Gene action for morphological, growth, biochemical, yield and yield attributing characters in sesame (*Sesamum indicum* L.)

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Abstract : A full diallel cross was conducted to estimate the nature and extent of gene action for morphological, growth, biochemical and yield characters in sesame by using 6 x 6 cross. In case of biochemical, yield and yield attributing characters, like chlorophyll content, soluble protein content, number of capsules per plant, and 1000 seed weight the non-additive effects were more pronounced as $\hat{H}_1$ and $\hat{H}_2$ were greater than $\hat{D}$. For seed yield per plant additive genetic variance $\hat{D}$ (1.45) and dominances genetic variance $\hat{H}_1$ (0.64) and $\hat{H}_2$ (0.68) were significant indicated that both additive and non-additive components were contributed to the variation in the hybrids. 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, days to first senescence, leaf area index, seed yield per plant and oil content. Pedigree selection is an appropriate method to improve these characters.

Introduction

Sesame is an important source of high quality edible oil. The seed contains 50-60 per cent oil, which has excellent stability due to the presence of natural antioxidants such as sesamolin, sesamin and sesamol (Brar and Ahuja, 1979). Sesame seeds are digestive, rejuvenative, anti-ageing and rich in vitamins E, A and B complex. Sesame oil is used as a cooking oil in Southern India. It is also used for anointing the body. The major sesame growing countries are Sudan, Nigeria, Ethiopia, Uganda, Mexico, Venezuela, India, China, Pakistan and Myanmar. India ranks second in area (18.62 lakh ha) and production (8.13 lakh tones) among the sesame growing countries (FAOSTAT, 2013).

In sesame, the yield is a complex character and the lower productivity could be attributed to the interplay of different yield related, biochemical, growth and morphological characters. In the bygone decades, the sesame improvement was solely based on the selection of morphological characters and less importance was given to physiological 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 makeup 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 a considerable extent. An insight into the genetics of morphological, growth, biochemical traits

would be the best prospects for breeding for higher yield. However, little is known about the morphological, growth and biochemical characters that appear highly promising in improving performance of this crop.

In this context, the knowledge of mode of gene action provide the basis for effective selection, utilization and development of superior sesame varieties. Diallel analysis can be used to elucidate genetic architecture more reasonably in terms of gene effects of additive, dominance and non-allelic interactions using various genetic parameters. Information on nature and magnitude of genetic components of variation of a character is essential for making an effective breeding strategies of the improvement of a crop. The present investigation was carried out with the objective of assessing the nature and magnitude of gene action for morphological, growth, biochemical, yield and yield attributing characters. Therefore, an experiment was undertaken to study the gene action using 6 x 6 diallel set of crosses in sesame.

Material and Methods

The present study was carried out with a view to know the nature and extent of gene action controlling the inheritance of yield and its components for obtaining better recombinants. the experiment was conducted at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar during 2012-2013. Six sesame genotypes namely VRI 1, VRI 2, TMV 3, TMV 4, TMV 6 and CO 1 were selected and were obtained from Regional Research Station, Vridhachalam. Six parents were crossed in all possible combinations and the resulting thirty cross combinations inclusive of reciprocal crosses along with the parents form an effective complete diallel set for the study. Thirty hybrids along with six parents were sown in rows with a spacing of 30 $\square$ 30 cm. In each cross, 20 plants were maintained. A randomized block design with three replications was adopted. Border rows were grown all around the experimental block. Recommended fertilizer schedule, cultural operations and plant protection measures were carried out. The observations were recorded on 10 plants in parents and hybrids for the following morphological traits viz., days to 50% flowering, plant height at maturity, number of branches per plant and days to first senescence, growth traits like leaf area index (LAI), drymatter production (DMP) and harvest index (HI), biochemical traits like total chlorophyll content and soluble protein content, yield characters like number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant. The statistical analysis was made for diallel based on Griffing (1956) Method 1 Model 1. The component of variation $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$ and $\hat{E}$ were calculated on the basis of Hayman (1954) theory.

Results and Discussion

The knowledge of gene action can help in proper planning and selection of appropriate breeding method. The results of the analysis of variance showed that all the characters studied were significant except 1000 seed weight indicated the genetic diversity of the parents selected for the present study (Table. 1).

Regarding the morphological characters, for days to 50 per cent flowering, number of branches per plant and days to first senescence the characters $\hat{H}_1$ and $\hat{H}_2$ were greater than $\hat{D}$ indicating the role of dominant factors which implies that the allelic interaction was well within the range of over dominance. For plant height at maturity the effect of gene with additive, properties appeared to be more as $\hat{D} > \hat{H}_1$ and $\hat{H}_2$.

