

Hayman's diallel analysis of elite x elite crosses in sesame (*Sesamum indicum* L.)

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ABSTRACT

The present investigation was carried out to study the genetic components of yield and its ancillary characters in a 8 x 8 full-diallel cross between elite sesame cultivars grown in different geographical regions of India. Hayman's analysis of variance indicated the presence of both additive and dominance genetic variance for all six characters studied. Ambidirectional dominance was indicated for all the characters with asymmetrical gene distribution except for seed yield and number of capsules/plant and residual dominance effects for all the characters studied. Branches/plant and test weight indicated epistasis. Seed yield, plant height and oil content showed over dominance while capsules/plant were under partial dominance. Parents *viz.*, HT-1, VRI-3 and TKG-22 had dominant genes with positive effects for seed yield; Phule til, Swetha til and RT-351 for capsule number/plant and crosses between HT-1, TKG-22 and E-8 results in segregants with high oil content. Estimates of components of variance demonstrated the involvement of additive gene effects for seed yield and capsule number, additive and dominant effects for plant height and oil content. Influence of the environment was strong on these characters, which followed simple additive-dominance inheritance.

Keywords: Additive, Diallel, Dominance, Gene action, Hayman, Sesame

Sesame (*Sesamum indicum* L.) is considered as 'Queen of Oilseeds' for its high oil content and better quality and is grown widely in tropical and subtropical conditions. The quality edible oil and seeds produced from this crop are widely used since time immemorial. Globally, sesame is cultivated in 12.05 m ha distributed across 79 countries, accounting for the production of 6.4 million tonnes and the productivity is 535 kg/ha. Sudan, India, Myanmar and United Republic of Tanzania are the top four sesame producing countries (FAOSTAT, 2020). India is the second largest producer of sesame, cultivated in 1.56 million hectares to produce 0.784 m tonnes, with average productivity of 502 kg/ha (Anonymous, 2018). Sesame is cultivated in 21 states of the country in a considerable area across different agro-climatic regions, under both rainfed and irrigated conditions. The top 4 states with the maximum area under sesame are Madhya Pradesh, Uttar Pradesh, West Bengal, and Rajasthan. The majority of the area under sesame is during kharif in northern and western parts of India. In eastern and southern parts of India, sesame is a summer crop.

The average yield potential of the released varieties is 700-800 kg/ha (Ranganatha, 2014). The genetic gain for yield in sesame is considerably low among other oilseed crops. Genetic improvement through mass selection from a locally adaptive population was followed to develop improved cultivars. Currently, hybridization between two purelines followed by pedigree or bulk selection is the most

popular method. However, the current data on productivity clearly indicates, very poor improvement in seed yield. Yield being a complicated quantitative trait needs to be addressed by operating different improved technologies for selection. Operating appropriate selection in a population is possible by understanding the inheritance pattern of the trait. The insight into the inheritance of characters is useful to plant breeders for, 1) selection of parents for hybridization, 2) choosing appropriate breeding and selection procedures for the genetic improvement of various quantitative traits, and 3) estimating the other genetic parameters.

Comprehensive studies on the inheritance pattern of yield and its attributes are limited in sesame and more information is required on these aspects. Diallel analysis of crosses is one most informative technique to understand the gene action of the traits. The pattern of inheritance for yield and its attributing characters along with phenological characters were studied through combining ability studies by Griffing's method of diallel analysis (Ravindran and Raghinam, 1996; Saravanan and Nadarajan, 2003; Banerjee and Kole, 2009; Pandey *et al.*, 2018). The above studies reported additive or non-additive gene action and identified crosses with high GCA and SCA, but further elucidating the other parameters of additive and dominance effects was lacking. Hayman's diallel analysis is robust in providing information on additive and dominance effects of genes, the proportion of dominance, the average degree of dominance, the direction of dominance, genes distribution among parents, maternal and reciprocal effects, the ratio of dominant to recessive

