GENERATION MEAN ANALYSIS FOR YIELD AND YIELD COMPONENTS IN INDIAN MUSTARD /BRASSICA JUNCEA /L./ CZERN AND COSS/

J.N.Sachan and B.Singh

Department of Plant Breeding
G.B.Pant University of Agriculture
and Technology, Pantnagar /Nainital/ U.P.,India

Abstract

Components of generation means were partitioned for yield and yield components, siliquae/plant, seeds/siliqua and 1000-seed weight in three crosses: Varuna x PR-5, Cross I; Varuna x YRT-3, Cross II and BRR63 x YRT-3, Cross III, of Indian mustard /Brassica juncea /L./ Czern and Coss/ cultivars using parents, F_1, F_2, F_3, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s, B_2s, B_1xF_1, B_2xF_1, B_{1bip}, B_{2bip}, F_2xP_1, F_2xP_2, F_2xF_1 and F_{2bip} generations. Additive-dominance model was adequate for siliquae/plant and 1000-seed weight in Cross I and seeds/siliqua and seed yield/plant in Cross III; digenic interactions model for seeds/siliqua in Crosses I and II and 1000-seed weight in Cross II and trigenic interactions model for siliquae/plant in Cross II.

Linked digenics model adequate for siliquae/plant in Cross III and seed yield/plant in Crosses I and II detected the importance of /i/, /j/ and /l/ interactions among linked pairs of genes. Complete association among the genes of greater effects in P_1 /higher mean parent/ was observed for siliquae/plant in Cross III and seed yield/plant in Cross I, whereas coupling phase of linkage was observed for seed yield/plant in Cross II.

Duplicate epistasis was evident for siliquae/plant in Cross II and seeds/siliqua in Cross I. Inadequacy of all the models fitted indicated the presence of higher order interactions for 1000-seed weight in Cross III.

The importance of fixable as well as nonfixable effects for different yield contributing characters in most cases suggested that the selection programme to improve yield in these cases should accumulate favourable genes and simultaneously maintain heterozygosity in the population for manifestation of non additive effects. Reciprocal recurrent selection /Comstock et al., 1949/ and Diallel selective mating system /Jensen, 1970/ for autogamous crops appear to be the best available methods to meet this requirement.

Introduction

The knowledge of mode of inheritance of complex quantitative characters is essential in deciding the most appropriate breeding method for faster improvement. Such information is inadequate and inconclusive in Indian mustard /*Brassica juncea* /L./ Czern and Coss/. Diallel line x tester and partial diallel techniques have usually been used for estimating gene effects with the assumption that epistatic effects are negligible. Additional evidences of the presence of components of epistatic gene effects in the inheritance of various quantitative attributes and their importance in genetic variation is however, required. Very few studies have been made allowing the partitioning of epistatic effects in Indian mustard. Therefore, present investigation was undertaken to estimate gene effects including the interactions among linked pairs of genes for yield and important yield component characters in Indian mustard /*Brassica juncea* /L./ Czern and Coss/.

Material and methods

The material included 21 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}, $B_2 x F_1$, $B_1 x F_1$, B_{1bip}, B_{2bip}, $F_2 x P_1$, $F_2 x P_2$, $F_2 x F_1$ and F_{2bip}/ of three crosses, viz; 'Varuna x PR-5'/Cross I/, 'Varuna x YRT-4' /Cross II/ and 'BRR-63 x YRT-4' /Cross III/. Notations for generations used are according to Jinks and Perkins /1969/. These progenies /generations/ were grown in a compact family block design with 3 replications at Crop Research

Centre, G.B.Pant University of Agriculture and Technology, Pantnagar during 1980-81. The crosses were randomized among the main plots within replication, and the progenies were randomized within these family main plots. The number of rows /2-10/ was different for different progenies depending upon the expected variances of generations. Each plot thus consisted of different number of rows, each of 3 meter length with spacing of 30 cm between rows and 15cm between plants was maintained by thinning. The two border rows on either side of main plots were sown with an early strain of mustard /Pant Rai 1D/ and were treated as non - experimental. Depending upon the expected variances of generations 5 to 30 plants were selected randomly from each plot, for recording the observation on number of siliquae/ plant, seeds/siliquae, 1000-seed weight and yield per plant.

