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Genetic analysis of seed yield in sesame (*Sesamum indicum* L.)

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Genetics of seed yield was studied in a set of 12 x 12 half diallel crosses of sesame which indicated importance of both dominant and additive gene action. E 8, Phule Til 1 and CST 785 emerged as a good general combiner for high seed yield. Among the crosses, PratapxRT103, CST 785xE8, BS5-18-6xPhule Til-1, T13x E8 exhibited positive and significant SCA effect indicating non-additive gene action for high seed yield. Study of various genetic parameters revealed that a number of groups of genes or loci having recessive alleles with increasing effect might be involved in realization of high seed yield and involvement of modifiers in the background genotype could not be ruled out.

Key words: Oil content, Diallel analysis, Gene action, *Lathyrus sativus* (L).

INTRODUCTION

Sesame (*Sesamum indicum* L. Family: Pedaliaceae) is one of the oldest oilseed crops grown throughout the tropical and sub-tropical regions of the world. Sesame oil is considered as the queen of high quality vegetable oil (44-58% of dry seed weight) for human consumption as it contains high levels of unsaturated fatty acids and antioxidants e.g., sesamol, sesamin, sesamolin and sesaminol (Nupur *et al.,* 2010). India is the second largest producer of sesame in the world but suffers a serious setback in terms of productivity (368kg/ha) as compared to world average (489kg/ha). Low productivity of sesame in India is mainly due to cultivation of varieties with poor yield potential and inconsistent yield performance under varied environmental conditions. Hence, there is a need to augment the productivity of crop through crop improvement programme.

Seed yield in sesame is a complex trait and it is determined by mutual relationship among the component morpho-economic traits. Each of these component traits follows polygenic inheritance. Indiscriminate selection of

plants on a massive scale in any crop often results in an immense wastage of time and resources. In this context, the knowledge of the mode of gene action underlying per se seed yield can provide the basis for effective selection and successful utilization of germplasm resources in the development of superior sesame varieties. Analysis of generation means (Hayman, 1958; Jink and Jones, 1958) and diallel analysis (Griffing, 1956; Hayman 1954a, b) are in vogue used for genetic analysis of quantitative traits. A limitation of the former is that (i) the measures of gene effects are first degree parameters which are subjected to internal cancellation and so a non-significant value of an effect does not necessarily mean absence of that kind of gene action and (ii) the method provides no measure of relative contribution of different types of gene effects to genetic variance (Sprague, 1966). However, the latter approach 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. There exists a wide array of variation in *per se* seed yield among the available genotypes (Tripathy et al. 2016). But, there is no conclusive information on the pattern of inheritance and the number of genes controlling seed

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yield although many researchers (El-Bramawy and Shaban, 2008; Vekaria *et al.,* 2015 and Madhusudan and Nadaf, 2009) addressed this problem using different base materials. Therefore, an effort was undertaken to study the gene action underlying seed yield using a 12x12 half - diallel set of crosses in sesame.

MATERIALS AND METHODS

Twelve diverse and popular parental genotypes of sesame collected from different states of India were tested along with all possible cross combinations in RBD with three replications to raise F_1 generation. Emasculation and pollination were carried out in late afternoon using Fevicol method (Das, 1990) for all possible combinations of parental genotypes in a 12x12 half -diallel mating design. Each parental genotype and cross was grown in five rows of 3.5m length with a spacing of 30 x 10 cm. Observations on seed yield/plant (gm) was recorded single plant-wise and averaged over ten plants in each replication.. The data were subjected to combining ability analysis for diallel matting design (Parents + crosses without reciprocals) as per the standard statistical methods of Griffing (1956) and Hayman (1954 a, b) for genetic interpretation on the nature of inheritance of seed yield.

RESULTS AND DISCUSSION

Seed yield is the articulated manifestation of a number of ancillary quantitative traits. Seeds of F_1 plants carry F_2 embryos. Obviously, performance of F_1 plant is reported (Snoad and Arthur, 1974 and Prakash et al., 1977) to be dependent on F_1 genotype, genotype of individual embryos and possible cytoplasmic factors, even if the influence of environmental factors is ignored.

The knowledge of gene action for expression of seed yield can help in proper planning and selection of appropriate breeding method. In this context, the diallel analysis could be a powerful tool to study the variance components of the genetic systems controlling a quantitative trait. Analysis of variance (Table-1) revealed significant difference among parents and crosses for seed yield/plant indicating that parents were genetically highly diverse and those also produced highly diverse F1 hybrids. Significance of parents vs. F1's envisaged the presence of higher quantum of overall heterosis in seed yield. Further, a perusal of Table 2 showed importance of both additive and dominant gene action for inheritance of seed yield as revealed from the significant value of GCA and SCA. However, the ratio of GCA variance to SCA variance (0.278) suggests the relative importance of non-additive gene action for expression of seed yield indicating effectiveness of selection of segregants in advance generations. These observations are in

conformity with the findings of Azeez and Morakinyo (2014), Mishra *et al.* (2009) and Kumar and Vivekanandan (2009). In contrast, the report of Ramesh et al. (2000) and Shafie (2010) highlighted the predominance of additive gene action for this trait. While, Ahmed and Adam (2014), and Kavitha *et al.* (1999) indicated equal importance of both additive and non-additive gene actions for inheritance of the trait.

