Indian Journal of Agricultural Sciences **82** (10): 881–4, October 2012

Genetics of yield and yield-contributing traits in Indian mustard (*Brassica juncea*)

V V SINGH[1], J S CHAUHAN[2], BHAGIRATH RAM[3], MAHARAJ SINGH[4] and M L MEENA[5]

Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur, Rajasthan 321 303

Received: 5 May 2012; Revised accepted: 2 July 2012

ABSTRACT

Generation mean analysis was performed using two crosses Maya × BPR 543-2 and BPR 543-2 × BPR 2 to study the nature and magnitude of gene effects for yield and its component characters in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. The F_1, F_2, BC_1 and BC_2 of these crosses alongwith P_1 and P_2 were studied for fourteen morphological traits. Additive × dominance (*j*) type interaction was observed for plant height, main shoot length, primary branches/plant and seed yield/plant and (*h*) gene effect was found to be predominant in the expression of these traits. The cross BPR 543-2 × BPR 2 showed (*d*) and (*j*) effects for main shoot length, a simple additive-dominance model being adequate for the other cross to have a positive shift in the expression of the phenotypic means, it is essential to harness both the additive and non-additive gene effects prevalent in the main shoot length strength. The seed yield/plant in the cross Maya × BPR 543-2 showed (*d*), (*h*) and additive × additive (*i*) type gene interaction indicate, that this trait is under the control of both fixable and non-fixable gene effects. The additive × additive (*i*) type gene interaction and duplicate epistasis seen in this trait suggest the possibilities of obtaining transgressive segregants in later generations. The study revealed the importance of both additive and non-additive types of gene interaction for all the traits studied.

Key words: Bi-parental mating, *Brassica juncea,* Gene effect, Quantitative trait

Rapeseed–mustard group of crops are grown in diverse agro-climatic conditions ranging from north-eastern/north-western hills to down south under irrigated/rainfed, timely/late-sown, saline soils and mixed cropping. Indian mustard is predominantly grown species in this group and accounts for 80% of the cultivated area in India. There are two distinct and genetically diverse gene pools in *B. juncea*, the east European and the Indian gene pools (Srivastava *et al.* 2001). Being native to India, it possesses vast genetic variability for seed and drought tolerance characters. Despite this fact, limited efforts have been made in the past for improvement of this crop. Determination of suitable breeding method and selection strategy for improvement of a trait would depend on knowledge of gene effects operating in the breeding population. Generation mean analysis is an efficient tool to understand the nature of gene effects involved in the expression of a character. The generation mean analysis utilizes six different generations of a cross, viz parents P_1, P_2, their F_1, F_2, backcross BC_1 and BC_2 for estimation of gene effects and components of genetic variation in interacting and non-interacting crosses. Though generation mean analysis has been extensively used to understand the gene effects in different crops, but very few reports are available on the use of this technique for understanding the gene effects in Indian mustard. In view of this fact, present study was undertaken to estimate different kinds of gene effects playing important role in inheritance of seed yield and its contributing traits.

MATERIALS AND METHODS

Three Indian mustard genotypes namely; Maya, BPR 543-2 and BPR 2 were used for generating breeding material which resulted into six basic generations (P_1 and P_2 parent cultivars, the F_1 and F_2 first and second filial generations, and the BC_1 and BC_2 first and second back crosses) of two cross combinations, these combinations being Maya × BPR 543-2 and BPR 543-2 × BPR 2. The parental populations were grown in crossing block. Parents of the respective crosses were used as P_1 and P_2 and the F_1 generations of the particular cross was used as the female parent and back crossed to P_1 to produce the BC_1. F_1 was again backcrossed to P_2 to produce BC_2 and the F_1 hybrids were selfed to obtain F_2 seeds. All these six generations were produced during two consecutive cropping season, i e 2008–09 and 2009–10. P_1, P_2, F_1, F_2, BC_1, and BC_2 were evaluated in randomized block design with two replications during 2010–11 at research farm of Directorate of Rapeseed-Mustard Research,

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[1] Principal Scientist (e mail: vvs_71@yahoo.co.in); [2] Director (e mail: js_chau@ yahoo.com); [3] Senior Scientist (e mail: bhagirathram_icar@yahoo.com); [4] Senior Scientist (e mail: ms_drmr @rediffmail.com); [5] Technical Officer (e mail: meethalaldrmr@ gmail.com)

