

GENETIC ARCHITECTURE FOR SEED YIELD AND ITS COMPONENTS IN INDIAN MUSTARD, *BRASSICA JUNCEA* (L.) (CZERN AND COSS)

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ABSTRACT

Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of two crosses namely PRQ-9701-46 × Kranti (C_1) PRQ-9701-46 × Pusa Bold (C_2) were evaluated in compact family block design with 3 replications under two set of environments viz., timely sown condition (TS) and late sown condition (LS). Observations were recorded on fourteen important quantitative traits namely, days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, length of main shoot, number so siliquae on main shoot, number of primary branches, number of secondary branches, siliqua length, number of seeds per siliqua, seed per plant, 1000-seed weight, oil content and harvest-index. Additive effects were found to be more impotent in the inheritance of days to flower initiation.

Additive × additive effect was relatively more important for all characters except days to flower initiation, days to 50% flowering, number of primary branches and number of secondary branches, dominance for plant height, length of main shoot, number of siliquae on main shoot, seeds per siliqua, seed yield per plant, 100-seed weight, oil content and harvest index, dominance × dominance for days to flower initiation, number of primary branches, additive × dominance for number of secondary branches and plant height.

Key words: Mustard, Generation means, Gene action, Yield components

INTRODUCTION

In recent years though there has been an increase in the area and production of rapeseed mustard, the average productivity in India is quite low in comparison to that in some of the developed countries. In India, however production of edible oils is about 50% of the requirements. Consequently, large quantities are being imported to make the shortfall, which in turn, is a heavy drain on foreign exchange resources, Vigorous efforts, therefore, are needed to increase the yield levels and to achieve self-sufficiency. Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. Hence, in the present investigation, an effort has been made to find out the inheritance of yield and its attributes for their further utilization in the breeding programme.

MATERIAL AND METHODS

Six generations namely, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of each of these two crosses viz.; PRQ 9701-46 × Kranti (C_1), PRQ 9701-46 × Pusa Bold were evaluated in a compact family block design with three replications in 5m long rows spaced 30cm, apart with plant to plant distance of 10cm during rabi 2003-04. The distance of 10cm between plants was maintained by thinning. One border row on either side of main plots was sown with a variety of mustard (Vardan) and were treated as non-experimental. The whole experimental was planted at two sowing dates viz., 22.10.2004 for timely sown condition (TS) and 13.11.2004 for late sown condition (LS). The numbers of rows were different for different progenies. Each plot thus consisted of different number of rows i.e., single row for parents (P_1 and P_2) and F_1 's three rows for backcrosses (BC_1 and BC_2) and seven rows for F_2 generations. Ten randomly selected plants each of P_1 , P_2 and F_1 , 40 plants of F_2 and 20 plants each of BC_1 and BC_2 generations were utilized for recording observations on various characters. Observations were recorded on important quantitative traits namely, days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, length of main shoot, siliquae on main shoot, number of primary branches, number of secondary branches, siliqua length, number of seeds per siliqua, seed yield per plant, 1000-seed weight, oil content and harvest index. The normal packages of agronomic practices were followed in raising the crop in experiment. The data were subjected to scaling test (Mather, 1949) to detect the presence of epistasis and genetic parameters m , d , h , l , j , and 1 were estimated. In case of significance of scaling tests, data were then subjected to the estimation of various genetic components as per Jinks and Jones (1958). More precise estimates of these parameters were then obtained by using joint scaling tests (Cavalli, 1952). Adequacy of two models i.e., additive-dominance (3 parameters) and digenic interactions (5 parameters) model was tested by joint scaling tests. In case, where additive-dominance (3 parameters) and digenic interaction (5 parameters) models were inadequate, parameters of complex model, digenic interactions (6 parameters) model have been described.

RESULTS AND DISCUSSION

The scaling test A, B, C and D revealed significance deviation from zero in all the crosses for all the characters except C_1 (LS) for days to flower initiation; C_1 (LS) and C_2 (TS) for days to 50% flowering; C_2 (TS and LS) for days to maturity; C_1 (LS) for length of

