# GENETIC ANALYSIS OF SEED YIELD AND ITS IMPORTANT COMPONENT TRAITS IN RAPESEED (BRASSICA CAMPESTRIS L.)

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The knowledge of genetic architecture of yield and its components is necessary for deciding an effective and efficient breeding strategy. A survey of pertinent literature on rapeseed showed that, by and large, line x tester and diallel across approaches have been used in elucidating the gene effects, though the detection, estimation and interpretation of non-allelic interactions is relatively better understood at the level of first degree statistics (Mather and Jinks, 1971). An elaborate study was, therefore, carried out using generation mean analysis in crosses between yellow sarson and toria. The information on nature and magnitude of various gene effects controlling the inheritance of number of seeds/siliqua, number of siliquae/plant and seed yield/plant in Brassica campestris L. constitute the subject of this paper.

## MATERIALS AND METHODS

The experimental material for the present investigation comprised 15 generations ($P_1$, $P_2$, $F_1$, $F_2$, $F_3$, $B_1$, $B_2$, $B_{11}$, $B_{12}$, $B_{21}$, $B_{22}$, $B_1S$, $B_2S$, $B_1F_1$ and $B_2F_1$) of each of the two crosses ; A (Pant YS-6 x M-3) and B (Pant YS-6 x P.T. 303). The parent Pant YS-6 was yellow seeded and belonged to Brassica campestris Var. yellow sarson and other two parents were the brown seeded strains of B. campestris var. toria. The seed colour differences of the parents were utilized to raise two types of $F_3$'S (from brown and yellow seeded $F_2$ segregants). Consequently, two families were formed in each cross for the purpose of analyses. A (b) and A (y) were the two families of cross A, having 14 generations in common and differing in only $F_3$ (brown seeded) and $F_3$ (yellow seeded) respectively. Similarly B (b) and B (y) were the two families of cross B. Experimental material was evaluated in compact family block design with three replications. Different

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generations were represented by 3 to 7 rows of 3 m. per replication depending upon the expected variance.

Joint scaling test (Cavalli, 1952) was employed for detection and estimation of gene effects and testing the adequacy of models. Four genetic models, additive-dominance (AD), digenic interactions (DI), trigenic interactions (TI) and linked digenic interactions (LD), were applied in the order of increasing complexity, and inferences were drawn from the most adequate model (Mather and Jinks, 1971).

## RESULTS AND DISCUSSION

There were significant differences amongst generations for all three characters. However, differences among families were significant for number of seeds/siliqua and number of siliquae/plant only.

The outcome of the goodness-of-fit test for number of seeds/siliqua showed that DI model was adequate in all the four families (Table-1). The estimates of mean (m) and additive ('d') effects were highly significant in all the families. However, dominance effects were non-significant. Epistatic effects appeared to be important in all the families, except in family A(b). With regard to individual epistatic gene effects, interaction due to average effect of non-allelic genes ('$i_{ab/}$') contributed significantly in family A(y) whereas additive x dominance effect ('$j_{a/b}$') appeared to contribute more in families B(b) and B(y). The relative magnitude of ('$j_{a/b}$') was several times higher than corresponding standard errors and the additive effects. Patnaik and Murty (1978), however, noticed the higher magnitude of dominance x dominance effects ('$1/_{ab}$').

For number of siliquae/plant the fitness test for different genetic models revealed the adequacy of DI model in respect of A(b) and A(y) and TI model for B(b) and B(Y) families (Table-2).

The DI model identified the estimates of m, 'd', '$i_{a/b}$', and '$j_{a/b}$' parameters to be highly significant which indicated the predominance of fixable effects. For family A(y), additive effects, dominance effects ('h') as well as all the digenic-interactions ('$i_{ab/}$', '$j_{a/b}$', '$l_{/ab}$') were highly significant which revealed the importance of both fixable as well as non-fixable effects. However, in terms of relative magnitude the preponderance of non-fixable effects was evident. The TI model which was found adequate in families B(b) and B(y), detected the significant estimates of 7 out of 10 parameters (Table-2). The relative magnitude and direction of each parameter was similar in both the families. It was clear from the significant estimates of different parameters that the gene effects due to dominance and all interactions involving dominance ('h', '$l_{ab/}$', '$l_{abc/}$', '$j_{a/b}$', '$j_{ab/c}$', '$j_{a/bc}$') were more important for the expression of number of siliquae/plant. By and large the above findings are in conformity with the earlier reports (Labana _et al_., 1978 and Singh _et al_., 1982) where preponderance of non-fixable effects have been reported in Indian rapeseed.

