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Genetic Analysis of Yield and Its Components in F_1 Generation of Brown Mustard (*Brassica juncea* L. Czern and Coss)

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Abstract: A 6x6 diallel cross experiment on F_1 generation of Brown mustard [*Brassica juncea* (L.) Czern and Coss] was conducted to explore the inheritance pattern of various yield and its components. The data obtained from the experiment were subjected to analysis of variance. The analysis of variance indicated highly significant differences among parents and their hybrids in F_1 generation for all the characters studied in this experiment except seed yield plant^{-1}, which was found to be significant. The genetic analysis revealed that the characters, plant height, number of primary branches, siliqua main^{-1} inflorescence and seed yield plant^{-1} have shown the additive type of gene action. While the inheritance of number of secondary branches was found to be operated by an over dominant type of gene action. So far as the regression analysis is concerned the non-significant deviation of the regression line from unit slope indicated the absence of non-allelic interaction, which was presented in all the characters.

Key words: *Brassica juncea,* genetic analysis, yield and its components, analysis of variance

INTRODUCTION

Over the past couple of decades *Brassica* oilseeds production has increased to become one of the most important world sources of vegetable oil. Oilseed *Brassica* crops annually occupy about 22 Million hectares of the world 's agricultural land and provide over 30 Million tons of the world's oilseed production which is the third most commonly traded vegetable oilseed in the world after soybean and cotton (F.A.O., 1996). Edible oil is an important part of a balance human diet. Rapeseed, (primarily *Brassica napus, Brassica campestris* and *Brassica juncea*) is grown world wide as a source of edible oil. (Downey and Rakow, 1987). These annual crops can be successfully grown in the different types of soils (French, 1977).

Young tender leaves of mustard greens are used in salads or mixed with other salad greens. Older leaves with stems may be eaten fresh, canned or frozen, for potherbs and to a limited extent in salads. Although widely and extensively grown as a vegetable, it is being grown more for its seeds, which yield an essential oil and condiment. Mustard oil is one of the major edible oils in India, the fixed oil content of rai varying between 28.6% and 45.7%. Oil is also used for hair oil, lubricants and, in Russia, as a substitute for olive oil. Seed residue is used as cattle feed and in fertilizers (Reed, 1976).

In Pakistan rapeseed and mustard are the second most important source of vegetable oil after cottonseed. They occupy an area of 301,000 ha with annual production of 229,000 Metric tones, contributing about 20% to the domestic production of edible oil (Anonymous, 1996). Mustard (*Brassica juncea*) is also one of the major oil seed crop in the Indian sub-continent. It is mainly self-pollinating crop having 7.5to 30% out crossing under natural field conditions.

Mustard belongs to the family crucifereae (Brassicaceae), Genus *Brassica* (Wiess, 1983). Allied species of mustered include, White mustard [*Sinapis alba* (L)] or *Brassica hirta* (L) Moench, Brown mustard (*Brassica juncea*), Black mustard (*Brassica nigra*) and Ethiopian mustard *(Brassica carinata)***.**

The presence of a wide range of brassica species, types and cultivars i.e., *Brassica campestris, Brassica napus, Brassica nigra, Brassica carinata, Brassica oleraceae, Brassica hirta* and *Brassica juncea* that can be intercrossed, providing considerable germplasm to plant breeders for the development of new cultivars (Weiss, 1983).

Brown or Indian mustard (*Brassica juncea*) is one of the most important species in the genus Brassica. It is the predominant cruciferous species and has been widely grown throughout the rain-fed areas of Dera Ismail Khan. It has great yield potentials for semi arid conditions and known to be more droughts tolerant and shattering resistant then *Brassica napus* and *Brassica campestris.* It matures earlier than *Brassica napus* and consequently escapes the attack of aphids and hairy caterpillar. It is also more lodging resistant as compared to rapeseed (*Brassica napus* and *Brassica campestris*). There is much scope of developing new mustard varieties, containing low levels of erusic acid and glucosinolates. However one limitation of *Brassica juncea* is that the available genotypes contain higher glucosinolates and erusic acids content, restricting their use as edible oil corp. In addition the oil content of these species is also lower than would be desired. Therefore there is great need to screen out breeding lines for lower levels of erusic acid percentage and glucosinolates content and higher yield potential.

