Asian J. of Bio Sci. (2007) Vol. 2 No. 1 : (47-52)

Genetics of yield and other quantitative traits in Indian mustard

SHWETA*, P. SINGH AND RANJEET
Department of Genetics and Plant Breeding, C.S. Azad University of Ag. & Tech., KANPUR (U.P.) INDIA

(Accepted : March, 2007)

Experiment comprising 100 treatments (10 parents + 45 F_1s + 45 F_2s) generated from 10 parent diallel mating design was conducted in Indian mustard. Graphical representation reflected the over dominance with non- additive gene action for the characters number of siliquae on main raceme in both the generations, number of secondary branches per plant in F_1, number of primary branches per plant and oil content in F_2 generation whereas, rest of the characters reflected the partial dominance.

Key words : Diallel, Graphical analysis, Over dominance, Partial dominance.

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] being a self-fertilized crop, had primarily been handled through pure line selection or pedigree method of breeding. Such routine methods have failed to bring about any significant shift in the yield potential of this crop. The limited improvement in this crop has been mainly due to narrow genetic base and arbitrary choice of parents without understanding their genetic architecture. The success of breeding programme depends upon choice of superior parents for hybridization and the information on the nature and magnitude of genetic components. In the present investigation, efforts have been made to understand the genetic components based on graphical approach.

MATERIALS AND METHODS

The experimental material comprised ten diverse genotypes of Indian mustard, viz., Varuna, Rohini, RK 02-3, RK 02-4, RK 02-5, RK 02-6, RK 03-1, RK 03-2, RK 01-3 and SEJ-2. The parents were crossed in diallel fashion (excluding reciprocals) to develop the hybrid seeds of 45 crosses. All the 100 treatment (10 parent + 45 F_1s + 45 F_2s) were grown in a Randomized Block Design with three replications at Oilseed Research Farm of C. S. Azad University of Agriculture and Technology, Kanpur. The parents and F_1s were grown in single row and the F_2s in two rows of five- meter length spaced 45 cm apart. The distance of 20 cm between the plants within a row was maintained by thinning. Ten plants each from parents and F_1s and twenty plants from F_2s were randomly selected for recording the observations on eleven characters (Table 1). The graphical analysis was based on variance and covariance (Vr and Wr graph) following the procedure developed by Jinks and Hayman (1953), Jinks (1954 and 1955) and Aksel and Johnson (1963).

RESULTS AND DISCUSSION

The validity of the assumption of diallel cross analysis in this study was tested by t^2 test (Hayman, 1954). Non-significant values of t^2 is exhibited for 10 out of 11 attributes is F_1 and 7 out of 11 attributes is F_2 generation which revealed the validity of hypothesis. Seed yield per plant is F_1 and days to 50 per cent flower, length of main raceme, 1000 seed weight and seed yield per plant in F_2 indicated significant values in both the generations which might be due to sampling error.

The regression coefficient 'b' deviated significantly from unity for all the characters in both the generations except plant height in F_2. Such significant deviations of regression coefficient (b) from unity indicated the presence of non-allelic gene interaction while the regression coefficient did not deviated significantly from unity indicating the involvement of additive gene action for plant height is F_1 generation.

Graphical representation for traits (Fig 1-11) reflected the partial dominance as regression line passed above the origin resulting into additive gene action for the characters days to 50 per cent flower, plant height, days to maturity, length of main raceme, number of seeds per siliqua, 1000-seed weight and seed yield per plant in both F_1 and F_2 generations, number of primary branches per plant and oil content in F_1 and number of secondary branches per plant in F_2 generation. Over dominance reflecting the non-additive gene action was observed for characters number of siliquae on main raceme in both the generations, number of primary branches per plant

