

Original Research Article

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Components of Genetic Variation and Graphical Analysis (Wr-Vr) in Indian Mustard (*Brassica juncea* L. Czern & Coss.)

T.M. Shrimali¹, R.M. Chauhan², R.A. Gami^{3*} and P.T. Patel⁴

¹Wheat Research Station, S.D. Agricultural University, Vijapur, Gujarat, India

²Seed technology, S. D. Agricultural University, Sardarkrushinagar-385506, Gujarat, India

³Maize Research Station, S.D. Agricultural University, Bhiloda-383245, Gujarat, India

⁴Seed Spices Research Station, S.D. Agricultural University, Jagudan, Gujarat, India

*Corresponding author

ABSTRACT

Keywords

Diallel analysis, Graphical analysis, Additive and non-additive gene effects, *Brassica juncea*.

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Hayman diallel analysis was performed excluding reciprocal in Indian mustard, the experimental material consisted of morphological diverse but genetically homozygous genotypes/varieties and their 45 direct crosses *i.e.*, the F₁ populations. The traits days to flowering, days to maturity, plant height, number of siliquae per plant, 1000-seed weight, harvest index, and linolenic acid explored additive type of gene effects. The correlation between parental order of dominance (Vr + Wr) and parental mean (Yi) was positive and significant for days to flowering, days to maturity, plant height, number of siliquae per plant, seed yield per plant, 1000 seed weight and erucic acid which indicated involvement of recessive alleles for increasing a value of respective traits. Whereas dominant genes were involve in increasing number of branches per plant and oil content. Based on comparison of both Griffing and Hayman approaches revealed over dominance for all the characters. The Hayman s' analysis was found invalid due to significant values of t² for number of siliquae per plant, seed yield per plant, oleic acid, linoleic acid and erucic acid. In these cases, Griffing analysis showed over dominance.

Introduction

Indian mustard (*Brassica juncea*) is a naturally autogamous species, accounting the environmental condition and frequency of pollinating insect *i.e.* bees, 5-30% out crossing takes place Based on ploidy level, Indian mustard is an amphidiploid (2n=36), derived from interspecific cross between two diploid species *i.e.*, *Brassica rapa* (2n=20) and *Brassica nigra* (2n=16) followed by natural chromosome doubling. The improved mustard seeds contain 39-44% oil. For International acceptance, erucic acid content

should be <2%. Seed quality, Seed yield and other yield related parameters of *Brassica* oil seed crop has been tried to improve by several researchers (Monpara, 2007). Many authors applied different strategies for improving seed yield and quality attributed of *Brassica* (Singh *et al.*, 2003; Gami *et al.*, 2012). Gami and Chauhan (2013) and Patel *et al.*, (2013) have also reported difference types of gene action and combining abilities in different sets of material studies. The various mating designs have been used for assessing the breeding

value of the parents through the estimation of variance and combining ability effects.

Diallel mating design has been extensively used in both self and cross pollinated species to understand the nature of gene action involved in the expression of quantitative traits. In the breeding of high yielding varieties of crop plants, the breeder is confronted with the problem of choice of parents. Elimination of poor yielding crosses on the basis of their performance in early generation had been recommended, but it was felt that knowledge of the genetic architecture of yield and its attributes will help to sort out the better crosses more efficiently. Several reports in past have appeared which indicate that diallel analysis is the quickest method of understanding the genetic nature of quantitatively inherited traits and to ascertain the prepotency of parents. Kearsey (1965) noted that Hayman and Jinks' diallel analysis provide more information than other methods, but has more necessary assumptions. The analyses proposed by Griffing (1956) do not provide any test to detect epistasis or linkage. Hayman and Jinks' analysis does provide such test. When using Griffings' analysis to estimate variance components, it has been suggested that simple tests, such as the W_r - V_r evaluation found in Haymans' (1954b) model, be used to ascertain the presence of epistasis and/or linkage disequilibrium (Pooni *et al.*, 1984; Wright, 1985). Keeping these in view the present investigation was undertaken to make an assessment of component of genetic variance and graphical analysis in Indian mustard.

