

ORIGINAL ARTICLE

Study of gene action for seed yield and oil content in sesame using Hayman's numerical and graphical approach

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ABSTRACT

A set of 28 F₁ hybrids derived from 8 x 8 half-diallele mating design along with all parents were evaluated for diallel analysis following Hayman's numerical and graphical approach for eight quantitative traits including seed yield and oil content. The t² test indicated non-significant t² value for all traits under study, whereas the deviation of b from unity was non-significant for days to 50% flowering, plant height, plant height up to first capsule, internode length and seed yield per plant indicating validity of the assumptions. The dominance variance was found to be greater in magnitude than additive variance for all the traits indicating role of over dominance with excess of dominant alleles for all traits except seed yield per plant. However, direction of dominance was strongly in positive direction except branches per plant and oil percentage. Distribution of +ve and -ve alleles were asymmetric with more involvement of negative alleles than positive alleles for almost all traits among parents. Graphical analysis also demonstrated similar mode of gene action. Days to 50% flowering (44.41%) followed by yield per plant (41.85%) and oil percentage (35.49%) displayed comparatively higher estimates of narrow-sense heritability indicating more reliable effective selection based on such traits. VRI-1 was shown to be highly concentrated with dominant alleles while, Krishna and Prachi were rich in recessive alleles for seed yield. In contrast, Rama and GT-10 were rich with dominant alleles, but rest others had shown more or less balanced proportion of dominant and recessive alleles for oil content.

Key words: Hayman's graphical approach, Genetic parameters, Wr-Vr graph, Gene action, Sesame

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INTRODUCTION

Oilseeds crops serve as the second most economically important target group of the Indian agriculture next to cereals accounting for 19% of the global area with around 2.7% of global production[1]. India is the fourth largest oilseed producing country in the world after the USA, China and Brazil[2]. There are nine oilseeds crops grown in India, out of which seven are of edible oilseed crops (soybean, groundnut, rapeseed mustard, sunflower, sesame, safflower, and niger) and two (castor and linseed) are of non-edible oilseed crops [3]. Among the minor oilseeds crop (castor, niger, safflower and sesame), sesame occupies the fifth position in terms of production after soybean, groundnut, sunflower and mustard [4]. Worldwide, it is cultivated in an area of 117 lakh ha with production of 60.16 lakh MT and productivity of 512 kg/ha[5]. Asia and Africa contribute nearly 97% of the world's total production of sesame. In India, it is cultivated in an area of 17.30 lakh ha which occupied 26 states and 1 Union territory with the production of 7.46 lakh MT and productivity of 413 kg/ha[6] which is far below the global average productivity. The low productivity may be attributed to various factors like its cultivation in un-irrigated areas, cultivation of low yielding dehiscent varieties, lack of varietal replacement through the development of hybrids, lack of improved varieties with tolerant to biotic and abiotic stresses[7].

Furthermore, sesame is a typically neglected crop or an 'Orphan crop' or under-exploited oilseed crop since it is not mandated to any one of the international agricultural research centers till now and the paradigm of sesame parallels to many minor crops. Most of the varieties under cultivation are selections from local cultivars or closely related populations under low levels of management. Besides, less emphasis has given on researches related to yield structure as a basis for progress in sesame breeding which in turn yielded low productivity potential of cultivars grown in India. This indicates that there is a need to enhance the productivity of this crop by developing high yielding varieties and hybrids varieties. Study of nature of gene action helps to obtain information on the genetic systems governing the inheritance of characters to be improved and predict the performance in subsequent generations by assessing the potential of different crosses[8,9,10]. Hence, an attempt was undertaken to study the mode of gene action for eight important quantitative traits including seed yield and oil content in a 8 x 8 half-diallel crosses following Haymen's numerical and graphical approach.

MATERIAL AND METHODS

Plant materials :Twenty eight F₁ crosses involving eight genetically diverse sesame genotypes (Rama, AT-382, VRI-1, GT-10, Krishna, Nirmala, Prachi and Uma)(Table 1) following 8 × 8 half diallel mating design were grown in *Kharif* 2017 to study mode of gene action using Hayman's numerical and graphical approach.