Bharatpur. All the genotypes were grown in row of 3 metre length. However number of rows varied for different generations, i e three rows, for the non-segregating generation P_1, P_2 and F_1; 20 rows for the F_2; and 15 rows for the BC_1 and BC_2 generations. Since the non-segregating generations represent the homogeneous population while the segregating generations represent the heterogeneous population the sample (i e number of plants analysed) varied as follows: 10 plants for the P_1, P_2 and F_1 generations; 40 plants for the F_2 generations; and 30 plants for the BC_1 and BC_2 generations. The traits assessed were days to 50% flowering, plant height (cm), primary branches/plant, secondary branches/plant, main shoot length (cm), siliqua on main shoot length, days to maturity, dry matter per plant, siliqua length (cm), siliqua per plant, seeds per siliqua, seed yield per plant (g), 1 000-seed weight (g) and oil content (%). The mean values, standard errors and variances of the different generation were subjected to weighed least-squares analysis using the scaling test and joint scaling test to estimate gene effects. The genetic effects were estimated using the models suggested by Mather and Jinks (1971). The significance of the scales and gene effects were tested by using the t-test (Singh and Chaudhary 1985). The scaling tests of A, B, C and D (Mather 1949) were performed for all the characters under study to judge the adequacy of additive- dominance model.

RESULTS AND METHODS

The values of six generations for the joint scaling tests and their interaction effect being presented in Table 1. The additive, dominance and epistatic types of gene interaction in each cross for different traits were found to be different from each other. The dominance × dominance (*l*) interaction was larger than the additive × additive (*i*) and additive × dominance (*j*) effects put together, while for the main effect the dominance component (*h*) was greater than the additive (*d*) component. The dominance (*h*) and dominance × dominance (*l*) effects were in opposite direction, suggesting that duplicate-type epistasis occurred in most cases and indicating predominantly dispersed alleles at the interacting loci. Dominance gene effects were found to be relatively more important, as indicated by the fact that in all cases the dominance (*h*) values were higher than the additive (*d*) values.

The days to 50% flowering trait for the BPR 543-2 × BPR 2 cross showed a pronounced additive × additive (*i*) and dominance × dominance (*l*) type gene interaction. For this trait additive × additive (*i*) and dominance × dominance (*l*) gene interaction were found to play a major role. Duplicate epistatis for this trait has also been reported by Kemparaju *et al*. (2009).

Kemparaju *et al*. (2009) reported that additive (d), dominance (h) and additive × additive (i) gene effects were found to be negative and high in primary crosses NPJ 102 × Laxmi, NPJ 102 × Pusa Jagannath, NPJ 102 × BEC 144 and Pusa Agrani × Pusa Jagannath for days to 50% flowering. It indicates that additive and additive × additive effects in these crosses can be fixed by any simple selection procedure and non- additive and dominance × dominance (l) epistasis components of genetic variance can be improved by recurrent or reciprocal recurrent selection for this trait.

In the case of the plant height trait, the dominance (*h*) and additive × dominance (*j*) effects were significant in the Maya × BPR 543-2 and BPR 543-2 × BPR 2 crosses. This trait showed complementary and duplicate type epistasis in all cases. The additive × dominance (*j*) effect was higher than either dominance (*h*) or additive (*d*) effects, although, dominance (*h*) was significant for the plant height. In the case of primary branches per plant trait the dominance × dominance (*l*) non-allelic interaction was significant and higher than additive x dominance (*j*) effects in the Maya × BPR 543-2 cross, while additive × dominance (*j*) and dominance × dominance (*l*) non-allelic interaction were significant in the BPR 543-2 × BPR 2 cross. Singh *et al* (2007) reported duplicate epistasis for this trait. In regard to secondary branches/plant trait all the gene interaction effects were non-significant except additive × dominance (*j*) effect negative significant for the Maya × BPR 543-2 and BPR 543-2 × BPR 2 crosses. Maya × BPR 543-2 cross showed complementary type epistasis, while BPR 543-2 × BPR 2 cross observed duplicate epistasis for this trait. For the main shoot length trait the additive × dominance (*j*) effects was negative significant in the Maya × BPR 543-2 cross, while the additive (*d*) and additive × dominance (*j*) effects were significant in the BPR 543-2 × BPR 2 cross. This trait showed duplicate-type epistasis in both the crosses.