In the present studies an effort was made to ascertain the gene action and magnitude of contribution of various quantitative characters in a six parent diallel cross experiment of Brown mustard to evolve new high yielding genotypes through genetic recombination to face global challenges.

MATERIALS AND METHODS

A field experiment was conducted at Faculty of Agriculture Gomal University, D. I. Khan to study the gene action regarding the parameters of yield and its related components in F_1 generation of Brown mustard. The experimental material comprised of F_1 hybrid seed resulted from 6x 6 diallel cross of four varieties R.L-18, B.M-1, Early raya, S-9 and two breeding lines, 91421and 91416, including self and reciprocals. All the varieties and breeding lines belonged to *Brassica juncea.*

The varieties and breeding lines were crossed in diallel fashion during October 2000-2001. The F_1 seeds of these crosses along with their parents were spaced during October 2001-02 in the experimental field using randomized complete block design with three replications. Each replication comprised of 6 parents and 30 F_1s, having single row of 5 meters length per each treatment and about one meter apart from one an other, by this way each treatment had the size of 1 x 5 m. Sowing was done with hand drill. All agronomic activities and plant protection measures were kept normal and uniform for the entire experiment, weeds were controlled by hoeing.

At maturity10 plants by leaving one plant on either side of each treatment were randomly selected in each replication. The data were recorded on the following plant parameters, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of siliqua main^{-1} inflorescence and seed yield plant^{-1} (gm).

Statistical analysis: The data regarding different plant characters were averaged and subjected to statistical manipulation for the analysis of variance technique to establish the level of variability among F_1 hybrids and their parental lines (Steel and Torrie, 1980).

Previous results of the genetic materials under study revealed a significant variation in parents and their F_1 hybrids in all the characters like, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, plant height (cm), number of siliqua main^{-1} inflorescence and seed yield plant^{-1} (gm). Further analysis for the diallel cross technique developed by jinks (1953, 1954 and 1956) was adopted for genetic analysis. All the crosses were arranged into arrays in the form of diallel tables and the two statistics, the variance (Vr) of the family mean within an array and the covariance (Wr) of these means with the non-recurrent parental values were calculated from each diallel table by the following methods.

Estimation of variances and covariances:

a: Variance was calculated by the following formula.

$$Vr = \frac{\Sigma X_i^2 - (\Sigma X_i)^2/n}{n-1}$$

b: Covariance (Wr) was calculated by the following formula.

$$Wr = \frac{\Sigma x_i Yi - (\Sigma X_i)\ (\Sigma Y_i)\ / n}{n-1}$$

Calculation of limiting parabola: The information on gene action was inferred by plotting the covariance (Wr) of each array against its variance (Vr). The slope and the position of the regression line fitted to the array points within the limiting parabola ($Wr^2 = Vp^{--}.Vr$) indicated the degree of dominance and the presence or absence of gene interaction.

The limiting parabola was constructed on the basis of formula, $Wr^2 = Vr \text{ x } Vp^{--}$ by plotting Vr, $(Vr \text{ x } Vp^{--})^{1/2}$ points. The corresponding values of Wr for all observed Vr values were calculated as $(Vr \text{ x } Vp^{--})^{1/2}$; where Vp^{--} = Variance of the parents. The different arrays (varieties) were fitted within the limits of the parabola using the individual variance and co-variance as their limiting point. Array nearest to the point of origin possessed most of the dominant genes, while the array that lay the farthest from the origin possessed the most recessive genes and the intermediate position signified the presence of both dominant and recessive genes in the array. The standard error for the regression line slope was estimated according to Snedecor (1962).