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Table 2. Cont

Crosses	Environment	m	d	h	i	j	l	χ^2	Type of epistasis
Days to flower initiation									
C ₁	TS	-2.26* ±0.56	-0.033±0.13	29.43** ±1.35	7.53**±0.54	-1.33*±0.40	-18.99*±0.83	-	Duplicate
LS	16.46*±4.52	-1.18±0.95	-15.01±12.98	-11.09±4.39	-	-	8.18±8.62	0.13(ns)	-
C ₂	TS	4.90**±0.49	0.46**±0.04	6.06**±1.05	-0.59±0.48	0.46* ±0.18	-5.33**±0.60	-	Duplicate
LS	16.45**±1.88	0.05±0.42	-19.88*±5.48	-12.01**±1.80	-	-	7.97±3.63	3.58(ns)	-
Number of siliqua length									
C ₁	TS	3.85* ±0.33	0.56±0.07	1.16±0.85	0.79*±0.30	-	-0.15±0.55	1.61(ns)	-
LS	4.45**±0.11	0.07±0.11	0.16±0.21	0.93±0.63	-	-	0.30±0.79	7.41(ns)	-
C ₂	TS	4.38**±0.63	-0.01±0.07	0.55±1.41	0.48*±0.14	-	-	0.01(ns)	-
LS	4.66**±0.07	0.09 ±0.06	0.48*±0.14	-	-	-	-	3.80(ns)	-
Number of seeds per siliqua									
C ₁	TS	9.78* ±0.63	0.21±0.07	7.78*±1.81	2.73**±0.62	-1.16±0.59	-4.16*±1.25	-	Duplicate
LS	13.16**±0.16	-0.01±0.18	0.51±0.45	-	-	-	-	6.38(ns)	-
C ₂	TS	12.89**±0.10	0.43**±0.10	0.38±0.16	-	-	-	6.99(ns)	-
LS	12.66**±0.14	0.30±0.14	0.66±0.30	-	-	-	-	4.88(ns)	-
Number of seed yield per plant									
C ₁	TS	-8.76±6.17	0.18±0.89	52.47*±17.61	12.58±6.07	-	-34.55*±11.67	0.61(ns)	Duplicate
LS	5.28** ±0.37	-1.08±0.56	2.32*±0.67	-	-	-	-	7.53(ns)	-
C ₂	TS	7.88*±0.80	1.77*±0.71	2.14±1.76	-	-	-	6.00(ns)	-
LS	-0.47±1.53	0.37±0.34	17.35**±4.01	3.47*±1.42	-	-	-13.67**±2.54	2.39(ns)	Duplicate
1000-seed weight									
C ₁	TS	3.04**±0.09	0.07±0.09	0.003±0.09	-	-	-	4.49(ns)	-
LS	2.86*±0.10	0.004±0.09	-0.02±0.16	-	-	-	-	0.24(ns)	-
C ₂	TS	1.71*±0.44	-0.21*±0.03	4.36*±0.98	1.58*±0.44	-	-2.82**±0.57	0.67(ns)	Duplicate
LS	3.08**±0.06	-0.10±0.05	-0.84±0.12	-	-	-	-	1.73(ns)	-
Oil content									
C ₁	TS	39.20**±0.50	1.09±0.47	1.94±1.00	-	-	-	4.12(ns)	-
LS	28.53**±2.43	-0.84 ±0.50	21.25*±6.71	6.83*±2.39	-	-	-12.44**±4.44	0.23(ns)	Duplicate
C ₂	TS	36.88**±1.30	-0.96±0.45	10.43*±3.84	3.06*±1.25	-	-7.18*±2.76	0.68(ns)	Duplicate
LS	28.25**±1.58	-0.79±0.41	23.40**±4.45	7.27**±1.40	-	-	-15.24**±3.49	0.46(ns)	Duplicate
Harvest index									
C ₁	TS	1.40± 6.74	0.72± 1.33	50.76* ±15.91	12.35±6.30	-	-30.28* ± 9.70	0.24(ns)	Duplicate
LS	5.61± 3.21	-0.29±0.51	23.26*± 7.31	9.77**±3.20	-	-	-9.04 ± 4.32	0.09(ns)	-
C ₂	TS	13.15± 6.78	-0.75± 0.88	17.52 ± 14.36	7.32±6.72	6.82±2.59	-8.72 ± 7.81	-	-
LS	0.42± 4.65	-0.85 ± 0.70	46.59** ±10.45	11.96 ± 4.50	-	-	-33.66**±6.08	0.26(ns)	Duplicate

TS=Timely sown condition; LS=Late sown condition; ns=Non-significant
 * Significant at 5% level
 ** Significant at 1% level

dominance effect. Significant additive \times additive action fraction of intra allelic interaction however indicated the possibility of manipulating these traits by selection in subsequent generations.

Considering overall results it was apparent that most of the characters in either of the crosses were found to be under the control of additive and non-additive gene effects coupled with duplicate type of epistasis indicating that heterosis breeding and recurrent selection would be more fruitful for the improvement of most of the characters. The duplicate epistasis for most of the characters showed their complex nature of inheritance. Therefore, breeding strategies should be designed accordingly to get desired results. Use of reciprocal recurrent selection has been suggested to improve the characters when both additive and non-additive genes are involved in expression of traits. (Comstock *et al.*, 1949).

Acknowledgement

The author thanks GBPUA & T, Pantnagar (Uttarakhand) and Indian Council of Agricultural Research (ICAR) New Delhi for providing financial assistance for the research work.

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