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Diallel analysis for yield and contributing traits in Sesame (*Sesamum indicum* L.)

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Abstract
Genetic information is estimated for yield and its component traits using full diallel analysis of 8 x 8 diverse parents of sesame. The combining ability analysis revealed that the genotype mean sum of the square were highly significant for all the traits. The t^2 test was non-significant which validated the use of simple additive dominance model for the traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, length of capsule, 1000-seed weight and oil content. The D component was significant for all the traits excluding the traits *viz.*, days to 50 per cent flowering, days to maturity, number of capsules per plant and seed yield per plant. The estimated components of H_1 and H_2 were significant for all the traits except days to maturity, 1000-seed weight and oil content disclosed the importance of additive and non-additive components. The unbalanced distribution of genes at the parents loci confirmed by the greater value of H_1 than H_2 and the ratio of $H_2/4H_1$ (<0.25) indicating dominance for all the traits except days to maturity, 1000-seed weight and oil content. The component F was significant for plant height, number of branches per plant and length of capsule. The Vr-Wr graphical analysis revealed the regression line intercepted Wr axis below the origin displayed over dominance for days to 50 per cent flowering, days to maturity, plant height, number of capsules per plant, length of capsule, number of seeds per capsule, 1000-seed weight, seed yield per plant and oil content. The regression line passed above the origin of Wr axis for number of branches per plant which indicated the presence of partial dominance.

Keywords: Hayman's diallel analysis, additive, dominance components, sesame

Introduction
Sesame (*Sesamum indicum* L.) is one of the world's oldest oilseed crop grown across the globe. It is an important and ancient oil-yielding crop cultivated for its flavour some, edible protein-rich seed and high-quality oil (Bhat *et al.*, 1999) [1]. Sesame seed contains high oil content (46 to 50%) with 83 to 90% unsaturated fatty acids, 20-25% proteins and various minor nutrients such as vitamins and minerals, a large number of characteristic lignans (sesamin, sesamol and sesamolin) and tocopherols (Fukuda *et al.*, 1985) [5]. Therefore, sesame seeds with high amounts of nutritional components are consumed as a traditional health food for their specific antihypertensive effect, anti-carcinogenic, anti-inflammatory and anti-oxidative activity (Yakota *et al.*, 2007) [21].

Parental selection is a challenging job of plant breeder during breeding of high yielding varieties. Even though, plant breeders eliminates inferior cross combinations in early generations on the basis of their progeny performance, but information on the genetic architecture of yield and attributing traits will help to find out the improved crosses more competently. Many plant breeders suggested diallel analysis is one of the best method of understanding the genetic nature of biometric traits and to ascertain the prepotency of parents. Kearsey (1965) [11] noted that Hayman and Jink's diallel analysis (1953) [10] remit more affirmation than other mating design, but with more necessary assumptions. The studies forecasted by Griffing (1956) [7] unafford any test to detect epistasis or linkage. However, Hayman and Jink's analysis had furnished such test. Using Griffing's analysis to estimate variance components, it has been advocated the Wr-Vr evaluation found in Hayman (1954b) [9] model, may be used to find out the presence of epistasis and/or linkage disequilibrium (Pooni *et al.*, 1984; Wright, 1985) [16, 20]. This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The confirmation of the hypothesis of additive-dominance model was tested by unit slope of regressions of Wr and Vr and by non-significant value of t^2 as advised by Hayman (1954b) [9].

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The diallel analysis given by Jinks and Hayman (1953) [10] and Hayman (1954a) [8] was employed catch on the genetic constitution of the parents with respect to various traits in the sesame.

The present investigation was an attempt to estimate the genetic nature of quantitatively inherited traits and to ascertain prepotency of parents in Sesame.

