



ISSN (E): 2277- 7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2021; SP-10(12): 920-925  
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[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 10-10-2021  
Accepted: 12-11-2021

**Ravinder Kumar**  
Department of Genetics and  
Plant Breeding, C. P. College of  
Agriculture, S. D. Agricultural  
University, Sardarkrushinagar,  
Gujarat, India

**Jagdish A Patel**  
Cotton Research Station, S. D.  
Agricultural University, Talod,  
Gujarat, India

**RS Solanki**  
Department of Genetics and  
Plant Breeding, C. P. College of  
Agriculture, S. D. Agricultural  
University, Sardarkrushinagar,  
Gujarat, India

**Parthsinh M Rahevar**  
Department of Genetics and  
Plant Breeding, C. P. College of  
Agriculture, S. D. Agricultural  
University, Sardarkrushinagar,  
Gujarat, India

**Corresponding Author**  
**Ravinder Kumar**  
Department of Genetics and  
Plant Breeding, C. P. College of  
Agriculture, S. D. Agricultural  
University, Sardarkrushinagar,  
Gujarat, India

## Diallel analysis using hayman method to study genetic parameters of yield components in sesame (*Sesamum indicum* L.)

**Ravinder Kumar, Jagdish A Patel, RS Solanki and Parthsinh M Rahevar**

DOI: <https://doi.org/10.22271/tpi.2021.v10.i12Sn.9583>

### Abstract

Seven sesame (*Sesamum indicum* L.) genotypes were crossed in a half diallel mating fashion. The analysis of variance revealed that the parents and their hybrids under study possessed sufficiently high amount of genetic variability. The component D measures the additive effects of genes. Greater values of  $H_1$  than  $H_2$  and the ratio of  $H_2/4H_1$  ( $< 0.25$ ) confirmed the unbalanced distribution of gene at the loci in the parents implying dominance for all the traits. It was also confirmed by greater than one value of KD/KR components for all the traits which suggested the higher frequency of dominant genes than recessive genes in the parents. The component F was indicating the presence of an excess of dominant alleles than recessive alleles. In graphical analysis, the regression line intercepted  $W_r$  axis below the origin indicating over dominance for all the traits except plant height.

**Keywords:** sesame, Hayman's diallel analysis, fixable and non-fixable components

### Introduction

Globally known as 'sesame' and in India as 'Til', sesame (*Sesamum indicum* L.;  $2n = 2x = 26$ ) belongs to an order Lamiales and family Pedaliaceae. The genus *Sesamum* contains most of wild species supposed to be originated in Africa while the cultivated type (*S. indicum*) originated in India (Bedigian, 2010 and Zohary *et al.*, 2012) [4, 29]. Cultivated sesame evolved from wild species in the Indian subcontinent during Harappan civilization as per recent archaeological data and spread west to Mesopotamia before 2000 B.C (Fuller, 2003) [7] whereas according to some reports sesame was first domesticated in Africa and later spread to India at a very early time (Alegbejo *et al.*, 2003; Purseglove, 1969) [3, 22]. Sesame is a vital source of high quality oil and protein (IPGRI and NBPGR, 2004) [13]. Sesame is called as the "Queen of oilseeds" due to its excellent qualities of the seed, oil and meal. Sesame seeds have nutritional as well as medicinal value due to its rich protein, carbohydrate, fat, fiber, vitamins E, A and B complex and minerals viz., calcium, phosphorus, iron, copper, magnesium, zinc and potassium with high unsaturated fatty acid (linolenic and tocopherol) (Pathak *et al.*, 2014) [20]. Breeders are continually challenged with the problem of parent selection during breeding of high yielding varieties of crop plants. Information on the genetic architecture of yield and its components will help to sort out the improved crosses more competently, though elimination of poor crosses on the basis of their performance in initial generation has been suggested. Kearsy (1965) [16] noted that Jink and Hayman's diallel analysis (1953) [15] deliver more evidence than other methods, but has more necessary assumptions. The studies anticipated by Griffing (1956) [9] do not afford any test to detect epistasis or linkage. Jink and Hayman's analysis do provide such test. When using Griffing's analysis to estimate variance components, it has been suggested that simple tests, such as the  $W_r$ - $V_r$  evaluation found in Hayman (1954b) [11] model, may be used to ascertain the presence of epistasis and/or linkage disequilibrium (Pooni *et al.*, 1984; Wright, 1985) [21, 28]. This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The diallel analysis given by Jinks and Hayman (1953) [15] and Hayman (1954a) [10] was employed in to present study to find out the genetic constitution of the parents with respect to various traits in the sesame.