RESULTS AND DISCUSSION

The results for the analysis of variance are presented in Table 1. The average performance of 30 hybrids along with their parents in 6x6 diallel cross for number of primary branches plant^{-1}, number of secondary branches plant^{-1}, plant height (cm), number of siliqua main^{-1} inflorescence, seed yield plant^{-1} (gm) shown in the tables (2-6) and Vr/Wr graphic illustration for each trait are presented in Figs. (1-5). All above characters are discussed as follows.

Plant height (cm): The analysis of variance for plant height given in Table 1 revealed highly significant variation due to various genotypes including parents and F_1 hybrid.

Contemplation to Fig. 1 and Table 2 indicated the additive type of gene action as the regression line cuts the Wr-axis above the origin on the positive side.

From the position of array points along the regression line it is quite obvious that Breeding line 9141 has maximum dominant genes. It was closely followed by Breeding line 9142. While the genotypes S-9 and Early Raya contains the maximum number of recessive alleles, as they are distantly located from the origin. Additive type of gene action suggests that selection in early generation may be fruit full for this character. The regression line does not deviate significantly from the unit slope thus indicating the absence of non-allelic interaction.

These results are in agreement with the findings of Sheikh *et al.* (1998) and Pathak (2000), who found the presence of additive type of gene action responsible for this trait.

Number of primary branches plant^{-1}: The analysis of variance for number of primary branches plant^{-1} given in Table 1 revealed highly significant variation due to various genotypes including parents and F_1 hybrids.

A study of Fig. 2 and Table 3 depicts that the regression line cuts the Wr-axis on the positive side showing additive type of gene action. From the array position on the regression line, it is evident, that Early Raya closely followed by S-9 have got the maximum number of dominant genes, while the Breeding line 9142 and R.L-18 contains the recessive genes being away from origin point Fig. 3. The regression line does not deviate significantly from the unit slope thus indicating the absence of non-allelic interaction. Additive with partial type of gene action suggest that the selection will be beneficial in early segregating generations and there is every possibility of having transgressive segregation. These results are supplemented with findings of Pathak *et al.* (2000). These results do not agree with the findings of Kumar *et al.* (1994) and Patel *et al.* (1993). Contradiction for the manifestation of this character might be due to different breeding materials of their parents utilized in the conduct of this experiment and different environmental conditions.

Number of secondary branches plant^{-1}: The analysis of variance for number of secondary branches plant^{-1} given in Table 1 revealed highly significant variation due to various genotypes including parent and F_1 hybrids.

It is obvious from Vr/Wr graph Fig. 3 and Table 4 for number of secondary branch plant^{-1} that regression line intercepts the Wr-axis below the origin indicating over dominant type of gene action responsible for this character. From the position of array points on the regression line it is clear that RL-18 possesses maximum dominant genes because of its proximity to the point of the origin, while Early raya contains the recessive genes being away from the point of origin. From the observed gene action it can be concluded that selection in early generation will be ineffective for this character while using them in any breeding program. The regression line does not deviate significantly from the unit slope thus indicating the absence of non-allelic interaction.

These results confirm the finding of Kumar *et al.* (1994) and Patel *et al.* (1993). The present results are

Table 1: Mean squares and degree of freedom for various traits of brown mustard (*Brassica juncea*)

S.O.V.	D. F	Plant height	Number of primary branches	Number of secondary branches	Siliqua main^{-1} Inflorescence	Seed yield plant^{-1}
Genotypes	35	2724.00	1.900	300.83	36.415	11.308
Errors	70	90.50	0.312	48.95	2.716	6.754
F. ratio		30.11**	6.09**	6.14**	13.41**	1.67*

** = Highly significant

Table 2: 6x6 Diallel average for plant height

Parents	R.L-18	B.M-1	B.L9141	B.L9142	Early Raya	S-9	(Vr)	(Wr)
R.L-18	209.00	208.50	258.667	258.667	211.667	210.66	633.96	875.00
B.M-1		197.00	245.333	248.000	197.167	197.50	599.52	843.64
B.L9141			265.000	269.167	263.167	262.66	68.98	173.63
B.L9142				267.333	265.833	268.66	68.44	136.42
Early Raya					196.333	196.50	1129.6	1158.3
S-9						197.66	1160.4	1174.1