Material and Method

The present experiment comprised of 56 F_1 crosses made by using 8 x 8 diallel mating design including reciprocals and their 8 parents along with three standard checks *viz.*, AKT-101, JLT-408 and GT-2. The cross combinations were attempted during *kharif* 2019 at Oilseed Research Station, Latur. A set of 67 genotypes were evaluated in Randomized Block Design (RBD) with two replications during summer 2020 at Parbhani. The experiment was sown in 3.0 m length in two rows with 45 cm row to row and 15 cm plant to plant spacing. The advocated packages of practices were endorsed for raising a good crop. The observations were recorded on quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, the number of capsules per plant, capsule length, the number of seeds per capsule, 1000 seed weight, seed yield per plant and oil content. The data were recorded replication wise based on mean values of each entry for the 10 traits and analyzed as suggested by Sukhatme and Panse (1985) [18]. Genetic components of variance were computed by employing diallel cross method as per Hayman (1954a) [8] for the traits where additive– dominance model fitted well. Acceptability of the additive dominance model was tested with the help of 't² test as given by Hayman (1954a) [8]. The graphical analysis was made according to Hayman (1954b) [9]. The material used in this experiment was tested for the treaty with assumptions basic to Hayman diallel analysis. The parents in the present experiment were genetically homozygous and diverse, 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.

Result and Discussion

The analysis of variance was highly significant due to the genotypes for all the characters indicated the genetic variability in the parents and hybrids. Moreover, partitioning of mean sum of square due to parents hinted that the differences among the parents were significant for plant height, number of branches per plant and number of capsules per plant, indicating greater diversity for these traits in the parental lines. The t^2 test specified the accomplished assumptions required under diallel analysis for all the traits under study excluding number of capsules per plant and seed yield (Table 2). The non-fulfillment of assumption in these traits showed the unjustifiability of the hypothesis of simple additive-dominance model of gene action and involvement of epistasis and/ or linkage disequilibrium. Vekariya *et al.* (2015) [19] disclosed non-significant t^2 value in sesame diallel analysis for days to flowering, days to maturity, plant height, number of capsules per plant, seed yield per plant and oil content. Similarly, the non-significant t^2 value have also been reported by Fahmy *et al.* (2015) [4] for days to flowering, days to maturity, plant height, number of capsules per plant, 1000-seed weight, seed yield per plant and oil content.

In the present investigation the component D was significant for plant height, number of branches per plant, length of capsule, 1000-seed weight and oil content (Table 2). This indicated that these traits can be easily fixed in early generation. These results are in accordance with the earlier findings of Mothilal and Manoharan (2005) [15], Lavanya *et al.* (2006) [12], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19], El-Kadar *et al.* (2017) [3] and Gami *et al.* (2020) [6]. The estimated components of H_1 and H_2 were significant for all the characters excluding days to maturity, 1000-seed weight and oil content (Table 2). The significant H_1 component disclosed non-additive (dominance or epistasis) gene effects, which plays a major role in the inheritance of these characters. Similar outcomes have been declared earlier by Mothilal and Manoharan (2005) [15], Lavanya *et al.* (2006) [12], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19], El-Kadar *et al.* (2017) [3] and Gami *et al.* (2020) [6] for seed yield per plant and one or more component traits in sesame.

Significant values of additive (D) and non-additive components (H_1 and H_2) exhibited predominance of fixable and non-fixable components. In this investigation the extent of non-additive (H_1) component was higher than additive (D) component for all the traits excluding 1000-seed weight and oil content indicating more important role of over dominance for these traits. Similar finding for seed yield per plant and one or more component traits in sesame are in agreement with the results reported earlier by Mothilal and Manoharan (2005) [15], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19], El-Kadar *et al.* (2017) [3] and Gami *et al.* (2020) [6]. However, as per the Comstock and Robinson, (1952) [2] the observed over-dominance may not be considered as index of true over-dominance could be biased due to linkage, epistasis or both.

The plant breeders are aided in choosing precise desirable traits by the equal distribution of positive and negative alleles in the parents. The value of H_1 was higher than H_2 for all the traits except number of seeds per capsule revealed the frequency of gene distribution in the parental lines was unequal and this was also confirmed by the ratio of $\hat{H}_2/4\hat{H}_1$ (< 0.25) which confirmed the unbalanced distribution of gene at the loci in the parental lines revealed dominance for all the traits except number of seeds per capsule (Table 2). Similar results were earlier reported by Mothilal and Manoharan (2005) [15], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19] and Gami *et al.* (2020) [6].