Experimental site : A field experiment was conducted in the EB-II section of the Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar. The experimental site is located at an altitude of 45 m above sea level (latitude 20.26°N and longitude 85.81°E) which is nearly 64 km west of the Bay of the Bengal, coming under the humid and subtropical climate zone of the state.

Experimental design and data collection : Eight parents and 28 F₁ hybrids were grown in Randomized Block Design(RBD) with three replications. Each net plot consisted of three rows of two-meter length with spacing of 30 cm × 10 cm. One border row on either side of each plot was laid to avoid the border effect. Observations on eight characters *viz.*, days to 50% flowering, plant height, plant height up to 1st capsule bearing node, branches per plant, internode length, capsules per plant, yield per plant and oil percentage were recorded.

Statistical analysis : The data were subjected to genetic analysis as per Singh and Choudhury[11] following Hayman's [8,9] numerical and graphical approach for study of gene action. Assumptions laid down for additive-dominance model (Haymen's Approach) was verified for goodness fit using t²- test (or F-test) against table value of F at 4 and (n-2) degrees of freedom, where, n is the number of parents involved. Besides, significance test for deviation of b (regression coefficient of W_r on V_r) from unity was carried out to verify the validity of the hypothesis.

RESULTS AND DISCUSSION

A perusal of Table 2 indicated significance of variances due to genotype as well as for GCA and SCA component of variances except internode length for GCA which envisaged presence of appreciable genetic variation among the present set of parents and crosses in terms of both additive and non-additive gene which is in agreement with Sankar and Kumar[12], Krishnaiah *et al.*[13] and Devi *et al.*[14].

As a follow-up step, Hayman's graphical analysis was conducted to assess the mode of gene action and genetic relationships among the parents. Two adequacy tests was followed to check the validity of the additive-dominance model. The first test was the t² test or F- test. If the t² test is significant, the additive-dominance model is not a good fit. The second test is the statistical significance of the deviation of b from unity. The data will be only valid for genetic interpretation if the value of the regression coefficient b deviates from zero but not from the unit. The t² test indicated non-significant t² value for all traits under study, whereas the deviation of b from unity was non-significant for days to 50% flowering, plant height, plant height up to first capsule, internode length and seed yield per plant indicating validity of the assumptions (**Table 3**). The failure of assumption (test for b-value) for a few traits could be due to diverse composition of parental materials, non-allelic interactions, correlated gene distribution (linkage disequilibrium) and multiple alleles.

Components of genetic variation : Gene action (additive and non-additive) for a trait is assessed on the basis of components of genetic variances. However, the estimates are highly influenced by the method of sampling, mode of pollination and genetic composition of the population[15]. Additive gene action is fixable in form of homozygosity, whereas non-additive gene action is inter-allelic and amenable for exploitation of heterosis in form of hybrids.

Table -1: Parents used and their origin

Parent	Pedigree	Origin
Rama	Selection from Khosla local	ORS, Berhampore (WB)
AT-382	G.Til 3 × G.Til 4	Agricultural Research Station (JAU)Amreli, Gujrat
VRI-1	Pureline selection from Tirukkattupalli local	TNAU, Coimbatore (TN)
GT-10	Selection from TNAU-17	RAS, GAU, Amreli (Gujarat)
Krishna	M-3-2 × Venezuela 17/4	RAU, Dholi (Bihar)
Nirmala	Mutant of Tilottama (B 67)	OUAT, Bhubaneshwar (Orissa)
Prachi	Mutant of Tillottama (B 67)	OUAT, Bhubaneshwar (Orissa)
Uma	Mutant of Kanak	OUAT, Bhubaneshwar (Orissa)

Table -2: Analysis of variance for combining ability for fourteen characters in 8 × 8 half diallel crosses in sesame

