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Studies on genetic components for seed yield and its contributing traits in Indian mustard (*Brassica juncea*)

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Abstract

An experiment was conducted to know the inheritance pattern of seed yield and its components in a 10 ´ 10 half diallel cross set of Indian mustard *[Brassica juncea* (L.) Czern and Coss.] The analysis of variance indicated highly significant differences among parents and F'_{1s} for almost all the characters. The estimates of components of variance were significant for all the characters except days to flowering, primary branches/plant and 1000-seed weight. The component studies revealed that both additive and non-additive gene action play their role in inheritance of various characters in Indian mustard.

Key words: *Brassica juncea, diallel, gene action, quantitative and qualitative traits*

Introduction

Rapeseed-mustard is an important group of oilseed crops which is grown in subtropical and tropical countries in the world. The estimated area, production and productivity of rapeseed-mustard in the world was 30.74 million ha, 59.93 million tones and 1,950 kg/ha, respectively in 2009-10. In India the estimated area, production and productivity of rapeseed-mustard is 5.77 million ha, 6.59 million tones and 1,142kg/ha, respectively during the 2009-10. It is mainly cultivated in Rajasthan, Uttar Pradesh, Madhay Pradesh, Gujarat, Haryana, West Bengal, Assam, Bihar and Punjab. Oilseed crops hold a sizeable share of the country's gross cropped area (14 per cent) and contribute around 1.4 per cent of Gross National Product and 7 per cent of the value of all agricultural commodities (Anonymous, 2011). The contribution of Uttar Pradesh in rapeseed-mustard acreage and production is 13.1 and 13.4 per cent respectively at national level. Enhancement of yield through appropriate breeding programme is a product of multiplicative interaction, which may be the ultimate objective. Breeding method to be used for genetic improvement of a crop depends upon the nature and magnitude of gene action responsible for the expression of quantitative traits. Keeping in view these facts, the present study was undertaken to know the gene action for seed yield and other contributing characters in Indian mustard.

Materials and Methods

Ten diverse genotypes of Indian mustard, viz., Varuna, Durgamani, RH-30, NDR-8501, RLM-198, Kranti, Pusa Bold, Pusa Basant, Sej-2, and RK-9807 were selected as parents for the present study. All possible crosses were made in diallel mating design excluding reciprocals to obtain F_1 during 2006-07. Resultant F1s were grown during 2007-08 and advanced to F_2. During 2008-09, 10 parents, 45 F'_1s and 45 F'_2s were evaluated in complete randomized block design with three replications. Each parent and F'_1 was grown in single row of 5m length with spacing of 45 cm x 15 cm sown at Oilseeds Research Farm of C.S. Azad University of Agriculture and Technology, Kanpur (UP). Recommended cultural practices were adopted in order to raise healthy crop. A sample of five representative plants were taken from each plots for recording data on days to flowering, days to maturity, plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae on main raceme, seed yield / plant, 1000-seed weight, and oil content, whereas 15 plants were selected for recording the data in F'$_2$s for all the characters under study. Statistical analysis was carried out as suggested by Jinks and Hayman (1953) and Hayman (1954).

Results and Discussion

The mean sum of squares due to genotypes (treatments) were found highly significant for all the characters, namely, days to flowering, days to maturity, plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae on main raceme, seed yield / plant, 1000-seed weight and oil content. The analysis of variance was analysed for parents, F$_1$ and F$_2$ generations for different characters (Table1). The analysis of variance in F$_1$ and F$_2$ were significant for all the characters except primary branches/plant and 1000-seed weight. The analysis of variances for parent v/s F'$_1$s and parents v/s F'$_2$s were significant for most of the characters except 1000-seed weight and oil content in parents v/s F'$_1$s and primary branches/plant, siliquae on main raceme and 1000-seed weight in parents v/s F'$_2$s indicating much genetic variability.

Table 1: Analysis of variances for 10 characters in Indian mustard

		Mean Squares									
Sources of variation	D.F. flowering	Days to 50% maturity	Days to branches	Plant height branches	No. of primary raceme	No. of secondary main raceme	Length of main per plant	No. of silique on weight	Seed yield	1000 seed	Oil content
Parents(P)	9	89.6**	104.2**	189.9**	1.1*	33.5**	288.9**	178.5**	6.0	0.5	6.8**
F'$_1$s	44	78.2**	28.6**	6.4**	1.1**	12.8**	61.7**	49.4**	17.2**	0.5**	4.2**
Parents vs F$_1$	1	422.4**	230.3**	44.9**	0.001	57.2**	58.5**	90.9*	118.4**	0.5	1.6
F'$_2$s	44	82.0**	37.5**	1.6**	1.0	14.6**	56.6**	27.9**	23.7**	0.3	6.9**
Parents vs F'$_2$s	1	1735.0**	185.9**	79.8**	0.1	59.1**	53.8**	24.7	125.7**	1.0	7.6**
Replication	2	91.5	35.1	3.5	2.0	51.1	3.9	93.9	170.4	3.6	11.4
Error	198	7.9	3.9	2.0	0.6	5.2	22.4	21.0	6.2	0.4	1.1