### Material and Methods

The experimental material consisted of seven parents (excluding check GT04) and their 21 half-diallel crosses.

The half diallel crosses were made during summer, 2019 and a set of 28 genotypes comprising of seven parents one check G.TIL 4 and 21 F1 hybrids were sown in Randomized Block Design (RBD) with three replications, during kharif, 2019 at 'Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar, Gujarat. The agronomical practices and plant protection measures were adopted as per recommendation for raising a good crop. The observations were noted both as optical assessment (days to flowering and days to maturity) and on randomly selected five competitive individual plants (plant height, the number of primary branches per plant, the number of capsules per plant, capsule length, the number of seeds per capsule, 1000 seed weight, seed yield per plant, harvest index and oil content). The replication wise mean values of each entry for the 11 traits were analyzed using Randomized Block Design (RBD) as suggested by Panse and Sukhatme (1985) [24]. Genetic components of variance were computed by employing diallel cross method suggested by Hayman (1954<sup>a</sup>) [10] for the traits where additive – dominance model fitted well. The graphical analysis was made according to Hayman (1954<sup>b</sup>) [11]. The replicated mean data were analyzed statistically using the software INDOSTAT version 8.1. The material used in this experiment was tested for the treaty with assumptions basic to Hayman diallel analysis viz., Sesame is normally selfpollinated. The parents in the study were homozygous and diverse in their origin, while the maternal effects were presumed to be absent in the studied material.

## Results and Discussion

The ANOVA from the mean data was carried out as per Randomized Block Design of the field experiment. The results (Table 1) revealed highly significant differences due to the genotypes for all the traits. Further, partitioning of mean sum of square due to genotypes implied that the differences among the parents were significant for plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, capsule length (cm), 1000 seed weight (g), seed yield per plant (g) and harvest index (%). Significant differences among parents showed greater diversity in the parental lines (Table 1). The component D measures the additive effects of genes; it was significant for all the traits except days to maturity, number of primary branches per plant, capsule length (cm) and 1000 seed weight (g) (Table 2). This suggests that these characters can be easily fixed in early generation. These results are in harmony with those reported by Sedeck and Shafie (2013) [23], Aldaji *et al.* (2014) [2], Vekaria *et al.* (2015) [27], El-Kadar *et al.* (2017) [6] and Ibrahim *et al.* (2021) [12] for seed yield per plant and one or more component traits whereas Tripathy *et al.* (2016b) [26] and Aldaji *et al.* (2015) [1] observed similar result for oil content. The estimates of  $H_1$  and  $H_2$  were significant for all the traits except days to maturity, number of primary branches per plant, capsule length (cm) and 1000 seed weight (g) (Table 2). The significant  $H_1$  component denotes non-additive (dominance or epistatic) genetic effects, which plays a major role in the inheritance of these traits. This finding is in agreement with the results reported by Sedeck and Shafie (2013) [23], Aldaji *et al.* (2014) [2], Vekaria *et al.* (2015) [27], Tripathy *et al.* (2016a) [25], El-Kadar *et al.* (2017) [6] and Ibrahim *et al.* (2021) [12] for seed yield per plant and one or more attributes in sesame. Significant values of additive (D) and non-additive components ( $H_1$  and  $H_2$ ) clearly assert the predominance role of both fixable and non-fixable

