primary branches per plant and 1000-seed weight in F_1 generation, whereas days to 50 per cent flowering, plant height, number of primary branches per plant, number of capsule per plant, days to maturity and 1000-seed weight in F_2 generation.

Conclusion

The present investigation to understand the nature and magnitude of gene action was indicated that both the additive and non-additive components were important in the inheritance of seed yield per plant and its major component characters. It is, therefore, suggested that biparental mating or few cycles of recurrent selection followed by pedigree selection may give fruitful results.

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