Regression coefficient = 0.940, ± = 0.087, t value at b0 = 9.639, t value at b1 = 0.608

Table 3: 6x6 Diallel average for number of primary branches plant^{-1}

Parents	R.L-18	B.M-1	B.L9141	B.L9142	Early Raya	S-9	(Vr)	(Wr)
R.L-18	9.600	10.133	11.433	10.317	9.3000	9.6667	0.5799	0.7952
B.M-1		9.4000	10.967	10.783	9.6333	9.4000	0.4807	0.7789
B.L91416			11.767	11.450	9.9667	6.9167	0.6357	0.7583
B.L91421				11.200	9.7167	9.8833	0.4959	0.7535
Early Raya					9.0667	10.000	0.1364	0.1970
S-9						9.0000	0.1466	0.2435

Regression coefficient = 1.265, ± = 0.174, t value at b0 = 7.229, t value at b1 = -1.515

Table 4: 6x6 Diallel average for number of secondary branches plant^{-1}

Parents	R.L-18	B.M-1	B.L9141	B.L9142	Early Raya	S-9	(Vr)	(Wr)
R.L-18	30.0250	37.0250	39.3125	38.3500	33.3750	34.550	12.071	-14.263
B.M-1		21.0000	26.9250	29.4500	35.5000	30.700	34.158	34.053
B.L9141			32.6250	47.1500	46.6500	33.362	66.534	21.152
B.L9142				20.3750	45.7500	40.950	106.08	84.286
Early Raya					45.9500	27.000	64.054	2.8533
S-9						36.900	23.453	-25.975

Regression coefficient =0.921, ± = 0.329, t value at b0 = 2.798, t value at b1 = 0.236

Table 5: 6x6 Diallel average for siliqua main^{-1}inflorescence

Parents	R.L-18	B.M-1	B.L9141	B.L9142	Early Raya	S-9	(Vr)	(Wr)
R.L-18	55.466	55.316	60.866	60.416	54.100	54.000	9.3719	11.563
B.M-1		52.800	59.866	60.133	53.600	54.216	10.336	12.087
B.L9141			60.066	61.350	56.183	57.950	3.8126	5.1436
B.L9142				60.833	60.283	55.933	3.8285	4.1794
Early Raya					52.5333	54.266	7.7101	9.3015
S-9						52.733	3.3456	5.8519

Regression coefficient = 1.049, ± = 0.108. t value at b0 = 9.678, t value at b1= -0.453

Table 6: 6x6 Diallel average for seed yield plant^{-1} (gm)

Parents	R.L-18	B.M-1	B.L9141	B.L9142	Early Raya	S-9	(Vr)	(Wr)
R.L-18	27.143	27.283	30.836	31.261	27.358	26.995	3.994	5.170
B.M-1		26.020	30.360	29.913	25.918	27.328	3.643	4.956
B.L9141			31.330	30.968	30.530	29.970	0.231	0.957
B.L9142				31.943	29.865	30.423	0.664	1.730
Early Raya					26.133	27.101	3.743	5.018
S-9						27.040	2.564	4.135

Regression coefficient = 1.11252, ± = 0.0643. t value at b0 = 17.2357, t value at b1 = -1.7430

