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S Suganthi
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar, Tamilnadu, India

Estimation of genetic parameters in sesame (*Sesamum indicum* L.) through diallel analysis

S Suganthi

Abstract
Six parents and their 30 hybrids were involved in a diallel mating design to estimate various genetic parameters in sesame. The traits like plant height at maturity, number of capsules per plant, number of seeds per capsule and seed yield per plant showed additive gene action. Pedigree selection is an appropriate method to improve these characters. Over dominance was observed for number of branches per plant, number of capsules per plant, 1000 seed weight and seed yield per plant. Negative F value was observed for days to 50 percent flowering and number of capsules per plant indicating the recessive genes were more frequent than dominant genes in the manifestation of these traits.

Keywords: genetic parameters, diallel mating, capsules per plant

Introduction
Sesame (*Sesamum indicum* L.), belongs to the family Pedaliaceae, a self pollinated crop, is an ancient cultivated oil crop and thought to have originated in Africa. It is called as the "Queen of Oil Seeds" in view of its oil and protein which are of very high quality. Sesame is an important source of food worldwide and constitutes an inexpensive source of protein, fat, minerals and vitamins in the diets of rural populations, especially for children. Sesame is an important source of high quality edible oil. The seeds contains 50-60 per cent oil. Sesame oil contains vitamin E and several important antioxidant constituents such as sesamol, sesamin and sesamolin, which are believed to promote the integrity of body tissues in the presence of oxidizing compounds.

Moreover similar to other crops, in sesame, the yield is a complex character and the lower productivity could be attributed to the interplay of different yield related, growth and morphological characters. In spite of rapid increase in the area under the crop, the productivity has declined over the years. The major constraints identified for lower productivity may be due to instability of yield, lack of wider adaptability, lack of availability of quality seeds and also due to genetic make up of the crop, indeterminate growth, abscission of floral parts, poor seed setting and cultivation under rainfed conditions.

Even though some of these factors have been already overcome, still there is scope to enhance the productivity to considerable extent. An insight into the genetics of morphological and growth characters would be the best prospects for breeding for higher yield. However, little is known about the morphological and growth characters that appear

The task of the sesame breeder is to improve and stabilize the sesame yield, by a further breakthrough in our understanding in the genetics of the yield and yield components of sesame. Information on the genetics of seed yield and yield contributing characters and their breeding value must always be a pre-requisite for selecting suitable parents for appropriate breeding programme to enhance seed yield. Evaluation of the sesame genotypes including popular high yielding varieties on the above lines would facilitate their use as donors.

Materials and Methods
Well filled, sound and plumpy, selfed seeds of sesame genotypes *viz*., TMV 5, TMV 6, CO 1, VRI 2, TMV 7 were obtained from the Regional Research Station, TNAU, Dindivanam. The genotype GOWRI was obtained from Directorate of Oil Seed Research Station in Rajendra Nagar, Andhra Pradesh.

The aforementioned six genotypes were sown on January season January – February, 2017. They were crossed in a diallel mating design (including both direct and reciprocal crosses). The observations were recorded on five randomly selected competing plants in each replication. These plants were tagged individually. Observations were recorded on days to 50 percent flowering, plant height at maturity, number of branches per plant, number of capsules

Correspondence
S Suganthi
Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar, Tamilnadu, India

per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant. The genetic components *viz.,* $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$ and $\hat{E}$ were estimated as described by Hayman (1954) using the second degree statistics and error mean squares. Heritability (in narrow sense) was calculated as per Crumpacker and Allard (1962)

Results and discussion

In genetic analysis study, various genetic parameters namely, $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$ and $\hat{E}$ along with their standard errors and the genetic ratios were estimated and were furnished in Table 1 and 2.

The breeding methodology depends considerably upon the nature and magnitude of gene action controlling the genetic behaviour of the most studied characters. An analysis based on large number of progenies from diverse parents, particular progenies of diallel set, is expected to give more reliable estimates. However, to have a clear picture of genetic mechanism of the sesame population, the absolute value of variances must be partitioned into its genetic components. Furthermore, knowledge regarding the nature and magnitude of gene action governing the inheritance of yield and yield components are essential for formulating efficient breeding strategies for the improvement of sesame crop.

Estimation of genetic parameters like $\hat{D}$, $\hat{H}_1$ and $\hat{H}_2$ was significant indicating the involvement of both additive and dominance gene effects in more number of characters. For plant height at maturity, number of capsules per plant, number of seeds per capsule and seed yield per plant, the dominance factors were less than additive factors elucidating greater contribution of additive factors in control of this trait. It implies that these characters can be easily fixed in the early generation. Similar report of additive factors for the control of traits was enunciated by Vidhyavathi *et al.* (2005), El-Bramawy and Shaban (2007), Georgive *et al.* (2011), Ramesh *et al.* (2014) and Musibau *et al.* (2014). For all other characters like days to 50 per cent flowering, number of branches per plant and 1000 seed weight, dominant factors was predominant for the inheritance of these traits.