Character	Mean sum of square			
	Genotype (35)	GCA (7)	SCA (27)	Error (70)
DF	11.21**	25.20**	7.77**	1.13
PH	296.27**	258.01**	305.83**	27.24
PHC	81.05**	118.83**	71.62**	10.57
B/P	1.11**	0.758*	1.20**	0.345
IL	1.89*	1.64	1.95*	0.967
C/P	469.94**	537.76**	452.99**	30.99
Y/P	9.65**	19.107**	7.30**	0.95
OP	63.65**	111.70**	51.64**	1.002

N.B: * and ** indicate significance at 5% and 1% levels of probability respectively. Figure in parentheses indicate degrees of freedom for corresponding sources of variation.

Table -3: Estimates of t^2 , a, b, SE(b), t_1 and t_2 .

Source	DF	PH	PHC	B/P	IL	C/P	Y/P	OP
t^2 value	0.30	1.08	2.45	1.59	0.058	0.77	5.99	6.08
A	-1.53	-103.7	-21.0	-0.37	-0.33	-47.1	-0.24	-12.4
b(wr, vr)	0.67	0.78	0.78	0.40	0.238	0.25	0.39	0.44
SE(b)	0.40	0.13	0.104	0.22	0.358	0.27	0.14	0.14
$t_1=b-0/SE(b)$	1.67	5.88**	7.49**	1.84	0.664	0.92	2.72*	3.14*
$t_2=1-b/SE(b)$	-0.79	-1.61	-2.11	-2.73*	-2.126	-2.71*	-4.13	-4.01**

N.B.: t_1 and t_2 refer to observed t-values for test of significant deviation of b from 0 and 1 respectively.

The estimates of genetic components of variation in respect of 8 quantitative characters including seed yield and oil content are presented in **Table 4**. It was observed that six genetic components of variation (D, H_1 , H_2 , E, F and h^2) were significant for all the 8 characters, except the D component was not significant for branches per plant and the h^2 component was not significant for branches per plant and oil percentage. This indicates importance of both additive and dominant component of variation for almost all characters as also reported by several researchers [16,17,18,19]. But, the relative magnitude of the dominance components (H_1 and H_2) was greater than the additive component (D) for all the characters indicating preponderance of non-additive gene action for their inheritance pattern. In this context, the h^2 estimate for all traits except branches per plant and oil percentage was highly significant and positive indicating that the overall direction of dominance was strongly positive for these characters. The F component, a measure of co-variance between additive and dominance effects was significant and positive for all traits except seed yield per plant indicating the excess of dominant alleles in the parents for these characters. However, significant negative F value for yield per plant suggested a higher frequency of recessive alleles for expression of the trait. It is worth to note that environmental component of variation was significant for all traits except oil content which envisaged greater role of environment for G x E interaction.

Table-4: Estimates of components of variation and others genetic parameters for eight characters in F₁ generation

Character/ Parameter	DF	PH	HC	B/P	IL	C/P	Y/P	OP
D	**7.2±1.11	*9.7±9.52 *	**0.8±2.89	2.0±5.0	**5.9±3.21	1.11±2.061 **6	**9.7±6.54	**6.81±5.44
H ₁	25.16±6.29**	774.59±86.12**	165.09±18.86**	2.82±0.62**	4.64±1.49**	159.7±255.61**	21.05±5.67**	226.44±42.28**
H ₂	20.48±5.48**	654.14±74.92**	138.86±16.40**	2.56±0.54**	3.02±1.29**	141.4±122.38**	19.17±4.93**	185.95±36.79**
F	6.40±6.47**	326.53±88.52**	53.53±19.38**	0.08±0.64**	2.55±1.53**	132.49±262.73* *	-1.78±5.82*	32.79±43.46*
h ²	33.35±3.68**	3253.04±502 5**	750.19±10.99* *	5.87±0.36	2.12±0.87**	158.7±149.14* *	42.87±3.30**	3.35±24.67
E	1.129±0.92**	27.23±12.49**	10.733±2.733* *	0.344±0.090**	0.967±0.216**	30.064±37.06 4**	0.948±0.821**	1.002±6.131
ADD	1.47	1.68	1.55	7.38	1.95	2.89	2.14	2.25
Uv	0.204	0.211	0.210	0.228	0.163	0.221	0.228	0.205
K _D /K _R	1.46	2.09	1.67	1.23	3.29	1.28	0.84	1.39
h ² (bs)	89.96	87.92	84.02	68.66	48.35	93.86	90.40	98.64
h ² (ns)	44.41	15.37	31.49	10.39	8.03	23.83	41.85	35.49