The estimated F component was significant for plant height, number of branches per plant and length of capsule, while for days to 50 per cent flowering and number of capsules per plant indicating the presence of an excess of dominant alleles than recessive alleles. The similar results are supported by the Mothilal and Manoharan (2005) [15], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19], El-Kadar *et al.* (2017) [3] and Gami *et al.* (2020) [6] for seed yield per plant and one or more component traits in sesame. The genetic information of number of gene/group of genes governing for particular trait is vital for the genetic progress through selection. The value of h^2/H_2 indicated that at least one group of gene operated for seed per plant and most of the other traits. These results are in agreement with the findings of Mothilal and Manoharan (2005) [15], Sedeck and Shafie (2013) [17], Vekariya *et al.* (2015) [19], El-Kadar *et al.* (2017) [3] and Gami *et al.* (2020) [6]. The values of h^2/H_2 did not furnish any valid interpretation for all the characters about the group of genes exhibiting dominance. The ratio could be underestimated when the dominance effect 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) [13, 14]. Environment component (E) was significant for all the traits except seed yield per plant, revealed the substantial role of environment in the expression of these traits. The narrow sense heritability was low for days to maturity, seed yield per plant and number of capsules per plant. However, the traits days to 50 per cent flowering, plant height, number of branches per plant, length of capsule, number of seeds per capsule, 1000-seed weight and oil content registered moderate heritability. Moderate to low levels of heritability indicated that all the traits were controlled by additive and non-additive genes with preponderance of non-additive genes. This reflects that selection would be rewarding in late generations.

Graphical analysis disclosed that the regression line intercepted Wr axis below the origin indicating over dominance for days to 50 per cent flowering (Fig 1), days to

maturity (Fig 2), number of branches per plant (Fig 4), number of capsules per plant (Fig 5), length of capsule (Fig 6), number of seeds per capsule (Fig 7), seed yield per plant (Fig 9) and oil content (Fig 10). The regression line cutting above the origin of Wr axis for plant height (Fig 3) reflecting the presence of partial dominance whereas the regression line cutting near the origin of Wr axis for 1000-seed weight (Fig 8) showing the complete dominance gene action. These results are in agreement with El-Kadar *et al.* (2017) [3] for days to maturity, 1000-seed weight and oil content. Substantial genetic variability was observed for days to 50 per cent flowering, days to maturity, number of capsules per plant, number of seeds per capsule, seed yield and oil content which was confirmed by the wide scattering of parental array points along the regression line in the Vr-Wr graph.

Table 1: Analyses of variance for experimental design in 8x8 diallel cross in Sesame.

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Number of capsules per plant	Length of capsule	Number of seeds per capsul	1000-seed weight	Seed yield per plant	Oil content
Replicates	1	43	3.73	0.29	0.05	0.21	0.004	0.92	0.07	0.13	0.74
Genotypes	63	64.27**	229.62**	287.7**	0.30 **	1368.39**	0.12 **	81.81***	0.25*	33.04***	35.99 **
Parents	7	4.77	14.77	783.56**	0.22 **	132.57 *	0.13	59.22	0.25	0.23	32.05
Hybrids	55	71.22**	258.16**	156.18**	0.31 **	1246.17 **	0.12 *	78.41**	0.25*	28.01**	37.156**
Parent Vs. Hybrids	1	98.68	163.78	4049.86**	0.18	16741.30 **	0.25	427.17**	0.04	538.92**	0.01
Error	63	31.72	73.74	80.03	0.06	48.44	0.06	34.82	0.15	1.70	17.74

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

Table 2: Estimation of genetic component of variance and other components for 10 characters in Sesame.