* Author for Correspondence

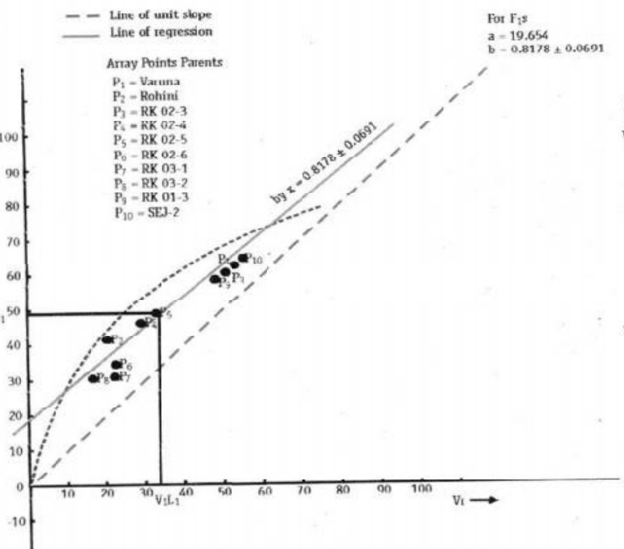

Fig. 1a. Wr, Vr graph for days to 50 per cent flower

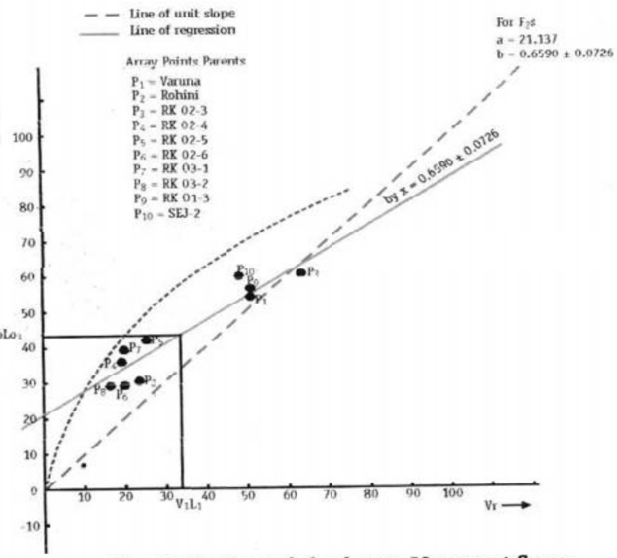

Fig. 1b. Wr, Vr graph for days to 50 per cent flower

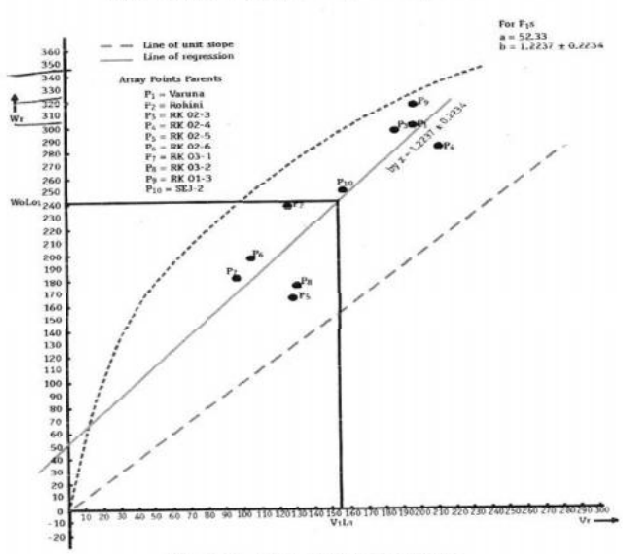

Fig. 2a. Wr, Vr graph for plant height

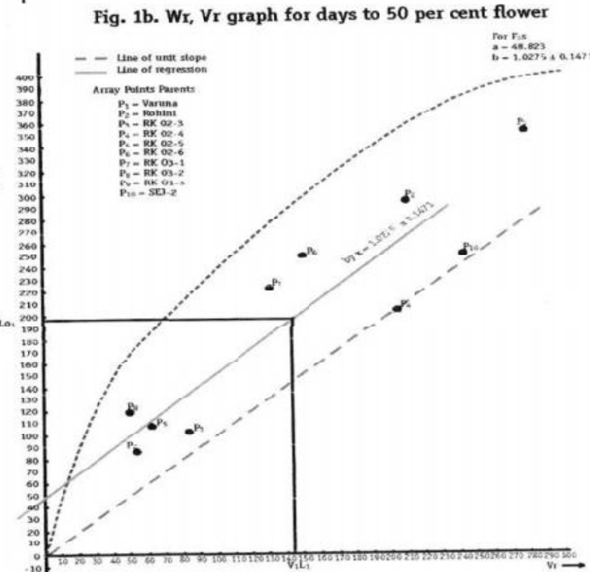

Fig. 2b. Wr, Vr graph for plant height

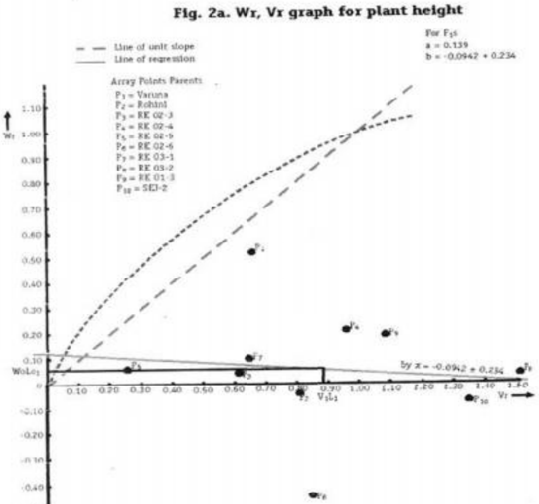

Fig. 3a. Wr, Vr graph for number of primary branches

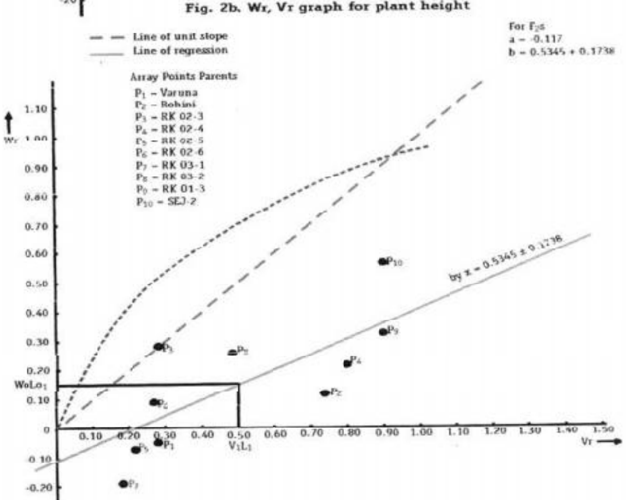

Fig. 3b. Wr, Vr graph for number of primary branches

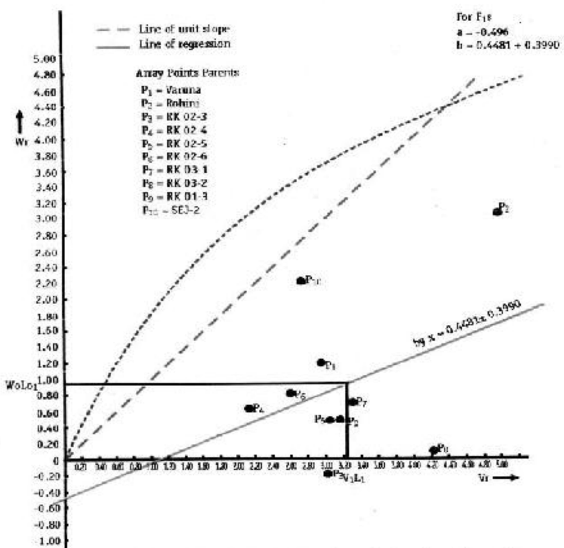