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alleles in all the parents, and broad sense (H^2) and narrow sense (h^2) heritability (Makumbi *et al.*, 2018). The use of this technique in sesame research is very limited (Vekaria *et al.*, 2015; Tripathy *et al.*, 2016; Suganthi, 2018; Dash *et al.*, 2020) and is gaining importance in present days. Sedack *et al.* (2013) used half diallel cross of 8 parents under Egyptian conditions to study the gene action for yield and its related characters. This study reported that both additive and dominance effects were significant for yield and yield contributing traits, where the magnitude of the dominant component was higher along with the predominant number of dominant alleles. The gene action depends on the distribution and expression of the genes present in the parents involved in developing diallel crosses. Parents may harbor favorable alleles at different loci, which need to be combined through crossing to develop an array of segregants with favorable genetic combinations expressing economically exploitable traits. Information on genetic systems governing the inheritance of characters by analyzing parents and cross combinations is necessary. Therefore, gene actions are particular to the parents and crosses studied. Knowledge of the genetic effects of the character in the crosses handled by the breeder helps in operating the right selection and generation advancement strategies of the segregating progenies. In the present study, an 8x8 full diallel cross was subjected to Hayman's method of diallel analysis (Hayman, 1954 a&b) to elucidate the genetic inheritance pattern and identify elite parents with dominant or recessive genes with positive and negative effects for yield and its attributing traits.

MATERIALS AND METHODS

Experimental site and plant material: The experiment was conducted at the experimental farm of ICAR-Indian Institute of Oilseeds Research, Hyderabad characterized with red sandy loam type of soil (17°15' N latitude and 78°18' E longitude at an altitude of 542m above mean sea level). Eight elite varieties *viz.*, E-8 grown in Karnataka (*khariif*), GT-2 in Gujarat (*khariif*), HT-1 in Haryana (*khariif*), Phule til in Maharashtra (*khariif*), RT-351 in Rajasthan (*khariif*), Swetha til in Telangana (summer), TKG-22 in Madhya Pradesh (*khariif*) and VRI-3 in Tamil Nadu (summer) were selected as parents. Eight parents were crossed in full diallel mating design (Hayman, 1954a) during summer 2018. All the 56 F_1 's including reciprocals and the parents comprising of 64 entries were raised in the plot size of 4.05 sq m to evaluate for yield and its attributes during *khariif* 2018. The experimental design adopted was a balanced block design with 2 replications. The standard recommended practices for sesame under the Telangana region were followed to raise a healthy crop.

Data recording: Data on number of capsules (NC); plant height (PH in cm); number of primary branches (PB) were collected from 5 randomly sampled plants in each replication. Seed yield (Sy in g) obtained from 4.05 sq m plot was quantified and the quantity obtained was divided by the number of plants/plot to obtain seed yield/plant (in g). 1000 seed weight (TW) was measured to obtain test weight (in grams) and oil content (OC in percentage) were estimated after harvesting using the Nuclear Magnetic Resonance (NMR) method.

Statistical analysis: The quantitative data recorded were analyzed for analysis of variance (ANOVA), where the total sum of squares is partitioned into different variance components *viz.*, a (additive), b (non-additive, which is further subdivided into b_1 , b_2 , and b_3), c (maternal) d (reciprocal differences other than maternal). The Vr-Wr graph was plotted following Hayman (1954 a&b). An approach of Jinks and Hayman (1953) based on Mather's notation (Mather and Jinks, 1982) was used to estimate components of genetic parameters. The analysis was done using SAS software version 9.4 (SAS Institute Inc., Cary, NC, USA) as per the programme code SASHAYDIALL (Makumbi *et al.*, 2018).

RESULTS AND DISCUSSION

Analysis of variance of 8x8 Diallel: The parents used in the study for diallel analysis were elite lines cultivated in different sesame regions of the country. The matrix mean of the characters studied for parents and F_1 is given in Table 1. Hayman's (1954a) analysis of variance for 8 x 8 diallel presented in table 2 indicates significant differences ($P < 0.0001$) among the genotypes for all the traits studied. Significant additive and non-additive effect were observed for all the characters studied. Dash *et al.* (2020) reported a non-additive effect for yield contributing traits in half diallel analysis. The magnitude of additive effects was high for all the characters except for number of primary branches/plant (PB). The mean deviation of F_1 from the mid parental value (b_1) was non-significant indicating ambidirectional dominance and therefore F_1 was intermediate between respective parents and hence, no heterosis effect for the characters studied. Ambidirectional dominance was indicated when the crosses specify dominance in the direction of high yield, but few crosses specified dominance in the opposite direction. In contrast, Aladji (2014) reported unidirectional dominance for capsule number in diallel analysis from the cross between local cultivars from Cameroon.

