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Research Article

Hayman's diallel analysis for yield and attributing traits in sesame (*Sesamum indicum* L.)

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Abstract

Eight sesame (*Sesamum indicum* L.) genotypes were crossed in a half diallel mating fashion. The analysis of variance for combining ability revealed that the mean sum of squares are due to the general combining ability were highly significant for all the traits. The t^2 test specified the fulfillment of assumptions required under diallel analysis for all the traits studied except the number of effective branches per plant, capsule length (cm) and harvest index (%). The component D measures the additive effects of genes. It was significant for all the traits except seed yield per plant and harvest index. The components H_1 and H_2 were significant for all the traits except days to maturity revealing the importance of fixable and non-fixable component. 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 significant for days to flowering, days to maturity, capsule length, oil content and leaf area per plant. The graphical analysis showed the regression line intercepted Wr axis below the origin indicating over dominance for plant height, the number of seed per capsule, oil content and leaf area per plant. The regression line intercepted the positive side of Wr axis for days to maturity which implies the presence of partial dominance.

Keywords

Sesame, Hayman's diallel analysis, fixable and non-fixable components

INTRODUCTION

Sesame (*Sesamum indicum* L.; 2n = 2x = 26) globally known as 'sesame' and in India as 'Til' belongs to an order Lamiales and family Pedaliaceae. It is one of the oldest and the most important traditional oilseed crops of the world. The genus *Sesamum* comprises most of wild species believed to be originated in Africa while the cultivated type *i.e., S. indicum* originated in India (Bedigian, 2010 and Zohary *et al.,* 2012). Recent archeological remnants suggest that the cultivated sesame evolved from wild species in the Indian subcontinent during Harappan civilization and spread west to Mesopotamia before 2000 B.C (Fuller, 2003). Some report claims sesame was first cultivated in Africa and later spread to India at a very early time (Alegbejo *et al.,* 2003; Purseglove, 1969). According to Tunde-Akintunde *et al.* (2012), sesame was grown as a main oil crop in Indus valley civilization and then spread to Mesopotamia around 2500 B.C. Sesame is an important source of high quality oil and protein (IPGRI and NBPGR, 2004). Due to excellent qualities of the seed, oil and meal, sesame is called as the "Queen of oilseeds". 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).

During breeding of high yielding varieties of crop plants, breeders are continually challenged with the problem of parent selection. Though elimination of poor crosses on the basis of their performance in initial generation has been suggested; but information on the genetic architecture of yield and its components will help to sort out the improved crosses more competently. Several reports in the past indicate that the diallel analysis is the hastiest method of understanding the genetic nature of quantitatively inherited traits and to ascertain the prepotency of parents. Kearsey (1965) noted that Hayman and Jink's diallel analysis (1953) deliver more evidence than other methods, but has more necessary assumptions. The studies anticipated by Griffing (1956) do not afford any test to detect epistasis or linkage. Hayman and Jink'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 Wr-Vr evaluation found in Hayman (1954b) model, may be used to ascertain the presence of epistasis and/or linkage disequilibrium (Pooni *et al.*, 1984; Wright, 1985). This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The validity of the hypothesis of additive-dominance model was tested by confirming unit slope of regressions of Wr and Vr and by non-significant value of t^2 as prescribed by Hayman (1954b). The diallel analysis given by Jinks and Hayman (1953) and Hayman (1954a) was employed to find out the genetic constitution of the parents with respect to various traits in the sesame.

MATERIAL AND METHODS

The experimental material comprised of eight parents (including check G.TIL 4) and their 28 half-diallel crosses. The half diallel crosses were made during *Kharif* **-** 2017 at Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar by manual crossing. The seeds of parental lines were maintained through selfing. A set of 36 genotypes comprising of eight parents (including check G.TIL 4) and their 28 F_1 hybrids were sown in Randomized Block Design (RBD) with three replications, during *Kharif* **-** 2018. Each entry was sown in 3.0 m length in two rows with 45 × 15 cm spacing. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. The observations were recorded both as visual assessment (days to flowering and days to maturity) and measurement on randomly selected five competitive individual plants (plant height, the number of effective 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 12 traits were analyzed using Randomized Block Design (RBD) as suggested by Panse and Sukhatme (1985). Genetic components of variance were computed by employing diallel cross method suggested by Hayman (1954a) for the traits where additive – dominance model fitted well. Adequacy of the additive dominance model was tested with the help of ' t^2 ' test as proposed by Hayman (1954a). The graphical analysis was made according to Hayman (1954b). The replicated mean data were analyzed statistically using the software WINDOSTAT version 8.1. The material used in this experiment was tested for the treaty with assumptions basic to Hayman diallel analysis. Sesame is normally self-pollinated. 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. For testing other assumptions, two general tests *i.e.,* t^2 test and regression of Wr on Vr were used.

