



# GRAPHICAL ANALYSIS FOR PHYSIOLOGICAL, GROWTH, BIOCHEMICAL AND YIELD CHARACTERS IN SESAME (*SESAMUM INDICUM* L.)

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## Abstract

A study was carried out in the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University with six sesame genotypes namely VRI 1, VRI 2, TMV 3, TMV 4, TMV 6 and CO 1 and thirty F1 crosses generated from them through 6 x 6 diallel mating design, it was found that a lot of diversity was present with respect to all the traits as depicted by scattered positions of parental arrays in the  $W_r$ - $V_r$  graphs. The regression line intersecting the  $W_r$  axis above the origin for days to first senescence, leaf area index, dry matter production, total chlorophyll content and seed yield per plant indicated partial dominance suggesting pedigree selection as an appropriate method to improve these characters. Position of the parental arrays on the graphs indicated the importance of both dominant and recessive alleles for different traits.

**Keywords:** Sesame, physiological, growth, biochemical, yield, diallel, graphical.

## Introduction

Sesame (*Sesamum indicum* L.) belonging to the family Pedaliaceae is one of the ancient indigenous oil seed crop and has been cultivated in India with the highest area, production and export in the world. The crop is grown primarily in the tropics by small landholders, of which 99.9 per cent is produced in developing countries (Ashri, 1994). Sesame is an important source of high quality edible oil. The seed contains 50-60 per cent oil, which has excellent stability due to the presence of natural antioxidants such as sesamol, sesamin and sesamol (Brar and Ahuja, 1979).

Moreover, similar to other crops, in sesame, the yield is a complex character and the lower productivity could be attributed to the interplay of different yield related, biochemical, growth and morphological characters. In the bygone decades, the sesame improvement was solely based on the selection of morphological characters and less importance was given to physiological characters. An insight into the genetics of morphological, growth, biochemical traits would be the best prospects for breeding for higher yield. However, little is known about the morphological, growth and biochemical characters that appear highly promising in improving performance of this crop.

Diallel analysis helps in understanding the genetic control of the trait, which guides the breeder to advance and select segregating populations. There are several approaches available for analysis of diallel crosses but the two main approaches being followed are Griffing's and Hayman's approaches. These two approaches are often used together for complementary data interpretation. Hayman (1954a), Jinks (1955 and 1956) and Whitehouse *et al.* (1958) demonstrated that an easier way of extracting information from a diallel cross was to plot the covariance ( $W_r$ ) of each array against its variance ( $V_r$ ). The slope and position of the

regression line fitted to the array points lying within limiting parabola ( $W_r^2 = V_p \cdot V_r$ ) indicated degree of dominance and presence or absence of gene interaction. The position of array points of regression line gave a measure of relative frequency of dominant or recessive alleles in an array. They further stated that yield per plant was controlled by over-dominance and that the interaction played a tremendous role in the expression of this character. Hayman (1954b) not only affirmed Jinks (1954) but also hypothesized six assumptions to be fulfilled for genetic analysis of diallel cross. The assumptions were (i) diploid segregation (ii) homozygous parents (iii) no reciprocal effects (iv) no epistasis (v) no multiple allelism and (vi) gene distribution independently between the parents. The statistics obtained from measurements of the progeny provided estimates of an overall degree of dominance of the parents and symmetry of gene distribution in the lines. The dominance relations were exhibited graphically. To test the validity of the assumption, relation between the variance ( $V_r$ ) and parent off-spring covariance ( $W_r$ ) of the same array and linear regression coefficient of  $W_r$  on  $V_r$  over arrays provides adequate means. The  $W_r$ ,  $V_r$  statistic provides an estimate of the relative number of dominance to recessive genes present in the common arrays of the parents, with the  $W_r$  and  $V_r$  statistics, calculated from diallel tables, graphs can be drawn and the geometric representation of these statistics can be interpreted. The position of the regression line in the graph indicates the degree of dominance and we can construct parabola limits in this graph. The interpretation of the results of this analysis is easy and straight forward if the main assumptions of the diallel analysis are fulfilled.

## Materials and Methods

The present investigation was carried out in the Plant Breeding Farm, Department of Genetics and Plant Breeding,

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Faculty of Agriculture, Annamalai University during 2015-2016. Six sesame genotypes namely VRI 1, VRI 2, TMV 3, TMV 4, TMV 6 and CO 1 were selected based on the commercial value and varying by pedigree and yield were obtained from Regional Research Station, Vridhachalam. Six parents were crossed in all possible combinations and the resulting thirty cross combinations inclusive of reciprocal crosses along with the parents form an effective complete diallel set for the study. Thirty hybrids along with six parents were sown in rows with a spacing of 30 x 30 cm. In each cross, 20 plants were maintained. A randomized block design with three replications was adopted. Border rows were grown all around the experimental block. Recommended fertilizer schedule, cultural operations and plant protection measures were carried out.