Stabilized selection for the characters among the parents would consequently result in either an absence of dominance or ambidirectional. Whereas, in the directional selection of genes, a dominant allele responsible for high yield could be favoured and thus gets fixed leading to unidirectional dominance (Crusio, 2007). Asymmetric gene distribution was

observed for significant values of b_2 for number of primary branches, test weight and oil content, reflecting that some parents harbored a considerable amount of dominant genes over other parents. For example, the array of F_1 developed with HT-1 as a parent resulted in significantly higher oil content than other arrays. Residual dominance which is unique to each F_1 (b_3) was significant for the characters studied, which indicated that some effect of unexplained dominant effect existed for all the characters. Diallel crosses of elite x elite crosses show the significant maternal effects and reciprocal differences other than maternal effects which are indicated by significant estimates of c and d , respectively (Table 2). Phule til, RT-351 and Swetha til can be used as female parents for improving capsule numbers, whereas HT-1 and Phule til are for oil content improvement. The block effect was non-significant, indicating homogeneity; therefore, all other components interacting with blocks are also non-significant. The diallel analysis for elite x elite crosses indicated that the capsule number/plant, number of primary and secondary branches/plant, plant height, seed yield, test weight and oil content are under the influence of both additive and non-additive effects in addition to maternal effects. Since the dominance effects were significant, further analysis to derive variance and covariance components was carried out.

Testing validity of the hypothesis: A test for the adequacy of the additive-dominance model was carried out using the ' t^2 ' test (Table 3). The non-significant values in all the characters indicated that V_r - W_r could be regarded as consistent over arrays, which implied that the additive-dominance model was satisfactory. Supplementing to the model, the regression coefficient with a unit slope in the absence of non-allelic interaction was observed for NC, PH, SY and OC. The slope was negative and the test value was significant, therefore the null hypothesis ($b=1$) was rejected for primary branches and test weight (Singh and Chaudary, 1985) reflecting the presence of non-allelic interactions for PB and TW. Kamala (1999) and Abd El-Kader *et al.* (2017) also reported non-allelic interactions for branches/plant, test weight and seed yield. Dominance being predominant, TW is under the influence of additive x dominance and dominance x dominance gene interaction (Sharmila *et al.*, 2007). Selection for these two traits should be postponed to advance generations. Therefore, the V_r - W_r graph and numerical approach (Hayman, 1954b) were carried out for seed yield/plant, capsule number/plant, plant height, and oil content.

V_r - W_r graph: The regression line for the array of parent-offspring covariance (W_r) on the array variance (V_r) with the unit slope crosses the W_r axis was above the origin (intercept =96.7) for NC indicating that this trait was under the influence of incomplete dominance. It was below the

origin for PH (intercept=-27.86), SY (intercept = -0.604) and OC (intercept= -0.436), indicating PH, SY and OC being under the influence of overdominance (Fig. 1). The reports are in agreement with Aladji *et al.* (2014), Mothilal *et al.* (2005) and Suganthi (2018). The regression coefficient (W_r on V_r) for NC and OC was low at 0.216 and 0.649 respectively, while for SY and OC it was high at 0.824 and 0.846 respectively (Fig. 1). The parents E-3, Swetha til, and TKG-22 possessed alleles dominant at most loci for NC; for PH parents RT-351 and E-8; for SY parents HT-1 and RT-351; and for OC parents HT-1, TKG-22 and Phule til harbored dominant alleles as indicated by position on the graph (Fig. 1) at near the origin. Plotting standardized values of parental means and (W_r+V_r) values for 8 arrays represented dominant and recessive alleles with positive and negative effects (Fig. 2) (Dabholkar, 1999). For NC, parents Phule til, Swetha til and RT-351 possessed most of the dominant genes with positive effects, while TKG-22 and E-8 possessed dominant genes with negative effects, VRI-3 possessed recessive genes with negative effects and GT-2 and HT-1 were neutral since they were at borderline (Figure 2a). For PH, dominant genes with positive effects were harbored in RT-351, negative effects in Swetha til and E-8, recessive positive effects in TKG-22, VR-3, Phule til and HT-1, recessive negative effect in GT-1 (Fig. 2b). Parental lines HT-1, Swetha til and VRI-3 possessed dominant genes with positive effects, while RT-351 possessed negative effects for seed yield, recessive genes with positive effects were observed in TKG-22 and negative effects in E-8, GT-1 and Phule til (Fig. 2c). Dominant genes with positive effects on oil content were found in HT-1, TKG-22 and recessive genes with positive effects in E-8 and negative effects in RT-351, while parental lines Swetha til, VRI-3, GT-2 and Phule til could possess an equal proportion of dominant and recessive genes (Fig. 2d). High frequency for segregants for increased capsule number could be expected in crosses between Phule til, RT-351 and Swetha til; for plant height from crosses between, HT-1, Phule til, RT-351 and VRI-3; for seed yield from crosses between HT-1, VRI-3 and TKG-22; for oil content, crosses between HT-1, TKG-22 and E-8. Riggs and Hayter (1973) identified parents with dominant and positive effects for increased grain number in spring barley. Sesame being a short-day plant (Weiss, 1983) and sensitive to photoperiod, localized varieties are grown in the major crop area. The varieties grown in one region do not perform to their potential in another region due to photo and thermo-sensitivity. The varieties are released specifically for *kharif* and summer and are also specific to the particular region. The local adaptation of the crop to season and location has gradually led to genetic variation among cultivated varieties. The diversity analysis using RAPD (Sharma *et al.* 2014) and microsatellites (Ramprasad *et al.*, 2017; Iqbal *et al.*, 2018) grouped the varieties into different clusters.

