

## Genetics of yield and other quantitative traits in Indian mustard

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Experiment comprising 100 treatments (10 parents + 45  $F_1$ s + 45  $F_2$ s) 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  $F_1$ s + 45  $F_2$ s) 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  $F_1$ s were grown in single row and the  $F_2$ s 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  $F_1$ s and twenty plants from  $F_2$ s were randomly selected for recording the observations on eleven characters (Table 1). The graphical analysis was based

on variance and covariance ( $V_r$  and  $W_r$  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 in  $F_1$  and 7 out of 11 attributes in  $F_2$  generation which revealed the validity of hypothesis. Seed yield per plant in  $F_1$  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 in  $F_1$  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

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