The observations were recorded on the physiological character like days to first senescence, growth characters like leaf area index, dry matter production and harvest index, biochemical characters like total chlorophyll content, soluble protein content and yield characters like number of capsules per plant, number of seeds per capsule, 1000 seed weight (g) and seed yield per plant (g). The data thus generated, was subjected to standard statistical procedures to generate the results. The variances and co-variances were estimated by following the graphic analysis as proposed by Jinks and Hayman (1953).

## Result

To assess the genetic relationships between parents, a Hayman graphical method was performed. In the diallel analysis, a Vr-Wr graph is drawn with the help of variances of array (Vr) and covariances between parents and their progeny (Wr). The graphical analysis is discussed as below.

A contemplation of the VrWr graph plotted for days to first senescence, the regression line cut the Wr axis above the origin which suggests partial dominance type of gene action. The distribution of array points along the regression line conceive that VRI 1 being nearer to the origin, contain maximum dominant genes, while VRI 2 and TMV 4 being further and had maximum recessive genes. The array points of VRI 2 and CO 1 were below the theoretical line in VrWr graph and which was above the regression line in WrWr graph suggesting complementary gene action. (Fig 1) (Table 1 & 2).

For leaf area index the parental array points were not much scattered under limiting parabola suggested narrow genetic base of parents. The expected regression line intercepted Wr axis above the origin indicating additive type of gene action with partial dominance controlling the inheritance pattern of the trait. (Fig 2.) (Table 1 & 2). The parents VRI 2, TMV 3 and TMV 6 were away from the origin possessing maximum recessive genes. The parents VRI 2 and TMV 6 were below the theoretical line in VrWr graph and were above the theoretical line in WrWr graph indicated complementary type of interaction for the above said. The

parent CO 1 which was below the theoretical line in VrWr graph was also below the line in WrWr graph indicated duplicate interaction.

The study VrWr graph for dry matter production revealed additive type of gene action with partial dominance controlling the inheritance pattern of the trait as the regression line passed positively through Wr above the origin. (Fig 3.) (Table 1 & 2). From the position of array points along the regression line, it was noted that VRI 1, TMV 4 and TMV 6 being nearer to the origin contain the maximum dominant genes. While VRI 2 being farther had maximum recessive genes. The slope of regression line (b) was 0.89. The array points of TMV 4 and TMV 6 was found to be located above the theoretical regression line of VrWr graph and below in WrWr graph suggested complementary type of interaction for this character

The relationship of VrWr and Fr values for harvest index, showed that the regression line cutting the Wr axis below the origin which revealed non-additive type of gene action with over dominance. From the position of array points on the regression line, it was observed that parents VRI 1, TMV 4, TMV 6 and CO 1 seemed to possess most of the dominant genes because of their nearest position to the origin, while the parent VRI 2 mostly had recessive genes being farthest from the origin. The array points of VRI 1, TMV 4 and TMV 6 were above the theoretical line of VrWr graph and WrWr graph indicated duplicate interaction for this character. In WrWr graph, the regression attained significance. (Fig 4.) (Table 1 & 2).

With reference to VrWr graph for total chlorophyll content indicated that the regression line intercepted the Wr axis above the origin and denoted additive type of gene action with partial dominance controlling the inheritance pattern of this character. (Fig 5.) (Table 1 & 2). From the position of array points on regression line it was found that VRI 1, TMV 4, TMV 6 and CO 1 possessed maximum dominant genes by virtue of their nearest position to the origin, while the parents VRI 2 and TMV 3 being away from the origin had the recessive genes. In WrWr regression failed to attain significance, the array points VRI 1 and CO 1 were below the regression line in both VrWr graph and WrWr graph indicated duplicate interaction for this character.

The analysis of VrWr graph for soluble protein content showed non-additive type of gene action with over dominance because the regressive line intercepted the Wr axis below the origin. From the position of array points on regression line it was observed that TMV 4 seemed to have maximum dominant genes being nearer to origin. The parents TMV 6 and CO 6 had equal frequencies of dominant and recessive genes by occupying the intermediate position while the parent TMV 3 being away from the origin assured the recessive genes for soluble protein content and these results were also confirmed by Wr + Vr and Yr graph. In WrWr regression failed to attain significance. The array points of TMV 3 and CO 1 were found below the theoretical

line in VrWr graph and WrWr graph indicated duplicate interaction for this character.(Fig 6.)(Table 1 & 2).

