SHORT COMMUNICATION

Genetics of Quantitative Traits in Indian Mustard [*Brassica juncea* L. Czern and Coss]

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36 F_1 s, 36F_2s and 9 parents were evaluated during rabi seasons 2003-2004 in randomized block design replicated thrice. The observation were recorded on ten metric traits and analyzed excluding reciprocals. The presence of epitasis was revealed for plant height, man raceme length, primary and secondary branches, siliquae on man raceme, seed yield and oil content per plant in F_1 and for day to flower, plant height, primary branches and siliqu length in F_2. The analysis of components of genetic variance reveled that the additive component (D) was significant for all the characters except primary and secondary branches in F_1. The two measures of non- additive components, & # 292; 1 and & # 292; 2 were significant for all the characters. Positively significant h^2 for different traits indicated that the average direction of dominance was positive and hence the characters were controlled by dominance genes in positive direction. The proportion of & # 292; 2/4 & # 292; 1 for most of the traits in both F_1 and F_2 population indicated nearly symmetrical distribution of positive and negative alleles among the parents. The proportion of dominant to recessive gene (KD/KR) exhibited an excess of dominant genes controlling most of the traits. The estimates on h^2/ & # 292; 2 varied from 0.05 (day to flower) to 3.74 (siliquaue on main receme) in F_1 indicating that siliquae an main receme is governed by 3 to 4 genes or group of genes. In F_2 estimate of & # 293; 2/ & # 292; 2 were lower than unity for all the characters and thus the number of dominant genes controlling the traits were underestimated.

Key Words: Indian mustard, Diallel, Genetic components, Epistasis, Dominance

Indian mustard (*Brassica juncea* (L.) Czern & Coss) is an important oilseed crop of the country covering more than six million hectares during the rabi season and yielding about 4.3 million tones of seeds. The country accounts for 13% of the world's oilseeds area and 7% of production. Oil seeds form the second largest agricultural commodity after cereals sharing 14% of the country's gross cropped area and accounting for nearly 5% of the gross national products and 10% value of all agricultural products [Hegde *et al.*, 2004]. The present average yield of Indian mustard in our country is low (<1000 kg/ha) as compared to the world average of more than 1333 kg/ha [Yadav *et al*., 2000]. As a result, production of edible oils in India, is grossly short of the requirements. Consequently large quantities have to be imported for making up the short fall, which in turn, is a heavy drain on foreign exchange resources. It, therefore, becomes essential to breed a variety having high yield potential. Hence, the present study was undertaken to understand gene action for seed yield, its contributing characters and oil content through diallel analysis, so that an effort could be made in right direction for the genetic improvement of mustard crop.

Nine diverse genotypes of Indian mustard, viz., T-59, RH-30, Pusa Bold, RL-1359, JGM-01-15, RW-351, CS-52, RK-1418 and Pant Rai-16 were selected as basic experimental material from breeding materials officially collected in October 2001 from National Research Centre on Rapeseed-Mustard, Sewar, Bharatpur (Raj.). During rabi 2002-2003, the nine strains cultivated in different states of India were grown and crossed in diallel mating design excluding reciprocals. The nine parents alongwith their 36F_1s and 36F_2s were grown during 2003-2004 and 2004-2005 in a randomized block design with three replications at the Agricultural Research Farm of Narain P.G. College (affiliated to Dr. BR Ambedkar University, Agra), Shikohabad (U.P.). The parents and F_1s were sown in single row and F_2s in three rows each of 4m length with 45 cm spacing between rows and 10-15 cm between plants. A fertilizers dose of 40 N : 20P : 20 K kg/ha was applied and normal cultural practices were followed for raising a good crop. Ten healthy vigorous plants in the parents and F_1s and 20 plants in F_2 populations were selected randomly for recording observations on 10 characters namely, days to first flower (mean in days on plot basis), plant height (cm), length of main raceme (cm), number of primary branches, number of secondary branches, number of siliquae on main raceme, siliqua length (cm), 1000-seed weight (g), seed yield/plant (g) and oil content/plant (%). The mean values of each

observation were used to determine genetic components of variation as per Hayman, (1954).