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Table 1 The matrix of mean values of six characters studied in 8 x 8 diallel cross along with parents (Parent values are in bold)

Parents	E-8	GT-2	HT-1	Phule til	RT-531	Swetha til	TKG-22	VRI-3
Number of capsules/plant								
E-8	68.5	69.3	73.3	84.0	78.5	84.0	61.0	67.5
GT-2	69.3	81.0	85.0	92.5	88.0	93.3	70.0	70.0
HT-1	73.3	85.0	85.0	114.0	90.3	77.5	74.0	92.0
Phule til	84.0	92.5	114.0	103.0	70.0	89.5	74.8	92.3
RT-531	78.5	88.0	90.3	70.0	110.0	92.5	84.5	116.5
Swetha til	84.0	93.3	77.5	89.5	92.5	106.0	83.5	88.3
TKG-22	61.0	70.0	74.0	74.8	84.5	83.5	61.5	65.3
VRI-3	67.5	70.0	92.0	92.3	116.5	88.3	65.3	63.5
Primary branches/plant (No.)								
E-8	6.0	4.5	6.0	6.0	4.5	5.0	4.5	4.5
GT-2	4.5	6.0	6.0	5.0	6.0	5.0	5.0	5.0
HT-1	6.0	6.0	5.0	4.5	6.0	6.0	6.0	5.0
Phule til	6.0	5.0	4.5	4.0	4.0	5.0	5.5	6.0
RT-531	4.5	6.0	6.0	4.0	6.0	5.0	6.0	6.0
Swetha til	5.0	5.0	6.0	5.0	5.0	4.0	5.0	5.0
TKG-22	4.5	5.0	6.0	5.5	6.0	5.0	6.0	4.5
VRI-3	4.5	5.0	5.0	6.0	6.0	5.0	4.5	4.0
Plant height (cm)								
E-8	124.5	124.8	138.0	138.5	140.0	143.8	122.5	133.8
GT-2	124.8	133.0	141.3	142.3	136.8	110.5	128.0	132.0
HT-1	138.0	141.3	154.5	153.0	134.5	130.8	149.5	152.5
Phule til	138.5	142.3	153.0	152.5	134.0	122.8	127.3	139.3
RT-531	140.0	136.8	134.5	134.0	149.0	135.3	143.0	126.8
Swetha til	143.8	110.5	130.8	122.8	135.3	123.5	137.0	126.3
TKG-22	122.5	128.0	149.5	127.3	143.0	137.0	143.0	120.8
VRI-3	133.8	132.0	152.5	139.3	126.8	126.3	120.8	148.0
Seed yield/plant (g)								
E-8	10.5	9.3	12.9	9.9	11.2	12.9	11.6	13.2
GT-2	9.3	10.2	12.7	10.7	11.0	10.8	11.2	14.1
HT-1	12.9	12.7	12.2	12.0	11.2	11.7	10.4	11.2
Phule til	9.9	10.7	12.0	11.3	12.2	14.8	13.4	11.8
RT-531	11.2	11.0	11.2	12.2	9.8	12.7	10.5	12.1
Swetha til	12.9	10.8	11.7	14.8	12.7	14.3	12.4	13.6
TKG-22	11.6	11.2	10.4	13.4	10.5	12.4	12.8	14.9
VRI-3	13.2	14.1	11.2	11.8	12.1	13.6	14.9	12.5
Test weight (g/1000 seeds)								
E-8	3.3	3.3	3.2	3.2	3.3	3.3	3.6	2.9
GT-2	3.3	3.0	3.6	2.9	3.1	3.3	3.2	3.0
HT-1	3.2	3.6	3.2	3.0	3.4	3.3	3.4	2.6
Phule til	3.2	2.9	3.0	2.8	3.0	3.3	3.2	2.9
RT-531	3.3	3.1	3.4	3.0	3.1	3.2	2.9	3.3
Swetha til	3.3	3.3	3.3	3.3	3.2	3.2	3.1	3.4
TKG-22	3.6	3.2	3.4	3.2	2.9	3.1	2.8	2.8
VRI-3	2.9	3.0	2.6	2.9	3.3	3.4	2.8	3.3
Oil content (%)								
E-8	46.2	45.6	45.4	47.0	42.6	45.0	45.4	45.4
GT-2	45.6	45.6	45.8	45.6	45.4	44.2	44.1	42.5
HT-1	45.4	45.8	47.8	47.8	47.7	47.0	46.9	46.5
Phule til	47.0	45.6	47.8	45.5	46.2	47.6	45.6	45.4
RT-531	42.6	45.4	47.7	46.2	41.8	45.4	45.8	45.5
Swetha til	45.0	44.2	47.0	47.6	45.4	45.3	43.8	42.9
TKG-22	45.4	44.1	46.9	45.6	45.8	43.8	45.6	45.3
VRI-3	45.4	42.5	46.5	45.4	45.5	42.9	45.3	45.3