Fig. 4a. Wr, Vr graph for number of secondary branches

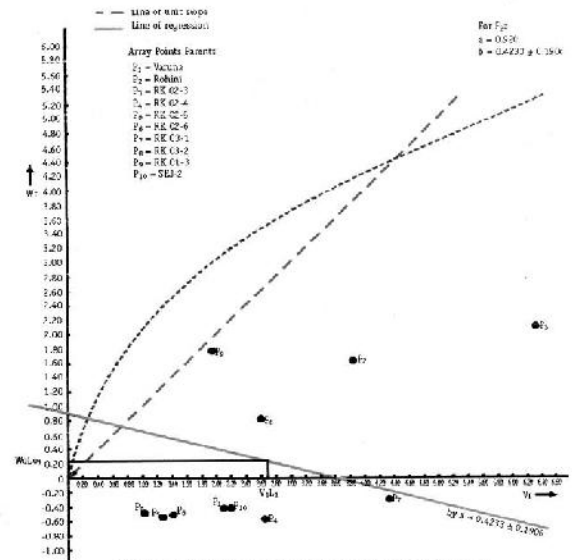

Fig. 4b. Wr, Vr graph for number of secondary branches

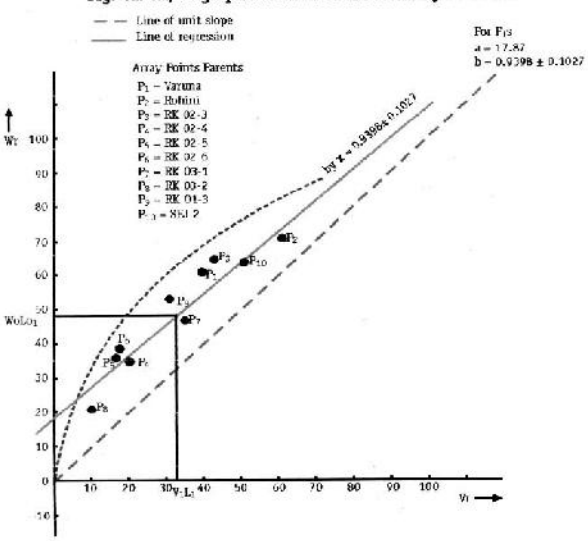

Fig. 5a. Wr, Vr graph for days to maturity

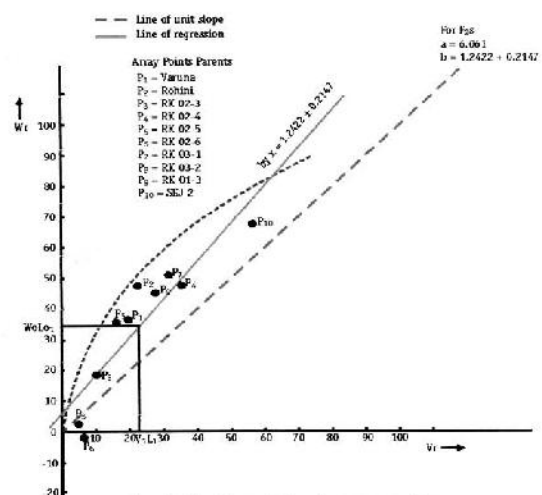

Fig. 5b. Wr, Vr graph for days to maturity

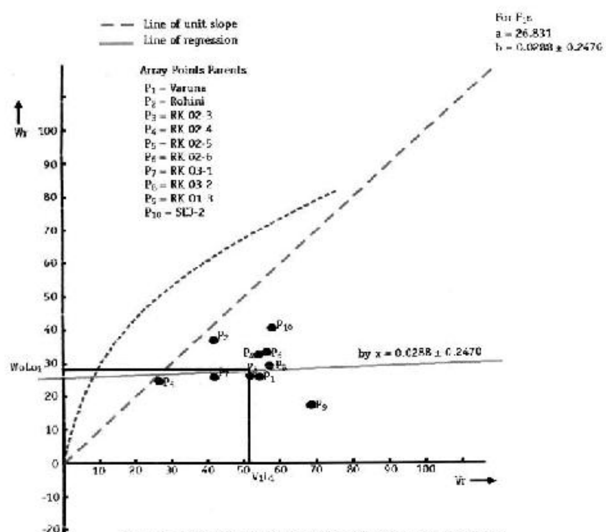

Fig. 6a. Wr, Vr graph for length of main raceme

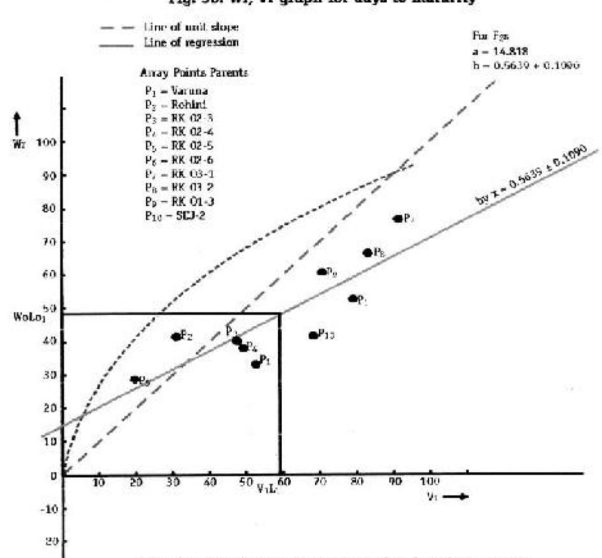

Fig. 6b. Wr, Vr graph for length of main raceme

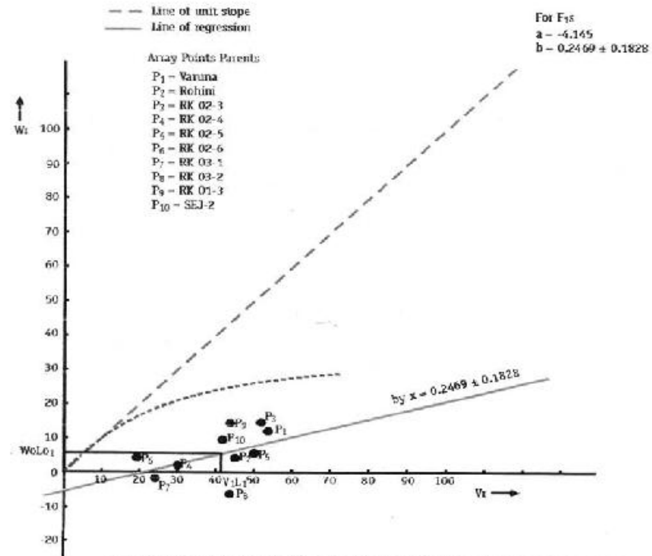

Fig. 7a. Wr, Vr graph for number of siliquae on main raceme

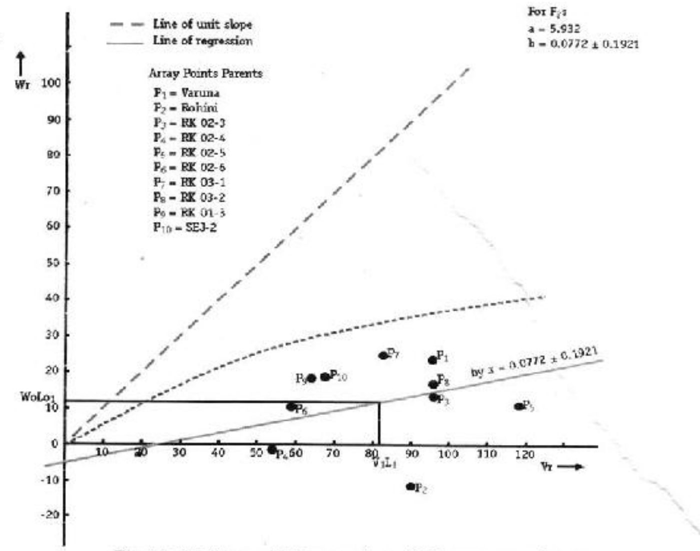