Materials and Methods

The experimental material consisted of morphological diverse but genetically homozygous genotypes/varieties *viz.*, GM 3, GDM 4, SKM 815, SKM 518, SKM 904, RH-0555, RGN-282, RGN-303, RW-1-02, RSK-

29 and their 45 direct crosses *i.e.*, the F_1 populations. All the 55 treatments (10 parents and 45 F_1 s) were grown in Randomized Block Design with three replications at S. D. Agricultural University, Sardarkrushinagar during *Rabi* 2014. The data was recorded on five randomly selected plants of each genotypes per replication and the mean data calculate from it for different traits *viz.*, plant height, number of branches per plant, number of siliquae per plant, days to flowering, days to maturity, seed yield per plant, harvest index, 1000-seed weight, oil content and fatty acid composition. Oil content of each sample was estimated in percentage by using Nuclear Magnetic Resonance Technique (Tiwari *et al.*, 1974), while fatty acids composition of each sample was estimated in percentage by using Fourier Transferable Near Infrared (FT-NIR) Technique. The material under present investigation was tested for the agreement with assumptions basic to Hayman diallel analysis (Hayman, 1954a). Mustard is a self-pollinated species. The parents included in the study were homozygous. The maternal effects are assumed to be absent in the present material. The multiple allelism might be present at certain loci controlling quantitative traits, but Hayman (1960) reported that it did not disturb measure of dominance critically. For testing other assumptions, two general tests *i.e.*, t^2 test and regression of W_r on V_r were used.

Genetic component analysis

Genetic component of variance were computed by employing diallel cross method suggested by Hayman (1954a) for the characters where additive – dominance model was fitted well. Adequacy of the additive dominance model was tested with the help of ' t^2 ' test as proposed by Hayman (1954a) as follows:

$$t^2 = \frac{n-2}{4} \frac{(\text{Var. } V_r - \text{Var. } W_r)^2}{\text{Var. } V_r \cdot \text{Var. } W_r - \text{Cov.}^2(V_r, W_r)}$$

The values were compared against table value of 'F' at 4 and (n – 2) degrees of freedom. Significant value indicates the failure of hypothesis, *i.e.*, $W_r - V_r$ are not constant over arrays. Where, n=Number of parents.

Estimation of genetic components

Following genetic components of variance were estimated according to Hayman (1954a).

- D = Component of genetic variance due to additive effects of the genes
- H₁ = Component of genetic variance due to dominant effects of the genes
- H₂ = Component of genetic variance due to dominance effects corrected for the genes distribution
- F = The mean of Fr over the arrays, where Fr is the dominance effects in single array and
- h² = Overall dominance effects of heterozygous loci

Graphical analysis

The graphical analysis was done according to Hayman (1954b). The V_r , W_r points for the parental were depicted along the V_r , W_r axes. For drawing parabola V_{ri} values and an initial value were calculated as per formula: $W_{ri} = (V_{ri} \times V_{0L_0})^{0.5}$

Where,

V_r = Variance of the rth array

V_{0L_0} = Variance of parental value.

For drawing regression line, expected W_{rei} values were calculated as per: $W_{rei} = W_r - bV_r + bV_r$

The point of interception (a) on W_r ordinate by the regression line is obtained by the formula: $a = W_r - bV_r$

The point of interception and the position V_r , W_r points for the different parents along the regression line would lead to draw the conclusion regarding degree of dominance and type of gene action involved in the parents.

Results and Discussion

This analysis is based on simple additive-dominance model of gene effects with certain assumptions. The validity of hypothesis of additive-dominance model was tested by confirming unit slope of regressions of W_r and V_r and by non-significant value of t^2 as prescribed by Hayman (1954b). Non-significant t^2 value indicated the validity of the additive-dominance model for days to flowering, days to maturity, plant height, 1000-seed weight (g) and harvest index (%). For traits *viz.*, number of branches per plant, oil content and linolenic acid the t^2 value was not significant but regression coefficient 'b' deviated significantly from unity (Table 1), indicating partial validity of the model. Therefore, for those cases only numerical analysis was carried out.

The regression coefficient deviated significantly from unity and t^2 values (Table 1) were significant for characters number of siliquae per plant, seed yield per plant, oleic acid, linoleic acid and erucic acid, which indicated non validity of the additive-dominance model for these traits and therefore, the genetical parameters of Hayman's diallel were invalid.