The joint scaling test suggested by Cavalli /1952/ was applied to test the adequancy of genetic models as well as for estimating the parameters of the models. Four genetic models /viz; additive-dominance, digenic interactions, trigenic interactions and linked digenics/ were fitted successively for all the characters according to Jinks and Perkins /1969/. Degree of dispersion /rd/ was computed following Jinks and Jones /1958/.

Results

The means of different generations for yield and yield components are presented in Table 1. F_1 mean was higher than both the parents for siliquae/plant in Cross I, seeds/siliqua in Cross II and III and yield/plant in all the crosses. But, the F_1 mean was lower than both parents for seeds/siliqua in Cross I. F_1 mean was higher than mid--parent and tended towards higher mean parent for 1000 - seed weight in Cross II. However, F_1 mean was lower than mid parent and tended towards lower mean parent for siliquae/plant in Cross II and 1000-seed weight in Cross II and III. F_1 mean was higher than F_2 mean in all the cases except for seeds/siliqua and 1000-seed weight in Cross I and III, respectively.

Means of backcrosses/B_1 and B_2/ were higher than both parents for siliquae/plant in Cross I. Mean of B_1 was higher than the better parent for siliquae/plant, seeds/ siliqua and yield/plant in Cross III while the B_2 mean was higher than the better parent for siliquae/plant and yield/ plant in Cross II.

The Chi-square tests of goodness of fit of various models fitted to the generation means for yield and yield components are given in Table 2. The Chi-squares for additive-dominance model were non-significant /$P > 0.01$/ for siliquae/plant in Cross I and 1000-seed weight and yield/plant in Cross III. Non-significant Chi-squares for digenic interactions model were observed for seeds/siliqua in Cross I and II, and 1000-seed weight in Cross II. For trigenic interactions model, non-significant Chi-squares were obtained in Cross II for siliquae/plant.

Non-significant Chi-squares for linked digenics model were observed for siliquae/plant in Cross III and yield/ plant in Cross II. However, for 1000-seed weight in Cross III Chi-squares were significant for all the models tested.

The estimates of gene effects under adequate model for yield and its component characters are given in Table 3. The main effects /d/ as well as dominance effect /h/ were important for seeds/siliqua in all the crosses and 1000 - seed weight in Cross I. Additive effects /d/ contributed significantly in the inheritance of siliquae/plant in Cross III, 1000-seed weight in Cross II and seed yield/plant in Cross I and III, whereas dominance effects /h/ were important for siliquae/plant in Crosses I and II.

Digenic interactions additive x additive /iab// were important for siliquae/plant and 1000-seed weight in Cross II. Additive x dominance interactions / ja/b / contributed significantly in the inheritance of seeds/siliqua in Cross II. Dominance x dominance interactions / 1/ab / were important for siliquae/plant and seeds/siliqua in Crosses II and I, respectively.

Trigenic interactions, additive x additive x additive / iabc/ / contributed significantly to the inheritance of siliquae/plant in Cross II.

Digenic interactions among linked pairs of genes, additive x additive /i/, additive x dominance /j/ and dominance x dominance /l/ were important for siliquae/plant and yield/plant in Crosses III and I, respectively. However, additive x dominance /j/ and dominance x dominance /l/ interactions among linked pairs of genes contributed significantly in the inheritance of yield/plant in Cross II.

The estimates of degree of dispersion presented in table 3 indicated coupling phase of linkage for yield/plant in Cross III and complete association for siliquae/plant in Cross III and yield/plant in Cross II.

Discussion

Presence of dominance and/or epistasis was evident from the deviation of F_1 means from mid-parent for siliquae/plant, seeds/siliqua, 1000-seed weight and yield/plant in all the crosses. This was further confirmed by the estimates of dominance effects /h/ and/or one or more epistatic effects in all the cases except for yield/plant in Cross III. Superiority of F_1 over better parent indicated the existance of heterobeltiosis for siliquae/plant in Cross I; seeds/siliqua in Cross II and III and yield/plant in all the crosses.
Higher values of F_1 mean over mid-parental value revealed the presence of standard heterosis for 1000-seed weight in Cross II. However, higher values of F_2 means over F_1 means observed for seeds/siliqua and 1000-seed weight in Cross I and III respectively may be because of sampling variance.