NB: * and ** indicate significance at 5% and 1% levels of probability respectively

D: Additive genetic variance

H₁: Dominance components of variation due to dominant gene effect

H₂: Symmetry or asymmetry of alleles

F: Covariance of additive and dominance effects in a single array

h²: Heritability

E: Environmental component

ADD: Average degree of dominance over all loci
 uv: Proportion of +ve and -ve alleles in the parents
 K_D/K_R : Proportions of dominant and recessive alleles in the parents
 h^2 (bs): Heritability in broad sense
 h^2 (ns): Heritability in narrow sense

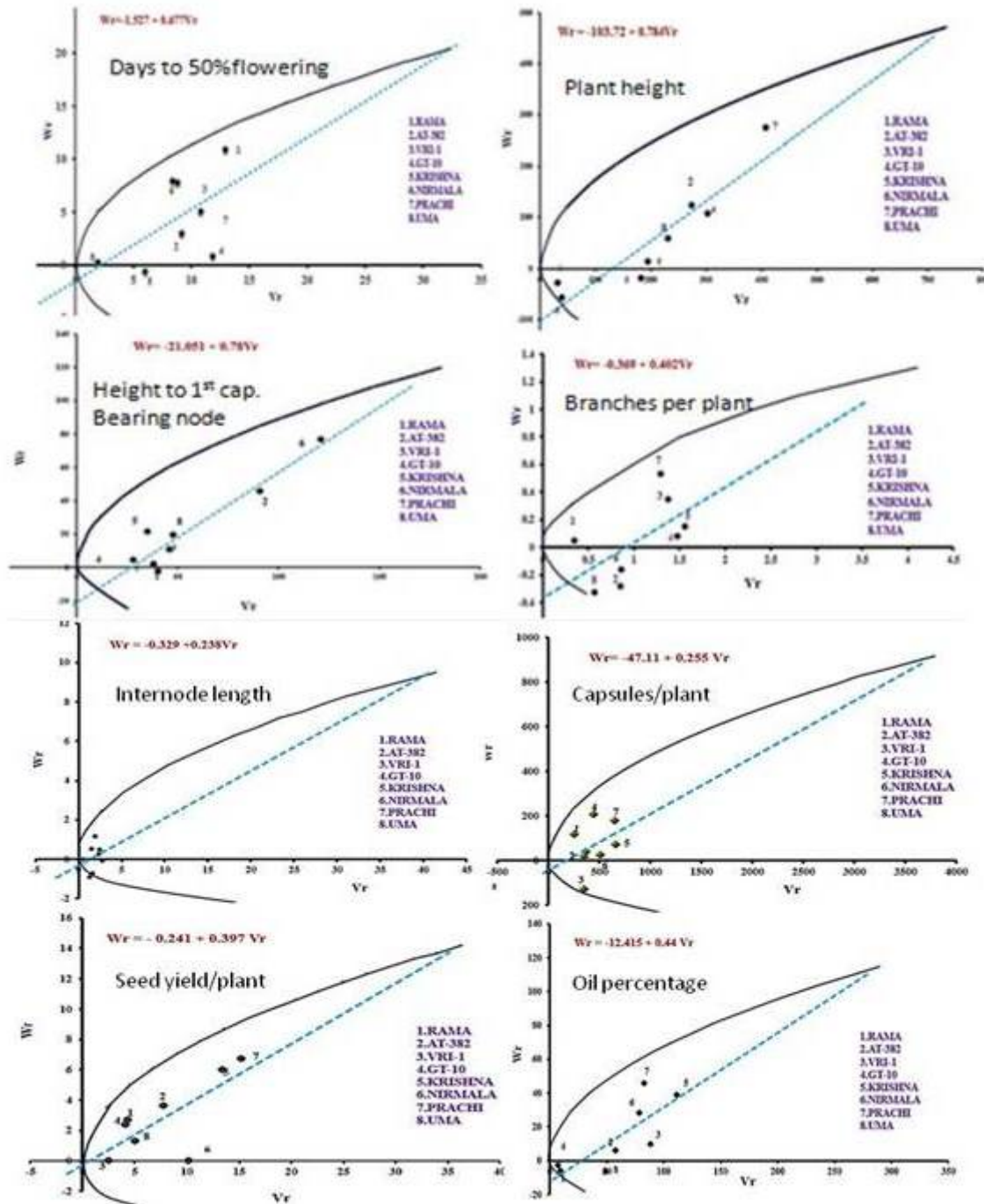


Fig-1: Regression of Wr on Vr graphs for eight agro-economic traits including seed yield and oil percentage in 8 x 8 half diallel mating design.

Table 5: Distribution of awareness given to participants by Antenatal Health Care providers

Characteristics	Frequency	Percentage
Nutrition		
Yes	50	39.1
No	78	60.9
Importance of TT injection		
Yes	27	21.1
No	101	78.9

Table 6: Distribution of guidance tips given to participants by Antenatal Health Care providers

Characteristics	Frequency	Percentage
Preferred place for delivery		
Yes	32	25
No	96	75
Transport arrangements		
Yes	13	10.2
No	115	89.8
Person accompanying her during delivery		
Yes	17	13.3
No	111	86.7
Travel time		
Yes	11	8.6
No	117	91.4
Cost of delivery		
Yes	20	15.6
No	108	84.4