The results of t^2 test indicated the fulfilment of assumptions required under diallel analysis for all the characters under study except number of siliquae per plant, seed yield per

plant, oleic acid, linoleic acid and erucic acid. Non-fulfilment of assumptions in these traits indicated the invalidity of the hypothesis of simple additive – dominance model of gene action and involvement of epistasis and/or linkage disequilibrium.

Days to flowering

In numerical analysis, components D, H_1 and H_2 were found significant (Table 1). The parameter F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The ratio $(H_1/D)^{0.5}$ (0.88) indicated partial dominance. The ratio KD/KR (1.31) indicated presence of higher proportion of dominant genes. The parameter h^2/H_2 (0.02) suggested that, at least one gene group was operating in the inheritance of this trait. The value of $H_2/4H_1$ was 0.22 near to 0.25 which indicated equal distribution of positive and negative alleles among the parents. The 'r' value (0.83) between Yr and (Wr + Vr) was significant and positive indicated the role of recessive genes in increasing the days to flowering. The narrow sense heritability was found high (0.71). The regression line intercepted for Wr axis below the origin which suggested over-dominance (Fig. 1).

The widely scattered array points of parents on the graph indicated considerable gene differences among the parental lines for this character. The parent SKM 518 occupied the nearest position to the point of origin hence possess dominant gene for early flowering. On the contrary the parents, RW-1-01 and RSK-29 occupied far away from the origin, which indicated that it contained maximum number of recessive genes among them.

Days to maturity

The t^2 value for days to maturity was non-significant and the regression value was 0.76

± 0.22 . The regression value deviated significantly from zero but did not deviated significantly from unity. The components D, H_1 and H_2 were found significant (Table 1) in numerical analysis of this trait. Non-significant value of F suggested equal proportion of dominant and recessive genes in the parents.

The ratio $(H_1/D)^{0.5}$ (1.08) indicated over dominance. The proportion of genes with positive and negative effects measured by $H_2/4H_1$ was 0.21 near to 0.25 showed symmetry of positive and negative alleles in the parental gene pool. The proportion of dominant and recessive loci estimated by KD/KR was more than unity (1.18) showed the excess of dominant genes. The parameter h^2/H_2 (0.39) suggested that, at least one gene group was operating in the inheritance of this trait. The 'r' value (0.77) between Yr and (Wr + Vr) was significant and positive indicated the role of recessive genes for earliness.

The heritability in narrow sense was low (0.32) for this trait. For graphical analysis, the regression line intercepted for Wr axis below the origin which suggested over-dominance (Fig. 2). Much scattered array points of parents on the graph indicated considerable gene differences among the parental lines for this character. The parent GM 3 occupied the nearest position to the point of origin hence possess dominant gene for earliness. The remaining parents had equal proportion of dominant-recessive alleles because their points lying middle in the graph.

Plant height (cm)

The t^2 value for plant height was non-significant and the regression coefficient not deviate from unity ($b=0.76$), therefore graphical and numerical analysis were carried out. The numerical analysis for plant height (cm) (Table 1) revealed that additive and non-

additive component were significant. The degree of dominance estimated was (1.06) indicated over dominance of gene effect. The environmental component was significant indicated the influence of environment for expressing for this trait. The value of F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The proportion of genes with positive and negative effects measured by $H_2/4H_1$ was 0.23 near to 0.25 showed symmetry of positive and negative alleles in the parental gene pool. The ratio KD/KR (1.22) indicated presence of higher proportion of dominant genes. The 'r' value (0.90) between Y_r and ($W_r + V_r$) was significant and positive indicated the role of recessive genes for dwarfness. The heritability in narrow sense was medium (0.51) for this trait. The V_r - W_r graph indicated the regression line intercepted for W_r axis below the origin which suggested over-dominance (Fig. 3). Much scattered array points of parents on the graph indicated considerable gene differences among the parental lines for this character. The parent GDM 4 occupied the nearest position to the point of origin hence possess dominant gene for dwarfness. The remaining parents had equal proportion of dominant-recessive alleles because their points lying middle in the graph.

Numbers of branches per plant

The slope of regression line deviating from unity and t^2 value was non-significant for this trait. Therefore, the graphical analysis was not performed but numerical analysis was carried out for this trait. The analysis revealed that only dominance components H_1 and H_2 were found significant which indicated non-additive type of gene action (Table 1). The value of F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The ratio $(H_1/D)^{0.5}$ (2.66) indicated over dominance.