Among twelve parents, CST 785, E8, Phule Til-1, Vinayak, TMV -5 and TC -25 exhibited high seed yield (≥3.0gm/plant) (Table 3). Among these, E 8 was also shown to be favourably good general combiner for high seed yield. Besides, Phule Til 1 and CST 785 were identified as good general combiner. In contrast, B67 and BS 5-18-6 exhibiting low seed yield (2.3gm/plant) was found to be the most poor general combiner for seed yield (GCA -appreciably higher negative value). In the present investigation, CST 785 x E8, T13 x E 8, Pratap x RT 103, Phule Til 1 x E 8 resulted high per se seed yield (≥ 6.5gm/plant) as compared to high yielding parents. These crosses included at least one high yielding parent with desirable general combining ability (E 8, CST 785 or Phule Til-1). Variability for seed yield in sesame was also reported by several workers (Singh *et al.,* 2000; Mukhekar *et al.*, 2003 and Sudhakar *et al.*, 2007).

Performance of crosses is often determined by specific combining ability of the parents used in the crossing programme. Unlike GCA, SCA effects are the result of non-additive gene interaction. Out of 66 cross combinations, only 12 crosses revealed significant positive SCA effects among which PratapxRT103, CST 785xE8, BS5-18-6xPhule Til-1, T13x E8 found to be best specific combiner for the trait. Barring PratapxRT103, all other cross combinations involved at least one favourable general combiner indicating substantial role of additive along with dominance and/or epistatic gene interaction for high seed yield in these crosses. Hybridization of selective parental genotypes followed by pedigree selection in the succeeding advance selfing generations can led to recovery of transgressive segregants with suitable gene combination for high seed yield.

The estimate of regression coefficient (b = 0.091) was not significant (Table 4) indicating uniformity of Vr and Wr leading to validity of the assumptions made by Hayman (1954a, b). The non-significant deviation of b-value clearly demonstrated the presence of non-allelic as well as allelic interactions for inheritance of the trait. The dominant effect (H1) was found to be much higher than additive effect (D) which implied that the allelic interaction was well within the range of overdominance. This was also evident from the mean degree of dominance (20.4) which was tremendously more than unity. However, the over-dominance observed may not be considered as index for true overdominance since the degree of dominance could be biased due to linkage, epistasis or both (Comstock and Robinson, 1952). The estimates of h2/H2 was >1.0 suggesting involvement of a number of

Table 1. Analysis of variance for mean seed yield of parents and crosses.

Source	df	Mean sum of square
Parents	11	1.0548*
F_1	65	3.9185**
Parents vs F_1	1	102.833**
Replication	2	52.812**
Error	154	0.5860

*, ** - significance at $P_{0.05}$ and $P_{0.01}$

Table 2. Analysis of variance for combining ability.

Source	df	Mean sum of square
gca	11	4.543**
sca	66	1.082**
Error	154	0.195

$\sigma^2_{gca}/ \sigma^2_{sca} = 0.278$

Table 3. *Per se* mean seed yield of parents(last column) & 66 crosses (upper half), estimates of general combining effects (diagonals) and specific combining effects (lower half).

Genotype	B 67	Vina-yak	TC 25	CST 785	Pratap	BS5-18-6	RT-103	TMV -5	T 13	Madh-abi	Phule Til-1	E8	Seed yield of parents (gm/plant)
B67	**-0.98**	2.64	2.73	4.69	3.49	3.15	3.43	2.88	3.50	3.43	4.35	4.81	2.3
Vinayak	-0.20	**-0.59**	3.43	4.02	4.62	3.0	3.38	3.83	3.79	4.15	3.86	6.15**	3.1
TC25	-0.55	-0.23	**-0.16**	6.26**	4.66	3.42	4.45	3.04	3.96	5.09*	5.97**	6.15**	3.0
CST 785	0.67	-0.40	1.41**	**0.59***	4.46	3.77	5.12**	5.39**	5.94**	4.94*	6.06**	7.82**	3.6**
Pratap	-0.20	0.54	0.15	-0.80	**0.25**	4.17	6.67**	5.71**	4.84	5.35**	6.25**	5.02*	2.9
BS 5-18-6	0.29	-0.25	-0.26	-0.66	0.07	**-0.58**	4.15	3.78	4.97*	3.40	6.03**	4.99*	2.3
RT 103	-0.07	-0.51	0.12	0.05	1.93**	0.24	**0.07**	5.48**	5.39**	3.85	5.53**	5.50**	2.7
TMV 5	-0.38	0.18	-1.04	0.56	1.21**	0.11	1.17**	**-0.18**	4.22	4.33	4.55	5.57**	3.1
T 13	0.02	-0.07	-0.34	0.90	0.13	1.09**	0.86*	-0.06	**0.04**	4.68	5.43**	6.95**	2.1
Madhabi	0.10	0.43	0.94	0.04	0.79*	-0.34	-0.52	0.20	0.33	**-0.11**	5.37**	5.86**	2.7
Phuletil 1	0.29	0.59	1.08**	0.42	0.95*	1.56**	0.42	-0.32	0.35	0.44	**0.63***	6.38**	3.2
E8	0.35	1.30**	0.86	1.79**	-0.68	0.13	-0.01	0.30	1.47**	0.53	0.31	**1.02***	3.3
Arrayvar.(Vr)	0.19	0.19	0.33	0.07	0.11	0.13	0.16	0.17	0.36	0.24	-0.02	0.09	-
ArrayCoVar(Wr)	0.65	0.83	1.65	1.47	1.16	1.05	1.34	1.07	1.57	0.91	1.05	1.33	-

