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Research Paper

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Genetic Analysis for Seed Yield in Sesame (*Sesamum indicum* L.)

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A B S T R A C T

Genetic analysis for of seed yield was studied in a set of 6 × 6 full diallel crosses of sesame which indicated importance of both dominant and additive gene action. Estimation of genetic parameters like D, H_1 and H_2 was significant indicating the involvement of both additive and dominance gene effects for more characters. For plant height at maturity, number capsules per plant, number of seeds per capsule and seed yield per plant, the dominance factor were less than additive factors elucidating greater contribution of additive factors in control of this trait. For all other characters like, days to 50 per cent flowering, number of branches per plant, capsule length and 1000 seed weight, dominant factor was predominant for the inheritance of these traits.

Key words: Sesame, Diallel analysis, Genetic parameters, Gene action

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 of edible oil and the seeds contain 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. In addition, sesame possesses some agricultural advantages such as, the ability to grow well under tropical and subtropical climates with minimum soil moisture, without rainfall or irrigation, and can be grown as mixed stands with diverse crop. However, it thrives best on well-drained soil with a moderate fertility and pH between 5.5 and 7.0 (Aladji *et al.* 2015).

In spite of rapid increase in area under the crop, the productivity has declined over the years. The major constraints identified for lower productivity are instability of yield, lack of wider adaptability, lack of availability of quality seeds and also the genetic makeup of the crop, indeterminate growth, abscission of floral parts, poor seed setting and cultivation under rainfed conditions. Sesame is genetically considered to be a self-pollinated crop in spite of varying degree of cross pollination reported in this crop. Improvement of this crop so far has been mostly confined to single plant selection. 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. The success in identifying such parents mainly depends on the gene action that controls the trait under improvement. Hence with the objective of to understand the genetics of seed yield in sesame, the present study was attempted.

MATERIALS AND METHODS

The present investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar during 2017-2019. The experimental material consisted of six genotypes of wide genetic diversity. The selected six genotypes viz. TMV 3, TMV 4, TMV 6, TMV 7, VRI 1 and VRI 2 were crossed in all

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possible combinations to produce 30 hybrids. The six genotypes were sown during January - February, 2018. They were crossed in a diallel mating design (including both direct and reciprocal crosses). The resultant 30 hybrids along with six selfed parents formed an effective complete diallel set for the present study. The observations like days to 50 percent flowering, plant height at maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, length of the capsule, 1000 seed weight and seed yield per plant were recorded on five randomly plants in each and every entry of each replication. The genetic components viz. D, F, H_1, H_2, h^2 and E were estimated as described by Hayman (1954) using the second-degree statistics and error mean squares as follows:

$\check{D}$= VoLo - E

F= 2 VoLo – 4 WoLo1 – 2(n - 1) E/n

$\hat{H}_1$= VoLo - 4WoLo1- 4VlL1-(3n - 2) E/n

$\hat{H}_2$= 4V1L1-4 VoL1 – 2E

$\hat{h}^2$= 4(ML1-MLo)2 – 4(n - 1) E/n2 and

E = Expected environmental variation obtained as sum of squares for blocks+ sum of squares for replication and progeny / degrees of freedom for both × number of replications.

Where,

$\check{D}$- Component of variation due to additive effect of genes

F- The mean value of Fr over arrays, Fr, being covariance of additive effect in the r^{th} array.

$\hat{H}_1$- Component of variation due to the dominance effect of the genes

$\hat{H}_2$- The proportion of dominance variance due to positive and negative effect of genes.

$\hat{h}^2$- Dominance effect expressed as the algebraic sum over all loci in heterozygous phase in all crosses.

The standard error for the above estimates were calculated using the equation S2 = ½ (var (Wr-Vr)) as the common multiplier and the term of the main diagonal of covariance matrix as corresponding multipliers.

These genetic parameters thus calculated were employed for the computation of proportional values mentioned below:

$$\text{Mean degree of dominance} = (H1/D)\ ½$$

The proportion of genes with positive and negative effects in the parents = H2 / 4H1

$$\text{The proportion of dominant and recessive genes in the parents} = \frac{[(4DH1)\ ½+F]}{[(4DH1)\ ½-F]}$$

Number of groups of genes which control the character and exhibit dominance k = h^2

$$h^2 \text{ Heritability in the narrow sense } h^2 (ns) = \frac{(1/2)D + (1/2)\ H1- (1/2)\ H2-(1/2)F}{(1/2)D + (1/2)H1- (1/4)H2 -(1/2)F+E}$$

RESULTS AND DISCUSSION

The ANOVA for yield and yield attributing characters of sesame were furnished in the (Table 1). The 'f' values were highly significant for all characters. The genetic characters namely, D, H_1, H_2 and h^2 were estimated and were furnished in (Table 2) and various ratios of genetic components variation are presented in (Table 3). For days to 50 percent flowering, the genetic characters H1 (12.27) and H2 (10.94) were greater than D (6.84), indicating the role of dominant factor. The positive values of F (6.07) indicates that the frequency of recessive alleles were less than the dominance. It was also confirmed by the proportion of dominance to recessive alleles in the parent [(4D/H1)1/2 +F/ (4D/ H1)1/2 -F] which was greater than one (1.07). The h^2 value (31.97) was positive indicating the direction of dominance was towards the parents. The mean degree of dominance (H1/D)1/2 was greater than zero, which reflected partial dominance. The ratio of (H2/4H1) was of 0.22, indicating asymmetry of positive and negative alleles in parents. The ratio of h2/H2 (2.92) indicates that at least one block of gene is controlling this trait. Heritability in the narrow sense, a reflection of the amount of additive variation was estimated as 0.10 per cent.