components. Further, the magnitude of non-additive ( $H_1$ ) component was higher than additive (D) component for all the traits except days to maturity and oil content (%) showing more important role of over dominance for these traits. Similar interpretation can be also drawn from the mean degree of dominance ( $>1$ ) for all the traits except days to maturity demonstrating over dominance for most of the traits (Table 2). Similar results were reported by Sedeck and Shafie (2013) [23], Aldaji *et al.* (2014) [2], Vekaria *et al.* (2015) [27], El-Kadar *et al.* (2017) [6] and Ibrahim *et al.* (2021) [12] for seed yield per plant and its contributing traits in sesame. However, as the degree of dominance could be biased due to linkage, epistasis or both the over-dominance observed may not be considered as index of true over-dominance (Comstock and Robinson, 1952). The equal distribution of positive and negative alleles in the parents aids the breeder in choosing precise desirable traits without losing any desirable traits. The value of  $H_1$  was greater than  $H_2$  for all the traits (Table 2) indicating that the frequency of gene distribution in the parental lines was unequal and this was also proved by the ratio of  $H_2/4H_1$  ( $< 0.25$ ) which confirmed the unbalanced distribution of gene at the loci in the parents implying dominance for all the traits. The results are in accordance with Sedeck and Shafie (2013) [23], Vekaria *et al.* (2015) [27] and Ibrahim *et al.* (2021) [12]. Mather and Jinks (1971) [19], while discussing the short comings of numerical component analysis suggested that  $(H_1/D)0.5$  at each locus is true for major degree of dominance only, where the distribution of dominance and recessive genes is symmetrical. Asymmetrical distribution of genes may influence over estimation of mean degree of dominance. The values of estimates of F component was significant for all the traits except plant height (cm), no. of primary branches per plant, capsule length (cm) and 1000 seed weight (g) indicating the presence of an excess of dominant alleles than recessive alleles. The present findings are in accordance with those of Sedeck and Shafie (2013) [23], Vekaria *et al.* (2015) [27], El-Kadar *et al.* (2017) [6] and Ibrahim *et al.* (2021) [12] for seed yield per plant and one or more components in sesame. The information of number of gene/group of gene responsible for particular trait is vital for the genetic progress through selection. When the distribution of genes is correlated the ratio could be underestimated when the dominance effects of all the genes concerned are not equal in size and distribution (Jinks 1956) [14] or when complementary gene interaction occur (Liang *et al.* 1968; Marlatt *et al.* 1996) [17, 18]. Environment component (E) was significant for number of capsules per plant, number of seeds per capsule, harvest index (%) and plant height (cm) (Table 2). This signifies the considerable role of environmental factor in the expression of these traits. Estimated narrow sense heritability was low for seed yield per plant and most of the other traits except days to flowering, days to maturity, no. of primary branches per plant, number of capsules per plant and seed yield per plant (g) which registered moderate heritability. Moderate to low levels of heritability indicated that all the traits were controlled by additive and non-additive genes with preponderance by non-additive genes which helps in selection at late generation. The correlation between parental order of dominance ( $V_r + W_r$ ) and parental mean ( $Y_i$ ) was positive and significant for days to maturity, number of cluster per plant, plant height and capsule length explicating contribution of recessive alleles for increasing the mean values. Thus, recessive genes are accountable for early days to maturity, high number of cluster per plant, higher plant height and

longer capsule length. The regression of  $W_r$  on  $V_r$  was desirable and near to unity for most of the traits. In graphical analysis, the regression line intercepted  $W_r$  axis below the origin indicating over dominance for all the traits except plant height (Fig. 1, 2 and 3). Regression line intercepted at near origin of  $W_r$  axis for plant height showing the presence of dominance gene action. The results are in agreement with

Ibrahim *et al.* (2021) [12] for capsule length, primary branches and oil content. The wide scattering of parental array points along the regression line in the  $W_r$ - $V_r$  graph for number of capsules per plant, seed yield per plant, number of primary branches, oil content and test weight suggests considerable genetic diversity among the parents for these traits.

**Table 1:** Analysis of variance (mean sum of square) for experimental design of 11 traits in sesame

Sources of variation	d. f.	Days to flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	Capsule length (cm)	1000 seed weight (g)	Seed yield per plant (g)	Harvest index (%)	Oil content (%)
Replications	2	32.42*	11.62*	55.2	1.00**	160.69**	37.99	0.01	0.01	8.94**	5.54	5.72
Genotypes	28	19.37**	11.56**	187.28**	0.35**	373.00**	93.84**	0.18**	0.52**	26.81**	35.79**	20.51**
Parents	6	28.93**	19.60**	105.46	0.09	217.27**	15.33	0.04	0.50**	7.40**	4.22	31.19**
Hybrids	20	17.99**	10.17**	225.27**	0.46**	451.10**	126.16**	0.21**	0.57**	34.7**	47.55**	18.75**
Parents Vs Hybrids	1	8.76	0.89	97	0.01	145.76*	11.61	0.47**	0.02	11.56*	3.59	0.01
Error	56	5.31	3.39	52.55	0.13	29.2	14.32	0.05	0.06	1.7	11.46	7.55