The negative value of $\hat{F}$ indicated the frequency of recessive alleles were more than dominance. It was also confirmed by the proportion of dominance to recessive alleles in the parents $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F)]$ was less than one for the traits days to 50% flowering, number of branches per plant and days to first senescence. (Mather and Jinks, 1971).

Table 1. Analysis of variance for morphological, growth, biochemical, yield and yield attributing characters

Source	DF	DFF	PH (cm)	NBP	DFS	LAI	DMP (g pl⁻¹)	HI	TCC (mg.g⁻¹)	SPC (mg g⁻¹)	NCP	NSP	TSW (g)	SYP (g)	OC (%)
Replication	2	51.07	84.49	24.58	32.76	0.01	4.95	0.65	0.01	1.35	15.18	5.80	0.23	0.73	1.42
Genotypes	35	17.68**	270.63**	3.99**	34.49**	0.02**	14.58**	31.51**	0.01**	2.31**	187.40**	22.41**	0.017	3.11**	11.80*
Error	70	7.11	69.56	1.99	5.54	0.01	3.98	4.49	0.01	0.79	7.22	3.94	0.02	0.43	6.48

** - Significant at 1% level

DFF- Days to 50 per cent flowering   LAI – Leaf area index
PH – Plant height at maturity   DMP – Dry matter production
NBP – Number of branches per plant   NSP – Number of seeds per capsule
DFS – Days to first senescence   SYP – Seed yield per plant
HI - Harvest Index   TSW – 1000 seed weight
TCC – Total chlorophyll content   OC- Oil content
NCP – Number of capsules per plant   SPC – Soluble protein content

Positive $\hat{F}$ value (43.43) indicated that there was more dominant alleles than recessive for plant height and positive h^2 showed that direction of dominance was towards the parents. For all the morphological traits, the mean degree of dominance $(H_1/D)^{1/2}$ was greater than zero but less than one, which reflected partial dominance for the characters. The ratio of $H_2/4H_1$ was of 0.55 indicating asymmetry of positive and negative alleles in parents for the characters to days 50 percent flowering, number of branches per plant and days to first senescence. The ratio of h^2/H_2 (0.83) indicated atleast one block of gene controlling this morphological trait except plant height at maturity. However, this parameter can be underestimated 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).   Heritability in the narrow sense, a reflection of the amount of additive variation was estimated as 0.12 per cent. (Table 2)**.** Regarding growth characters viz., leaf area index, dry matter production and harvest index the parameter $\hat{D}$ was significant and greater than $\hat{H}_1$ and $\hat{H}_2$ indicating additive factors in these traits. Negative $\hat{F}$ (-0.002) value showed that frequency of recessive alleles was more than the dominant alleles in case of leaf area index. Negative value of F could be an indication for preponderance of recessive alleles for leaf area index (Mather and Jinks, 1971). Positive $\hat{F}$ value was observed for dry matter production and harvest index indicating that frequency of dominant alleles were more than the recessive.

Table 2. Estimates of genetic characters for morphological, growth, biochemical, 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)	-1.59±0.80*	-3.47±1.95	1.08±2.02	2.36±1.81	1.96±1.22	2.78±0.30*
2.	Plant height at maturity (cm)	107.02±5.62*	43.43±13.74*	32.10±14.27*	32.00±12.75*	13.14±8.58*	23.33±2.13*
3.	Number of branches per plant	0.14±0.43	-0.14±1.04	1.56±1.08	0.92±0.97	-0.25±0.65	0.87±0.16*
4.	Days to first senescence (days)	8.72±1.08*	-3.22±2.65	4.02±2.75	4.44±2.46	0.84±1.65	2.09±0.41*
5.	Leaf area index	0.008±0.0002*	-0.002±0.00005*	-0.001±0.0006	-0.001±0.00005*	-0.003±0.00003*	0.001±0.0001*
6.	Dry matter production (g plant^{-1})	5.57±0.54*	1.86±1.32	1.68±1.37	1.52±1.23	3.34±0.83*	1.32±0.20*
7.	Harvest index	4.55±1.59*	1.00±3.89	24.26±4.05*	21.15±3.62*	63.32±2.43*	1.46±0.60*
8.	Total chlorophyll content (mg g^{-1})	0.002±0.0008*	0.0004±0.002	0.008±0.002*	0.006±0.002*	0.011±0.001*	0.0009±0.0003*
9.	Soluble protein content (mg g^{-1})	0.36±0.09*	0.01±0.22	0.86±0.23*	0.82±0.21*	3.10±0.14*	0.27±0.03*
10.	Number of capsules per plant	9.76±5.24	-3.61±12.79	124.53±13.29*	116.21±11.87*	190.23±7.99*	2.48±1.98
11.	Number of seeds per capsule	6.73±0.79*	-2.95±1.93	6.71±2.00*	4.91±1.79*	3.70±1.21*	1.33±0.30*
12.	1000 seed weight (g)	-0.005±0.0008*	-0.009±0.002	-0.019±0.002*	-0.01±0.002*	-0.004±0.001*	0.009±0.0003
13.	Seed yield per plant (g)	1.45±0.07*	0.19±0.18*	0.64±0.18*	0.68±0.16*	2.23±0.11*	0.15±0.03*
14.	Oil content (%)	1.02±0.33*	-3.68±0.81*	-2.04±0.85*	-1.60±0.76*	-0.03±0.51	2.11±0.13*