In case of siliqua on main shoot length trait the dominance × dominance (*l*) non-allelic interaction was higher and significant in the Maya × BPR 543-2 cross, while additive × additive (*i*) and dominance × dominance (*l*) non-allelic interaction were significant in the BPR 543-2 × BPR 2. This trait also showed duplicate type epistasis in both crosses. Singh *et al.* (2007) reported duplicate epistasis for this trait. In the case of siliqua length trait all the gene interaction effects were non-significant for the Maya × BPR 543-2 and BPR 543-2 × BPR 2 crosses and complementary epistasis were observed for this trait. For the siliqua per plant trait the additive (*d*) and dominance (*h*) gene effect were significant in the BPR 543-2 × BPR 2 cross, while only the additive (*d*) effect was significant in the Maya × BPR 543-2 cross. This trait also showed duplicate type epistasis in both crosses. For days to maturity trait Maya × BPR 543-2 cross showed additive (*d*) significant negative gene interaction. For this trait additive (*d*) and dominance (*h*) gene interaction were found to play a major role. Duplicate epistasis for this trait has also been reported by Kabdal and Singh (2010).

In regard to the seeds per siliqua trait all the gene interaction effects were non-significant except the dominance (*h*) effect for the Maya × BPR 543-2 cross. These results indicate that seeds per siliqua are predominantly controlled

Table 1 Estimates of components of generation means for different morphological characters under moisture stress condition in Indian mustard

Character	Crosses	Gene effects						Type of epistasis
		[m]	[d]	[h]	[i]	[j]	[l]	
Days to 50% flowering	(Maya × BPR 543-2)	57.68**	0.5	-0.54	-0.68	-15**	1.40	D
	(BPR 543-2 × BPR 2)	42.12**	-0.40	-0.78	4.51**	-23.55**	6.71**	D
Plant height (cm)	(Maya × BPR 543-2)	206.9**	-6.32**	12.72**	-0.01	199.15**	0.50	C
	(BPR 543-2 × BPR 2)	188.32**	-10.56**	8.92**	-0.02	205.13**	-0.87	D
Primary Branches/ plant	(Maya × BPR 543-2)	32.87**	-0.73	-54.51**	-26.48**	8.3**	26.49**	D
Secondary branches/ plant	(BPR 543-2 × BPR 2)	42.13**	-0.87	-36.16**	-23.11**	9.39**	41.56**	D
	(Maya × BPR 543-2)	7.71**	0.51	0.01	-0.2	-8.26**	0.04	C
Main shoot length (cm)	(BPR 543-2 × BPR 2)	4.69**	-0.69	2.11	0.3	-9.78**	-0.05	D
	(Maya × BPR 543-2)	64.41**	2.21	-2.12	0.02	-62.15**	0.02	D
Siliqua on main shoot length	(BPR 543-2 × BPR 2)	39.11**	8.13**	-5.59**	2.13	40.98**	2.46	D
	(Maya × BPR 543-2)	48.12**	2.36	-0.53	0.01	0.01	93.36**	D
Siliqua/plant	(BPR 543-2 × BPR 2)	61.25**	-2.56	-10.15**	6.35**	0.03	72.13**	D
	(Maya × BPR 543-2)	173.91**	22.43**	-7.24**	0.02	-0.01	0.01	D
	(BPR 543-2 × BPR 2)	105.45**	14.26**	10.55**	0.41	0.05	-4.85**	D
Siliqua length (cm)	(Maya × BPR 543-2)	4.4**	-0.14	0.13	-0.01	0.01	0.01	C
	(BPR 543-2 × BPR 2)	8.12**	-0.12	-0.10	0.52	2.15	1.12	C
Days to maturity	(Maya × BPR 543-2)	140.97**	2.67*	152.39**	0.02	0.01	-0.02	D
	(BPR 543-2 × BPR 2)	112.21**	-2.96*	102.41**	0.15	0.02	-0.01	D
Dry matter/plant	(Maya × BPR 543-2)	45.51**	8.29**	5.53**	0.02	0.01	-0.03	D
	(BPR 543-2 × BPR 2)	68.25**	24.21**	-4.29**	0.05	0.05	3.56*	D
Seeds/siliqua	(Maya × BPR 543-2)	45.19**	-0.09	-13.76**	0.02	-0.01	0.17	D
	(BPR 543-2 × BPR 2)	36.47**	-0.07	26.98**	0.09	-0.09	-0.56	D
Seed yield/plant (g)	(Maya × BPR 543-2)	-22.83**	-2.75*	44.55**	16.3**	41.74**	-16.28**	D
	(BPR 543-2 × BPR 2)	47.72**	-2.11	24.13**	28.36**	30.48**	-9.54**	D
1000-seed weight (gm)	(Maya × BPR 543-2)	-3.71*	-0.39	0.29	0.01	-0.01	20.09**	C
	(BPR 543-2 × BPR 2)	2.85*	1.23	0.22	1.05	9.11*	26.27**	C
Oil content (%)	(Maya × BPR 543-2)	41.41**	0.05	-0.52	-0.02	78.26**	0.84	D
	(BPR 543-2 × BPR 2)	33.14**	-0.06	-5.61**	2.54*	84.11**	2.25	D