Table-1 : Estimates of genetic parameters and chi-square value for the most adequate model for number of seeds/siliqua.

| Parameters | Families | | | |
|---|---|---|---|---|
| | A(b) | A(y) | B(b) | B(y) |
| | DI | DI | DI | DI |
| m | 13.26** ± 0.70 | 12.42** ± 0.66 | 15.31** ± 1.39 | 14.83** ± 0.76 |
| 'd' | 1.23** ± 0.39 | 1.43** ± 0.39 | 1.98** ± 0.21 | 1.98** ± 0.21 |
| 'h' | −2.11 ± 2.21 | −0.13 ± 2.13 | −5.20 ± 3.67 | −4.07 ± 2.40 |
| 'iab/' | 0.85 ± 0.82 | 1.88* ± 0.77 | −0.35 ± 1.39 | 0.12 ± 0.76 |
| 'ja/b' | −2.24 ± 1.28 | −2.47 ± 1.28 | −8.61** ± 1.24 | −8.63** ± 1.24 |
| 'l/ab' | 1.39 ± 1.78 | 0.22 ± 1.75 | 2.59 ± 2.37 | 1.93 ± 1.74 |
| No. of parameters | 6 | 6 | 6 | 6 |
| D.F. | 9 | 9 | 9 | 9 |
| Chi-square value | 14.597 | 19.471 | 23.112 | 21.461 |
| Probability | 0.103 | 0.022 | 0.008 | 0.515 |

*DI : Digenic interaction model.*

**, ** : Significant at 5% and 1% levels, respectively.*

Table-2 : Estimates of genetic parameters and chi-square value for the most adequate model for number of siliquae/plant.

| Parameters | Families | | | |
|---|---|---|---|---|
| | A(b) | A(y) | B(b) | B(y) |
| | DI | DI | TI | TI |
| m | 370.15** ± 35.96 | 480.12** ± 32.87 | 619.63** ± 12.68 | 638.25** ± 30.50 |
| 'd' | 54.35** ± 5.70 | 54.80** ± 5.70 | −145.66 ± 131.52 | −153.25 ± 137.61 |
| 'h' | −144.81 ± 106.80 | −425.00** ± 100.16 | −1599.19** ± 361.26 | −1675.00** ± 608.71 |
| 'iab/' | −164.03** ± 35.22 | −271.81** ± 32.20 | −393.75** ± 52.29 | −411.31** ± 129.94 |
| 'ja/b' | −284.50** ± 42.87 | −244.43** ± 42.36 | 39.94 ± 304.63 | 56.38 ± 317.30 |
| 'l/ab' | 102.00 ± 76.37 | 274.06** ± 72.90 | 2558.00** ± 728.15 | 2662.00** ± 967.66 |
| 'iabc/' | | | 203.09 ± 130.95 | 210.00 ± 137.06 |
| 'jab/c' | | | 1005.94** ± 164.46 | 1044.81** ± 290.90 |
| 'ja/bc' | | | 631.06* ± 288.27 | 620.88* ± 293.84 |
| 'l/abc' | | | −1179.63** ± 455.75 | −1226.31* ± 528.68 |
| No. of parameters | 6 | 6 | 10 | 10 |
| D.F. | 9 | 9 | 5 | 5 |
| Chi-square value | 28.722 | 23.707 | 8.414 | 8.998 |
| Probability | 0.007 | 0.007 | 0.142 | 0.112 |

*DI : Digenic interaction model ; TI : Trigenic interaction model.*

**, ** : Significant at 5% and 1% levels, respectively.*

For seed yield/plant which is recognised as most complex trait, the results of joint scaling test for testing the validity of different models showed that DI model was adequate in family A(y) whereas in other three families TI model was adequate (Table-3). Of the main effects, dominance effects were found to be important in families A(b) and A(y) whereas additive effects were important in other two families. Non-allelic interactions due to average effects of genes were important in all the families. Dominance x dominance effects assumed importance in family A(y) only whereas 'j' type of interactions were important in other three families though with differing signs. In general, the magnitude of trigenic-interaction was pronounced in families B(b) and B(y). The results are in agreement with those of Labana *et al.*, 1978 ; Patnaik and Murty, 1978 ; Duhoon *et al.*, 1982 and Singh *et al.*, 1982, who found the preponderance of non-additive effects.

