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Genetic analysis for yield and its components and oil content in Indian mustard [*Brassica juncea* (L.) Zern & Coss]

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Abstract

Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of six crosses namely Pusa Basant/Bio 8 (3), Pusa Basant/81, Pusa Bahar/81, Pusa Bahar/Bio8(3), 113/Bio8(3) and 113/81 were evaluated for days to 50% flowering (DTF), days to 75% maturity (DTM), seed yield per plant (SYPP), thousand seed weight (TW) and oil content (OC) in a randomized block design under timely sown and late sown conditions. The data of six generations were subjected to scaling tests to detect epistasis and genetic parameters m, d, h, i, j and l were estimated. Additive effects were found to be more important in the inheritance of DTF, SYPP, TW and OC, additive × additive for DTF, DTM, SYPP and OC, dominance for DTM, SYPP and OC and dominance × dominance for DTF, DTM and TW.

Key words : Mustard, generation means, gene action, yield components, oil content

Introduction

Rapeseed (*Brassica campestris*) and mustard (*Brassica juncea*) are the most important *rabi* oilseed crops of India. Indian mustard [*Brassica juncea* (L.) Zern & Coss], is the most important member of the group, accounting for more than 70% of the area under rapeseed-mustard. 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 grossly short of the requirements. Consequently, large quantities have to be imported for making up 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 character 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.

Materials and methods

Six generations namely, P_1, P_2, F_1, F_2, BC_1 and BC_2 of each of these six crosses viz.; Pusa Basant/Bio 8(3) (C_1), Pusa Basant/81 (C_2), Pusa Bahar/81 (C_3), Pusa Bahar/Bi 8(3) (C_4), 113/Bio 8(3) (C_5) and 113/81 (C_6). were raised in a randomized block design with two replications in 2.25 M long rows spaced 40 cm. apart with plant to plant distance of 15 cm. The whole experiment was planted at two sowing dates, timely sown (TS) and late sown (LS). Five 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. Data were recorded on days to 50% flowering (DTF), days to 75% maturity (DTM), seed yield per plant (SYPP), thousand seed weight (TW) and oil content (OC). The data were subjected to scaling tests [1] to detect the presence of epistasis. In case of significance of scaling tests, data were then subjected to the estimation of various genetic components as per Hayman [2]. More precise estimates of these parameters were then obtained by using weighted joint scaling tests [3]. Wherever five parameters were found significant a 5 parameter model was fitted and adequacy of it was tested by χ^2 (1 df). In the event of the scaling tests being non significant (i.e. absence of non allelic interactions), the three parameter model of Cavali [3] which is based on least square estimates (joint scaling test) was used to estimate main effects, m, d and h. The adequacy of 3 parameter model was tested by χ^2 (3df). The individual plant data over 2 replications were pooled to calculate the mean of a generation.

Results and discussion

The estimates of gene effects and interactions for the best fit model with respect to different traits in six crosses of Indian mustard are given in table 1-5. The inheritance pattern varied with cross, chracter and

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*Present address : Crop Improvement Division, VPKAS (ICAR), Almora 263 601 sowing condition under consideration. Means of F_1's for DTF were found to be either intermediate or closer to lower parent (desirable), indicating dominance of genes for early flowering. Mean values of F_1's for TW were intermediate or in some cases approaching the higher parent indicating balancing of the effects of negative and positive alleles or dominance of genes for higher TW. Mean values of F_1's for OC and DTM were found to be closer to or higher than those of the higher parent suggesting dominance of genes for higher oil content (desirable) and later maturity period (undesirable). In general, OC under LS condition was higher than that under TS and DTM mean values were inconsistent under the two planting dates (TS and LS conditions). In most of the crosses, F_1 means of SYPP were higher than those of the higher parent. BC_1 and BC_2 means for SYPP are invariably higher than those of the parents and F_1's. Same is the casewith OC particularly in LS condition. It may be extrapolated from these results that an extra back cross dose of parent leads to the accumulation of favourable alleles in this set of materials.

In general, additive effect (d) was more pronounced and in desirable direction for the inheritance of DTF in TS condition (Table 1). Whereas, in LS condition, dominance effect was relatively more important. The role of G × E interaction was indicated as 3 parameter model fitted under LS but not under NS condition. Among the interactions additive × additive (i) and dominance × dominance (l) were important. Opposite sign of h and l parameters indicated duplicate type of epistasis for this character. Negative sign of significant effects indicated that the genes for earlyness were dominant over the genes for lateness. Inadequacy of additive-dominance model in almost all crosses under TS indicated that, either gene interaction or linkage or both are playing an important role in the expression of this character.