An examination of VrWr graph plotted for number of capsules per plants, showed that the regression line intercepted the Wr axis negative side below the origin, thus indicated the phenotypic manifestation of this parameter in  $F_1$  generation was conditioned by non-additive type of gene action with over dominance. (Fig 7.)(Table 1 & 2). The Fr values and position of array points on the regression line revealed that VRI 1, VRI 2, TMV 3, TMV 6 and CO 1 had an intermediate position render them as carrier of equal frequencies of dominant and recessive genes whereas TMV 4 located away from the origin and had the recessive genes and these results were also accentuated by the  $Wr + Vr, Yr$  graph. The array points of TMV 3, TMV 4 and CO 1 were below the theoretical line in both graphs. The array point of VRI 2 was below theoretical line in VrWr graph and it was above the line in WrWr graph. It suggested duplicate type of interaction for TMV 3, TMV 4 and CO 1 and complementary type of interaction for VRI 2.

The VrWr graph for number of seeds per capsule exhibited the regression line passing the Wr axis below the origin and indicated non additive type of gene action with over dominance. (Fig 8.)(Table 1 & 2). From Fr values and the position of array points on the regression line, it was obvious that the parents TMV 4 and CO 1 being nearest to the origin had the maximum dominant genes, while VRI 2 and TMV 6 proved as carrier of recessive genes due to their distance from the origin. The array points of VRI 1 and CO 1 which were above the theoretical line in VrWr graph was below the theoretical line in WrWr graph indicated complementary type of interaction.

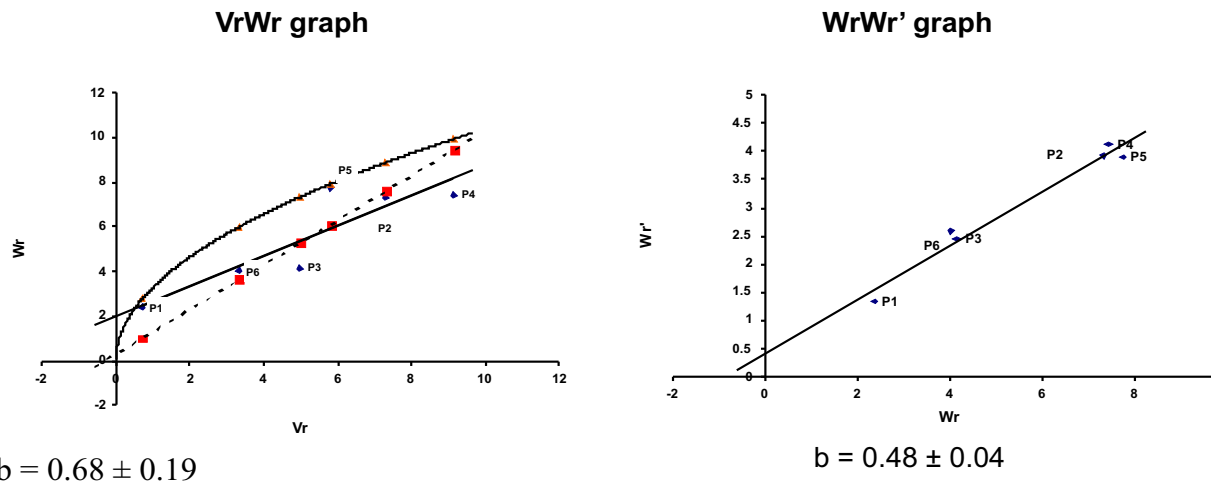
The VrWr graph for 1000 seed weight indicated non-additive type of gene action with over dominance as regression line passed through the Wr axis below the origin. Position of array points and Fr values disclosed that the parent CO 1 had maximum genes due to closeness to the origin. The parents VRI 2 and TMV 4 had equal frequencies of dominant and recessive gene due its intermediate position from the origin. While the parents VRI 1 had recessive genes due to their farthest position from the origin. The array points of VRI 2 and TMV 4 were above the

theoretical line of both VrWr graph and WrWr graph suggested duplicate type of interaction. In WrWr regression failed to attain significance. (Fig 9.)(Table 1 & 2). Similar trends also observed by Rai *et al.* (2005) and Shrimali *et al.* (2017) found over dominance for 1000 seed weight which were according with present findings.