*, **Significant at 5 and 1 per cent levels, respectively

The estimates of component of variation (D, H$_1$, H$_2$, F, E, h^2) along with their standard errors and related statistics were compared (Table 2). Estimates of additive (D) and dominance (H$_1$) components were significant for all the characters except days to flowering, primary branches/plant and 1000-seed weight, where additive component was non-significant. Similar findings were earlier reported by Singh (2005) and Singh *et al*. (2006). The components of dominance (H$_1$, H$_2$) were higher than additive component for all the characters that reflected predominant role of non-additive gene action in the inheritance of these characters. These findings are in agreement with earlier reports by Singh and Lallu (2004), Tahir *et al.* (2007). Relative magnitude of H$_1$ component was higher than H$_2$ component indicating unequal distribution of dominance genes. Positive and significant estimates of F for almost all the characters revealed that dominant genes were more frequent. Estimates of h^2 component exhibited more or less same trend as F component for all the characters except primary branches/plant reflecting role of dominance. The estimates of average degree of dominance (H$_1$/D) were also found more than unity for all the characters indicating over-dominance. The values of H$_2$/4H$_1$ were close and almost equal to theoretical value for seed yield and 1000-seed weight, respectively indicating symmetrical distribution of positive and negative alleles. The difference between H1 and H2 components was very small and hence, supported the above conclusion. However the proportion of dominant and recessive alleles (KD/

Table 2: Genetic components and related statistics in Indian mustard

Character	Estimates of Genetic compounds and related statistics in Indian mustard										
	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	$\hat{h}$	$\hat{E}$	$(\hat{H}_1/\hat{D})^{1/2}$	$\hat{H}_2/4\hat{H}_1$	$\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}$	$\hat{h}^2/\hat{H}_2$	r
Days to 50% flowering	22.7	359.6**	266.4*	53.2	54.8**	2.7	3.6	0.2	1.7	0.20	-0.64
SE ±	12.3	104.6	88.9	21.7	14.9	3.7					
Days to maturity	33.4**	239.5**	151.9**	96.9**	29.9**	1.3	2.7	0.2	3.4	0.19	0.38
SE ±	3.3	27.8	23.6	15.0	3.9	1.0					
Plant height	56.7**	611.5**	350.3**	231.3**	56.9**	6.6	3.3	0.1	4.3	0.16	-0.81
SE ±	13.5	115.3	98.0	62.5	16.4	4.8					
No. of primary branches	0.2	5.6**	3.8*	1.1	-0.1	0.2	5.7	0.2	3.4	-0.02	-0.67
SE ±	0.2	1.7	1.5	0.9	0.2	0.1					
No. of secondary branches	9.4**	91.7**	54.6**	33.2**	6.9**	1.8*	3.1	0.2	3.6	0.12	0.40
SE ±	1.9	15.9	13.5	8.6	2.3	0.6					
Length of main raceme	88.8**	544.0**	306.7**	271.0**	50.0*	7.5	2.5	0.1	4.2	0.17	-0.88
SE ±	15.1	128.5	109.2	69.7	18.3	4.6					
No. of siliquae on main raceme	52.5**	320.3**	163.9**	151.2**	9.5	7.0**	2.5	0.1	3.8	0.05	-0.79
SE ±	4.9	41.3	35.1	22.4	5.9	1.5					
Seed yield per plant	20.1**	75.5**	71.1**	20.4	14.9**	2.1	1.9	0.2	-	0.20	-0.35
SE ±	2.6	22.5	19.1	12.2	3.2	0.8					
1000-seed weight	0.0	1.3*	1.3*	0.0	0.0	0.1	5.5	0.3	1.0	0.015	0.32
SE ±	0.1	0.6	0.5	0.3	0.1	0.0					
Oil content	1.9**	22.4**	16.2**	5.4*	0.1	0.4	3.4	0.2	2.4	0.005	-0.005
SE ±	0.4	3.7	3.1	2.0	0.5	0.1					

*, ** Significant 5 and 1 per cent levels, respectively

KR) in parents revealed excess of dominant alleles showing estimates more than unity for all the traits. The estimates of h^2/H_2 that provides information about number of effective gene groups, which control the character expression and exhibit dominance indicated that single group of polygenes was responsible for the inheritance of all the characters. Since, in present study, alleles were not distributed symmetrically, hence, a greater reliance could not be placed on gene group. The correlation coefficient between parental order dominance and parental order of measurement was negative for almost all the characters except days to maturity, secondary branches/plant and 1000-seed weight indicating dominance and recessive alleles contributing towards expression of the traits with negative and positive values, respectively. Thus, considering the gene action and over-dominance, which attributed major effect in controlling the inheritance of characters, it can be concluded that method such as reciprocal recurrent selection could hold promise for genetic improvement of days to maturity, plant height, secondary branches/plant, length of main raceme, siliquae on main raceme, seed yield and oil content.

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