Negative $\hat{F}$ value was observed in days to 50 per cent flowering, number of capsule per plant, suggested that recessive genes were more frequent than dominant genes in the manifestation of these characters. These results were in harmony with the findings of Swain *et al.* (2001), Thirugnanakumar *et al.* (2006), Thiyagu *et al.* (2007), Yamunara *et al.* (2009), Ramesh *et al.* (2014) and Tripathy *et al.* (2016)

The estimates for mean degree of dominance $(H_1/D)^{1/2}$ showed over dominance for the characters like number of branches per plant, number of capsule per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant. Partial dominance was noticed for days to 50 per cent flowering and plant height maturity. These results were in agreement with Mothilal *et al.* (2005), Lavanya *et al.* (2006) and Thirugnanakumar *et al.* (2006).

It is worthy to mention that value of h^2 as a measure of overall dominance effects of heterozygous loci, was significant and positive for only days to 50 per cent flowering. These results indicated that the mean direction of dominance was positive for the character. The non-significant values of h^2 for the characters, plant height at maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant did not indicate any direction of dominance. These findings were in agreement with results reported by Mothilal *et al.* (2005) and El-Bramawy and Shaban (2007).

The value of h^2/H_2 was less than unity for all characters *viz.,* days to 50 per cent flowering, plant height at maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant suggested that the values of h^2/H_2 did not provide any valid interpretation for all the traits about group of genes exhibiting dominance. The ratio could be under estimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes is correlated (Jinks, 1954) or when complementary gene interactions occur (Mather and Jinks, 1971).

The conclusion drawn from the results manifested that both additive and non-additive components of genetic variances were involved with predominance of dominance variances for most of the yield characters. As additive variance is predominant for the characters, plant height at maturity, number of capsule per plant, number of seeds per capsule and seed yield per plant. Pedigree selection is an appropriate method to improve these characters. As selection based on progeny performance exploits only additive component of genetic variances, bi-parental mating or diallel selective mating, which allows intermating among selected segregants in the different cycles, would be useful to recover superior homozygotes in later generations. Besides, the greater contribution of dominance and over dominance indicated the scope of heterosis breeding in sesame which exploits non-additive gene action.

Table 1: Estimates of genetic characters for yield and yield attributing characters

S. No.	Characters	D	F	H_1	H_2	h^2	E
1	Days to 50 per cent flowering (days)	2.73 ± 0.83 *	-0.03 ± 2.04	8.79 ± 2.12 *	7.59 ± 1.90 *	5.42 ± 1.27 *	0.18 ± 0.31
2	Plant height at maturity (cm)	90.90 ± 1.64*	23.45 ± 4.02*	14.98 ± 4.18*	12.30 ± 3.24 *	0.78 ± 2.51	0.18 ± 0.62
3	Number of branches per plant	1.13 ± 0.55 *	1.80 ± 1.35	6.36 ± 1.41 *	5.45 ± 1.26 *	-0.05 ± 0.84	0.17 ± 0.21
4	Number of capsules per plant	11.77 ± 5.98	-11.10 ± 14.61	76.50 ± 15.18 *	72.00 ± 13.56 *	13.71 ± 9.13	1.00 ± 2.26
5	Number of seeds per capsules	1.67 ± 7.58	2.95 ± 18.51	132.83±19.24 *	111.54±17.19 *	1.65 ± 11.57	1.68 ± 2.86
6	1000 seed weight (gm)	0.03 ± 0.02	0.05 ± 0.05	0.49 ± 0.05 *	0.42 ± 0.05 *	0.01 ± 0.03	0.006 ± 0.008
7	Seed yield per plant (gm)	0.06 ± 0.06 *	0.08 ± 0.14	0.40 ± 0.15 *	0.32 ± 0.13 *	0.06 ± 0.09	0.01 ± 0.02

Table 2: Ratio of genetic characters for yield and yield attributing characters

S. No.	Characters	$(H_1/D)^{1/2}$	$H_2/4H_1$	$[(4DH_1)^{1/2} +F] /[(4DH_1)^{1/2} -F]$	h^2/H_2	Heritability (N.S)%
1	Days to 50 per cent flowering (days)	1.78	0.22	0.99	0.68	0.47
2	Plant height at maturity (cm)	0.40	0.20	1.93	0.05	0.56
3	Number of branches per plant	2.36	0.21	2.00	-0.009	0.03
4	Number of capsules per plant	2.54	0.23	0.68	0.19	0.66
5	Number of seeds per capsules	8.90	0.21	1.22	0.01	0.24
6	1000 seed weight (gm)	4.05	0.21	1.64	0.02	0.09
7	Seed yield per plant (gm)	2.56	0.20	1.68	0.21	0.15

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