Table 2 Analysis of variance of a 8 x 8 diallel table for number of capsules (NC), primary branches (PB), secondary branches (SB), plant height (PH), seed yield (SY), test weight (TW) and oil content (OC) in sesame

Components	Df	NC	PB	PH	SY	TW	OC
Rep	1	122.07*	0.125	21.13NS	0.23	0.024	1.54*
Entry	63	722.78**	1.681**	400.30**	9.71**	0.210**	5.67**
total	63	722.78**	1.681**	400.30**	9.71**	0.210**	5.67**
a	7	1799.36**	1.536*	748.76**	13.85*	0.298**	17.56**
b	28	418.74**	1.719**	287.26**	5.25**	0.166**	4.73**
b ₁	1	51.59	0.161	601.29	1.61	0.151	0.16
b ₂	7	222.69	1.655**	118.63**	1.43	0.124**	5.97**
b ₃	20	505.71*	1.819**	330.57**	6.77**	0.181**	4.53**
c	7	1925.60**	1.786*	1299.82**	26.41**	0.199**	5.75**
d	21	368.37**	1.643**	135.04**	8.71**	0.242**	2.91**
total x Block	63	32.72	0.252	18.62	1.73	0.012	0.33
a x Block	7	8.61	0.393	26.84	2.71	0.011	0.11
b x Block	28	26.93	0.219	15.16	1.57	0.010	0.36
b ₁ x Block	1	5.31	0.446	27.16	1.87	0.007	0.62
b ₂ x Block	7	63.66	0.131	5.61	1.49	0.014	0.28
b ₃ x Block	20	15.16	0.238	17.90	1.59	0.009	0.38
c x Block	7	87.94*	0.357	47.89	2.14	0.013	0.07
d x Block	21	30.07	0.214	10.73	1.49	0.014	0.45
Residuals	63	32.72	0.252	18.62	1.73	0.012	0.33

*, ** - Significant at 0.01 and 0.05 probability levels respectively; Df - Degrees of freedom; a - additive effect; b - dominance effect; b₁ - measures of directional dominance; b₂ - measure of ambidirectional dominance; b₃ - residual dominance, c-average maternal effect of each parent; d- residual reciprocal variation

Estimation of components of variation: Estimates of genetic components were computed for the characters studied (Table 3). A significant estimate of additive variance indicated that the capsule number in the plant was controlled by additive effects of genes. The parents under study carried different proportions of dominant and recessive genes with uneven allelic frequencies. The correlation between mid parents and F₁ hybrids was negative, low and non-significant, thus parents contained the most dominant genes with both increasing and decreasing effects. Positive correlation indicated that recessive genes were in favor of capsule number/plant (Nassar, 1965; El-Bramawy and Shaban, 2008). Parents could not be classified as dominant or recessive since the measure of proportion of the dominant to recessive genes was not less than unity. The narrow-sense heritability was high at 47.2% (Robinson, 1966), therefore, the response to selection could be high for the trait. Crosses made between Swetha til, Phule til and RT-351 can produce an array of segregants with high NC. Selection can be made in early segregating generations and the trait can be fixed by further re-selection in every generation for characters with additive effects with moderate heritability (Tanaka and Niikura, 2006).