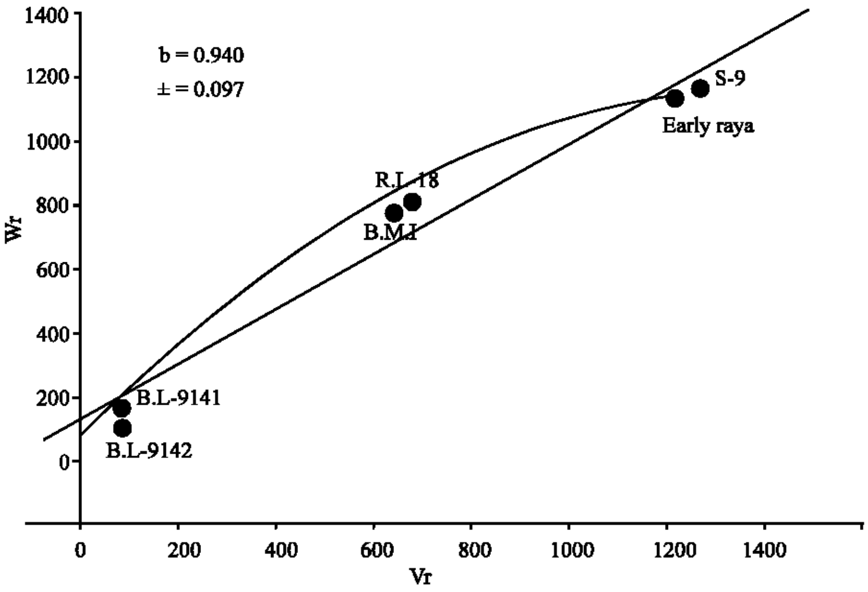

Fig. 1: Vr/Wr graph for Plant Height (F1)

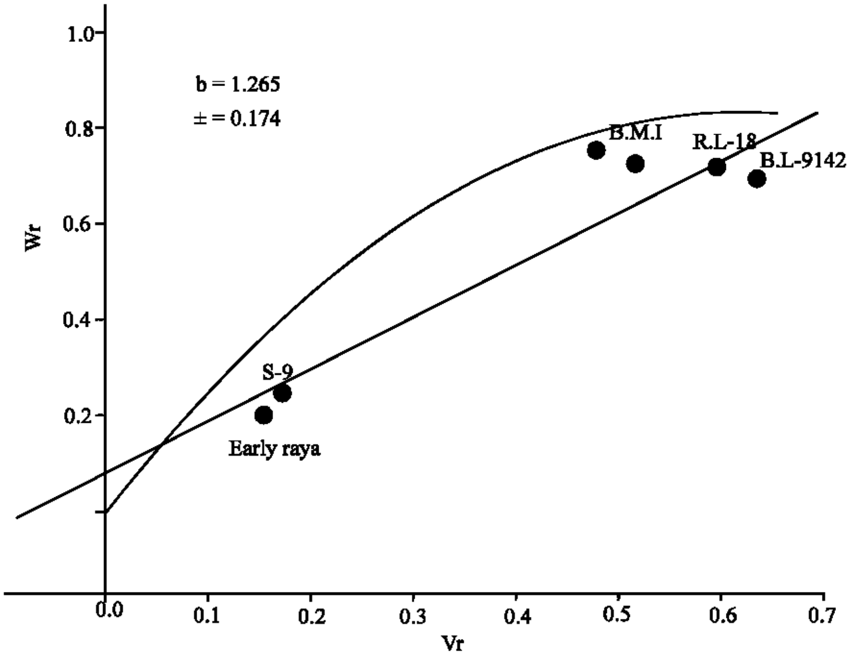

Fig. 2: Vr/Wr graph for number of primary branches $plant^{-1}$(F1)