RESULTS AND DISCUSSION

The analysis of variance 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. This supports that the parents and their hybrids under study possessed sufficiently high amount of genetic variability. Further, partitioning of mean sum of square due to genotypes implied that the differences among the parents were significant for all the traits excluding harvest index. Significant differences among parents showed greater diversity in the parental lines.

Table 1. Analysis of v ariance (mean sum of square) for experimental design of 12 traits in sesame

Sources of variation	d.f.	Days to flowering	Days to maturity	Plant height	Number of effective branches per plant	Number of capsules per plant	Capsule length	Number of seeds per capsule	1000 seed weight	Seed yield per plant	Harvest index	Oil content
Replications	2	0.56	1.44	143.59	0.56	37.39	0.03*	2.06	0.00	5.90	9.41	0.05
Genotypes	35	14.28**	3.99**	246.26**	0.95**	223.06**	0.10**	165.19**	0.42**	17.59**	25.11**	32.43**
Parents	7	26.99**	11.23**	343.21**	1.31**	290.68**	0.23**	234.32**	0.48**	8.35*	3.02	63.09**
Hybrids	27	8.11**	2.18	221.54**	0.78**	211.20**	0.07**	147.38**	0.39**	20.38**	31.15**	24.62**
Parents *Vs* Hybrids	1	92.02**	2.15	234.93*	2.97**	70.03	0.13**	162.00**	0.68**	7.08	16.74*	28.45**
Error	**70**	**1.74**	**1.59**	**57.24**	**0.25**	**53.13**	**0.01**	0.80	0.00	3.06	3.69	0.26

*** P ≤ 0.05, ** P ≤ 0.01**

The results of t^2 test specified the fulfillment of assumptions required under diallel analysis for all the traits under study except the number of effective branches per plant, capsule length and harvest index (**Table 2**). The non fulfillment of assumption in these traits shows the unjustifiability of the hypothesis of simple additive-dominance model of gene action and involvement of epistasis and/or linkage disequilibrium. Non-significant t^2 value in sesame diallel analysis has been reported by Vekaria *et al.* (2015) for days to flowering, days to maturity, plant height, the number of capsules per plant, seed yield per plant and oil content. The non-significant t^2 values have also been reported by Fahmy *et al.* (2015) for days to flowering, days to maturity, plant height, the number of capsules per plant, 1000 seed weight, seed yield per plant and oil content. El-Kadar *et al.* (2017) observed non-significant t^2 values for days to flowering, the number of capsules per plant, 1000 seed weight and seed yield per plant.

The component D measures the additive effects of genes; it was significant for all the traits except seed yield per plant and harvest index (**Table 2**). This implies that these traits can be easily fixed in early generation. These results are in harmony with those reported by Mothilal and Manoharan (2005), Lavanya *et al.* (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Aldaji *et al.* (2014), Vekaria *et al.* (2015), El-Kadar *et al.* (2017) for seed yield per plant and one or more component traits, and Tripathy *et al.* (2016b), Aldaji *et al.* (2015) for oil content and Tripathy *et al.* (2016b) for seed yield per plant in sesame.

The estimates H_1 and H_2 were significant for all the traits except days to maturity in which only H_1 component confirmed significant effects **(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 Mothilal and Manoharan (2005), Lavanya *et al.* (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Aldaji *et al.* (2014), Vekaria *et al.* (2015), Tripathy *et al.* (2016a), El-Kadar *et al.* (2017) 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 showing more important role of over dominance for these traits. This was also evident 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 Mothilal and Manoharan (2005), El-Bramawy and Shaban (2007), El-Kadar *et al.* (2017), Aldaji *et al.* (2014), Sedeck and Shafie (2013), Vekaria *et al.* (2015) for seed yield per plant and its contributing traits in sesame. However, the over-dominance observed may not be considered as index of true over-dominance as the degree of dominance could be biased due to linkage, epistasis or both (Comstock and Robinson, 1952).