Fig. 7b. Wr, Vr graph for number of siliquae on main raceme

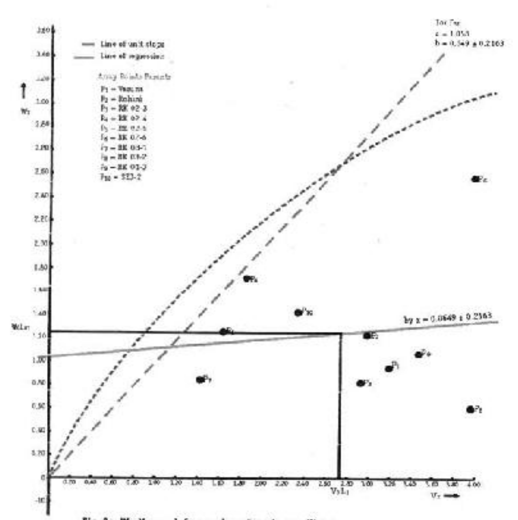

Fig. 8a. Wr, Vr graph for number of seeds per siliqua

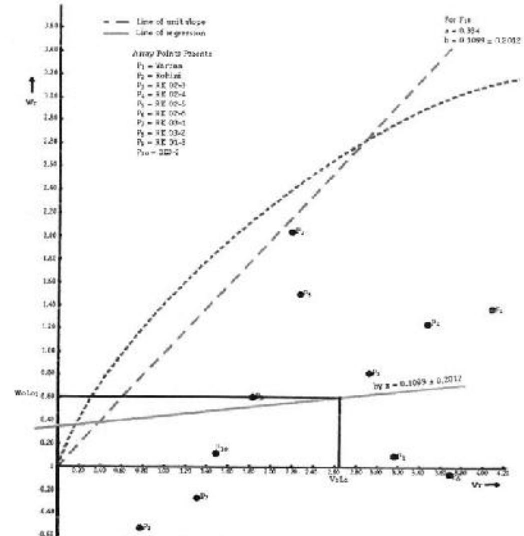

Fig. 8b. Wr, Vr graph for number of seeds per siliqua

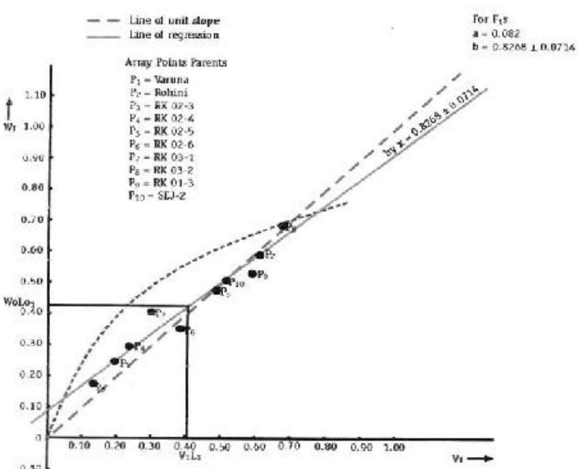

Fig. 9a. Wr, Vr graph for 1000-seed weight

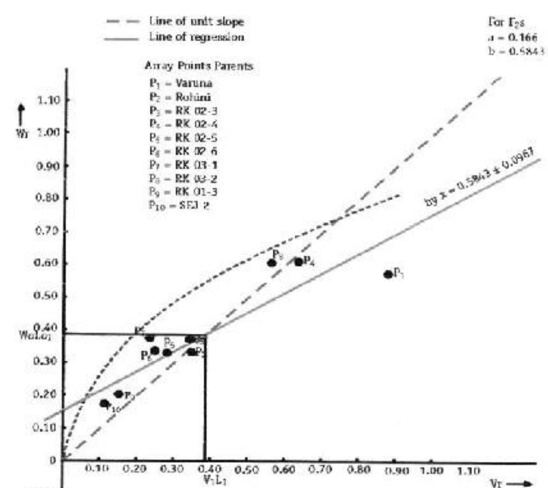

Fig. 9b. Wr, Vr graph for 1000-seed weight

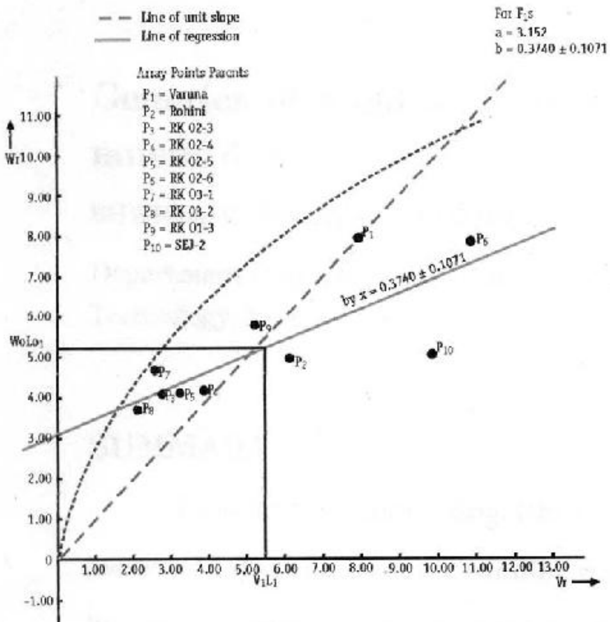

Fig. 10a. Wr, Vr graph for seed yield per plant

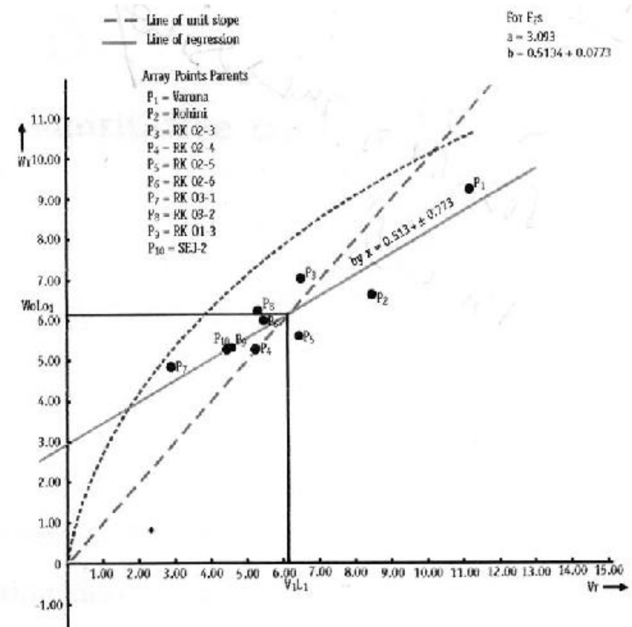

Fig. 10b. Wr, Vr graph for seed yield per plant

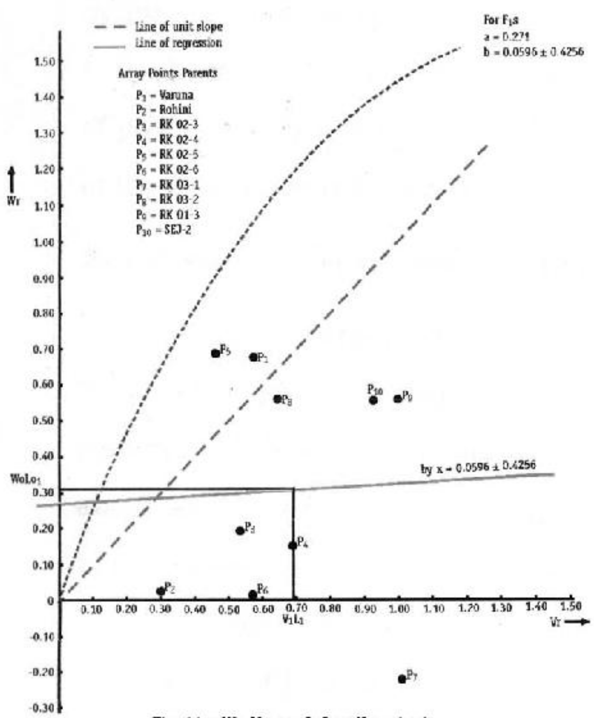