Non-significant Chi-squares for additive-dominance model for siliquae/plant in Cross I, and seeds/siliqua, 1000-seed weight and yield/plant in Cross III revealed its adequacy and indicated that epistatic effects have no significant role in the inheritance in these cases. On the other hand significant Chi-squares for additive-dominance model for siliquae/plant and 1000-seed weight in Cross II and III; and seeds/siliqua and yield/plant in Cross I and II revealed its inadequacy and indicated the presence of epistatic effects in these cases.

Non-significant Chi-squares for digenic interactions model for seeds/siliqua in Cross I and II; and 1000-seed weight in Cross II indicated its adequacy and revealed that digenic interactions among unlinked genes are adequate to describe the generation means in these cases. Similarly, non-significant Chi-squares for trigenic interactions model for siliquae/plant in Cross II revealed its adequacy and indicated that nothing beyond trigenic interactions are involved in the inheritance of siliquae/plant in Cross II.

Non-significant Chi-squares for linked digenics model in Cross III for siliquae/plant and yield/plant in Cross I and II indicated its appropriateness and existance of linked epistasis in these cases. Significant Chi-squares for all the tested models in respect of 1000-seed weight for Cross III revealed the inadequacy of all the models and indicated the presence of higher order interactions.

Importance of fixable effects in the form of additive effects /d/ and/or additive x additive interactions /iab/ for siliquae/plant in Cross III; seeds/siliqua in all the crosses, 1000-seed weight in Cross I and II and yield/plant in Cross I and III indicated the potential for improvement in these traits through selection.

Desirable direction of dominance was evident from the positive values of /h/ for siliquae/plant in Cross I and seeds/siliqua in all the crosses. Considering the sign of /h/ and /l/, duplicate epistasis was evident for siliquae/plant in Cross II; seeds/siliqua in Cross I. Duplicate epistasis was also reported by Sachan and Singh /1986/ for siliquae/plant and Chaudhary and Sharma /1982/ for seeds/siliqua in Indian mustard. While the sign of the /l/ type of interactions is negative for siliquae/ plant in Cross III and yield/plant in Cross II, we have no direct estimates of /h/ because it is confounded with those of m and /l/.

The results of degree of dispersion revealed that higher mean parent /P_1/ contains all the genes of greater effect /rd=1/ for siliquae/plant in Cross III and yield/plant in Cross I. However, coupling phase of linkage /rd=0.62/ was observed for yield/plant in Cross II.

Presence of marked dominance effects and/or epistatic effects for siliquae/plant and seeds/siliqua in all the crosses:, 1000-seed weight and yield/plant in Crosses I and II emphasizes the need for maintaining heterozygosis in breeding populations. This is quite possible and practicable in Indian mustard where considerable amount of cross pollination does occur.

The importance of fixable as well as non fixable effects for yield and yield component characters suggested that the selection programme to improve yield in these populations should accumulate favourable genes and simultaneously maintain heterozygosity in the population for manifestation of non additive effects. Reciprocal recurrent selection /Comstock et al., 1948/ and diallel selective mating system /Jensen, 1970/ for autogamous crops appear to be the best available methods to meet the requirements. The method proposed by Singh et al. /1981/ in which selections in early generations may be intermated in biparental fashion, and ultimately the best families may be bulked to produce phenotypically uniform but genetically buffered population, may also be used with success.

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Table 1. Generation means over replications for yield and yield component characters in three crosses of Indian mustard cultivars.