**Table 2:** Estimation of genetic components of variance and other parameters for 11 traits in sesame

	Parameters	Days to flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	Capsule length (cm)	1000 seed weight (g)	Seed yield per plant (g)	Harvest index (%)	Oil content (%)
Additive effect	D	7.490**	5.268	17.230**	-0.025	60.540**	-0.076**	-0.003	0.150	1.824**	-2.417**	8.051**
Dominance effect	$H_1$	8.611**	3.106**	173.86**	0.217	289.630**	124.48**	0.216	0.760	29.008**	35.048**	20.90**
Proportion of dominance due to positive and negative effect of genes	$H_2$	7.080**	2.887**	163.86**	0.200	270.670**	122.78**	0.203	0.590	26.076**	31.811**	17.08**
Fr mean	F	0.991**	0.214**	-22.568	-0.137	-79.630**	-11.84**	-0.011	0.220	-4.329**	-9.020**	8.550**
Environment	E	2.154	1.265	18.129**	0.056	11.881**	5.188**	0.018	0.020	0.645	3.825**	2.345
Mean degree of dominance	$(H_1/D)0.5$	1.072	0.768	3.196	2.947	2.187	40.321	8.440	2.260	3.988	3.807	1.611
Proportion of positive to negative genes	$H_2/4H$	0.206	0.232	0.236	0.231	0.234	0.246	0.235	0.190	0.225	0.227	0.204
The proportion of dominant to recessive genes	KD/KR	1.132	1.055	0.656	0.036	0.538	-0.314	0.630	2.010	0.541	0.342	1.983
Number of groups of genes	$h^2/H_2$	0.082	-0.157	0.056	-0.133	0.079	-0.003	0.392	-0.010	0.071	-0.038	-0.067
Coefficient of correlation (r)	$r(P, W_r + V_r)$	0.705	0.694	0.441	0.726	0.936	0.712	0.355	0.290	0.878	0.541	0.878
Heritability in Narrow Sense	Heritability (ns)	0.506	0.570	0.296	0.376	0.510	0.163	0.137	0.220	0.388	0.295	0.201
Estimation of Most Dominant Parent		40.782	89.328	94.326	3.856	1.373	57.450	3.980	3.920	8.069	23.363	34.204
Estimation of Most Recessive Parent		51.789	99.476	108.303	3.863	8.478	59.950	3.100	3.950	8.946	23.552	74.590