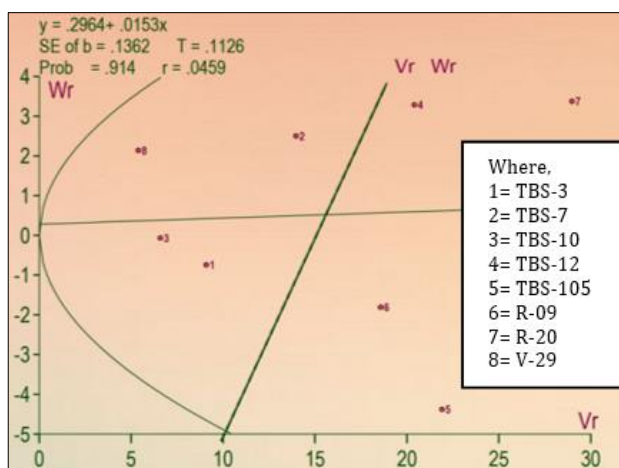| Parameters	Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Number of capsules per plant	Length of capsule	Number of seeds per capsule	1000-seed weight	Seed yield per plant	Oil content
b (Wr, Vr)	0.42	0.78	0.88	1.11	0.29	0.65	0.45	0.97	0.004	0.65
T^2	2.74	0.12	0	1.52	0.64	0.14	5.32*	0.03	105.73**	0.09
D	0.38	-0.38	352.38*	0.08*	42.44	0.03*	12.46	0.05*	-0.72	7.28*
H_1	3.18*	-6.82	606.6.28*	0.19*	1450.32*	0.08*	44.38*	-0.03	35.58*	-2.89
H_2	2.73*	-2.69	369.01*	0.09*	1231.56*	0.05*	45.13*	-0.01	30.00*	-1.72
F	0.79	-7.05	560.68*	0.15*	115.55	0.05*	-10.67	-0.06	-0.58	-7.70
E	2.00*	7.77*	39.39*	0.02*	3651.72*	0.04*	17.14*	0.07*	0.83	8.73*
h^2/H_2	4.07	-3.20	2.35	0.26	2.96	0.706	1.90	1.90	3.91	2.21
$\hat{H}_2/4\hat{H}_1$	0.21	0.09	0.15	0.12	0.21	0.17	0.25	0.08	0.21	0.14
Heritability	0.04	-0.01	0.92	0.47	0.09	0.20	0.12	0.14	-0.06	0.16

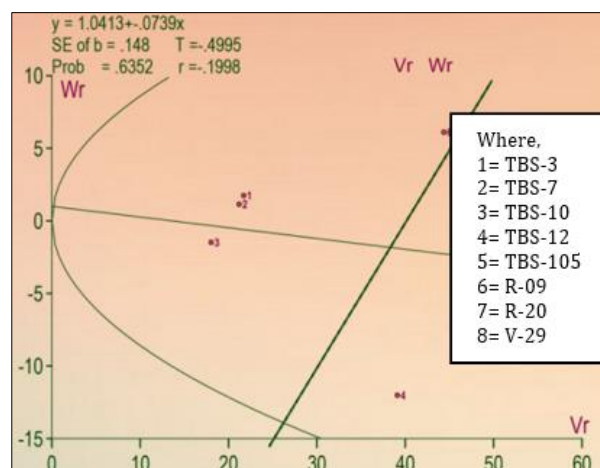**Fig 1:** Vr, Wr graph for days to 50% flowering