Generation	Siliquae/plant /No/			Seeds/siliqua /no./			1000 seed weight /g/			Yield/plant /g/		
	CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII
P1	165,00	170,26	177,60	13,24	13,32	13,00	2,98	2,37	2,37	4,62	3,99	2,58
P2	171,13	253,66	319,99	13,84	9,61	10,20	2,23	2,17	2,26	2,48	2,38	2,43
F1	235,03	196,23	233,93	12,84	14,04	13,61	2,31	2,73	2,24	4,87	4,40	3,82
F2	201,56	175,85	169,30	14,86	13,26	12,57	2,19	2,38	2,62	4,08	2,86	2,83
F3	221,22	300,95	219,17	12,93	12,40	11,89	2,26	2,26	2,24	4,11	3,50	2,71
B1	202,50	186,86	232,86	13,19	12,96	13,37	2,44	2,73	2,26	4,29	3,63	3,10
B2	193,40	256,96	194,90	12,96	13,95	12,60	2,14	2,46	2,06	3,35	4,95	2,03
B11	197,13	185,63	168,40	13,19	12,91	12,75	2,49	2,73	2,29	4,43	3,33	2,48
B12	262,66	199,50	176,63	11,79	12,77	13,27	2,43	2,54	2,35	4,13	4,12	2,88
B21	177,86	162,66	175,00	13,82	12,62	12,73	2,32	2,62	2,11	4,22	3,21	1,89
B22	235,40	291,46	272,43	13,82	12,48	13,13	2,25	2,27	2,14	4,59	3,57	3,60
B1S	184,50	211,03	178,16	13,34	12,55	11,92	2,71	2,52	2,02	3,45	3,19	1,82
B2S	180,73	284,89	214,73	14,33	12,66	12,09	2,35	2,42	2,18	3,16	4,32	2,21
B1 x F1	187,93	208,02	238,84	13,21	11,96	11,86	2,62	2,84	2,16	3,55	3,39	2,67
B2 x F1	208,02	235,37	212,49	15,54	12,44	13,03	2,42	2,41	2,01	4,93	3,12	2,33
B1bip	199,57	287,33	295,84	13,70	11,63	12,85	2,53	2,43	2,22	4,65	4,66	4,14
B2bip	244,95	371,73	236,99	14,04	12,54	12,29	2,42	2,10	2,21	4,40	5,68	2,25
F2 x P1	205,80	174,10	196,14	13,71	15,26	12,88	2,32	2,45	2,02	5,32	3,33	2,40
F2 x P2	223,25	193,86	242,75	14,06	12,95	11,71	2,26	2,50	2,11	5,02	3,17	2,27
F2 x F1	209,88	230,21	278,05	13,97	13,70	11,24	2,23	2,39	2,14	4,68	4,25	3,27
F2bip	228,95	226,30	352,84	14,39	12,15	11,80	2,38	2,21	1,98	4,66	3,24	4,42
S.EN±	17,38	16,72	17,76	0,31	0,34	0,32	0,06	0,05	0,04	0,27	0,24	0,28
C.D./at 5%/	34,34	46,34	49,24	0,87	0,94	0,90	0,18	0,15	0,14	0,76	0,67	0,79

Table 2. χ^2 test of goodness of fit of various models for yield and yield components in three crosses of Indian mustard cultivars.

Model	No.of para-meters	χ^2 degrees of freedom	χ^2 values											
			Siliquae/plant /no./			Seeds/siliqua /no./			1000-seed weight /g/			Yield/plant /g/		
			CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII	CrossI	CrossII	CrossIII
Additive-dominance	3	18	24,27 /0.160/	44,62^{xx}	135,02^{xx}	43,61^{xx}	84,78^{xx}	32,60 /0.020/	33,06 /0.016/	43,39^{xx}	108,97^{xx}	71,79^{xx}	169,58^{xx}	30,76 /0.032/
Digenic interactions	6	15	-	43,81^{xx}	110,15^{xx}	29,61 /0.014/	28,37 /0.021/	-	-	30,17 /0.010/	73.26^{xx}	51,47^{xx}	113,81^{xx}	
Trigenic interactions	10	11	-	21,98 /0.025/	92,64^{xx}	-	-	-	-	-	46,22^{xx}	48,05^{xx}	65,15^{xx}	
Linked digenics	12	9	-	-	15,20 /0.088/	-	-	--	-	-	34,95^{xx}	12,83 /0.230/	21,78 /0.250/	

xx χ^2 $P < 0.001$

Figures in parenthesis indicate the probability

Table 3. Estimates of parameters with standard errors under adequate model for yield and yield contributing characters in three crosses of Indian mustard cultivars.