Av. seed yield of parents =2.86gm/plant, Av. seed yield of F1's =4.42gm/plant, SE(gi) = 0.115, SE(gi-gj) = 0.167, SE(sij) = 0.39, SE(sij-sik) =0.58, SE(sij-skl) = 0.57   *, **-Significance at $P_{0.01}$ and $P_{0.05}$

groups of genes showing dominance. 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), or when complementary gene interactions occur (Mather and Jinks, 1971). In the present study, B67 had very high concentration of dominant alleles owing to lower value of both Vr and Wr , whereas, TC 25 and T13 with concomitant higher magnitude of Vr and Wr values showed high concentration of recessive alleles. On similar

consideration, Madhabi had equivalent proportion of dominant and recessive alleles.

Non-significant correlation coefficient value (r =0.012) between (Wr + Vr) and (Yr) evidenced that dominance was shared between the increasing alleles at some loci and the decreasing alleles at others. Further, h2 being positive and significantly higher in magnitude which envisaged that the total magnitude of increasing alleles surpassed than that of the decreasing alleles controlling seed yield. Negative value of F (Table 4) could be an indication for preponderance of recessive alleles for seed

Table 4. Component of variation with standard errors in F_1 generation for seed yield in sesame.

Sl. No.	Component of variation	Estimated value ±S.E
1.	D = Variance due to additive effect	0.01±0.22
2.	H_1= The component of variation due to dominance effect	3.67±0.44
3.	H_2 = The component of variation due to dominance effect (where, $H_2=H_1$ [1-(u-v)^2)]) where, u and v are freq. of increasing and decreasing alleles	2.65±0.36
4.	h^2 = Dominance effect (as the algebric sum over all the loci in heterozygous phase in all crosses).	11.3±0.24
5.	F = Mean of the covariances of additive and dominance effects over the arrays	-0.59±0.49
6.	E = The expected environmental component of variation	0.20±0.06
7.	**Other parameters:** :	
a)	Mean degree of dominance $\{(H_1 / D)^{1/2}\}$	20.4
b)	b= Regression of Covariance(Wr) on the variance(Vr)	0.091± 0.106
c)	Proportion of genes with +ve and –ve effects in the parents($H_2/4H_1$)	0.18
d)	Proportion of dominant and recessive genes in parents= $\{(4DH_1)^{1/2} + F/ (4DH_1)^{1/2} – F \}$	0.24
e)	r = Co-efficient of correlation between parental order of 0.012(NS) dominance (Wr + Vr) and parental measurement (Yr)	
f)	r^2 =Prediction for measurement of completely dominant and recessive parents	0.001
g)	h^2/H_2 = No. of groups of genes that exhibit dominance	4.264
h)	Narrow sense heritability (Hns)	17.48%
i)	Broad sense heritability (H_b)	64.1%

yield (Mather and Jinks, 1971) in sesame. In the present investigation, the proportion of genes with + ve and - ve effects (H2/4H1) was about 1: 5.5 (0.18) while the ratio of dominant and recessive alleles was estimated to be approximately 1:4 (0.24). So, high yielding sesame varieties can be bred by increasing the concentration of recessive alleles with positive effects through rigorous selection in the segregating population. Such a selection may also be helpful to get a residual genetic background where there is more expression of the gene(s) governing seed yield.

Seed yield was found to be inherited with a narrow sense heritability of 17.48% and broad sense heritability of 64.1% reaffirmed the fact that seed yield in the present set of materials is governed by lower proportion of additive component of genetic variation compared to non-additive components. Besides, Vekaria et al. (2015) also revealed lower estimates of narrow sense heritability (11%) in a 6x6 F_2 diallel in sesame This envisaged that the genetic nature of seed yield expression is largely under non-additive components of genetic variation and therefore, improved breeding methods e.g., single seed descent (SSD) method may be considered useful for recovery of high yielding plants. Besides, genetic improvement for high seed yield could be better handled by identification and monitoring of quantitative trait loci (QTL) for increased seed yield in succeeding segregating populations.

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