Estimation for the component of variance for the plant height suggests that estimates of environmental component of variance (1.41) were non-significant and the additive genetic variance $\check{D}$ was significant. The effect of gene with additive properties appeared to be more as D<H1 and H2 (43.28, 60.29, and 47.25) respectively. Positive F value (34.03) indicated that there were more dominant alleles than recessive for plant height and the positive h^2 showed the direction of dominance was towards the parents. The mean degree of dominance (H1/D)1/2 was greater than zero but less than one which showed the presence of partial dominance. H1 (60.29) was greater than H2 (47.25) showing the occurrence of non-equal gene frequency at all loci. This was also confirmed from the ratio of (H2/4H1) having values less than one (0.19). This estimates the ratio of dominance to recessive alleles [(4D/H1)1/2 +F/ (4D/ H1)1/2 -F] having value greater than one (1.01) which showed more dominant genes than recessive in the parents. The heritability in narrow sense was 0.19 per cent.

For number of branches per plant, the parameters H1 (3.66) and H2 (3.01) were greater than D (1.01), indicating dominant factors in this trait. The contribution of environmental components $\hat{E}$ (0.02) was non-significant. The positive F value (1.26) indicated that the frequency of recessive alleles were less than dominant alleles. The inference drawn from the F value was also confirmed by the proportion of dominance to recessive alleles in the parents measured by [(4D/H1)1/2 +F/ (4D/ H1)1/2 -F] which was greater than (1.41). The ratio of (H2/4H1) was (0.20) indicating asymmetry of positive and negative recessive alleles in the parents.

In case of number of capsules per plant, the additive D (164.53) dominance H1 (466.05) and H2 (355.74) were significant and h^2 (6.56) and E (2.45) were non-significant. The additive component D (164.53), was less than dominance component H1 (4.66.65) indicating the involvement of additive gene action. The value of H1 being greater than H2 indicated the complete asymmetrical distribution of positive and negative genes as confirmed by the value of (H2/4H1) (0.19). Additive effects and their control on the trait were also confirmed by [(4D/H1)1/2 +F/

(4D/ H1)1/2 -F] (1.00) ratio. Estimates of components of variance for capsule length suggested that environmental component of variance E (0.002) did not played any role in the inheritance of capsule length. The additive genetic variance was non-significant whereas dominant genetic variances were significant. But the contribution of non-additive effects were more pronounced as H1 greater than D. the ratio of (H1/D)1/2 was (105.5) indicated over dominance. The ratio of (H2/4H1) (0.22) suggested asymmetry of positive and negative alleles in the parents. The ratio of (h^2/H2) (0.43) suggested at least one pair of genes controlling this trait.

Table 1 Analysis of variance for yield and yield attributing characters in sesame

Source	df	Mean sum of squares							
		Days to 50 per cent flowering	Plant height at maturity	No. of branches per plant	No. of capsules per plant	Capsule length	No. of seeds per capsule	1000 Seed weight	Seed yield per plant
Replication	2	1.6931	0.6667	0.0284	1.1111	0.00032	0.5425	0.0083	0.1550
Genotype	35	12.9428**	85.7074**	3.7699**	411.5462**	2.1457**	80.2889**	1.7629**	4.8349**
Error	70	0.7326	4.3566	0.0723	7.5348	0.0076	4.0809	0.0068	0.2245

**Significant at 1 percent level

Table 2 Estimation of genetic characters for yield and yield attributing characters

Characters	D	F	H1	H2	h^2	E
Days to 50% flowering	6.84±0.91*	6.07±2.24*	12.27±2.33*	10.94±2.08*	31.97±1.40*	0.25±0.34
Plant height at maturity	43.28±6.62*	34.03±16.18*	60.29±16.81*	47.25±15.02*	3.47±10.11	1.41±2.50
No. of branches per plant	1.01±0.36*	1.26±0.90	3.66±0.93*	3.01±0.83*	0.56±0.56	0.02±0.13
No. of capsules per plant	164.53±48.22*	236.05±117.82*	466.65±122.43*	355.74±109.37*	6.56±73.61	2.45±18.22
Capsule length	0.01±0.32	0.04±0.80	2.11±0.83*	1.89±0.74*	0.83±0.50	0.002±0.12
No. of seeds per plant	6.45±12.00	10.59±29.33	68.52±30.48*	56.43±27.23*	5.76±18.32	1.32±4.53
1000 seed weight	0.11±0.10	-0.14±0.25	1.39±0.26*	1.34±0.23*	0.76±0.15*	0.0023±0.03
Seed yield per plant	2.36±0.46*	1.90±1.14	2.76±1.19*	2.16±1.06*	0.08±0.71	0.07±0.17