The dominance variation component, indicating asymmetry of positive and negative effects of genes (H₂) was significant for seed yield, indicating that the character was under the influence of additive effects of genes. The mean degree of dominance (1.34), >1 indicated over dominance supporting the graphical analysis. The proportion of dominant and recessive genes in parents was equal to unity, indicating symmetry in the distribution of increasing and decreasing alleles in the parents. A negative and non-significant correlation coefficients for seed yield (-0.197) indicated both increasing and decreasing effects of dominant genes among parents. The parents in the study are elite lines that were historically selected for their higher yield possessing alleles with increasing effects, due to the symmetry in the distribution of genes that was observed in the study. Narrow sense heritability for seed yield was medium (Robinson, 1966). Seed yield is a complex character, and non-allelic interactions have been reported with additive-dominance gene effects (Kumar and Sivasmy, 1996; Kamala, 1999; Solanki and Gupta, 2003; Swain *et al.*, 2001; Abd El-Kader *et al.*, 2017).

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Table 3 Genetic component estimates for number of capsules/plant (NC), primary branches/plant (PB), plant height (PH), seed yield/plant (SY), test weight (TW) and oil content (OC) in sesame

Parameter	NC	PB	PH	SY	TW	OC
	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE
Additive variation (D)	351.92±95.53*	0.73±0.19*	134.81±26.50*	0.56±0.35*	0.03±0.03	2.46±0.5*
Dominance variation (H1)	412.26±219.60	1.65±0.43*	280.55±60.91*	1.017±0.81	0.18±0.07*	6.07±1.15*
Dominance variation component indicating asymmetry of positive and negative effects of genes (H2)	353.23±191.05	1.22±0.37*	250.02±53.00*	1.78±0.71*	0.14±0.06*	4.08±1.0*
Overall mean dominance effect of heterozygous loci (h2)	0.000±128.13	0.000±0.25	123.39±35.54*	0.000±0.45	0.03±0.04	0.000±0.67
Relative frequency of dominant and recessive alleles in the parents (F)	194.14±225.72	1.03±0.44*	76.4±62.61	0.000±0.84	0.03±0.07	2.34±1.18*
Environmental variation (E)	32.72±31.84	0.25±0.06*	18.62±8.83*	1.73±0.12*	0.01±0.10	0.33±0.17*
Mean Degree of Dominance	1.08	1.50	1.44	1.35	2.48	1.57
Proportion of dominance	0.21	0.18	0.22	0.44	0.2	0.17
Proportion of dominant and recessive genes in parents	1.68	2.78	1.49	1.000	1.57	1.87
Correlation between W_r+V_r and Y_r	-0.53	0.16	0.26	-0.2	-0.404	-0.87*
Prediction for measurement of completely dominant and recessive parents	0.28	0.03	0.07	0.04	0.16	0.76
Heritability in narrow sense	0.47	0.10	0.35	0.00	0.26	0.44
Broad-sense Heritability	0.86	0.59	0.85	0.17	0.82	0.86
Intercept of regression line (b V_r , W_r)	96.71	-	-27.86	-0.60	-	-0.43
t^2	0.02	0.37s	1.61	0.14	1.05	0.26
$H_0 : b=1$	1.85	2.53*	0.33	0.53	4.05 *	1.48

W_r , covariance between families within the i^{th} array and their nonrecurrent parent; V_r , the variance among family (F_1 +reciprocal) means within an array; Y_r , mean parental value; ** significant at $p<0.05$

The significant estimates of additive and dominance variance for PH and OC indicated the additive and dominance components of genotypic variance, and also the influence by the environment in the variation observed. Variation due to dominance component indicating asymmetry of positive and negative effects of genes was significant, indicating both high and low values for PH and

OC that were controlled by dominance effects of the genes at different loci. Hence, the dominant genes were preponderant exhibiting the dominance effect of genes of OC. The mean degree of dominance ratio was more than 1 indicating over dominance of alleles in a heterozygous state (Comstock and Robinson, 1952). The ratio, dominant and recessive genes in parents was >1 and dominant genes were preponderant

resulting in an asymmetrical distribution of dominant and recessive genes among the parental genotypes. Provided that the dominant genes were preponderant, the proportion of alleles with increasing and decreasing effects was also asymmetrically distributed and skewed towards increasing effects since the ratio was less than 0.25. The correlation between the degree of dominance of parents and the mean of a common parent was negative, high and significant for OC (-0.873). The prediction for measurement was not less than unity, so completely dominant or recessive parents were not identified. Over dominance was involved in PH and OC as indicated by the mean degree of dominance and the Vr-Wr graph (Fig. 1 b&d). When over dominance is involved, gene action can be best exploited by biparental mating with

pedigree selection in every segregating generation in the direction of high oil content, which is likely to lead to substantial improvement in the character. Population improvement through simple recurrent selection is also a better approach for improving the traits under the influence of over dominance gene action in self-pollinated crops since the exploitation of heterosis is laborious. The selection favoring heterozygotes over both homozygotes facilitate equilibrium in allele frequencies. The heritable variation is high at 86.3%, consequently, recurrent selection for high oil content from early generation (F₂) and a subsequent generation may be carried out to fix the dominant genes. Tripathy *et al.* (2016) reported dominant gene action with an increasing effect at one locus for high oil content.