Fig. 11a. Wr, Vr graph for oil content

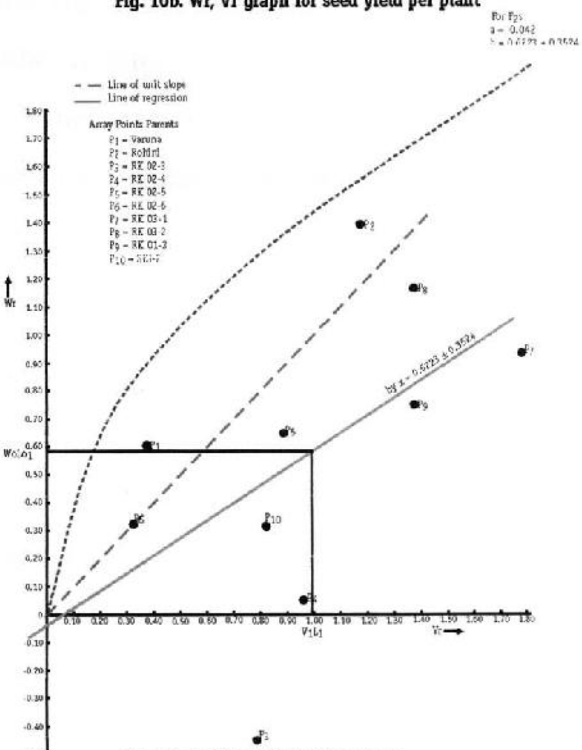

Fig. 11b. Wr, Vr graph for oil content

and oil content in F_2 and number of secondary branches per plant in F_1 generation as regression line passed below the origin.

On the basis of computed genetic variances from graphical analysis it is suggested that characters reflecting additive gene action can be improved by simple selection or pedigree method of breeding and traits governed by non additive gene action can be improved through biparental mating followed by recurrent selection.

Table 1: Uniformity test of Wr, Vr by t^2 and b for 11 characters in Indian mustard

