

GENE EFFECTS FOR SEED YIELD, YIELD COMPONENTS AND DEVELOPMENTAL TRAITS IN INDIAN MUSTARD (Brassica juncea (L.) Czern and Coss.)

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SUMMARY

Nature of gene action for seed yield, yield components and two developmental traits, viz. synchrony of branching, and synchrony of flowering in Indian mustard were analysed through estimates of gene effects from generation means of three intervarietal crosses, RLM 514 x RH 761, RLM 198 x RLM 752 and RLM 356 x Pant Rai 15. Additive, dominance and epistatic gene effects were involved though dominance and epistatic gene effects were predominant for a number of traits. Considering the individual epistatic gene effects, the additive x additive gene action was higher for seed yield, days to flower, primary branches, number of siliquae on the main raceme, synchrony of branching and synchrony of flowering; additive x dominance gene action for seeds per siliqua and dominance x dominance gene action in case of plant height. The complementary type of epistasis played an important role for the direct yield components except for seeds per siliqua. Among the three crosses, two crosses, viz. RLM 514 x RH 761 and RLM 356 x Pant Rai 15 were identified as promising for exploitation of fixable gene effects through the use of biparental mating.

INTRODUCTION

Amongst Brassicaceae, Indian mustard (Brassica juncea (L.) Czern and Coss.) has the maximum area and production in Indian subcontinent. However, studies on genetics of developmental traits related to productivity of yield attributes for planning an effective breeding programme are still inconclusive. The present study is an attempt to determine the nature of gene action for such traits from the means of six basic generations.

MATERIAL AND METHODS

The experimental material consisted of P_1 , P_2 , F_1 , F_2 , B_1 and B_2 generations of three intervarietal crosses (Table 1) involving five genetically diverse parents, viz. RLM 514, RLM 198, RLM 356, RH 761 and Pant Rai 15. The six generations of the crosses were sown in compact-family block design, with three replications,

during 1979-1980. The material was evaluated for eight characters including two developmental traits, viz. synchrony of branching and synchrony of flowering. Synchrony of the developmental traits was scored by using a scale of 1 (indicating lowest level of expression of the traits) to 10 (indicating highest level of expression of traits). The scaling tests of Mather (1949) were performed to detect non-allelic interactions. The components of gene effects were estimated from generation means according to the formulae of Jinks and Jones (1958).

RESULTS AND DISCUSSIONS

Additive gene effects were significant in the inheritance of days to flower, primary branches, synchrony of branching, synchrony of flowering and siliquae on the main raceme (Table 1). Both additive and dominance effects were significant for days to flower and plant height. Among the interaction components, additive x additive interaction (i) was significant for seed yield, days to flower, primary branches, siliquae on the main raceme, synchrony of branching and synchrony of flowering. Additive x dominance interaction (j) was important for seeds/siliqua and dominance x dominance interaction (l) for plant height. The presence of significant additive (d) and additive x additive (i) effects coupled with complementary epistasis for some traits in some crosses exhibited the fixable nature of the characters, if selection is practised in advanced generations.

Transgressive segregants may occur in later generations due to complementary epistasis. The presence of additive gene effects (d) for developmental traits showed potential for their breeding manipulations (Patnaik and Murty, 1978). The similarity in the nature of gene action of developmental traits to that of direct yield attributes might have originated as a result of simultaneous selections in nature for constellation of characters related to development and productivity (Ram, Murty and Doloi, 1969). In such cases, favourable additive genes can be accentuated by intermating the early segregation isolates. Among the three crosses, two crosses, viz. RLM 514 x RH 761 and RLM 356 x Pant Rai 15 were identified as promising for exploitation of fixable gene effects through the use of biparental mating.

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Table 1 : Estimates of gene effects for eight characters in three crosses, A. RLM 514 x RH 761
B. RLM 198 x RLM 752 and C. RLM 356 x Pant Rai 15.

Cross No.	m	(d)	(h)	(i)	(j)	(l)	Type of epistasis
1. Days to flower							
A.	64.73**	-12.04**	16.04**	6.45**	-4.32**	8.82**	C
B.	67.45**	-17.50**	-12.44**	-5.06**	4.82**	11.46**	D
C.	60.30**	-10.22**	6.42*	5.34**	12.34**	6.25	D
2. Plant height							
A.	185.50**	-6.82**	22.14**	14.66**	-2.40	19.22**	C
B.	192.36**	3.16**	-14.48*	10.08**	11.50*	12.20**	D
C.	140.34**	20.42**	28.60**	22.38**	-21.06**	-10.40**	D
3. Number of primary branches/plant							
A.	10.28**	4.30**	-5.86*	3.28**	6.02*	3.95*	C
B.	8.75**	-2.04	10.60**	6.16**	10.24*	-14.21**	D
C.	7.48**	3.20**	-6.37*	8.30**	5.61	-9.30*	C
4. Synchrony of branching							
A.	5.80**	1.85**	0.90	1.68**	-0.56	1.64	C
B.	5.04**	0.56	1.06	1.10	0.68	-1.02	D
C.	6.40**	1.96**	0.80	0.88*	2.16*	3.82*	C
5. Synchrony of flowering							
A.	5.78**	1.94**	-2.04**	1.92**	0.63	8.44*	D
B.	5.11*	-0.86*	-1.10	-0.84	-2.02	3.04	D
C.	6.04**	0.92*	-1.87*	1.86**	-0.64	6.32*	D
6. Number of siliquae on the main raceme							
A.	42.21**	2.24*	18.46**	14.62**	2.82	-18.10**	D
B.	48.30**	8.08**	-14.04**	13.30**	-8.36**	-12.32*	C
C.	30.12**	6.12*	24.80**	22.10**	-12.86**	14.41*	C
7. Seeds per siliqua							
A.	10.88**	-0.36	0.86	0.94	3.48**	-4.85**	D
B.	12.04**	0.64	1.46*	-1.02*	10.96**	-2.92*	D
C.	9.95**	1.08*	0.82	0.93	2.04**	-2.04	D
8. Seed yield per plant							
A.	22.32**	6.40**	-28.62	62.21**	7.32*	-72.14**	C
B.	26.10**	3.22	48.30*	51.86**	-9.54**	-83.02**	D
C.	18.54**	5.30*	32.18*	44.04**	4.66	22.37	C

* and ** represent 5% and 1% level of significance respectively.