Additive as well as dominance effects were important for the inheritance of SYPP and OC, dominance being more in magnitude (Tables 2 & 3). The fixable component, additive × additive (i) was found to be the most important interaction component being significant and in desirable direction. This suggested that selection for SYPP and OC would be more fruitful if selection is delayed till dominance component is reduced due to selfing. Opposite sign of h and l component indicated duplicate epistasis for both characters. Inadequacy of additive-dominance model for both characters, in all cases except C_5 and C_6 for OC, indicated presence of gene interaction or linkage or both in the expression of these traits.

Additive effect (d) was the most important for TW, being significant higher in magnitude and in desirable direction in both TS and LS condition (Table 4). Among the interactions, dominance × dominance (l) was relatively more important component by virue of its higher magnitude and desirable direction. Opposite sign of h and l component indicated the presence of duplicate epistasis for TW, which would hinder the progress in selection. Presence of gene interaction or linkage or both was indicated by inadequacy of additive-dominance model for this character.

Considering the magnitude and direction, dominance component (h), dominance × dominance (l) and additive × additive (i) were relatively important in the inheritance of maturity period (Table 5). Positive sign and later magnitude of h and l parameters

Table 1. Estimates of gene effects and interactions for days to flowering (DTF)

Cross	Condition	m	d	h	i	j	l	χ^2
C1	TS	80.30**±6.58	–8.85**±1.42	10.90±17.34	–8.15±6.33	26.25**±5.64	–0.90±11.59	-
	LS	80.73**±0.55	–2.33**±0.55	–4.89**±1.00	-	-	-	**3.35**(ns)
C2	TS	82.50**±6.57	–12.10**±1.30	2.91±16.79	–7.10±6.44	41.80**±5.14	–22.40*±10.73	-
	LS	77.87**±0.80	0.12±0.74	–3.92*±1.62	-	-	-	**6.73**(ns)
C3	TS	82.19**±1.73	–7.00*±1.27	1.92±2.00	–2.58±2.28	17.92*±3.64	-	**1.29**(ns)
	LS	74.78**±0.79	–1.82*±0.79	–3.96**±1.35	-	-	-	-
C4	TS	87.81**±21.6	–4.84**±1.37	–9.77**±2.74	–10.14**±2.71	7.69±4.29	-	**2.81**(ns)
	LS	72.40**±3.34	–3.95**±0.81	25.94**±8.28	6.95*±3.24	10.00**±2.47	–27.85**±6.10	-
C5	TS	88.69**±2.89	0.22±1.49	–4.93±4.49	–8.69**±3.24	–6.41±4.48	-	**2.35**(ns)
	LS	81.65**±0.42	–1.75**±0.41	–4.28*±1.04	-	-	-	**4.24**(ns)
C6	TS	88.75**±7.28	–3.50±1.41	–39.20*±19.34	–4.75±7.14	-	25.95±12.51	**8.07**(ns)
	LS	71.90**±1.88	2.25**±0.78	–2.99±3.06	6.28**±2.01	–5.60 ±3.34	-	**0.24**(ns)

*Significant at 5% level, **Significant at 1% level

Table 2. Estimates of gene effects and interactions for seed yield per plant

Cross	Condition	m	d	h	i	j	l	χ^2
C1	TS	24.78**±2.84	6.15*±2.74	5.91±5.64	26.55*±11.44	-	-	6.77(ns)
	LS	–18.80±11.50	33.35*±1.21	129.35**±29.66		–14.20±8.53	–96.75**±19.28	-
C2	TS	17.80*±8.37	11.82**±3.18	15.62±13.40	–0.35±5.48	10.48±8.85	--	0.16(ns)
	LS	12.31**±1.40	–0.52±1.36	12.99**±3.25		–29.93±9.82		4.57(ns)
C3	TS	23.56**±3.91	7.29*±3.64	–7.40±5.62	0.35±5.48	–29.93±9.82	–45.25**±15.49	1.07(ns)
	LS	–13.20±8.77	–0.80±1.37	81.05**–22.98	24.60**±8.67	7.65±6.91	–56.80*±25.39	-
C4	TS	–13.30±12.88	4.65±4.15	99.80**±35.09	36.05**±12.19	–3.95±12.54	–90.25*±27.20	-
	LS	–15.13**±6.82	2.76**±1.11	64.85**±11.82	23.14**±6.80	–12.37*±5.99	-	1.04(ns)
C5	TS	–24.95*±12.48	5.95±3.55	146.60**±34.06	49.00**±11.97	–2.35±11.39	–90.25*±27.20	-
	LS	11.56**±1.67	6.01**±1.62	26.06**±3.93	-	-	-	6.43(ns)
C6	TS	54.90**±13.34	6.80*±3.41	–77.50*±33.52	–31.70*±12.89	3.60±10.37	58.90*±24.27	-
	LS	–30.30**±9.51	4.05*±2.00	129.30**±26.38	46.55**±9.30	–13.95±8.67	–71.60**±18.77	-