Table 2. Estimation of genetic components of variance and other parameters for 12 traits in sesame

Parameters	Days to flowering	Days to maturity	Plant height (cm)	Number of effective branches per plant	Number of capsules per plant	Capsule length (cm)	Number of seeds per capsule	1000 seed weight	Seed yield per plant	Harvest index	Oil content
b (Wr, Vr)	0.78	0.89	0.51	0.13	0.25	1.4	0.5	0.22	-0.13	-0.11	0.83
t_{b-0}	-5.91**	-2.59*	-1.51	-1.09	-1.30	-5.73**	-1.11	-0.45	0.61	2.15	-3.10*
t_{1-b}	1.68	0.35	1.43	7.41**	3.85**	-1.64	1.13	1.60	5.508**	21.76**	0.65
t^2	1.2	0.47	0.003	14.67**	3.34	7.33**	0.24	0.25	3.23	90.85**	0.05
D	8.43**	3.22**	94.53**	0.35**	79.32*	0.07**	77.82*	0.16*	1.74	-0.28	20.95**
H_1	9.91**	2.27**	181.83*	0.69*	268.45**	0.10**	256.96**	0.53**	23.35**	34.41*	53.62**
H_2	7.06**	1.11	144.45*	0.55*	184.77*	0.07**	200.92**	0.35*	19.87*	28.06*	34.84**
F	6.82*	3.22**	54.82	0.22	116.42	0.08**	118.23	0.21	2.57	1.20	35.78*
h^2	14.84**	0.12	29.85	0.45*	3.81	0.02*	26.45	0.11	0.70	2.16	4.63
E	0.57	0.53*	19.88*	0.09*	17.56	0.03	0.28	0.00	1.05	1.28	0.08
$(H_1/D)^{0.5}$	1.08	0.84	1.39	1.40	1.84	1.19	1.82	1.82	3.67	11.19	1.60
$H_2/4H_1$	0.18	0.12	0.20	0.20	0.17	0.17	0.20	0.17	0.21	0.20	0.16
KD/KR	2.19	3.96	1.53	1.58	2.33	2.77	2.43	2.13	1.51	1.49	3.29
h^2/H_2	2.10	0.11	0.21	0.81	0.02	0.28	0.13	0.32	0.04	0.08	0.13
r (P,Wr +Vr)	0.92**	0.73	0.52	0.41	0.47	0.92	0.41	0.18	-0.24	-0.66	0.78*
Heritability	0.49	0.42	0.40	0.37	0.27	0.37	0.13	0.41	0.18	0.23	0.18

*** $P \leq 0.05$, ** $P \leq 0.01$**

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 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 (**Table 2**). The results are in accordance with Mothilal and Manoharan (2005), Sedeck and Shafie (2013), Vekaria *et al.* (2015). Mather and Jinks (1971) 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 days to flowering, days to maturity, capsule length, oil content and leaf area per plant, while for rest of the traits it was positive indicating the presence of an excess of

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dominant alleles than recessive alleles. This was also confirmed by greater than one value of KD/KR components for all the traits suggesting higher frequency of dominant genes than recessive genes in the parents. The present findings are in accordance with those of Mothilal and Manoharan (2005), Lavanya *et al.* (2006), El-Bramawy and Shaban (2007), Sedeck and Shafie (2013), Vekaria *et al.* (2015), El-Kadar *et al.* (2017) 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. The value h^2/H_2 indicated that at least one group of gene operated for seed yield per plant and most of other traits in the present study. These result are analogous with the results reported by Mothilal and Manoharan (2005), El-Bramawy and Shaban (2007), Lavanya *et al.* (2006) and Vekaria *et al.* (2015).

The values of h^2/H_2 did not provide any valid interpretation for all the traits about the group of genes exhibiting dominance. The ratio could be underestimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes are correlated (Jinks 1956) or when complementary gene interaction occur (Liang *et al.* 1968; Marlatt *et al.* 1996). Environment component (E) was significant for days to maturity, plant height and the number of effective branches per plant (Table 2). This signifies the considerable role