This was also confirmed by the proportion of dominance to recessive alleles in the parents measured by $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F)]$ which was more than one. The mean degree of dominance (0.35) suggested the partial dominance in this trait. The proportion of ratio $[(4DH_1)^{1/2} + F)/(4DH_1)^{1/2} - F)]$ (0.42) indicated the high frequency of recessive alleles. The ratio of h^2/H_2 (0.42) indicated atleast one gene group in controlling the character. The heritability in narrow sense was 1.95 per cent (Table 3).

In case of biochemical, yield and yield attributing characters, like chlorophyll content, soluble protein content, number of capsules per plant, and 1000 seed weight the non-additive effects were more pronounced as $\hat{H}_1$ and $\hat{H}_2$ were greater than $\hat{D}$. For seed yield per plant additive genetic variance $\hat{D}$ (1.45) and dominances genetic variance $\hat{H}_1$ (0.64) and $\hat{H}_2$ (0.68) were significant indicated that both additive and non-additive components were contributed to the variation in the hybrids.

Table 3. Ratios of genetic characters for morphological, growth, biochemical, 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)	0.82	0.55	0.14	0.83	0.12
2.	Plant height at maturity (cm)	0.55	0.24	2.18	0.42	0.38
3.	Number of branches per plant	3.29	0.15	0.74	0.27	0.84
4.	Days to first senescence (days)	0.68	0.28	0.57	0.19	1.58
5.	Leaf area index	0.35	0.19	0.42	0.42	1.95
6.	Dry matter production (g.plant^{-1})	0.55	0.23	1.87	2.20	0.46
7.	Harvest index	2.31	0.22	1.10	2.99	0.35
8.	Total chlorophyll content (mg.g^{-1})	1.93	0.18	1.11	1.81	0.51
9.	Soluble protein (mg.g^{-1})	1.54	0.24	1.02	3.75	0.47
10.	Number of capsules per plant	3.57	0.23	0.90	1.64	0.30
11.	Number of seeds per capsule	1.00	0.18	0.64	0.75	1.43
12.	1000 seed weight (g)	2.02	0.19	0.33	0.25	0.001
13.	Seed yield per plant (g)	0.66	0.27	1.22	3.27	0.63
14.	Oil content (%)	1.42	0.20	0.12	0.02	1.09

The role of additive effects were more as $\hat{D} > \hat{H}_1$. For oil content, Additive component $\hat{D}$ (1.02) was greater than dominance component $\hat{H}_1$ and $\hat{H}_2$ the average degree of dominance $(H_1/D)^{1/2}$ (1.42) was greater than one, suggested additive type of gene action with over dominance. The positive $\hat{F}$ for total chlorophyll content, soluble protein content and seed yield per plant indicated that frequency of dominant alleles was more than recessive alleles. The mean degree of dominance $(H_1/D)^{1/2}$ was greater than unity indicating over dominance for the traits total chlorophyll content, soluble protein, 1000 seed weight and oil content. For seed yield per plant, the value of mean degree of dominance $(H_1/D)^{1/2}$ was 0.66, which indicated that there was partial dominance type of gene action (Table 2 & 3). The estimates of narrow sense heritability for seed yield per plant was 0.63 per cent that was good for rapid improvement in seed yield per plant through meticulous selection. These results were in agreement with that of Swain *et al.* (2001), Lavanya *et al.* (2006) and Thirugnanakumar *et al.* (2006).

Vekaria *et al*. (2015) also revealed lower estimates of narrow sense heritability in sesame. This envisaged that the genetic nature of seed yield expression is largely under non-additive component of genetic variation and therefore, improved breeding methods like single seed descent method may be considered useful for recovery of high yielding plants (Tripathy *et al*, 2016).

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, days to first senescence, leaf

area index, seed yield per plant and oil content. 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.

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