M, Mid point; d, additive; h, dominance; i, additive × additive; j, additive × dominance; l, dominance × dominance. An asterisk (*) and (**) indicate that the value were significant by the t- test at the 5% and 1% probability level, respectively

by dominance type interaction effects and observed the duplicate epistasis for this trait. For the seed yield per plant trait the dominance (*h*) and additive x additive (*i*) effect were found to be the most important in both Maya × BPR 543-2 and BPR 543-2 × BPR 2 crosses. Duplicate epistasis was observed for this trait.

For the dry matter per plant trait the additive (*d*) and dominance (*h*) effects were significant in the Maya × BPR 543-2 cross, while the dominance × dominance (*l*) non-allelic interaction was significant in the BPR 543-2 × BPR 2. Duplicate epistasis was observed in both the crosses for this trait. In regard to the oil content (%) trait non-allelic additive × dominance (*j*) gene effects were found to be significantly and relatively more important because of higher than additive × additive (*i*) interaction effects in BPR 543-2 × BPR 2 cross and duplicate epistasis were observed for this trait.

In the case of 1 000-seed weight trait the dominance × dominance (*l*) non-allelic interaction was significant in the Maya × BPR 543-2 cross, while additive × dominance (*j*) effect was significant in the BPR 543-2 × BPR 2 cross and complementary – type epistasis were observed in both the crosses. Cheema *et al.* (2004) reported complementary epistasis for this trait. Additive × dominance (*j*) type interaction was observed for plant height, main shoot length, primary branches per plant and seed yield/plant and (*h*) gene effect was found to be predominant in the expression of these traits. These findings are in good agreement with those of Kumar *et al.* (2006), Tahir *et al*. (2007), Singh *et al* (2007), Prajapati *et al.* (2008), Upadhyay and Kumar (2008) and Yadav *et al*. (2011). The cross BPR 543-2 × BPR 2 showed (*d*) and (*j*) effects for main shoot length, a simple additive-dominance model being adequate for the other cross to have a positive shift in the expression of the phenotypic means it is essential to harness both the additive and additive and non-additive gene effects prevalent in the main shoot length strength. The seed yields per plant in the cross Maya × BPR 543-2 showed (*d*), (*h*) and additive × additive (*i*) type gene interaction indicate that this trait is under the control of both fixable and non-fixable gene effects. The additive × additive (*i*) type gene interaction and duplicate epistasis seen in this trait suggest the possibilities of obtaining transgressive segregants in later generations.

The additive effects and gene interaction dominance × dominance (*l*) or other type digenic complementary gene interaction can be exploited effectively by selection for the improvement of the characters. Use of reciprocal recurrent selection or bi-parental mating suggested improving the characters when both additive and non- additive gene effects are involved in the expression of these traits. Presence of non- additive gene effects for days to 50 % flowering, primary branches per plant, main shoot length, oil content and seed yield per plant indicating that conventional selection procedure may not be effective enough for improvement of yield. Therefore postponement of selection in later generation or intermating among the selected segregants followed by one or two generation of selfing could be suggested to break the undesirable linkage and allow the accumulation of favourable alleles for the improvement of this trait.

The different type of gene effects estimated provide a test for gene action and are useful for analyzing the genetic architecture of a crop so as to further improve desirable traits. The estimates obtained from each cross may be unique to that cross and may not be applicable to the parental population. Additive genetic variance formed the major part of genetic variance for the important yield component main shoot length trait. Therefore genetic improvement in the seed yield per plant trait would be easier through indirect selection for a component trait such as the main shoot length trait than through direct selection for seed yield itself.

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