It was evident from VrWr graph plotted for seed yield per plant, that additive type of gene action with partial dominance controlled inheritance of the trait as the regression line passed through the Wr axis above the origin. (Fig. 10) The array points position evidently showed that CO 1 was nearer to the origin thus possessed maximum dominant genes. Whereas VRI 2 and TMV 4 being away from the origin had recessive genes for the trait. The array points TMV 3 and TMV 4 were below the theoreticalline of both VrWr and WrWr graph indicated duplicate type of interaction. While the array point of VRI 2 which was below the theoretical line in VrWr graph was above the theoretical line in the WrWr graph indicated complementary type of interaction. These results are in accordance with the findings of Arifullah *et al.* (2013)(Table 1 & 2)

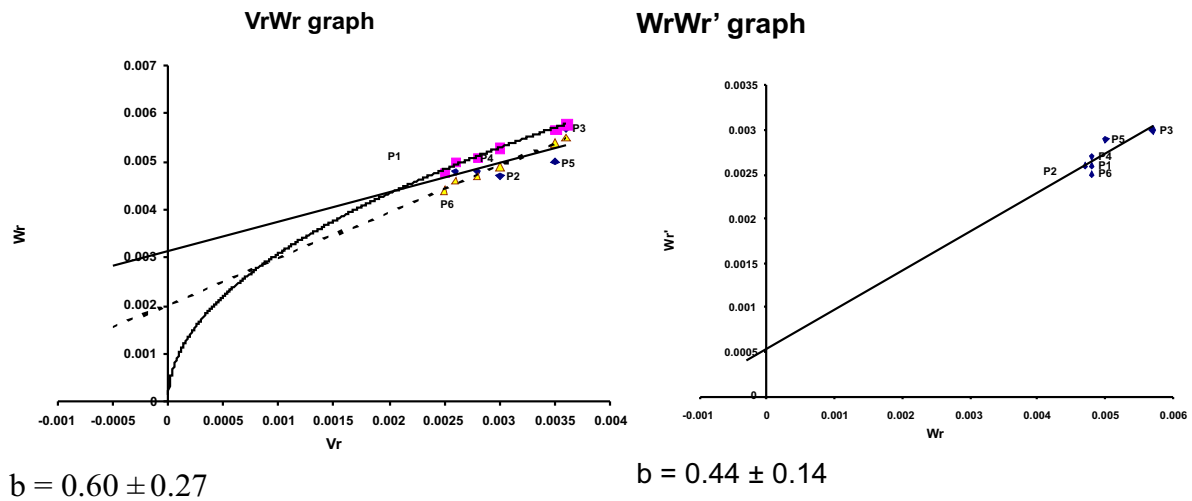
## Discussion

The role of additive gene action with partial dominance was observed for days to first senescence, leaf area index, dry matter production and seed yield per plant suggesting pedigree selection as an appropriate method to improve these characters. For all other characters dominant factor was predominant for the inheritance of these traits. The  $Wr/Vr$  graph suggest that due to more prominent role of non-additive effects and presence of over-dominance, selection could be delayed up to late segregating generations for all the traits except for days to first senescence, leaf area index, dry matter production, total chlorophyll content and seed yield per plant. Information on the maximum and minimum collection of dominant and recessive genes for a particular characteristic in distinct genotypes could be of considerable value for future use as donor parents. Thus, the current investigations make a significant contribution to determine the genetic control mechanism of different physiological, growth, biochemical and yield characteristics to accelerate the high yielding sesame selection and breeding program.



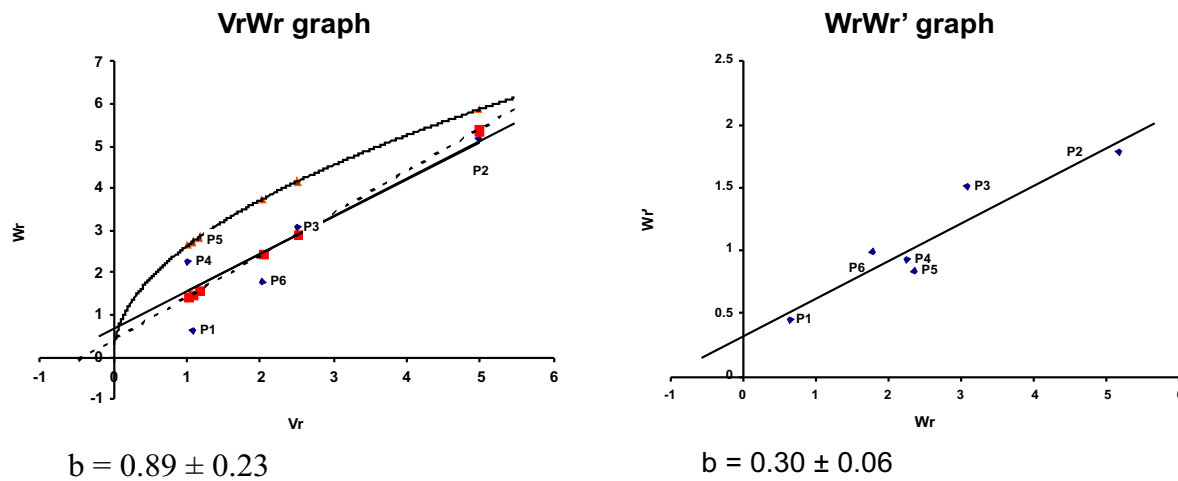
P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig 1. Graphical analysis for days to first senescence**