The estimates of components of genetic variances ($\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $\hat{F}$ and E) alongwith their standard errors and its different proportions for F_1s and F_2s are presented in Table 1. The estimated values of the components of variation due to additive effect of gene ($\hat{D}$) were highly significant for most of the characters in both F_1 and F_2 generations except for primary and secondary branches and seed yield per plant in F_1 generation. The magnitudes of $\hat{D}$ estimates in both the analysis were almost similar except for plant height. The estimates of dominance components, $\hat{H}_1$ and $\hat{H}_2$ were highly significant for most of the characters in F_1 and F_2 analysis. The relative magnitude of these components was higher for all the traits in the F_2s when compared with the F_1s except for the number of primary branches. The results are in agreement with the reports of Labana *et al.* (1984). It showed that both additive and non-additive gene action were important for the traits under study. The role of both additive and non-additive gene action to seed yield, its component characters and oil content in Indian mustard was also reported by Yadav *et al.* [1981] and Trivedi and Mukherjee [1986]. Components $\hat{H}_1$ and $\hat{H}_2$ were found higher than $\hat{D}$ for most of the traits which confirmed predominance of non-additive genetic variance. The observed positive values of $\hat{H}_1$ and $\hat{H}_2$ for all the traits of interest, indicated that there were unequal frequencies of alleles, i.e. $u \neq v$, at all the loci, where u is proportion of positive genes in the parents and v is proportion of negative genes in the parents.

Further proof for the unequal distribution of alleles over loci was obtained by the ratio of $\hat{H}_2/4\hat{H}_1$, which is the estimate of uv. In the present study, the uv estimates were in the range of 0.17 to 0.23, which is less than its maximum value of 0.250 (Table 1). The maximum value of 0.250 arises, when u = v = 0.5 i.e., the increaser (positive) and decreaser (negative) alleles at all these loci are in equal proportion in the parents. But, the low estimates of uv indicated that the positive and negative alleles at loci exhibiting dominance were not in equal proportions in the parents of interest. However, these estimates did not permit a determination as to which type of allel occurred more frequently. The proportion of positive and negative alleles ($\hat{H}_2/4\hat{H}_1$) were unequal. The positive F values showed that parents studied had more dominant alleles than recessive ones for these characters. Indeed, the proportion of dominant to recessive genes

$$\text{(KD/KR) i.e. } \frac{(4\hat{D}\hat{H}_1)^{0.5} + F}{(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}}$$

confirmed the above mentioned fact. The ratios were more than one for most of the characters except plant height where ratios were less than one in both the generations. Hence, it can be said that the nine parents used for study, carried more dominance than recessive genes and it was in conformity with the findings of Yadav *et al.* [1981].

The estimate of $\hat{h}^2$ were positive and significant for most of the characters in F_1 analysis except days to flower. In F_2 analysis, siliquae on main raceme, test weight, seed yield per plant and oil content per plant were the traits which recorded positive significant estimates of $\hat{h}^2$. This indicated that the direction of dominance for there characters was positive and dominance effect expressed as the algebric sum over all loci in heterozygous phases in all the crosses. The estimates of degree of dominance, as revealed by the ration of ($\hat{H}_1/\hat{D}$) 0.5 were higher than unity for all the characters except days to first flower in F_1s suggested that analyzed characters were under the influence of over dominance while days to first flower indicated partial dominance. The magnitude of the estimates of degree of dominance for most of the characters increased in the F_2s as compared with the F_1s except for number of primary branches, indicated an increase in the dominance effects and decrease in the additive effects in the selfed generation.

The ratio of $\hat{h}^2/\hat{H}_2$ denotes an approximate number genes or group of genes controlling the characters, exhibiting dominance were analyzed. The estimates ranged from 0.01 to 3.70 and therefore, indicated that at least 1 to 4 genes or groups of genes showing dominance were present for all the traits in F_1s except for days to flower and secondary branches. But in F_2, the estimates were less than one for all the characters, which is most likely an under estimation. This may be attributed to unequal effects of dominant genes in intensity and dependent on their direction as well as cancellation effects. Yadav *et al.* [1981], Trivedi and Mukherjee [1986] and Kant and Gulati [2001] also arrived at the same conclusion. According to Jinks [1954] non random distribution of genes may bring about this discrepancy. The lower values of the estimate would not mean absence of genes exhibiting dominance for the character as this estimate has no connection with Mather's [1949] definition of effective factors.