Character	Generation	b	SE ±	1-b/SE b	b-0/SE b	t^2
Days to 50per cent flower	F_1	0.8178	0.0691	38.21**	171.20**	3.4890
	F_2	0.6590	0.0726	64.74*	125.06**	13.0052**
Plant height	F_1	1.2237	0.2234	-4.47**	24.53**	3.0289
	F_2	1.0275	0.1471	-1.29	47.52**	0.6047
Number of primary branches per plant	F_1	-0.0942	0.2347	19.85**	-1.70	1.3764
	F_2	0.5345	0.1738	15.42**	17.66**	1.8485
Number of secondary branches per plant	F_1	0.4481	0.3990	3.46**	2.81**	0.3535
	F_2	0.4233	0.1906	15.89**	11.64**	1.9328
Days to maturity	F_1	0.9398	0.1027	5.74**	89.09**	0.0249
	F_2	1.2422	0.2147	-5.26**	26.97**	3.5093
Length of main raceme	F_1	0.0288	0.2470	15.91**	0.485	1.0713
	F_2	0.5639	0.1090	36.69**	47.43**	7.2537**
Number of siliquae on main raceme	F_1	0.2469	0.1828	22.54**	7.38**	3.3745
	F_2	0.0772	0.1921	25.04**	2.08	3.3114
Number of seeds per siliqua	F_1	0.0649	0.2163	19.97**	1.39	2.0658
	F_2	0.1099	0.2012	21.96**	2.73*	2.7224
1000-seed weight	F_1	0.8268	0.0714	33.89**	162.04**	3.7208
	F_2	0.5843	0.0967	44.46**	62.46**	9.1207**
Seed yield per plant	F_1	0.3740	0.1071	54.53**	32.58**	12.8682**
	F_2	0.5134	0.0773	81.50**	85.89**	19.8566**
Oil content	F_1	0.0596	0.4256	5.19**	0.329	0.2825
	F_2	0.6223	0.3524	3.03*	5.02**	0.2917

*Significant at 5 per cent level, ** Significant at 1 per cent level

REFERENCES

Aksel, R. and Johnson, L. P.C. (1963). Analysis of diallel cross : a worked out example. *Advancing Frontiers of Pl.*, **2 :** 37-53.

Hayman, B. I. (1954). The analysis of variance of diallel table. *Biometrics*, **10 :** 235-244.

Jinks, J. L. and Hayman, B. I. (1953). The analysis of diallel cross. *Maize Genet. Newsletter*, **27 :** 48-54.

Jinks, J. L. (1954). The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics*, **39 :** 767-788

Jinks, J. L. (1955). A survey of the genetical basis of heterosis in variety of diallel crosses. *Heredity*, **9 :** 223-238.