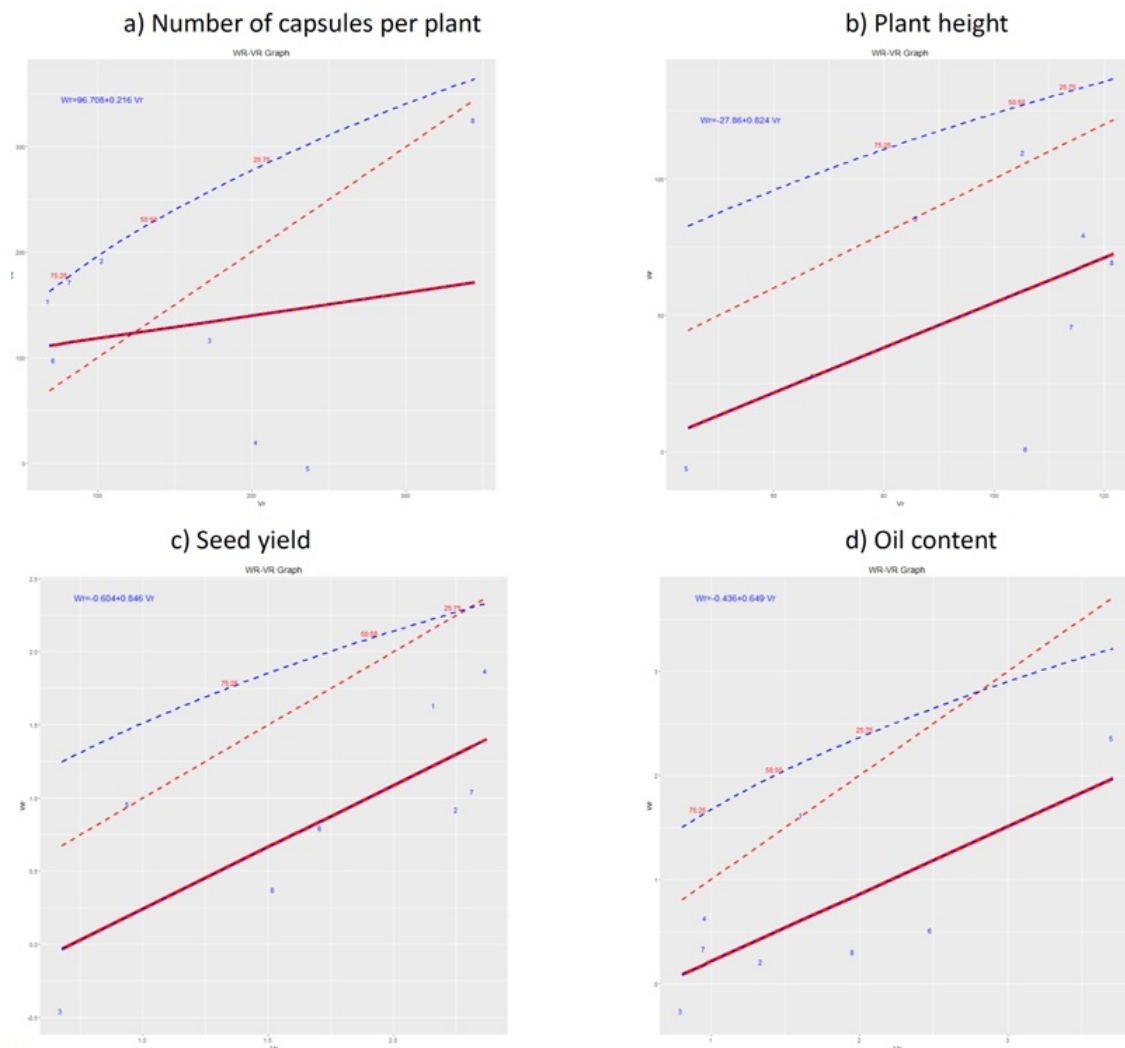


Fig. 1. (Vr,Wr) graph of (a) number of capsules/plant $Wr=96.708+0.216Vr$, (b) Plant height, $Wr=-27.86+0.824Vr$, (c) Seed yield/plant, $Wr=-0.604+0.846Vr$ and (d) Oil content, $Wr=-0.436+0.649Vr$. Solid line represents the best fitting regression of Wr on Vr and dotted line represents the regression with the theoretical slope of 1 expected in the absence of non-allelic interaction