Fig 2: Vr, Wr graph for days to maturity
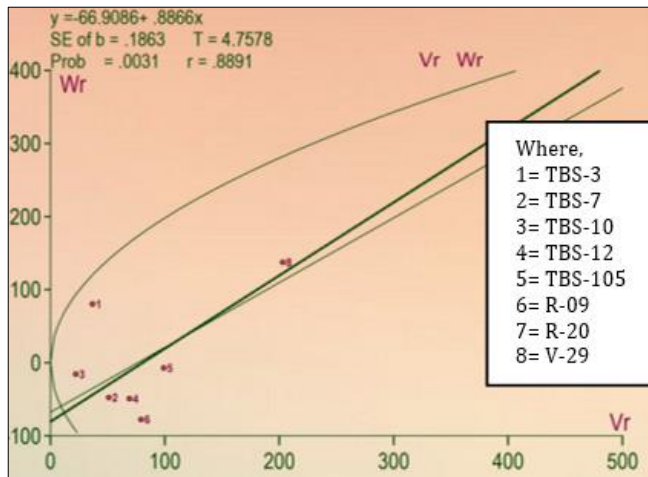
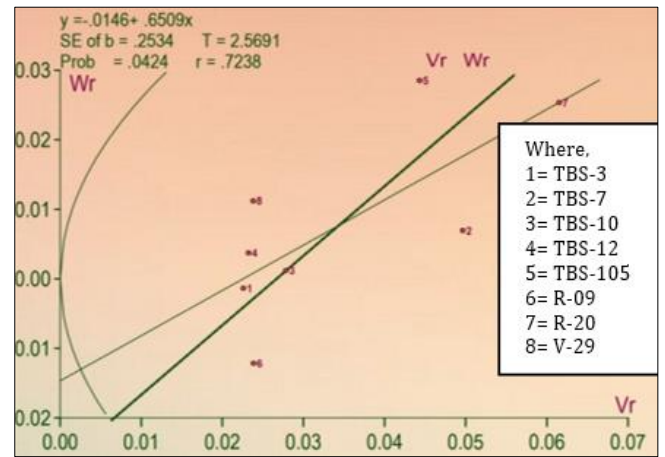**Fig 3:** Vr, Wr graph for plant height

Fig 6: Vr, Wr for length of capsule
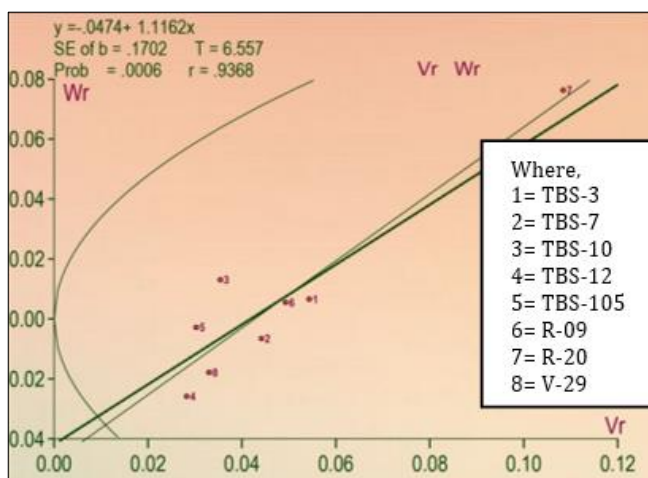

Fig 4: Vr, Wr graph for number of branches per plant
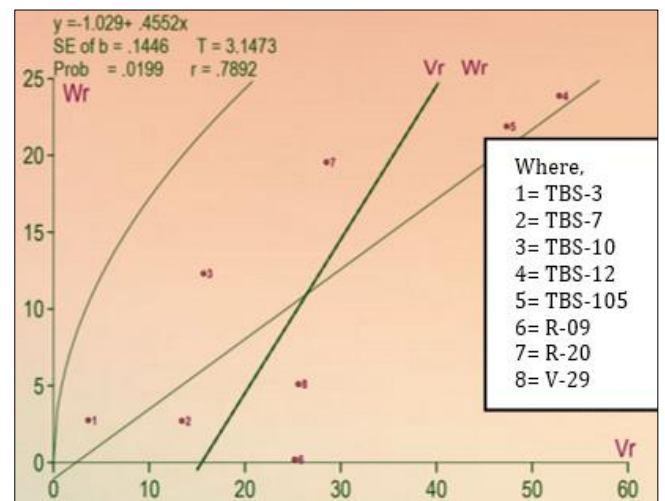