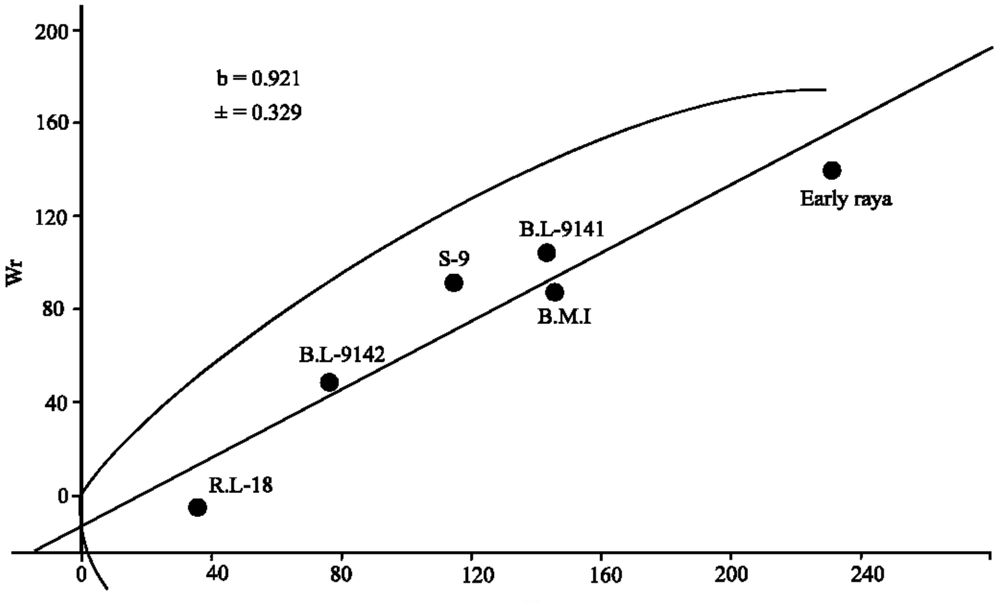

Fig. 3: Vr/Wr graph for number of secondary branches $plant^{-1}$(F1)

however not in accordance with the findings of Pathak *et al.* (2000), who reported the presence of additive type of gene action for this trait. These differences might be due to different source of germplasm used under different agro-climatic conditions.

Number of siliqua $main^{-1}$ inflorescence: The analysis of variance for siliqua $main^{-1}$ inflorescence given in Table 1 revealed highly significant variation due to various genotypes including parents and F_1 hybrids.

A study of Fig. 4 and Table 5 indicated that the regression line intercepts Wr- axis above the origin, on the positive side thereby showing the presence of additive type of gene action for siliqua $main^{-1}$ inflorescence.

From the position of array points on the regression line it is evident that the Breeding line 9141, Breeding line

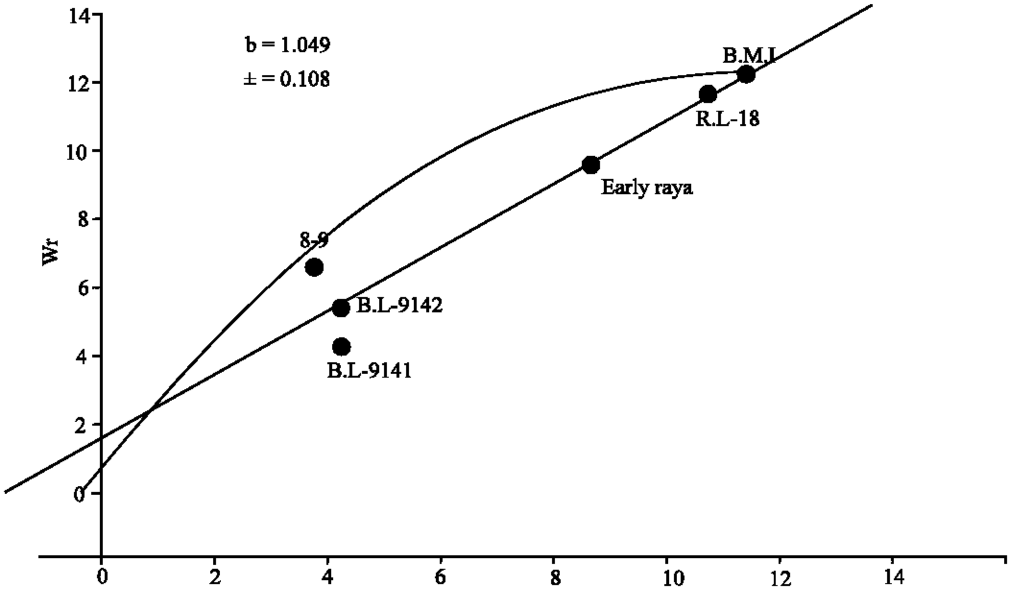

Fig. 4: Vr/Wr graph for siliqua main^{-1} inflorescence (F1)