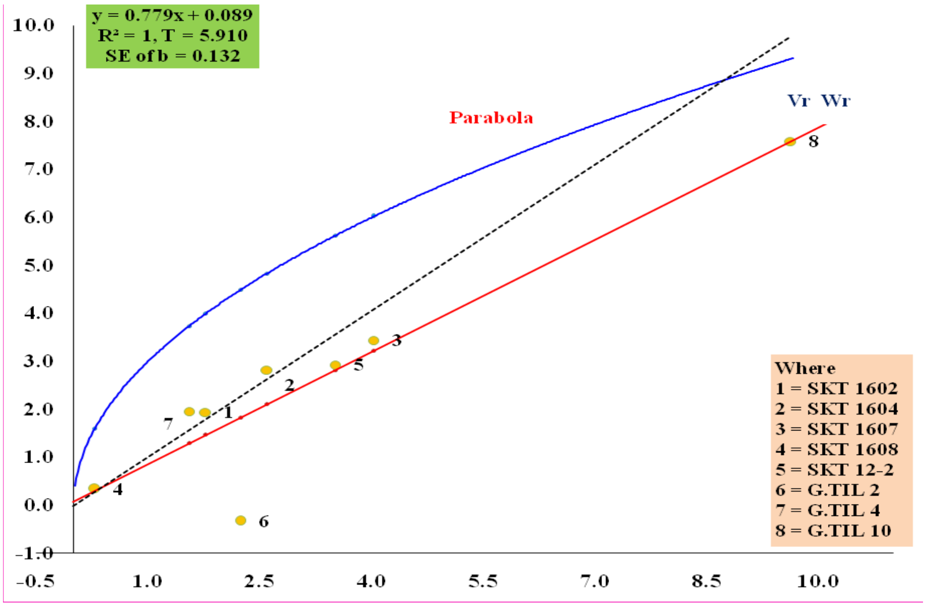

Fig. 1 Vr, Wr graph for days to flowering in sesame

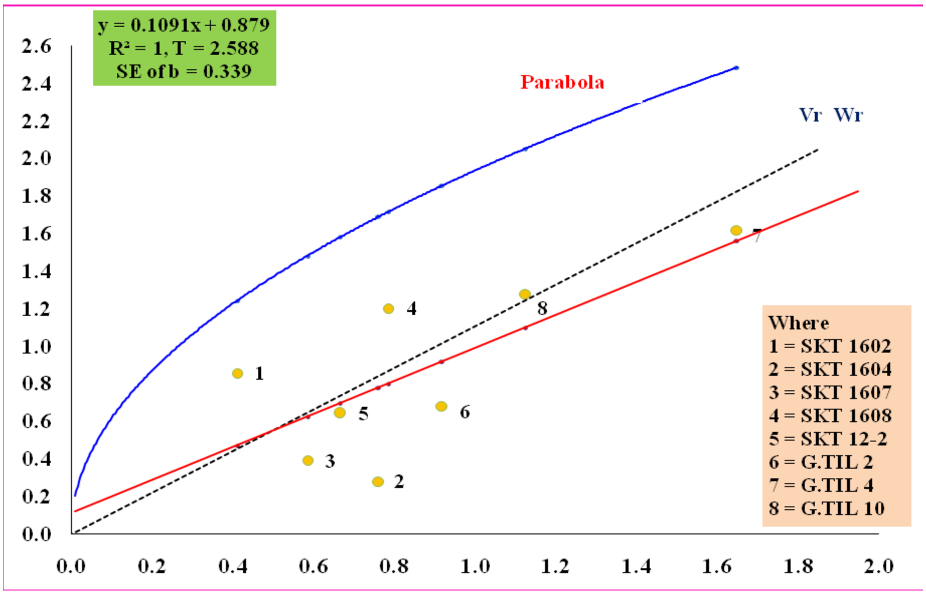

Fig. 2 Vr, Wr graph for days to maturity in sesame

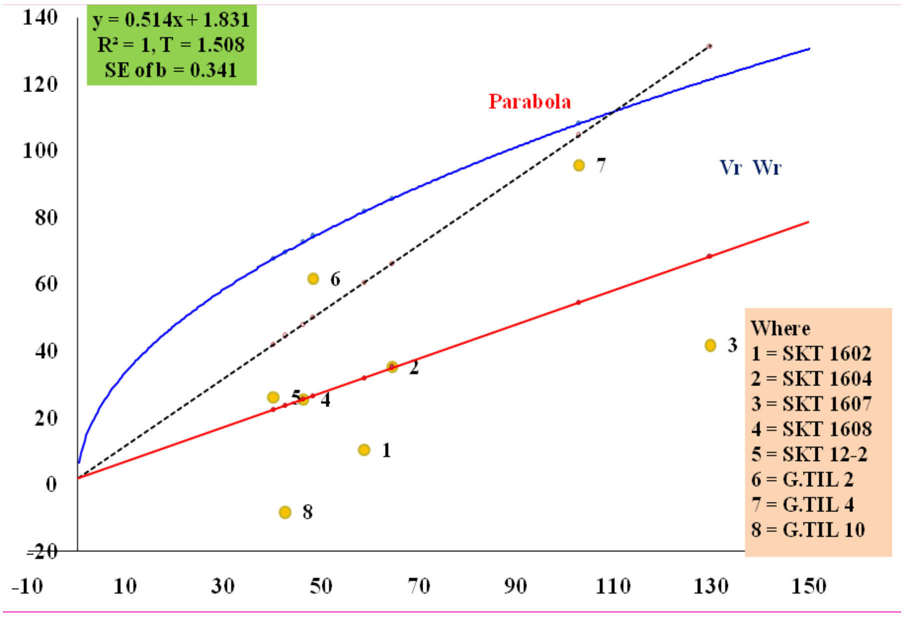

Fig. 3. Vr, Wr graph for plant height in sesame

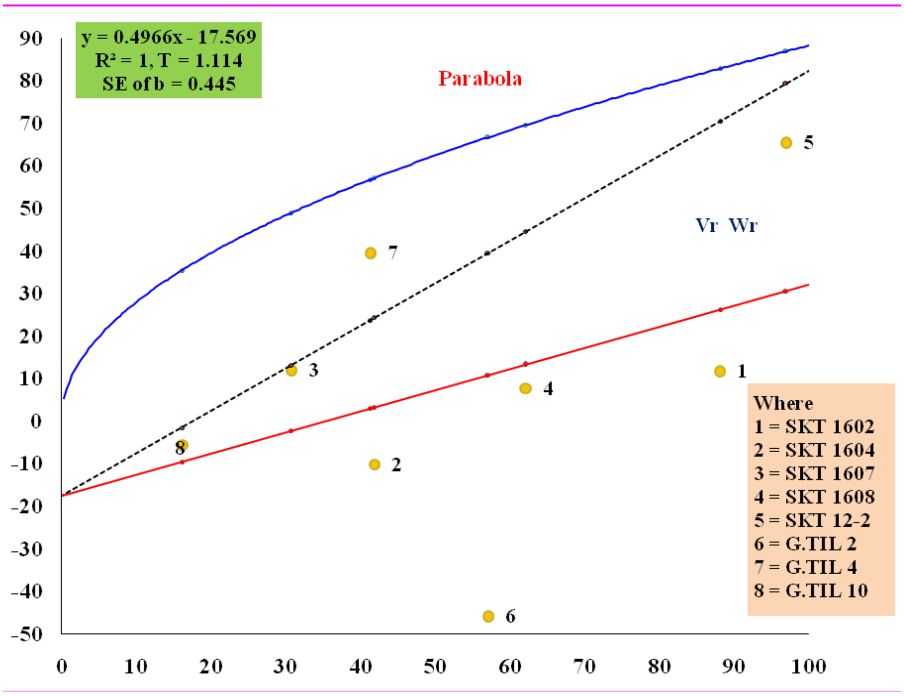

Fig. 4. Vr, Wr graph for number of seeds per capsule in sesame

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 and plant height 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. This shows that selection would be rewardable at late generation. The correlation between parental order of dominance (Vr + Wr) and parental mean (Y_i) was positive and significant for days to flowering and oil content, explicating contribution of recessive alleles for increasing the mean values (**Fig 1.**). Thus, recessive genes are accountable for early flowering and increasing oil content. El-Bramawy and Shaban (2007) also reported recessive genes for oil content. In case of seed yield per plant the negative correlation indicates role of dominant genes for increasing mean values.

