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Short communication

Genetics of seed yield and its attributes in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]

P. K. Goswami[1]

Department of Plant Breeding, CCS Haryana Agricultural University, Hisar 125 004

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Six generations namely, P_1, P_2 F_1, F_2, BC_1 and BC_2 of three crosses Indian mustard [*Brassica juncea* (L.) Czern & Coss.], namely, RH 9608 × RWH-1 (C_1), RH 9615 × RWH-1 (C_2) and RH 9621 × RWH-1 (C_3) were raised in a compact family block design with three replications. Ten randomly selected plants each of P_1, P_2 and F_1, 25 plants each of F_2, BC_1 and BC_2 generations were used for recording observations on quantitative characters namely, plant height, primary branches, secondary branches, siliquae/plant, seeds/siliqua, 100 seed weight and seed yield /plant. The data recorded were subjected to weighted analysis of Cavalli [1] to know the adequacy of additive-dominance models, in the presence of epistasis, the data, where any of the 4 or 5 parameters found adequate in the model of Jink and Jones [2] was subjected accordingly to sequential model in order to obtain more precise estimates for these parameters. The adequacy of these sequential models was tested by X^2 test at 2 and 1 degree of freedom, respectively.

Simple additive-dominance model was found to be adequate for plant height in all the three crosses (Table 1). Estimates of components of generation mean, i.e. d and h were significant suggesting the importance of both additive as well as dominance gene effects in the inheritance of plant height in C_1. However, only additive gene effects were important in the inheritance of plant height in C_2 and C_3 suggesting that additive effects can be exploited through simple progeny selection. Jain *et al.* [3] observed the importance of dominance gene effects influencing the trait.

Presence of epistasis was detected for primary branches in all the three crosses. Additive gene effects were important in inheritance of primary branches. Similar results were observed by Singh *et al.* [4] and Yaspal and Singh [5]. Moreover, in addition to additive dominance gene effects, non-allelic interactions such as additive × additive in C_1, additive × dominance C_2 and dominance × dominance C_3 were also influencing the inheritance of the trait. The negative value of dominance gene effects suggest the present of decreaser alleles for this trait in the two crosses, C_2 and C_3. In the cross C_3, dominance and dominance × dominance gene effects indicated duplicate epistasis.

Simple additive-dominance model was adequate for secondary branches in crosses C_1 and C_3, while in C_2, the digenic model revealed the significance of additive and additive × additive type of gene effect. Both additive and dominance gene effects were important for the inheritance of the trait in crosses C_1 and C_3. Singh *et al.* [4] observed that dominance gene effects were higher than additive effects for inheritance of secondary branches.

Only additive gene effects were important for inheritance of main shoot length in C_1. So, improvement can be achieved through simple pedigree selection. However, in crosses C_1 and C_3 in addition to additive and dominance gene effects, nonallelic interaction additive × additive was also influencing the trait.

Simple additive - dominance model was inadequate in all the three crosses for siliquae on main shoot. In cross C_1, both additive and dominance gene effects were significant along with non-allelic interaction, dominance × dominance. In cross C_2, dominance, additive × additive and dominance × dominance type of gene effects were important. Duplicate epistasis was observed in C_1 and C_2. While in cross C_3 dominance, additive × additive and additive × dominance gene effects were important. Singh *et al.* [4] also observed preponderance of non-additive gene effects influencing the trait. Additive gene effects were important in inheritance of siliqua length. However, in cross C_1, in addition to additive and dominance gene effects

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[1] Present address: Regional Agricultural Research Station, Assam Agricultural Univ., Garumuria Gaon, North Lakhimpur 787 001.

Table 1. Estimation of genetic parameters in Indian mustard.