The value of $H_2/4H_1$ was 0.21 near to 0.25 which indicated equal distribution of positive and negative alleles among the parents. The proportion of dominant and recessive loci estimated by KD/KR was more than unity (1.63) showed the excess of dominant genes. The heritability in narrow sense was low (0.22) for this trait.

1000 seed weight (g)

Haymans' diallel analysis for this trait was satisfactory as the regression coefficient of W_r on V_r and t^2 values were desirable. Thus both graphical and numerical analysis was carried out. The additive and non-additive components were found significant (Table 1) in numerical analysis of this trait. The value of F was significant, which suggested unequal proportion of dominant and recessive genes in the parents. The ratio $(H_1/D)^{0.5}$ (1.10) indicated over dominance. The proportion of genes with positive and negative effects measured by $H_2/4H_1$ was 0.20 near to 0.25 showed symmetry of positive and negative alleles in the parental gene pool. The proportion of dominant and recessive loci estimated by KD/KR was more than unity (1.92) showed the excess of dominant genes. The parameter h^2/H_2 (1.17) suggested that, many group of gene were operating in the inheritance of this trait. The 'r' value (0.82) between Y_r and ($W_r + V_r$) was significant and positive indicated the role of recessive genes in increasing the 1000 seed weight. The heritability in narrow sense was medium (0.49) for this trait. The regression line intercepted for W_r axis below the origin which suggested over-dominance (Fig. 4). The parent GDM 4 and SKM 815 occupied the nearest position to the point of origin hence possess dominant gene for test weight. On the contrary the parents, RGN-303 and RH-0555 occupied farthest position from the origin. Thus, indicating concentration of

maximum number of recessive genes among them.

Harvest index (%)

Haymans' diallel analysis was found valid due to non-significant t^2 value and unit slope of regression line (0.50 ± 0.37). In numerical analysis for this character, components D, H_1 and H_2 were found significant (Table 1). The parameter F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The ratio $(H_1/D)^{0.5}$ (1.32) indicated over dominance. The ratio KD/KR (1.48) indicated presence of higher proportion of dominant genes. The proportion of genes with positive and negative effects measured by $H_2/4H_1$ was far away to 0.25 showed asymmetry of positive and negative alleles in the parental gene pool. The narrow sense heritability was found high (0.60). The graphical analysis indicated that the regression line intercepted for Wr axis below the origin which suggested over-dominance (Fig. 5). Much scattered array points of parents on the graph indicated considerable gene differences among the parental lines for this character. The parents, GM 3 and RSK-29 occupied farthest position from the origin. Thus, indicating concentration of maximum number of recessive genes among them.

Oil content (%)

The regression coefficient deviation from unity and t^2 value was non-significant for this trait. Therefore, the graphical analysis was not performed and only numerical analysis was performed. The analysis revealed that only non-additive components (H_1 and H_2) were found significant indicating non-additive type of gene action (Table 1). The value of F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The ratio $(H_1/D)^{0.5}$ (1.79)

indicated over dominance. The value of $H_2/4H_1$ was 0.19 far away to 0.25 which indicated unequal distribution of positive and negative alleles among the parents. The proportion of dominant and recessive loci estimated by KD/KR was more than unity (2.11) showed the excess of dominant genes. The parameter h^2/H_2 (0.12) suggested that, at least one gene group was operating in the inheritance of this trait. The heritability in narrow sense was low (0.27) for this trait.

Linolenic acid (%)

The slope of regression line deviating from unity and t^2 value was non-significant for this trait. Therefore, the graphical analysis was not performed but numerical analysis was carried out for this trait. In numerical analysis for this character, components D, H_1 and H_2 were found significant (Table 1) showing involvement of both fixable and non-fixable effect of genes. The parameter F was non-significant, which suggested equal proportion of dominant and recessive genes in the parents. The degree of dominance (2.04) indicating major role of over dominance in expression of the character. The ratio KD/KR (1.90) indicated presence of higher proportion of dominant genes. The proportion of genes with positive and negative effects measured by $H_2/4H_1$ was far away to 0.25 showed asymmetry of positive and negative alleles in the parental gene pool. The narrow sense heritability was found low (0.29).