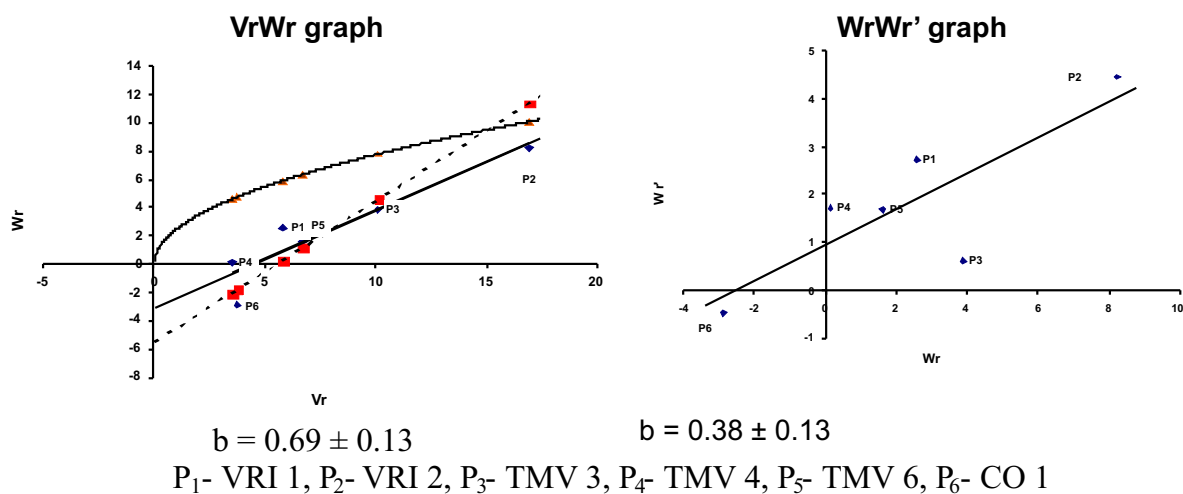
P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig. 2. Graphical analysis for leaf area index**