*Significant at 5% level, **Significant at 1% level

Table 3. Estimates of gene effects and interactions for oil content

Cross	Condition	m	d	h	i	j	l	χ^2
C_1	TS	43.10**±2.11	2.24**±0.70	–25.36**±5.41	–8.08**±1.99	–4.40*±1.83	18.57**±4.28	-
	LS	27.82**±2.18	1.39*±0.64	21.88**±5.50	6.81**±2.09	–3.67*±1.80	–13.21**±3.95	-
C_2	TS	31.78**±1.51	0.07±1.05	5.26*±2.49	5.67**±1.70	–4.39±2.61	16.03**±3.92	0.03(ns)
	LS	29.48**±2.27	–0.74±0.49	23.25**±5.84	7.50**±2.20	-	-	7.10(ns)
C_3	TS	36.25**±1.19	0.80±0.90	–1.48±1.88	1.91±1.46	–5.03*±2.44	-	0.04(ns)
	LS	33.78**±0.96	–1.10±0.74	6.61**±1.31	3.73**±1.23	2.65±2.38	-	1.11(ns)
C_4	TS	35.86**±0.47	2.71**±0.41	–0.25±0.95	-	-	-	1.75(ns)
	LS	27.10**±2.38	0.42±0.48	23.63**±5.84	7.72**±2.25	-	–14.80**±3.85	0.00(ns)
C_5	TS	35.84**±0.50	3.37**±0.39	2.38*±0.99	-	-	-	3.51(ns)
	LS	36.33**±0.63	2.29**±0.55	2.77*±1.24	-	-	-	2.77(ns)
C_6	TS	38.50**±0.67	–0.29±0.57	–2.04±1.24	-	-	-	1.23(ns)
	LS	38.50**±0.62	0.18±0.56	1.18±1.18	-	-	-	1.58(ns)

*Significant at 5% level, **Significant at 1% level

Table 4. Estimates of gene effects for 1000-seed weight

Cross	Condition	m	d	h	i	j	l	χ^2
C_1	TS	5.66**±0.46	1.71**±0.11	–6.56**±1.22	–1.79**±0.45	–0.54±0.37	5.14**±1.05	-
	LS	3.09**±0.39	0.95**±0.26	1.21±0.67	0.49±0.41	2.13*±0.62	-	1.77(ns)
C_2	TS	3.49**±0.36	0.79**±0.12	1.01±0.58	1.34*±0.37	–0.88*±0.45	-	1.45(ns)
	LS	4.04**±0.13	0.68**±0.12	0.17±0.23	-	-	-	0.23(ns)
C_3	TS	6.46**±0.58	0.62**±0.12	–6.74**±1.46	–1.84**±0.56	–0.17±0.44	4.45**±1.03	-
	LS	3.78**±0.12	0.50**±0.11	0.72**±0.23	-	-	-	7.46(ns)
C_4	TS	4.55**±0.53	1.54**±0.12	–3.14**±0.13	–0.85±0.51	–0.33±0.38	2.26*±0.95	-
	LS	5.33**±0.56	0.62**±0.24	–5.16**±1,47	–1.91**±0.51	1.60**±0.58	3.81**±1.05	-
C_5	TS	5.55**±0.60	1.73**±0.17	–4.43**±1.54	–1.66**±0.58	–0.73±0.50	2.54*±1.44	-
	LS	5.07**±0.62	1.13**±0.29	–4.06*±1.70	–1.15*±0.54	1.13±0.70	3.56**±1.38	-
C_6	TS	3.83**±0.37	0.78**±0.17	0.08±0.63	0.94*±0.39	–0.48±0.52	-	0.71(ns)
	LS	4.07**±0.16	0.66**±0.15	1.08**±0.32	-	-	-	7.23(ns)