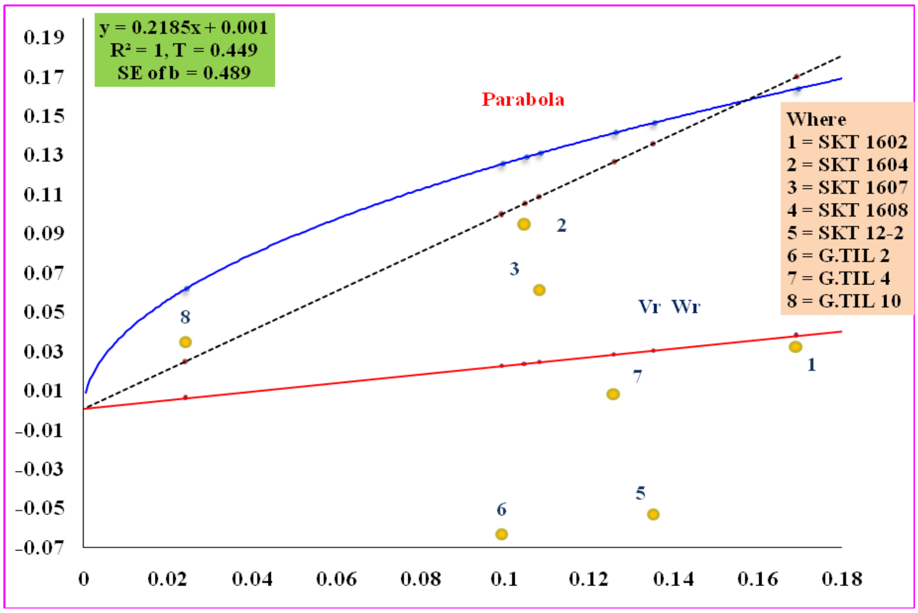

Fig. 5. Vr, Wr graph for 1000 seed weight in sesame

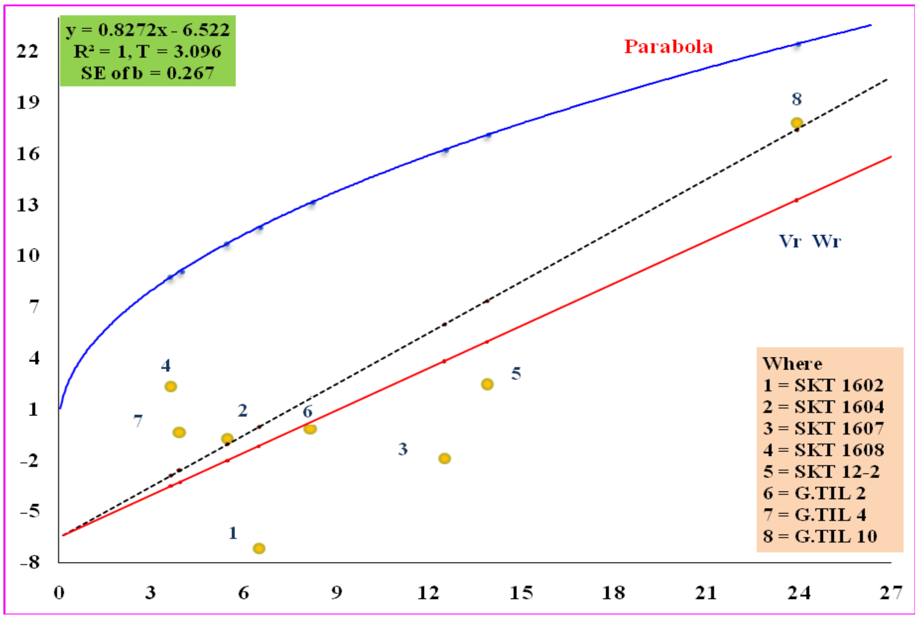

Fig. 6. Vr, Wr graph for Oil content in sesame

The regression of Wr on Vr was desirable and near unity for days to flowering, days to maturity, plant height, the number of seeds per capsule, 1000 seed weight, oil content and leaf area per plant. Hence, the graphical analysis was performed for these traits only. For the remaining traits including seed yield per plant, the Wr-Vr graph was much distorted and failed to give much information.

In graphical analysis, the regression line intercepted Wr axis below the origin indicating over dominance for plant height (**Fig 3**.), the number of seeds per capsule (**Fig 4**.) and oil content (**Fig 6.**). The regression line intercepted the positive side of Wr axis for days to maturity implying the presence of partial dominance (**Fig 2.**), while the regression line intercepted at near origin of Wr axis for 1000-seed weight showing the presence of dominance gene action (**Fig 5**.) The results are in agreement with El-Kadar *et al.* (2017) for plant height, days to maturity, 1000 seed weight and oil content. The wide scattering of parental array points along the regression line in the Wr-Vr graph for days to maturity, the number of seeds per capsule, 1000 seed weight and leaf area per plant suggests considerable genetic diversity among the parents for these traits. The parental line G.TIL 4 had maximum recessive genes for early maturity and dwarfness. Similarly, the parent G.TIL 10 had maximum recessive genes for early flowering and increased oil content, while it also possessed maximum dominant genes for the number of seed per capsule and 1000 seed weight.

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