Parameters	Siliqua/plant /no./			Seeds/siliqua /no./			1000-seed weight /g/			Yield/plant /g/		
	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III
m	179,05±6,70^{xx}	527,06±89,39^{xx}	-	12,40±0,51^{xx}	11,28±0,71^{xx}	12,16±0,20^{xx}	2,46±0,46^{xx}	2,20±0,10^{xx}	-	-	-	2,71±0,21^{xx}
/d/	2,32±5,89	-14,76±146,23	73,67±12,41^{xx}	0,76±0,35^{x}	1,62±0,34^{xx}	0,65±0,18^{xx}	0,22±0,04^{xx}	0,32±0,10^{xx}	0,09±0,03^{xx}	1,00±0,27^{xx}	0,50±0,27	0,37±0,18^{x}
/h/	50,80±14,18^{xx}	-1190,00±405,55^{xx}	-	4,99±1,93^{xx}	4,28±2,17^{x}	1,13±0,42^{xx}	-0,18±0,06^{xx}	0,15±0,36	-	0,22±0,98	-	0,54±0,42
/iab/	-	-314,13±90,54^{xx}	-	0,34±0,39	0,58±0,65	-	-	0,31±0,11^{xx}	-	-	-	-
/ja/b/	-	224,94±351,19	-	-1,45±1,20	-6,07±0,92^{xx}	-	-	-0,24±0,26	-	-	-	-
/l/ab/	-	1196,00±592,18^{xx}	-	-4,41±1,83^{x}	-2,08±1,83	-	-	0,40±0,31	-	-	-	-
/iabc/	-	59,90±46,03	-	-	-	-	-	-	-	-	-	-
/jab/c/	-	812,06±210,82^{xx}	-	-	-	-	-	-	-	-	-	-
/ja/bc/	-	-156,69±248,97	-	-	-	-	-	-	-	-	-	-
/l/abc/	-	-344,50±291,28	-	-	-	-	-	-	-	-	-	-
m+/h/+/l/	-	-	225,11±82,25^{xx}	-	-	-	-	-	2,22±0,13^{xx}	-	4,24±0,67^{xx}	-
m + /i/	-	-	253,73±82,51^{xx}	-	-	-	-	-	2,36±0,11^{xx}	3,61±0,18^{xx}	3,31±0,64^{xx}	-
/pi/	-	-	100,20±23,41^{xx}	-	-	-	-	-	0,14±0,06^{x}	2,60±0,49^{xx}	0,39±0,39	-
/p^{2}i/	-	-	29,43±32,16	-	-	-	-	-	0,43±0,12^{xx}	2,92±0,64^{xx}	-0,47±0,37	-
/pj/	-	-	116,19±25,93^{xx}	-	-	-	-	-	0,13±0,92	1,51±0,65^{x}	-2,07±0,49^{xx}	-
/p^{2}j/	-	-	-125,48±42,99^{xx}	-	-	-	-	-	0,32±0,15^{x}	-1,47±0,97	-2,64±0,64^{xx}	-
/pl/	-	-	-6,15±35,42	-	-	-	-	-	0,05±0,12	-0,54±0,74	-1,15±0,65	-
/p^{2}l/	-	-	24,52±36,57	-	-	-	-	-	0,28±0,36	1,89±0,75^{x}	-1,70±0,47^{xx}	-
/p^{3}l/	-	-	85,34±39,04^{x}	-	-	-	-	-	0,36±0,21	2,23±0,86^{xx}	-2,97±0,46^{xx}	-
/p^{4}l/	-	-	-100,16±44,64^{xx}	-	-	-	-	-	0,83±0,23^{xx}	2,50±0,91^{xx}	-2,32±0,55^{xx}	-
rd	-	-	1,00	-	-	-	-	-	-	1,00	0,62	-

$^{x}P = 0,05$, $^{xx}P = 0,01$ Parameters of complex model, as none of the model is adequate