*Significant at 5% level, **Significant at 1% level

Table 5. Estimates of gene effects for days to maturity

Cross	Condition	m	d	h	i	j	l	χ^2
C_1	TS	158.17**±1.79	2.46*±1.23	2.47±2.15	–5.43*±2.24	–8.56±4.58	-	2.68(ns)
	LS	160.18**±1.88	2.84**±0.33	–8.23**±3.13	–5.81**±1.89	–3.39±1.94	-	0.24(ns)
C_2	TS	167.31**±1.72	–0.96±0.81	–15.51**±2.45	–11.31**±1.93	3.73±2.78	-	2.64(ns)
	LS	144.25**±3.05	3.55**±0.73	25.00**±7.64	9.40**±2.96	–8.55**±2.34	–14.35**±4.93	-
C_3	TS	163.14**±2.10	–1.75*±0.79	–7.71*±3.48	–7.66**±2.20	8.65**±2.90	-	2.38(ns)
	LS	146.47**±1.64	1.68*–0.81	10.40**±2.68	5.67**±1.76	–2.84±2.35	-	0.83(ns)
C_4	TS	152.72**–0.94	–0.05±0.93	6.84**±1.60	-	-	-9.86*±4.95	5.66(ns)
	LS	162.70**–2.88	1.10*±0.50	–19.76**±7.64	–10.10**±2.84	–5.15*±2.39		-
C_5	TS	141.20**±4.28	3.15**±1.04	44.54**±10.81	12.95**±4.15	–6.40±3.441	–28.45**±6.81	-
	LS	147.75**3.33	0.30±0.44	17.07±8.17	4.05±3.30	–1.70±2.24	–11.25*±5.08	-
C_6	TS	157.24**±1.43	0.09±0.49	1.73±1.69	0.03±1.55	8.24**±2.60	-	0.84(ns)
	LS	153.10**±2.99	1.00±0.79	8.70±7.90	–2.00±2.89	0.60±2.67	–11.40*±5.11	-

*Significant at 5% level, **Significant at 1% level

suggested duplicate epistasis. Additive-dominance model was inadequate hence indicating the role of gene interaction or linkage or both for the control of DTM.

On over all basis additive (d) component is more important in the inheritance of DTF, SYPP, TW and OC whereas the other fixable component additive × additive (i) is important for DTF, DTM, SYPP and OC. These results are in agreement with the earlier studies in mustard and related *Brassica* spp [4, 5]. It should be possible to select for the increased manifestation of early flowering, higher seed yield per plant, early maturity, higher thousand seed weight and higher oil content. Dominance effect (h) is having important role in governing the inheritance of DTM, SYPP and OC. Dominance X Dominance (l) interaction component is important for DTF, DTM and TW. These results are in agreement with the findings in mustard & related Brassica spp [4, 6]. Although, additive and additive × additive gene effects were significant for these attributes investigated, non-additive gene effects and interaction appear to overpower them. In such conditions biparental mating or recurrent selection which generate more heritable variation may be helpful. These results while restricted to these parents suggest the use of biparental mating in segregating generations followed by conventional selection procedures as the breeding strategy to exploit this kind of gene action.

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References

1. **Mather K.** 1949. Biometrical Genetics. The study of continuous variation. Methun and Co. Ltd., London.
2. **Hayman B. I.** 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity, **12**: 371-396.
3. **Cavalli L. L.** 1952. An analysis of linkage in quantitative inheritance. In: "Quantitative inheritance", (Ed. E.C.R. Reeve and C. H. Waddington), HMSO, London, pp. 135-144.
4. **Singh S. P. and Singh D. P.** 1972. Inheritance of yield and other agronomic characters in Indian mustard (*Brassica juncea*). Can. J. Genet. Cytol., **14**: 277-233.
5. **Grami B. and Stefansson B. R.** 1977. Gene action for protein and oil content in summer rape. Can. J. Plant. Sci., **57**: 625-631.
6. **Patnaik M. C. and Murty B. R.** 1978. Gene action and heterosis in brown sarson. Indian J. Genet., **38**: 119-125.