Character	Cross	m	d	h	i	j	l	Epistasis
Plant height (cm)	C_1	204.85**±2.69	15.04**±2.66	20.03**±5.55	-	-	-	-
	C_2	195.13**±3.04	26.19**±3.13	5.49±3.06	-	-	-	-
	C_3	207.02**±2.48	13.08**±2.40	5.29±6.02	-	-	-	-
Primary branches	C_1	2.09*±0.96	1.86**±0.57	5.97**±1.35	5.55**±1.18	-	-	-
	C_2	6.69**±0.29	2.90**±0.30	-2.47**±0.69	-	−4.29**±1.35	-	-
	C_3	8.00**±0.50	1.40**±0.43	-9.93**±1.92	-	-	10.79**±1.88	D
Secondary branches	C_1	65.06**±3.97	14.17**±3.90	16.02**±7.2				
	C_2	33.24**±9.16	13.80**±3.09	56.58**±13.94	30.22**±9.84	-		
	C_3	67.03**±3.26	10.46**±3.15	15.32**±6.26	-	-	-	
Main shoot length (cm)	C_1	15.83**±1.64	4.78**±1.67	0.40±2.29	-	-	-	-
	C_2	5.55±3.17	7.47**±1.54	12.74**±4.27	8.37*±3.72	-	-	-
	C_3	7.28**±2.93	4.71**±0.94	9.56**±4.26	8.29**±3.15	-	-	-
Siliquae on main shoot	C_1	4.65**±0.11	0.75**±0.10	2.04**±0.62	-	-	−3.00**±0.60	D
	C_2	0.59±0.93	0.94**±0.17	12.81**±2.35	4.56**±0.91	-	−6.50**±1.55	D
	C_3	2.34**±0.44	1.12**±0.14	3.48**±0.52	2.19**±0.47	2.05**±0.63	-	-
Siliqua length (cm)	C_1	8.33**±0.89	0.95**±0.44	4.49±1.14	2.93**±1.03	-	-	-
	C_2	11.24**±0.35	0.77*±0.34	1.18±0.65	-	-	-	-
	C_3	10.26**±1.25	1.61**±0.35	2.91**±1.71	1.36**±0.32	-	-	-
Seeds/siliqua	C_1	11.76**±1.67	5.96*±2.15	37.19**±12.74	34.57**±10.15	-	-	-
	C_2	17.77**±1.59	5.13*±2.11	42.93**±13.46	33.73**±9.98	-	-	-
	C_3	40.26**±2.41	5.84**±2.38	10.19**±5.14	-	-	-	-
Seed yield/plant	C_1	3.56±4.69	1.71*±1.37	29.83**±5.91	15.56**±5.05	-	-	-
	C_2	17.86**±1.16	1.12±1.16	14.04**±2.74	-	-	-	-
	C_3	3.07±3.14	0.16±1.23	41.02**±5.16	22.73**±3.35	−10.32*±4.96	-	-
1000 seed weight (g)	C_1	4.05**±0.06	1.30**±0.06	0.49**±0.09	-	1.16**±0.26	-	-
	C_2	3.51**±0.13	1.77±0.11	2.19**±0.16	1.01**±0.18	-	-	-
	C_3	3.62**±0.06	0.94**±0.06	2.69**±0.35	-	-	−1.45**±0.36	D
Oil content (%)	C_1	39.27**±0.18	1.05**±0.18	0.97**±0.32	-	-	-	-
	C_2	41.32**±0.65	0.78±1.81	-5.64**±2.77	-	-	-	-
	C_3	40.50**±0.05	0.83**±0.07	1.55**±0.22	-	-	-	-

*C_1 = RH 9608 × RWH 1, C_2 = RH 9615 × RWH I and C_3 = RH 9621 × RWH 1

non-allelic interaction additive × additive was also influenced the inheritance. Simple additive-dominance model was found to be adequate in cross C_2 and additive gene effects were important in the inheritance of the trait. In cross C_3, additive, dominance and non-allelic interaction, additive × additive were significant. The existence of appreciable additive × additive gene effects in most of the crosses studied reflects the possibility of making effective improvement in the trait through simple selection.

Presence of non-allelic interaction was observed for inheritance of seeds/siliqua in crosses C_1 and C_2. In addition to additive and dominance gene effects, additive × additive interaction was also influencing the inheritance of the trait. In cross C_3, both additive and dominance gene effects were important for inheritance of the trait. Jain *et al.* [3] observed that dominant gene effects were more important for the inheritance of this trait.

Presence of epistasis was detected for seed-yield/plant in crosses C_1 and C_3. Analysis of cross C_1 indicated the presence of dominance and additive × additive type of inheritance and in C_3 dominance, additive × additive and additive × dominance type of interaction were observed. In cross C_2, the simple additive - dominance model was found to be adequate with predominance of dominant component in inheritance of this trait. Jain *et al.* [3] observed additive × additive, additive × dominance and dominance × dominance interactions for influencing seed-yield/plant. Singh *et al.* [4] reported that dominant gene effects were highly significant and much larger than additive gene effects for inheritance of the trait. Moreover, they observed additive × additive and dominance × dominance gene effects to play a major role.

Simple additive-dominance model was inadequate in all the three crosses for 1000-seed weight. In cross C_1, additive, dominance and additive × dominance gene effects were important. In cross C_2, dominance and additive × additive gene effects, while, in cross C_3 both additive and dominance gene effects were significant along with dominance × dominance type of non-allelic interaction. Duplicate epistasis was indicated by opposite sign of dominance and dominance × dominance interaction in cross C_3. Jain *et al.* [3] observed dominance × dominance and dominance type of gene actions, influencing the inheritance of the trait.

Simple additive-dominance model was adequate for oil content in all the three crosses. Both additive and dominance gene effects were important in C_1 and C_3. In C_2, only dominance effect was significant but in decreasing order. Ramdhari and Yadav [6] also observed that both additive and dominance effects were important for this trait.

The present study suggests that the nature and magnitude of gene effect vary with different crosses for different characters. So, specific breeding strategy has to be adopted for a particular cross to get improvement. In some crosses, pureline can be developed through hybridization following the pedigree method of selection. In other crosses, although high magnitude of dominance gene effects and dominance × dominance interactions were present, it is difficult to exploit them due to presence of duplicate epistasis, in such cases some form of recurrent selection like diallel selective or bi-parental mating may be an effective approach.

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