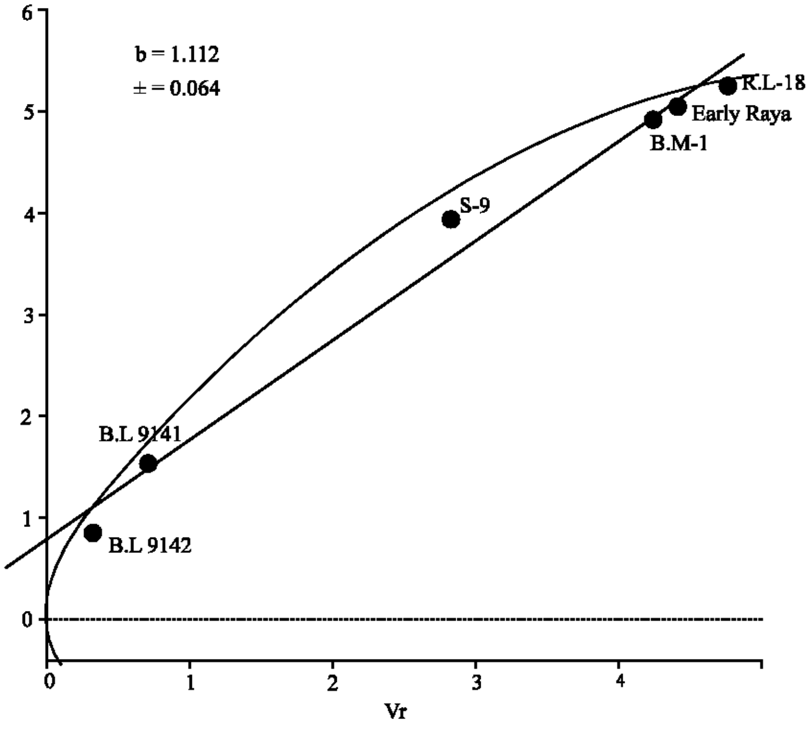

Fig. 5: Vr/Wr graph for seed yield plant^{-1} (F1)

9142 and S-9 contains the maximum dominant genes due to their nearest position from the origin, while B.M-1 contains the maximum recessive genes due to farthest position from origin. From such type of gene action, it is concluded that selection of desirable lines can be made in early generations, while using them in breeding program. The regression line does not deviate significantly from the unit slope thus indicating the absence of non-allelic interaction. These results confirm the findings of Pathak *et al.* (2000), who also reported the involvement of additive type of gene action for this trait. These results do not agree with the findings of Kumar *et al.* (1994), who reported the presence of non-additive type of gene action. This type of contradiction might be due to different genetic materials and climatic conditions under which these experiments were performed.

Seed yield plant $^{-1}$(gm): The analysis of variance for seed yield plant^{-1} among parents and their F_1 hybrids was significant. Table 1;

The inheritance pattern for seed yield/plant shows an additive type of gene action, as the regression line intercepts the Wr-axis above the origin Fig. 5.

Distribution of array points on the regression line suggest that Breeding line 9142 possesses the maximum number of dominant genes, while R.L-18 contains recessive alleles due to being the nearest and farthest positions respectively. Additive type of gene action with partial dominance indicates that progress should be made through more sophisticated and precise selection procedures for this character while using them in any breeding program. The regression line does not deviate significantly from the unit slope thus indicating the absence of non-allelic interaction. (Epistasis).

The results of Kant *et al.* (2001) and Kumar *et al.* (1994) are also in line with the present findings, which also showed additive type of gene action controlling seed yield in ***Brassica juncea.*** The present results are however contradicted with the reports of Khulbe *et al.* (1998), Kumar *et al.* (1994) and Sheikh *et al.* (1998), Who reported the non-additive type of gene action for the trait under reference. The variation in the research findings might be due to use of different genetic material and environmental effects.

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