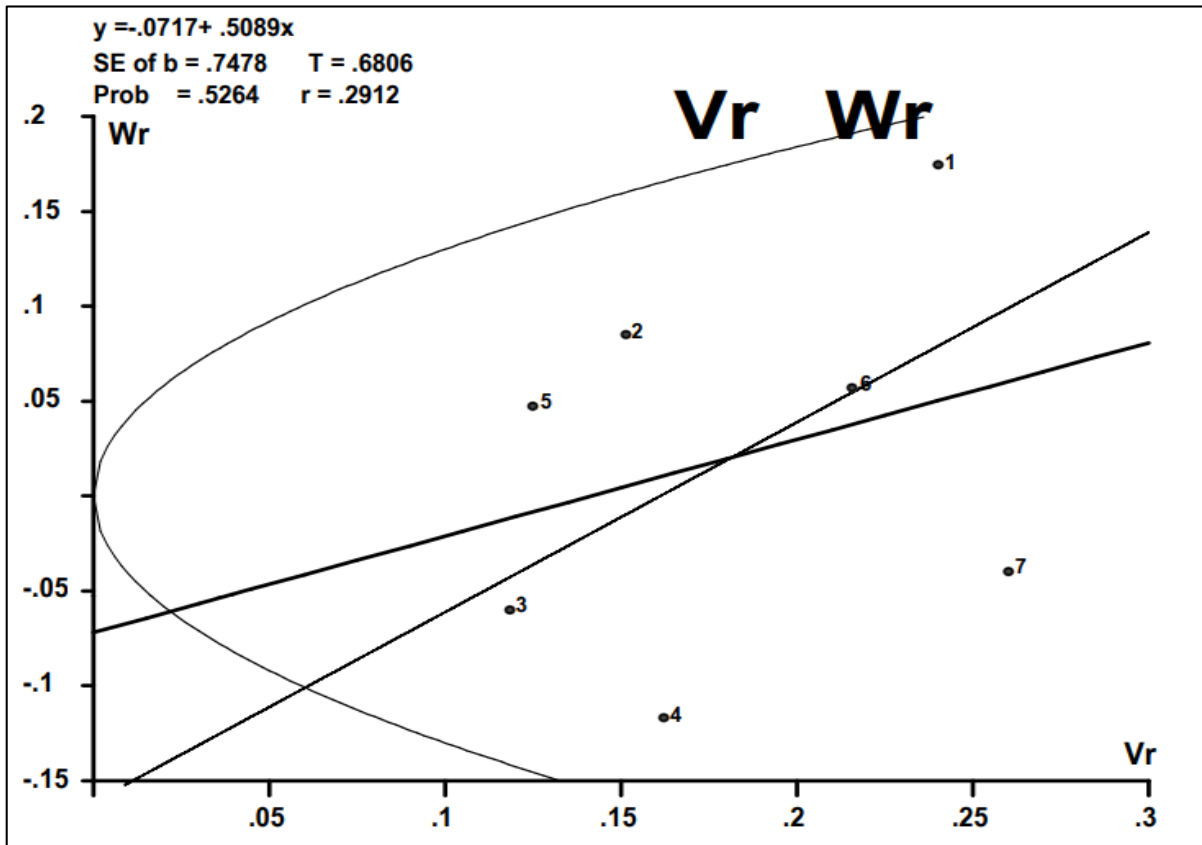


Fig 1: Vr, Wr graph for Seed yield per plant in sesame

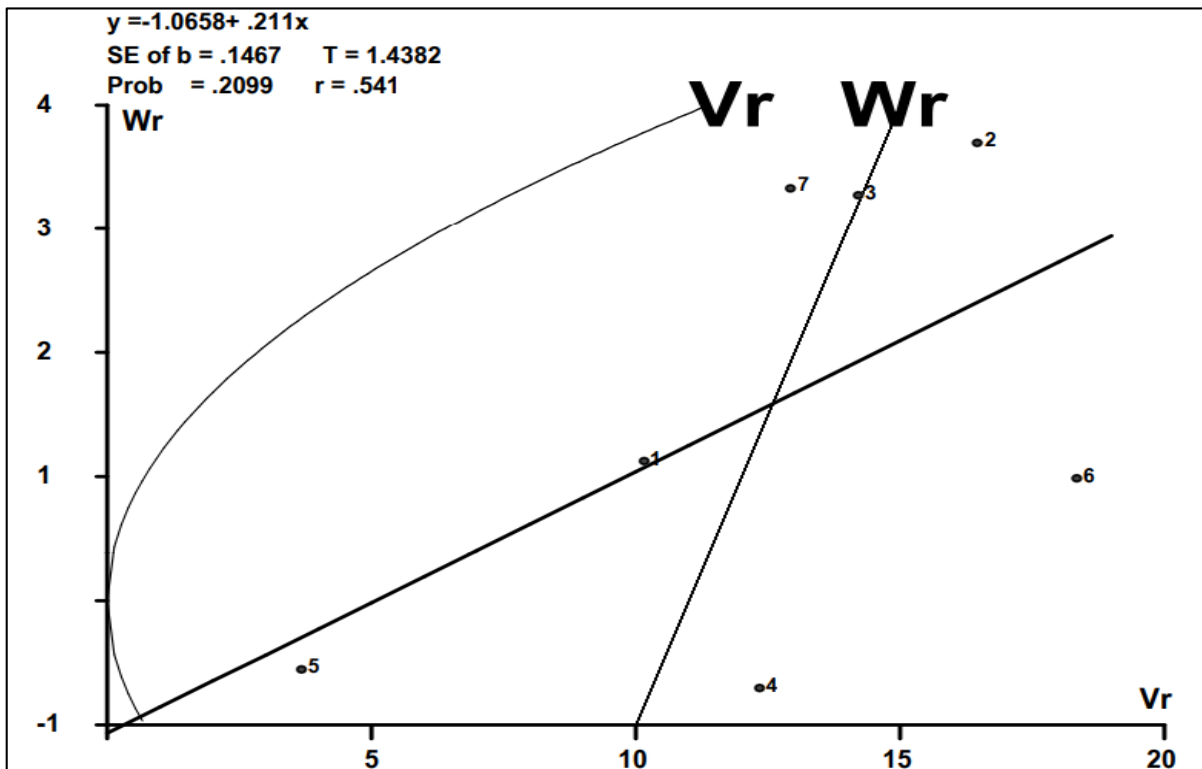


Fig 2: Vr, Wr graph for Oil content (%) in sesame

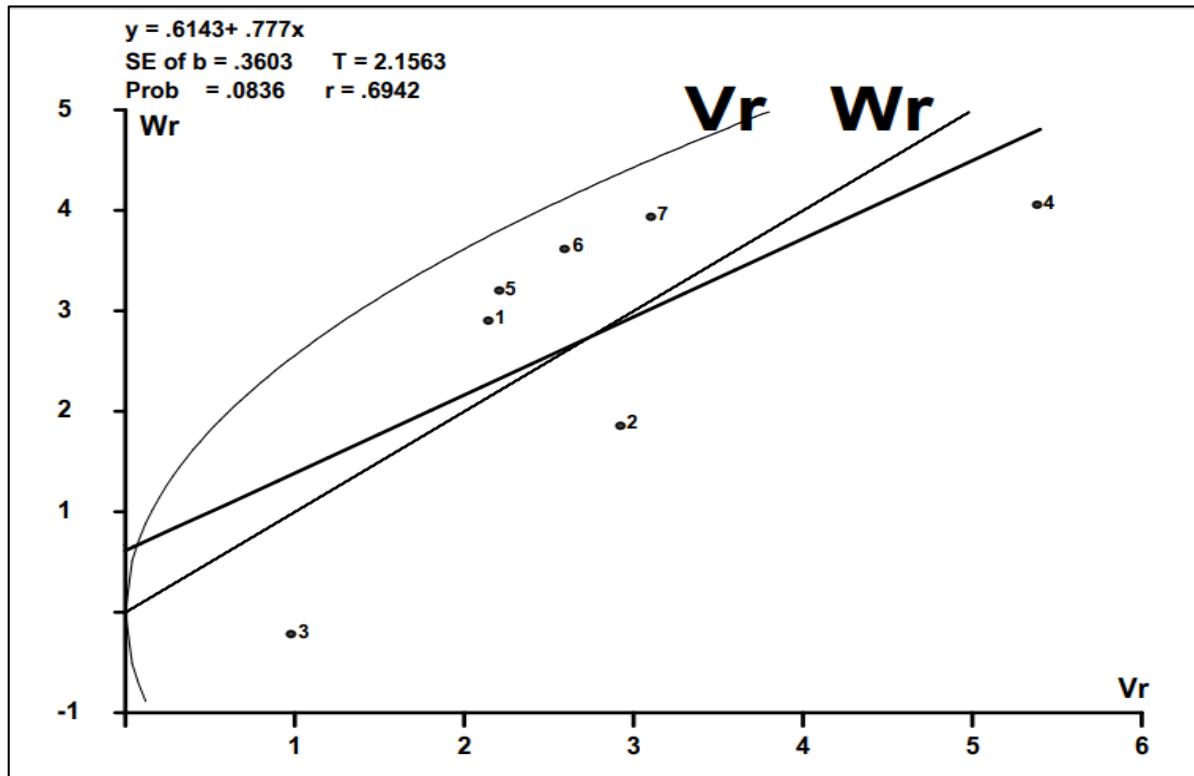


Fig 3: Vr, Wr graph for Plant height in sesame

#### Acknowledgment

We are thankful to Agronomy Instructional Farm, Sardarkrushinagar for providing resources and Directorate of research, S.D.A.U., along with C. P. College of agriculture for providing research facility and funding to conduct the trial.

#### Conclusion

In the latest research, graphical approaches were used. Seed yield and its components are expected to be governed by both non-additive and additive genetic components. As a result, selecting or modifying the trait in previous generations is difficult. Improved breeding methods, such as pedigree selection and single seed descent (SSD), may be considered for the recovery of high yielding segregants, in addition to genetic improvement for high seed yield, which could be better handled by identifying and monitoring quantitative trait loci (QTL) for increasing seed yield in succeeding segregation populations.

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