Further, different genetic ratios viz., ADD (Average degree of dominance), uv (Proportion of +ve and -ve alleles in the parents), K_D/K_R (Proportions of dominant and recessive alleles in the parents), h^2 (heritability) in broad sense and narrow sense (**Table 4**) derived from six genetic components of variation (D, H_1 , H_2 , E, F and h^2) can reflect more clarity for mode of inheritance for the quantitative traits under study. The estimated average degree of dominance (ADD) for 8 characters was in fact greater than 1.0 for all the characters indicating the existence of over-dominance. Whereas, the estimates of uv value were even less than 0.25 for all characters under study suggesting asymmetric distribution of +ve and -ve alleles with more involvement of negative alleles than positive alleles among parents.

In the present study, K_D/K_R value was shown to be greater than 1 for all characters except seed yield per plant indicating preponderance of dominant alleles than recessive alleles in the parents, whereas reverse was the case for yield per plant with K_D/K_R less than 1.0 suggesting excess of recessive alleles present among parents for expression of the trait.

Estimates of h^2 (bs) and h^2 (ns) among the characters revealed appreciable difference which may be accounted for involvement of non-additive gene action for all characters. The highest broad sense heritability was observed in oil percentage (98.64%) followed by capsules per plant (93.86%) and yield per plant (90.40%). Whereas, days to 50% flowering (44.41%) followed by yield per plant (41.85%) and oil percentage (35.49%) displayed comparatively higher estimates of narrow-sense heritability indicating reliability of such trait based-selection to achieve higher expected genetic gain in the subsequent generations.

