RESEARCH PAPER Asian Journal of Bio Science, Vol. 4 Issue 2 : 180-182 (October, 2009 to March, 2010)

Effect of Genetic variability on seed yield and oil content in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

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(Accepted : June, 2009)

Ten parents of wide phenotypic differences and their 45F_1S and 45F_2S progenies were studied to assess the genetic variability among the parents and progenies for seed yield and oil content attributes for improvement in Indian mustard. The seed yield and oil content related to days to flowering, number of primary and secondary branches / plant, 1000 grain weight, length of main fruiting branches, harvest index exhibited significant differences among parents and the progenies but 1000 grain weight did not show any significant difference among F_1S and F_2S. Therefore, the direct and indirect selection efficiency through desirable characters is to be fixed for high yield. The range and variability are the measurements of parents and progenies, which will be supporting analogs for selection.

Key words : Variability, *Brassica juncea*, Oil content

INTRODUCTION

Rapeseed - mustard crops occupy a prominent place being next in importance to groundnut. India has about 6 million hectares for rapeseed-mustard cultivation with an average yield of 1150 Kg/ha. The yield of Asian Countries are below the world average (1613 Kg/ha). In order to increase the seed yield and oil content it is essential to develop high yielding potential varieties along with better oil content. The knowledge of genetic system is important for the improvement programme in any crop. Hence, the present investigation was, carried out to find out the seed yield and oil content improvement contributed by different hybrids of Indian mustard.

MATERIALS AND METHODS

The base material comprised of ten widely diverse Indian mustard genotypes namely, CSR-1017, RL-18, LAHA-101, T-6342, RK-8901, RK-8601, RK-8608, RK-8701, A-11 and B-85. All possible single cross combinations were among all the parents in a diallel fashion. The experiment was sown in Randomized Block Design with three replications at Research farm of C.S.A. Univ. of Agriculture and Technology, Kanpur. All the treatments were grown in 5 m. long three rows plots. Twenty plants were taken at random from each of F_1S and F_2S and ten plants each of parent in each replication and data were collected and compiled for biometrical analysis.

RESULTS AND DISCUSSION

The data obtained from the present investigation on seed yield and oil content improvement for eight character *viz.*, days to flowering, number of primary and secondary branches / plant, length of main fruiting branch, seed yield / plant, harvest index, 1000 grain weight and oil content. The analysis of variance (Table 1) for all the characters were subjected for 'F' test to know the significant differences among the parents and offspring's for different attributes. The parent, F_1S and F_2S showed significant variation among all the traits except number of primary branches / plant for parent and 1000 grain weight for F_1S and F_2S. Parents vs crosses did not show any significant difference for the characters days to flowering, 1000 grain weight and oil content. F_1S and F_2S showed differences significantly for all the characters except 1000 grain weight and oil content. The data presented in Table 2 revealed the range and variability in the traits. The high variation in days to flowering in F_1S population was 45.27-69.83 as compared to parent and F_2S, which indicated presence of both additive and non – additive gene interactions (Asthana and Pandey, 1977). The maximum number (6.43-10.63) of primary branches in F_1S and secondary branches / plant (20.70-37.67) in F_1S indicated involvement of non-allelic gene interactions in the expression of this character. The large variations in length of main fruiting branch in F_1S (70.17 – 96.03) and F_2S (66.19 – 90.02) were observed. Such type of variability occurs due to non-additive gene effects (Anand and Rawat, 1978). The seed yield / plant exhibited higher mean values (36.24g) in F_1S populations over the F_2S (26.37g) and parents (21.21g). Such type of genetic variability is additive gene effects in the progenies (Varshney *et al*., 1990). The

Table 1 : Analysis of variance for parents, F_1S and F_2S of 8 attributes in a 10 parent – diallel cross of Indian mustard

Sources of variation	d.f.	Days to flowering	No. of primary branches/ plant	No. of secondary branches / plant	Length of main fruiting branch	Seed yield / plant	Harvest Index	1000 grain weight	Oil content
Replications	2	74.58**	0.89	118.24**	535.13**	609.02**	7.22**	0.03	73.51**
Treatments	99	100.73**	3.79**	87.47**	105.56**	282.55**	13.00**	1.40*	4.98**
Parents	9	98.94**	1.83	37.80**	204.90**	195.49**	30.41**	3.83**	5.66**
F_1S	44	123.61**	3.04**	64.33**	108.05**	200.51**	14.09**	1.33	5.11**
F_2S	44	75.71**	2.67**	77.95**	73.08**	183.40**	8.29**	1.02	4.82**
P vs. Cross	1	298.05	26.74**	629.84**	295.85**	2751.02**	22.80**	0.02	2.67
F_1s Vs F_2s	1	13.73**	80.80**	1429.54**	351.69**	6569.82**	5.74*	0.38	1.71
Error	198	11.10	1.51	48.27	34.51	156.66	4.69	0.12	1.72

* and **indicate significance of values at P=0.05 and 0.01, respectively

Table 2 : Mean and range of 8 attributes in parents, F_1s and F_2s of a 10 parent – diallel cross in Indian mustard

Attributes	Mean			Range					
	Parent	F_1	F_2	Parent		F_1		F_2	
				Min.	Max.	Min.	Max.	Min.	Max.
Days to flowering	54.84	57.94	58.39	47.38	64.15	45.27	69.83	48.57	68.02
No. of primary branch / plant	6.30	7.85	6.75	5.20	7.57	6.43	10.63	5.08	9.19
No. of secondary branch/plant	21.76	28.76	24.29	16.52	29.03	20.70	37.67	17.15	33.02
Length of main fruiting branch	77.22	81.67	79.39	64.36	87.15	70.17	96.03	66.19	90.02
Seed yield / plant (g)	21.21	36.24	26.37	11.53	40.75	22.33	57.33	15.47	48.29
Harvest Index	22.09	21.02	21.32	17.24	27.31	16.91	25.32	17.75	25.09
1000 grain weight (g)	3.89	3.82	3.90	2.31	5.72	2.62	5.28	2.66	5.18
Oil content (%)	36.40	36.17	36.01	34.81	38.49	32.32	38.70	33.48	38.52

harvest index in parents as compared to F_1S and F_2S were more considerable. The selection on the basis of 1000 grain weight for yield will be economical. The oil content was studied under laboratory condition in parents F_1S and F_2S which varied from 34.81 – 38.49 in parents, 33.48 – 38.52 in F_2S and 32.32 – 38.70 in F_1S. This was mainly controlled by non-additive gene reflects Singh and Yashpal (1991). Genetic variability, an important objective of any breeding programme, is to assess the variability in the material under important and utilize them efficiently for selection in target at direction. The choice of different parents with good general combining ability in a hybridization programme has assisted in substantial genetic advance in self as well as cross pollinated crops (Griffing, 1956). The selection of parents of wide genetic base will create variability for better procurement of genotype.

The analysis of variance for all characters revealed an appreciable variability among parents and their progenies (F_1S and F_2S) except 1000 grain weight. It reflected that the selections were genetically divergent and estimation of various genetic parameters will be awakable. Genetic variability (Gardner, 1963) is due to additive gene action and results of additive effects, while non-additive is due to dominance and epistasis (Hayman, 1958).

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