Considering the overall results it can be concluded that the genetic control of the characters, particularly siliquae number and seed yield/plant was quite complex. Linked digenic interaction model was not adequate in any of the cases which suggested the complete lack of interactions between linked pairs of genes. Epistatic effects were more important than additive as well as dominance effects for siliquae number and seed yield/plant. For number of seeds/siliqua, the additive genetic effects were more important in both the crosses but non-allelic interactions between additive and dominance effects were also important in cross B only. However, dominance appeared unimportant in both the crosses. This suggested that with the increasing complexity of the inheritance of a particular quantitative character, there is corresponding increase in the contributions made by epistasis (particularly the interactions involving dominance). Similar results were also obtained by Gamble (1962) in the inheritance of yield and yield attributes in maize.

The significant estimates of different parameters for siliquae number and seed yield/plant revealed the appreciable amounts of fixable effects, though lower in magnitude compared to non-fixable effects, which indicated the possibility of improvement through simple selections. However, fixable effects present in the form of '$i_{ab/}$' and '$i_{abc/}$' tend to suggest that selection in early segregating generations may not be effective. Therefore, selection has to be relaxed to the later generations so as to allow the fixation of these desirable epistatic combinations (Matzinger, 1963). A large portion of the genetic control which is due to dominance, and digenic and trigenic interactions involving dominance ('h', '$j_{a/b}$', '$l_{/ab}$', '$j_{ab/c}$', '$j_{ab/c}$' and '$l_{/abc}$') point to the need for exploitation of heterosis. The selection programme aiming to improve such traits in a population should accumulate the genes conditioning fixable effects and simultaneously maintain genetic heterogeneity in the population for manifestation of dominance and epistatic effects. One of the approaches to achieve the above objective may be to intermate the selections of early generations in bi-parental fashion which could hasten the settling of desirable epistatic combinations and finally the best families may be bulked to produce a phenotypically uniform and a genetically buffered variety. The improvement in seeds/siliqua shall automatically

Table-3 : Estimates of genetic parameters and Chi-square value for the most adequate model for seed yield/plant.

| Parameters | Families | | | |
|---|---|---|---|---|
| | A(b) | A(y) | B(b) | B(y) |
| | TI | DI | TI | TI |
| m | 0.79 ± 1.46 | 8.60** ± 1.09 | 5.69 ± 3.51 | 4.34 ± 3.71 |
| 'd' | −1.13 ± 3.47 | 0.21 ± 0.37 | 9.35* ± 3.75 | 8.83* ± 3.78 |
| 'h' | 20.57* ± 9.46 | −8.72* ± 3.44 | −6.68 ± 20.50 | −1.25 ± 21.06 |
| 'iab/' | 3.94** ± 1.48 | −4.07** ± 0.98 | −0.54 ± 3.51 | 0.01 ± 3.71 |
| 'ja/b' | 2.48 ± 8.26 | −1.31 ± 1.38 | −30.13** ± 8.89 | −29.13** ± 8.93 |
| 'l/ab' | −26.63 ± 18.48 | 6.35* ± 2.71 | 14.90 ± 35.02 | 7.98 ± 35.57 |
| 'iabc/' | 1.37 ± 3.43 | | −9.04* ± 3.73 | −8.52* ± 3.76 |
| 'jab/c' | −15.58** ± 5.24 | | 8.95 ± 12.26 | 6.35 ± 12.48 |
| 'ja/bc' | −3.95 ± 7.37 | | 36.46** ± 9.07 | 36.04** ± 9.08 |
| 'l/abc' | 11.40 ± 10.75 | | −5.32 ± 18.61 | −2.48 ± 18.79 |
| No. of parameters | 10 | 6 | 10 | 10 |
| D.F. | 5 | 9 | 5 | 5 |
| Chi-square value | 4.669 | 8.741 | 12.287 | 13.904 |
| Probability | 0.463 | 0.465 | 0.034 | 0.017 |

*DI : Digenic interaction model; TI : Trigenic interaction model.*

*, ** *Significant at 5 % and 1 % levels respectively.*

be effected through above procedure as it is predominantly under additive genetic control.

It was also gratifying that the classification of the material based on seed coat colour showed marked influence on the inheritance of these characters. It was more so for seed yield/plant.

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