HAYMAN'S DIALLEL ANALYSIS OF ELITE X ELITE CROSSES IN SESAME

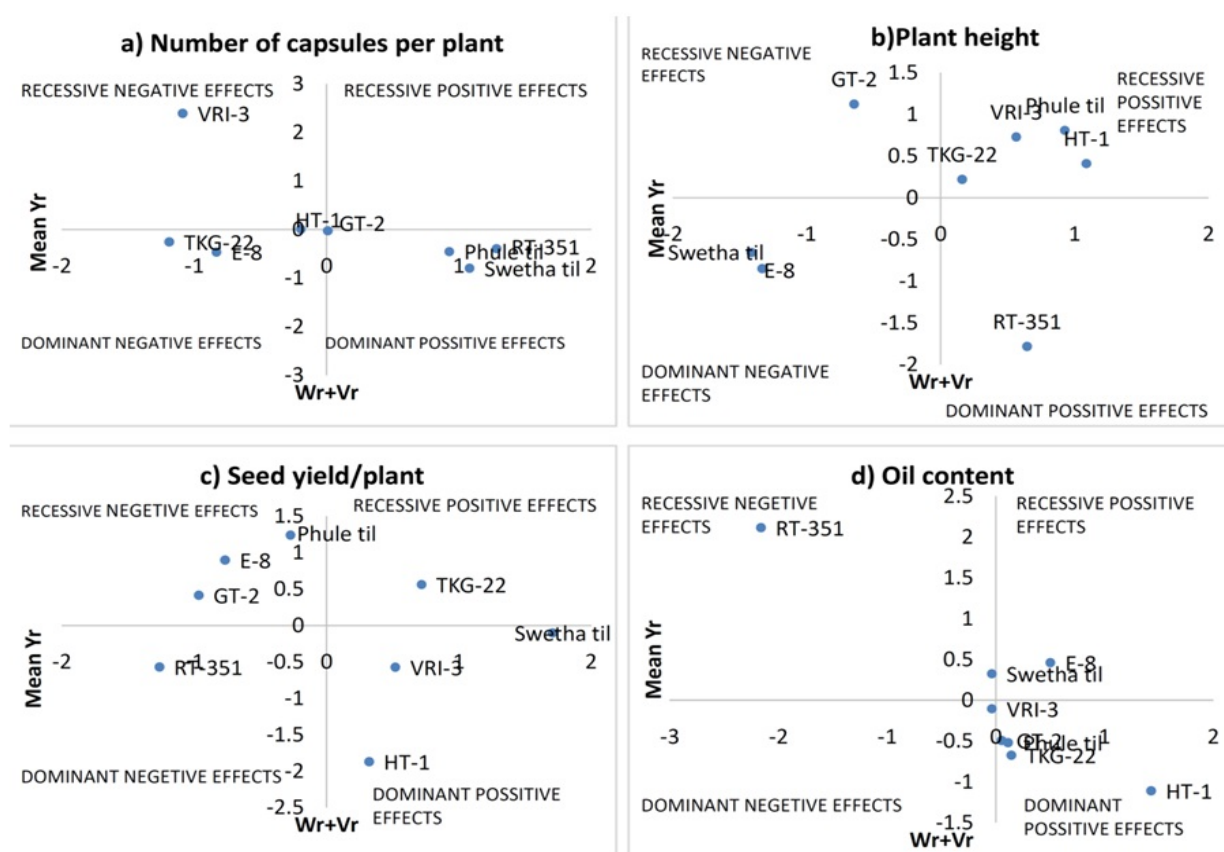


Fig. 2. Standardised deviation of mean Yr and Wr+Vr of (a) capsules number/plant, (b) plant height, (c) seed yield/plant and (d) oil content

The present study helps in understanding the gene action of sesame elite x elite combinations and deciding the selection procedure for the improvement of yield. The results showed that both additive and dominance gene actions influenced the yield and its attributing characters in sesame. The gene action for seed yield and its major attributing character, capsules number/plant was under additive effects of genes and under the absence of gene interactions, thus selection made for higher number of capsules/plant and high seed yield can be fixed. Selections for capsules number/plant can be accurate since it can be done by visual counting, consequently, seed yield will improve. Biparental mating and recurrent selection in segregating material is the best way to improve capsule number/plant and oil content by forwarding the F_1 's of crosses from Phule til and RT-351. The single seed descent method is appropriate for forwarding the generation in place of the bulk method.

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