The estimates of D which measure the variance due to additive gene effects were significant for characters *viz.*, days to flowering, days to maturity, plant height, number of siliquae per plant, 1000-seed weight, harvest index, and linolenic acid. Thus additive gene effects were significant for these characters. The H_1 , which measure the variance due to non-additive effects, was significant for all the characters except oleic

acid and erucic acid. This clearly indicates the predominance of non-additive gene action for all the characters under study. The estimates of dominance ratio $(H1/D)^{0.5}$ greater than unity for all the traits except days to flowering indicating over dominance for most of the characters. According to Singh *et al.*, (2008) and Arifullah *et al.*, (2013) both D and H component were played important role in genetic component of plant height. Over dominance for yield contributing traits also reported by Thakral *et al.*, (2000) and Arifulla *et al.*, (2013). The predominance of non additive gene action for number of branches per plant is also supported by Shweta *et al.*, (2007).

The equal distribution of positive and negative genes in the parents helps the breeder in selecting particular desirable trait without trailing any other desirable traits. In the present study more or less symmetrical distribution of genes in the parental lines was observed for most of the characters in present study as the value $H2/4H1$ was closer to 0.25. Mather and Jinks (1971) while discussing the short comings of numerical component analysis suggested that $(H1/D)^{0.5}$ 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 for may influence of over estimation of mean degree of dominance. The values of component KD/KR indicated unequal frequency of dominant and recessive genes with higher frequency of dominant genes for all the characters studied except oleic acid. Knowledge of number of genes/group of genes responsible for particular traits is important for the genetic progress through selection. The value $h^2/H2$ indicated at least one group of gene was

operating for all the traits. Estimated narrow sense heritability was low for linoleic acid and most of the other trait except days to flowering, days to maturity and harvest index which had moderate to high heritability.

The correlation between parental order of dominance $(Vr + Wr)$ and parental mean (Yi) was positive and significant for days to flowering, days to maturity, plant height, number of siliquae per plant, seed yield per plant, 1000 seed weight and erucic acid which indicated involvement of recessive alleles for increasing the mean values. For number of branches per plant and oil content the correlation was negative indicating role of dominant genes for increasing mean values. The regression of Wr on Vr was desirable and near unity for days to flowering, days to maturity, plant height and 1000 seed weight validity of simple additive-dominance hypothesis of gene action for these characters. Whereas significant t^2 value for number of siliquae per plant, seed yield per plant, oleic acid, linoleic acid and erucic acid leads to failure of hypothesis for these characters. The regression line intercepted Wr axes below the origin indicated over dominance for all the characters. The wide scattering of parental array points along the regression line in the $Wr-Vr$ graph for days to maturity and harvest index indicated considerable genetic diversity among the parents for these traits. Similar trends also observed by Rai *et al.*, (2005) found over dominance for 1000 seed weight which were according with present findings.

The information obtained from Griffing and Haymans' diallel analyses pertaining to the nature of gene action controlling different characters are summarized in table 2 for comparable evaluation.

Table.1 Estimation of genetic component of variance and other parameters for various characters in Indian mustard