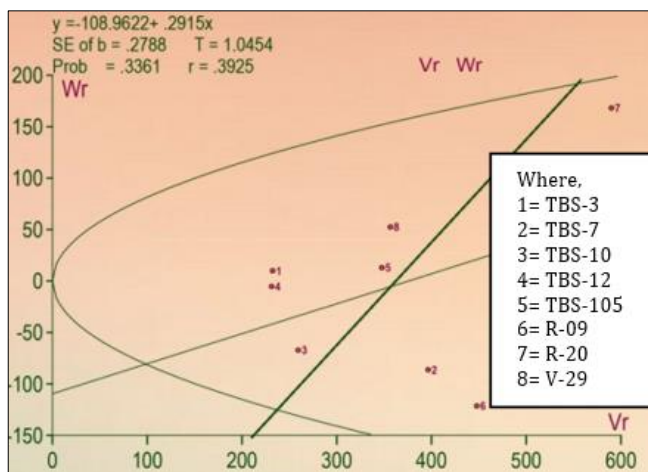**Fig 7:** Vr, Wr for number of seeds per capsule
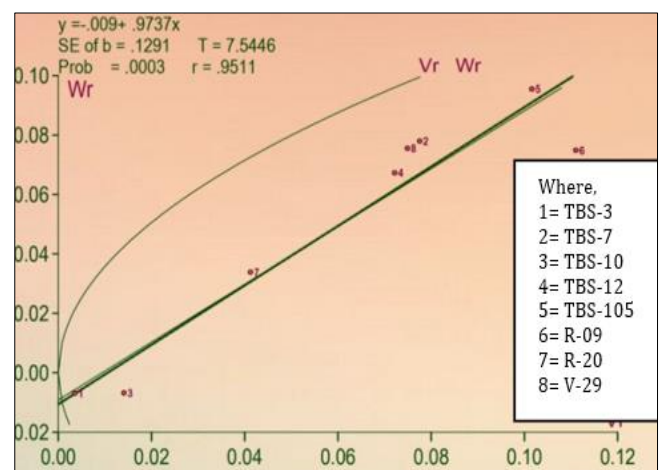

Fig 5: Vr, Wr for number of capsules per plant

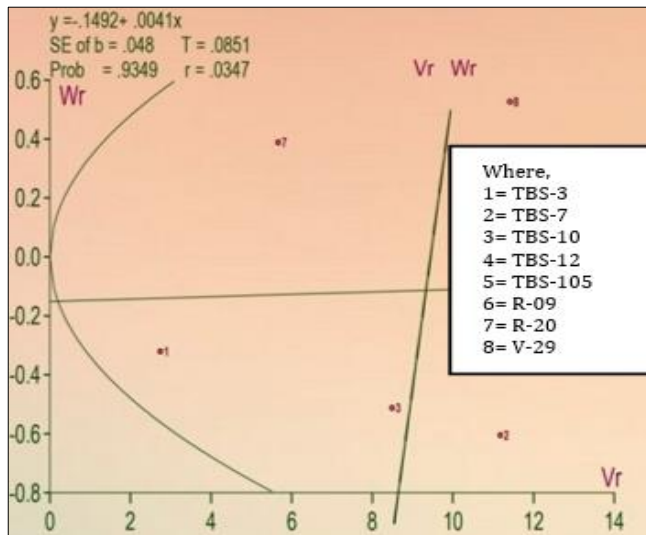**Fig 8:** Vr, Wr for 1000-seed weight
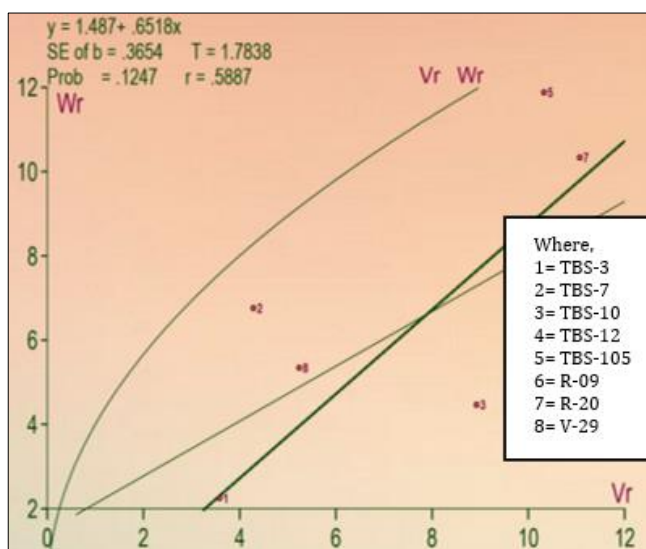
Fig 9: Vr, Wr for seed yield per plant

Fig 10: Vr, Wr for oil content

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