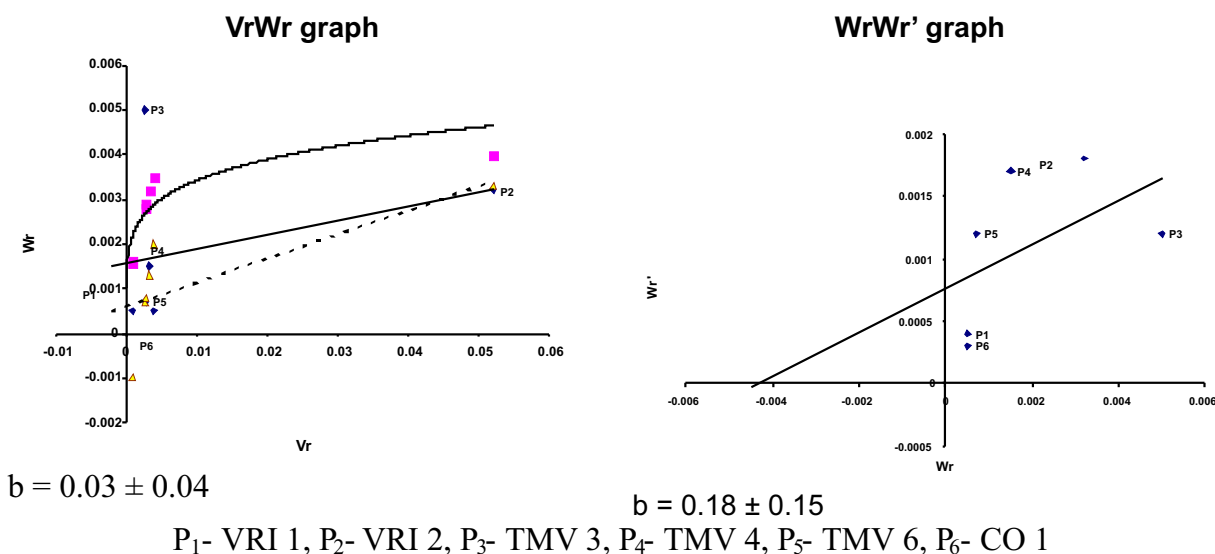


P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

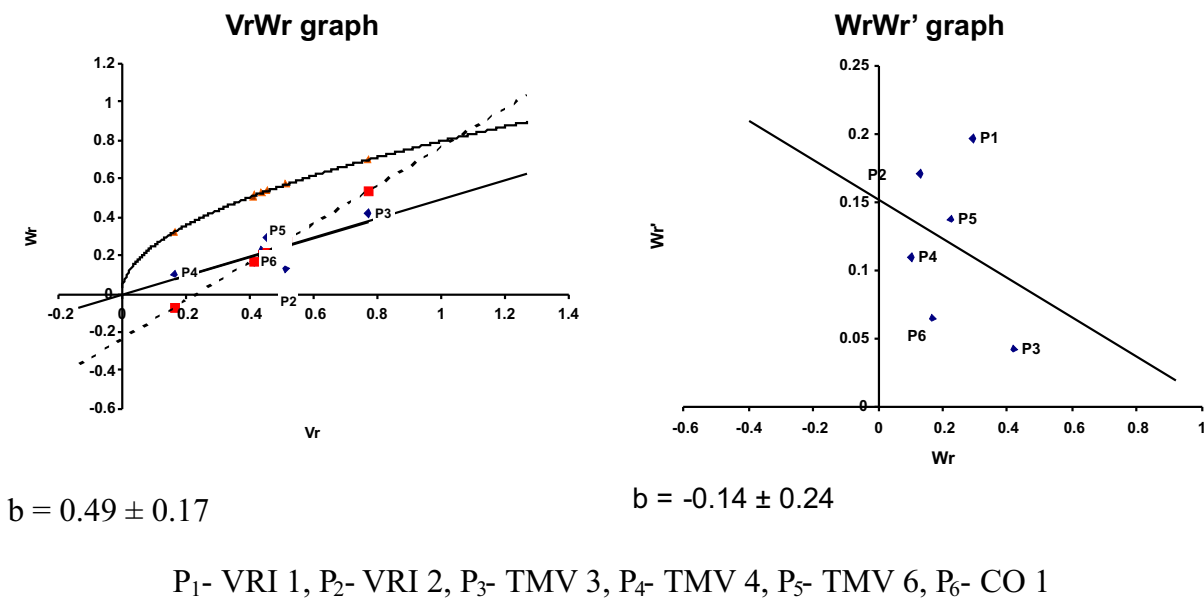
**Fig. 3. Graphical analysis for dry matter production**



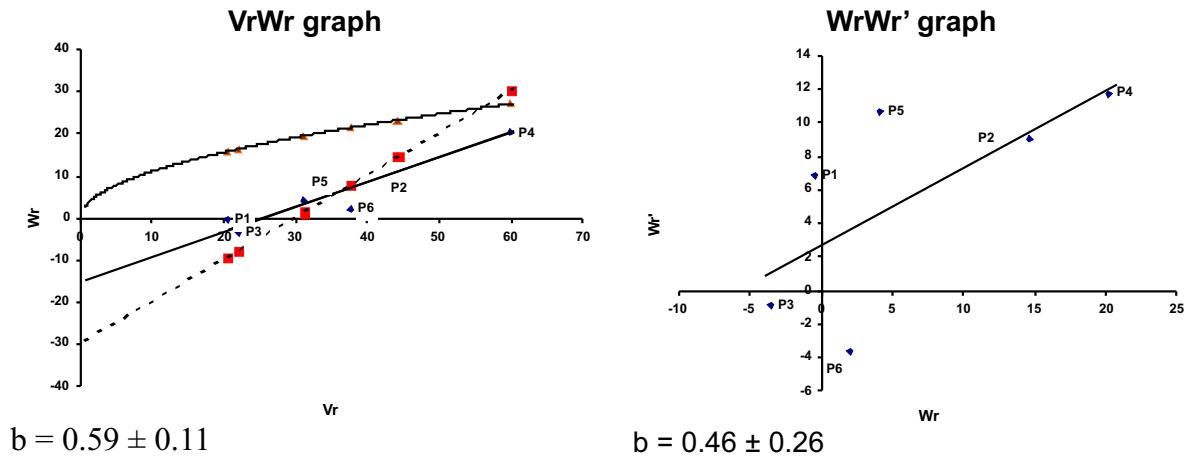
**Fig. 4. Graphical analysis for harvest index**