	Parameters	Days to flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of siliquae per plant	Seed yield per plant (g)	1000 seed weight (g)	Harvest Index (%)	Oil content (%)	Oleic acid (%)	Linoleic acid (%)	Linolenic acid (%)	Erucic acid (%)
1	b (Wr, Vr)	0.87	0.76	0.75	-0.09	0.21	0.12	0.96	0.50	-0.34	0.01	0.09	0.32	0.002
2	t _{b-0}	-4.16**	-3.41**	-5.67**	0.44	-1.62	-2.75*	-4.07**	-1.35	1.26	-0.08	-0.62	-1.34	-0.16
3	t _{1-b}	0.64	1.06	1.90	5.23**	6.20**	19.57**	0.19	1.38	4.94**	25.30**	6.35**	2.81**	86.79**
4	t ²	0.06	0.01	1.28	2.37	10.46**	116.81**	0.56	0.19	0.29	156.97**	8.30**	0.80	1885.84**
5	D	61.78*	20.16*	281.36*	6.13	-	-	0.67*	67.60*	5.96	-	-	1.47*	-
6	H ₁	47.27*	23.47*	316.40*	43.32*	-	-	0.82*	118.39*	19.16*	-	-	6.10*	-
7	H ₂	41.50*	19.55*	293.55*	36.16*	-	-	0.64*	82.69*	14.74*	-	-	4.72*	-
8	F	14.55	3.58	60.77	7.77	-	-	0.47*	34.51	7.64	-	-	1.85	-
9	h ²	0.73	7.76*	-13.34	-0.08	-	-	0.11	-0.88	1.78	-	-	0.11	-
10	E	0.59	0.95	41.36*	0.96	-	-	0.04	2.46	0.06	-	-	0.02	-
11	(H ₁ /D) ^{0.5}	0.88	1.08	1.06	2.66	-	-	1.10	1.32	1.79	-	-	2.04	-
12	H ₂ /4H ₁	0.22	0.21	0.23	0.21	-	-	0.20	0.18	0.19	-	-	0.19	-
13	KD/KR	1.31	1.18	1.22	1.63	-	-	1.92	1.48	2.11	-	-	1.90	-
14	h ² /H ₂	0.02	0.39	-0.05	-0.01	-	-	1.17	-0.01	0.12	-	-	0.02	-
15	r (P, Wr +Vr)	0.83**	0.77*	0.90**	-0.15	-	-	0.82**	0.43	-0.41	-	-	0.43	-
16	Heritability	0.71	0.64	0.51	0.22	-	-	0.49	0.60	0.27	-	-	0.29	-