Table 1. Estimates of genetic components of variation and their proportions in F_1 and F_2 diallel progenies for 10 characters in Indian mustard

Characters	Populations	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{h}^2$	$\hat{F}$	E	$\left(\frac{\hat{H}_1}{\hat{D}}\right)^{\frac{1}{2}}$	$\left(\frac{\hat{H}_2}{4\hat{H}_1}\right)^{\frac{1}{2}}$	$\frac{KD}{KR}$	$\frac{\hat{h}^2}{\hat{H}_2}$
Days to first flower	F_1	31.79**	29.36**	22.96*	1.08	11.14	0.72	0.96	0.19	1.44	0.05
	SE	±3.47	±7.67	±6.59	±4.41	±8.10	±1.09				
	F_2	31.77**	123.80	89.65**	1.53	36.85*	0.74	1.97	0.18	1.89	0.02
	SE	±2.88	±25.42	±21.86	±3.66	±13.43	±0.91				
Plant height (cm)	F_1	180.00**	186.20**	170.80**	494.43**	-130.30*	22.53*	1.01	0.22	0.47	2.85
		±21.62	±47.72	±41.03	±27.48	±50.44	±6.83				
	F_2	201.20**	401.20**	323.50	52.19	-72.15**	1.46	1.41	0.20	0.76	0.01
		±13.68	±120.84	±103.88	±17.39	±63.86	±4.32				
Main raceme length (cm)	F_1	83.39**	216.30**	176.80**	575.64**	93.24	00.08	1.61	0.20	2.06	3.24
		±24.97	±55.12	±47.38	±31.74	±58.25	±7.89				
	F_2	82.25	543.50**	390.40	36.74	172.10	1.22	2.57	0.17	2.35	0.09
		±13.22	±116.73	±100.34	±16.80	±61.68	±4.18				
No. of primary branches	F_1	0.62	6.66**	6.29**	8.30**	0.06	0.01	3.26	0.23	1.03	1.32
		±0.50	±1.11	±0.95	±0.64	±1.17	±0.15				
	F_2	0.62*	5.17*	4.75*	0.14	0.87	0.01	2.88	0.22	1.64	0.03
		±0.21	±1.85	±1.59	±0.26	±0.98	±0.06				
No. of secondary branches	F_1	2.22	14.41**	12.83**	7.96**	-0.07	0.02	2.97	0.22	0.98	0.62
		±1.38	±3.05	±2.62	±1.75	±3.22	±0.43				
	F_2	2.17**	20.38**	15.79**	0.55	4.09	0.03	3.05	0.19	1.88	0.04
		±0.38	±3.35	±2.88	±0.48	±1.77	±0.02				
No. of siliquae on main raceme	F_1	14.05*	107.20**	92.76**	347.14**	14.35	0.25	2.76	0.20	1.43	3.70
		±5.18	±11.44	±9.84	±6.59	±12.09	±1.64				
	F_2	14.07*	233.30**	174.30**	20.63**	24.58	0.24	4.07	0.17	1.52	0.12
		±4.34	±38.30	±32.95	±5.51	±20.26	±1.37				
Siliqua length (cm)	F_1	0.15**	0.35**	0.30**	0.92**	0.09	0.0007	1.48	0.22	1.52	2.94
		±0.02	±0.04	±0.04	±0.02	±0.05	±0.007				
	F_2	0.15**	1.51**	1.19**	0.02	0.21	0.0007	3.09	0.19	1.56	0.02
		±0.02	±0.23	±0.20	±0.03	±0.12	±0.008				
Test weight (g)	F_1	0.32**	0.42**	0.37**	1.22**	0.13*	0.001	1.14	0.21	1.43	3.28
		±0.02	±0.04	±0.04	±0.02	±0.05	±0.007				
	F_2	0.32**	1.39**	1.17**	0.22**	0.18	0.002	2.07	0.21	1.31	0.19
		±0.02	±0.25	±0.22	±0.03	±0.13	±0.009				
Seed yield/plant (g)	F_1	1.67	19.19**	16.61**	50.72**	-1.24	0.27	3.38	0.21	0.81	3.05
		±2.08	±4.60	±3.95	±2.65	±4.86	±0.65				
	F_2	1.91**	24.68	21.05**	10.42**	2.90	0.02	3.58	0.21	1.51	0.47
		±0.37	±3.34	±2.87	±0.48	±1.76	±0.11				
Oil content (%)	F_1	3.42**	31.23**	30.45**	65.36**	10.45	0.45	3.02	0.23	1.65	3.45
		±1.36	±5.18	±4.75	±6.75	±7.05	±0.26				
	F_2	3.15**	45.22**	33.23**	8.24**	16.25	1.01	3.79	0.22	2.12	0.35
		±1.84	±6.22	±2.48	±2.55	±4.15	±0.76				

*, ** significant at 5% and 1% level of probability, respectively.

Our results from diallel experiment demonstrate that seed yield, oil content and major yield components showed the significance of both additive and non-additive type of gene action in different cross combinations for different characters in mustard. Therefore, further improvement in important traits in this crop is not possible by simple pureline selection or modified pedigree methods. Continuous improvement can be obtained through recurrent selection like diallel selective or bi-parental mating.

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