**Fig. 5. Graphical analysis for total chlorophyll content**

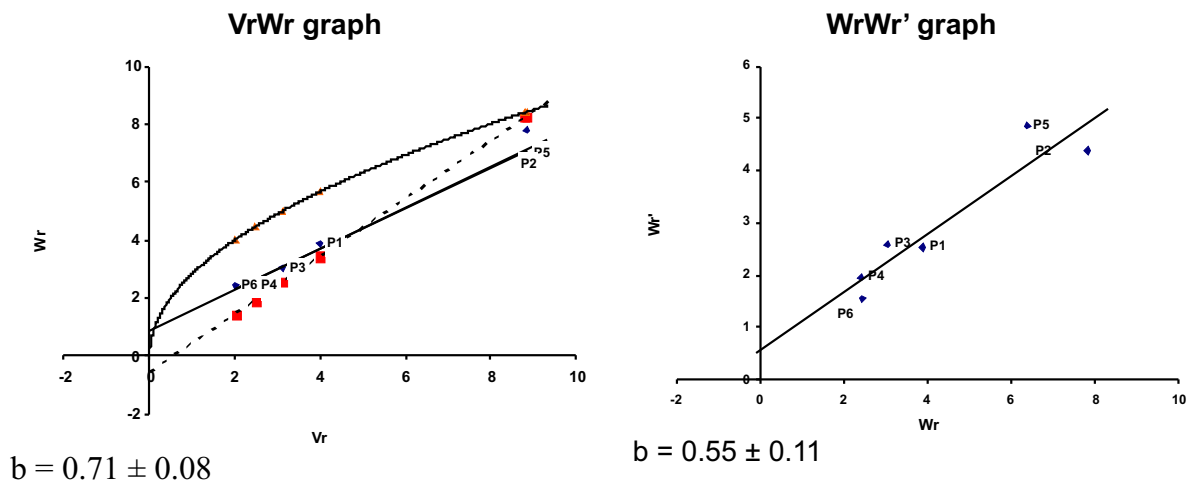


**Fig. 6. Graphical analysis for soluble protein content**



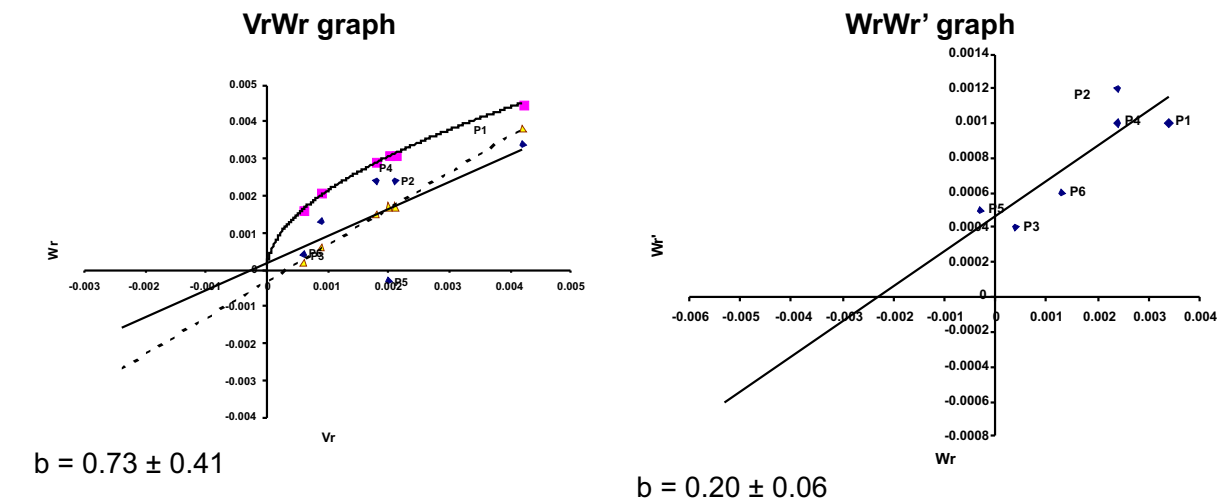
P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig. 7. Graphical analysis for number of capsules per plant**