Table 3 Ratio of genetic characters for yield and yield attributing characters

Character	$(H_1/D)^{1/2}$	$H2/4H_1$	$[(4DH_1)^{1/2}+F]/ (4DH_1)^{1/2}-F]$	h_2/H_2	Heritability (N.S)%
Days to 50 per cent flowering	0.89	0.22	1.07	2.92	0.10
Plant height at maturity	0.69	0.19	1.01	0.07	0.19
Number of branches per plant	1.81	0.20	1.41	0.18	0.09
Number of capsules per plant	1.41	0.19	1.00	0.02	0.05
Capsule length	105.5	0.22	37.36	0.43	0.15
Number of seeds per capsule	5.31	0.20	1.02	0.10	0.13
1000 seed weight	6.31	0.24	0.37	0.56	0.45
Seed yield per plant	0.58	0.19	1.34	0.03	0.17

For number of seeds per capsule, the parameters H1 (68.52) and H2 (56.43) were greater than D (6.45), indicating dominance factor of this trait. h^2 (5.76) and E (1.32) were non-significant for this trait. The additive D (6.45) was less than dominance component H1 (68.52) which indicated the involvement of additive gene action. The value of H1 being greater than H2 indicated asymmetrical distribution of positive and negative genes as confirmed by the value of (H2/4H1) (0.20). Additive effects and their control on trait were also confirmed by [(4D/H1)1/2 +F/ (4D/ H1)1/2 -F] (1.02) ratio. The heritability in narrow sense was 0.13. Estimates of the components of variance for 1000 seed weight suggested that environmental component of variance E (0.0023) did not played any role in the inheritance of 1000 seed weight. The ratio of (H2/4H1) (0.24) suggested asymmetry of positive and negative alleles in the parents.

For the trait seed yield per plant, the additive genetic variance D (2.36) and dominance genetic variance H1 (2.76) and H2 (2.16) were significant which indicated that both additive and non-additive components were contributed to the variation in the hybrids. The role of additive effects was as D>H1. The parameter F (1.90) was positive which showed that the frequency of dominant alleles were more than recessive alleles. Similar gene frequency was reflected by dominant to recessive alleles [(4D/H1)1/2 +F/ (4D/ H1)1/2 -F] which was more than one (1.34) showing the prevalence of more dominant genes than recessive genes. The estimate of narrow sense heritability was 0.17 per cent for seed yield per plant. 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 variances must be

partitioned into its genetic components. The genetic analysis of different characters were estimated by adopting the method suggested by Hayman (1954), Griffing (1956).

Estimation of genetic parameters like D, H1 and H2 was significant indicating the involvement of both additive and dominance gene effects for more characters. For plant height at maturity, number capsules per plant, number of seeds per capsule and seed yield per plant, the dominance factor were less than additive factors elucidating greater contribution of additive factors in control of this trait. Similar report of additive factors for the control of traits was enunciated by Musibau and Morakinyo (2014). For all other characters like days to 50 per cent flowering, number of branches per plant, capsule length and 1000 seed weight, dominant factor was predominant for the inheritance of these traits. The estimation of mean degree of dominance (H1/D)1/2 showed over dominance for the following characters viz. number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule and 1000 seed weight. These results were in agreement with the findings of Agarwal *et al*. (2017).

It is worthy to mention that the value of h^2 as a measure of overall dominance effects of heterozygous loci, was significant and positive for days to 50 per cent flowering and 1000 seed weight. These results indicated that the mean direction of dominance was positive for the characters. The non-significant values of h2 for the characters, plant height at maturity, number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule and seed yield per plant did not indicate any direction of dominance. These findings were in agreement with results reported by Tripathy *et al.* (2017).

The value of h2/H2 was more than unity only for days to 50 per cent flowering indicating that at least one block of gene is controlling this trait and for other characters like plant height at maturity, number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, 1000 seed weight and seed yield per plant, it was less than unity indicating that the value of h^2/H2 did not provide any valid interpretation for these traits about the group of genes exhibiting dominance. The ratio could be under estimated when the dominance effects of all genes concerned are not equal in size and distribution, when the distribution of genes are correlated (Jinks 1954) or when complementary gene interactions occur (Mather and Jinks 1971).

The conclusion drawn from the results inferred that both additive and no-additive components of genetic variances were involved with predominance of dominance variance for most of the yield characters. Additive variance is predominant for the characters, plant height at maturity, number of capsules 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, greater contribution of dominance and over dominance indicated the scope of heterosis breeding in sesame which exploits non-additive gene action.

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