Graphical analysis : The variance of the off springs in an array (V_r) and the covariance between the parents and their off-springs in each array (W_r) were computed for graphic representation (**Fig 1**). As shown by Hayman[8,9] and Jinks[10], in the absence of epistasis and with the independent distribution of genes among the parents, the linear regression of W_r on V_r has a unit slope. This assumption holds good when the W_r, V_r array points would remain along the regression line, $W_r = a + b V_r$ and within an

area delineated by parabola, $Wr^2 = Vp \cdot Vr$. The magnitude and sign of the intercept cut off by the regression line shows the level of dominance and scattering of Vr and Wr points along the regression line gives information about direction of dominance. The above information can be obtained from Vr - Wr graph only when the basic assumptions of diallel analysis by Hayman's method hold for the material under study. A regression graph of parent-offspring covariance and variance provides a useful means of assessing genetic relationships among the parents. The Vr - Wr graphs for 8 characters are presented in **Fig 1**. Magnitude and direction(+ve or -ve) of the intercept and relative distance of Wr , Vr points from the origin was used in drawing inference on the presence of epistasis, nature of allelic-interaction and relative concentration of dominant/recessive alleles in different parents for 8 characters.

The line of unit slope passed below the point of origin for eight characters indicating allelic interaction was within the range of over dominance (**Fig 1**). From the distribution of Wr and Vr data points, it was evident that all parents were very close to the origin for internode length and number of capsules per plant suggesting that much more concentration of dominant alleles in all parents. In contrast, it appears that all parents were distributed not beyond mid way along the regression line for branches per plant, oil content and seed yield per plant indicating no possibility of any parent with higher concentration of recessive alleles for such traits. On the other hand, the Wr , Vr data points of all parents were well distributed along all throughout the regression line for characters e.g., days to 50% flowering, plant height and plant height upto 1st capsule bearing node indicating proportionately different polygenic status among the parents under study. There is not enough report for gene action study for the characters, height up to 1st capsule bearing node and internode length.

From the distribution of Wr and Vr data points, it is clear that dominant alleles were very much concentrated in Uma and Krishna while recessive alleles were in Rama for days to 50% flowering. In the remaining five parents, the number of dominant and recessive alleles was relatively balanced. For plant height, dominant alleles were much concentrated in Rama and Nirmala, whereas in Prachi, more recessive alleles were concentrated. A balance of dominant and recessive alleles was observed in the remaining five parents. None of the parents with more number of the dominant allele for plant height up to 1st capsule bearing node was observed, whereas the concentration of recessive allele was more in AT-382 and Nirmala. In the other six parents, a balance between dominant and recessive alleles was observed for plant height up to 1st capsule bearing node.

For branches per plant, the concentration of more dominant allele was observed in Rama while in the other seven parents equal number of dominant and recessive alleles were present, whereas for internode length, in all the 8 parents the concentration of more dominant alleles than recessive alleles were present. The concentration of a more dominant allele was observed in parent, AT-382 and VRI-1 while in the other six parents there was an equal number of the dominant and recessive alleles was present for capsules per plant.

For yield per plant, dominant alleles were much concentrated in VRI-1 while recessive alleles were present in Krishna and Prachi, while other parents were shown to be relatively balanced for number of dominant and recessive alleles. Similarly, for oil percentage, concentration of dominant alleles were more in Rama and GT-10 while none of the parent with more concentration of recessive alleles. In the remaining six parents, the number of dominant and recessive alleles was relatively balanced. However, Swain *et al.*[20] reported symmetrical to nearly symmetrical distribution of genes for capsules/plant and seed yield. This contradictory finding with present research was due to genetic difference in the materials handled and the presence of genotype \times environment interactions. A similar finding has been reported by Swain and Dikhit[21], Sedek and Shafie[22] and Abd El-Kader *et al.*[23] in sesame, Alam[24] in groundnut, Nair and Ghorade[25] in sorghum, Eftekhari *et al.*[26] and Fellahi *et al.*[27] in wheat.

CONCLUSION

Since most of the character expression governed by non-additive gene action including seed yield, the pedigree method of breeding alone would not be effective. Recurrent selection and inter-se crossing in the inbred generation followed by pedigree selection may be useful in breaking tight linkage and bringing desirable recombination. So for improvement of these characters through heterosis breeding is the effective breeding method.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interests.

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