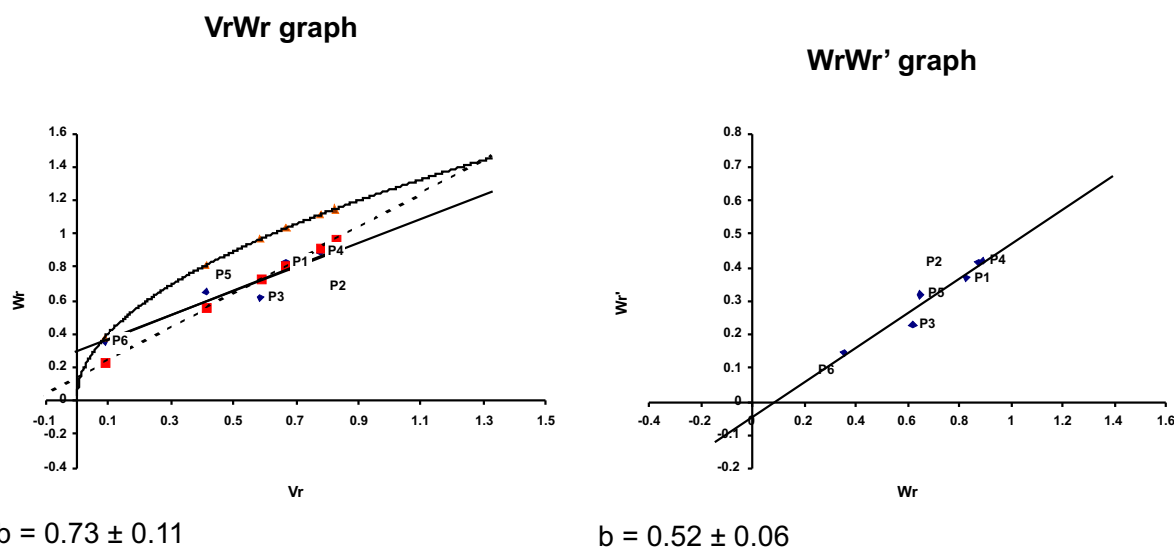
P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig. 8. Graphical analysis for number of seeds per capsule**



P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig. 9. Graphical analysis for 1000 seed weight**



P<sub>1</sub>- VRI 1, P<sub>2</sub>- VRI 2, P<sub>3</sub>- TMV 3, P<sub>4</sub>- TMV 4, P<sub>5</sub>- TMV 6, P<sub>6</sub>- CO 1

**Fig. 10. Graphical analysis for seed yield per plant**

**Table 1: Estimates of 'Y' intercept (a) and slope (b) of best fitting regression line for physiological, growth, biochemical and yield characters**

S. No.	Characters	VrWr		WrWr'	
		A	b	a	B
1.	Days to first senescence (days)	1.969	0.680±0.178	0.405	0.480±0.043
2.	Leaf area index	0.003	0.623±0.268	0.0008	0.389±0.144
3.	Dry matter production (g.plant <sup>-1</sup> )	0.648	0.891±0.227	0.322	0.298±0.062
4.	Harvest index	-3.091	0.687±0.132	0.932	0.377±0.135
5.	Total chlorophyll content (mg.g <sup>-1</sup> )	-0.0005	0.553±0.255	0.0006	0.439±0.153
6.	Soluble protein content (mg.g <sup>-1</sup> )	-0.003	0.492±0.174	0.152	-0.145±0.244
7.	Number of capsules per plant	-14.921	0.588±0.105	2.774	0.461±0.263
8.	Number of seeds per capsule	0.885	0.706±7.529	0.584	0.554±0.115
9.	1000 seed weight (g)	0.0002	0.719±0.407	0.0005	0.188±0.062
10.	Seed yield per plant (g)	0.294	0.728±0.106	-0.048	0.518±0.063

**Table 2: Significant of deviation of 'b' for Vr/Vr and Wr/Wr for physiological, growth, biochemical and yield characters**

S. No.	Characters	VrVr		Wr Wr $\phi$	
		b-0/SE	1-b/SE	b-0/SE	1-b/SE
1.	Days to first senescence (days)	3.820**	1.798	12.000**	13.000**
2.	Leaf area index	2.325*	1.407	2.779*	4.364**
3.	Dry matter production (g.plant <sup>1</sup> )	3.925**	0.480	4.967**	11.700**
4.	Harvest index	5.205**	2.371*	2.900*	4.792**
5.	Total chlorophyll content (mg.g <sup>-1</sup> )	2.169*	1.753	2.927*	3.740*
6.	Soluble protein content (mg.g <sup>-1</sup> )	2.828*	2.920*	-0.604	4.771**
7.	Number of capsules per plant	5.600**	3.924**	1.773	2.073
8.	Number of seeds per capsule	0.094	0.039	5.036**	4.055**
9.	1000 seed weight (g)	1.767	0.690	3.133*	13.533**
10.	Seed yield per plant (g)	6.868**	2.566*	8.633**	8.033**

\* - Significant at 5% level

\*\* - Significant at 1% level

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