* P ≤ 0.05, ** P ≤ 0.01

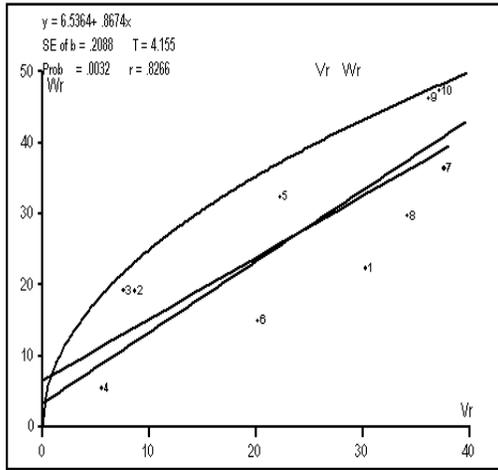


Fig. 1. Vr, Vr graph for Days to flowering

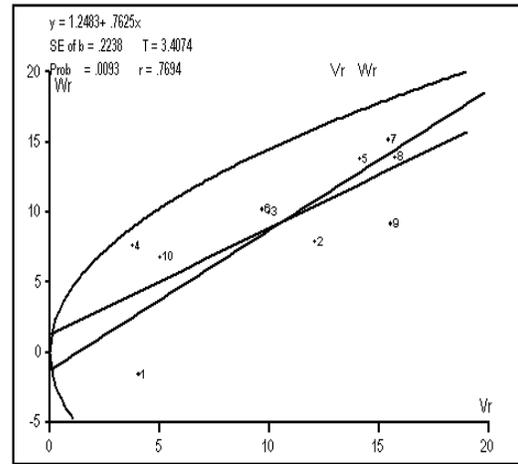


Fig. 2. Vr, Vr graph for Days to maturity

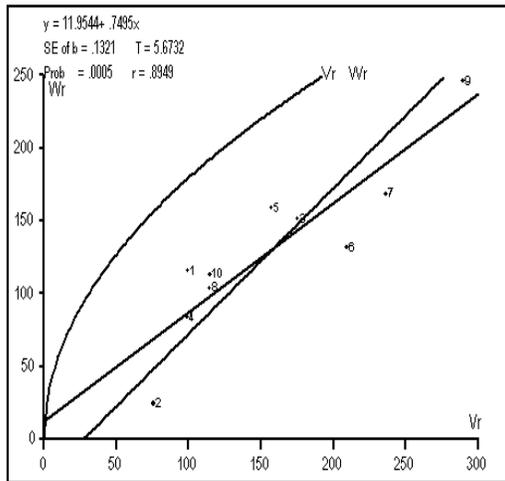


Fig. 3. Vr, Vr graph for Plant height

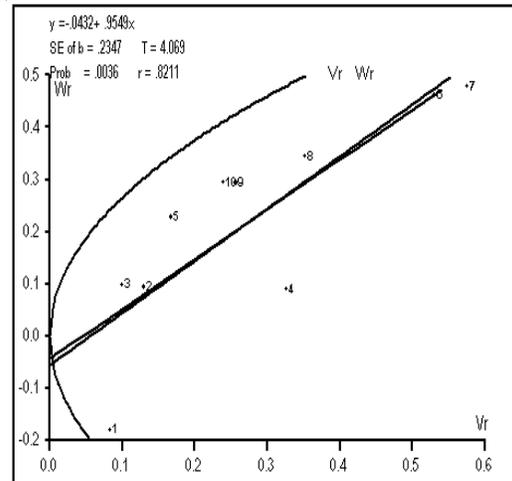


Fig. 4. Vr, Vr graph for 1000 seed weight (g)

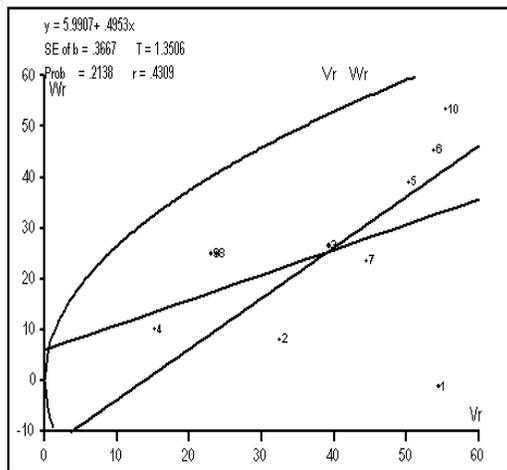


Fig. 5. Vr, Vr graph for Harvest index (%)

Where,

1. GM 3
2. GDM 4
3. SKM 815
4. SKM 518
5. SKM 904
6. RH-0555
7. RGN-303
8. RGN-282
9. RW-1-02
10. RSK-29

Table.2 Comparison of two diallel analyses for various traits in mustard

Characters	σ^2 GCA ————— σ^2 SCA	$[H_1/D]^{1/2}$	Status of Hayman's analysis
Days to flowering	Partial dominance (1.26)	Partial dominance (0.88)	Valid
Days to maturity	Over dominance (0.99)	Over dominance (1.08)	Valid
Plant height (cm)	Partial dominance (1.03)	Over dominance (1.06)	Valid
No. of branches per plant	Over dominance (0.12)	Over dominance (2.66)	Partially valid
No. of siliquae per plant	Over dominance (0.35)	Over dominance (1.83)	Invalid
Seed yield per plant (g)	Over dominance (0.17)	Over dominance (3.79)	Invalid
1000 seed weight (g)	Over dominance (0.62)	Over dominance (1.10)	Valid
Harvest index (%)	Over dominance (0.70)	Over dominance (1.32)	Valid
Oil content (%)	Over dominance (0.16)	Over dominance (1.79)	Partially valid
Oleic acid (%)	Over dominance (0.13)	Over dominance (6.44)	Invalid
Linoleic acid (%)	Over dominance (0.07)	Over dominance (3.17)	Invalid
Linolenic acid (%)	Over dominance (0.17)	Over dominance (2.04)	Partially valid
Erucic acid (%)	Over dominance (0.07)	Over dominance (10.76)	Invalid

Perusal of the table 2 leads to draw the conclusion that both the analyses gave more or less the same picture with regard to the magnitude of additive and non-additive genetic effects for respective characters. The Griffing and Hayman analyses (Table 2) revealed over dominance for all the characters. The Hayman s' analysis was found invalid due to significant values of t^2 for number of siliquae per plant, seed yield per plant, oleic acid, linoleic acid and erucic acid. In these cases, Griffing analysis showed over dominance. This situation can be interpreted as presence of epistasis (non-allelic interaction). Griffing (1956) has noted that this analysis provides simultaneous test for both general and specific combining ability and is more powerful in presence of non-allelic gene interactions. Thus, non-validity of Hayman s' analysis with over dominance in combining ability analyses in present investigation was most probably due to presence of epistasis, the direction or magnitude of which could not be ascertained through these diallel analyses. The perusal table 2 reveals existence of interrelationship between Griffing and Hayman diallel

analyses. The two analyses helped better interpretation of data as Hayman s' model helped to assume the presence of epistasis along with dominance for yield and some of the yield components.

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