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Genetic analysis for estimates components of genetic variance in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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Abstract
Highly significant differences were recorded among the treatments for all the characters. Analysis of variance further indicated highly significant differences among the parents except biological yield, F1s indicated highly significant differences except no. of secondary branches per plant, no. of seeds per siliqua and biological yield per plant, parent vs F1s for all the characters. The estimates of all genetic components were found highly significant for Days to 50% flowering, Days to maturity, plant height, no. of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, no. of seed per siliqua, 1000- seed weight, biological yield per plant, harvest index, oil content and seed yield per plant. The estimates of mean degree of dominance were more than unity for number of secondary branches per plant, no. of seeds per siliqua, 1000- seed weight, biological yield per plant, harvest index, oil content and seed yield per plant. The proportion of genes with positive and negative effects was near or equal to theoretical value for all characters except seed yield per plant.

Keywords: *Brassica,* genetic components and gene action

Introduction
Rapeseed-mustard is a group of crops comprising rapeseed (toria, brown sarson and yellow sarson) cultivar of *Brassica campestris;* Indian Mustard (*Brassica juncea*); black mustard (*Brassica nigra*) and taramira (*Eruca sativa*). Some exotic species of Brassicas like gobhi sarson (B. napus), Ethopian mustard or karan rai (B. carinata) and white mustard (Sinapis alba) have been brought into cultivation in India. The crops of rapeseed group are largely cross pollinated where as Indian mustard is largely self pollinated. Out of these cultivars Indian mustard fits well in cropping system of rainfed areas and accounts for >75% of the total area under rapeseed-mustard cultivation in India. Other cultivars like brown sarson and yellow sarson are under cultivation over a limited area in the Eastern part of the country including North-Easter States. Toria, a short duration crop is largely grown as a catch crop in tarai part of UP, Haryana, Assam and Odisha. Gobhi sarson is under cultivation over a limited areas in HP, J&K and Punjab under Irrigated ecologies.

Rapeseed & Mustard is widely grown in majority of Continents with largest area of 8 million ha in Canada followed by China (7 million ha) and India (6 million ha). Majority of the countries grow rapeseed, whereas, India has largest area under mustard. The productivity of India is the lowest among the major rapeseed mustard growing countries. As against the World average of 2144 kg/ha, highest productivity of 3640 kg/ha of European Union, the Indian average yield was only 1161 kg/ha during 2013-16. (Anonymous 2014-15) [1].

Materials & Methods
The material for the present investigation consisted seven varieties/ genotypes (Maya,NRCDR-2,NRCHB-101,RGN-73,Pusa M-21,Urvashi and Pusa Bold) of Indian mustard, [*Brassica juncea* (L.) *Czern & Coss*] which were selected on the basis of variation for various characters from available genetic material. Using seven diverse genotypes, a diallel set (excluding reciprocals) was made to obtain 21 crosses during *Rabi,* 2015-2016. Plan of layout-All the 28 treatments, (7 parents and 21 F1s) were grown in randomized complete block design with three replications at Oilseed Research Farm, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur during Rabi 2015-2016. The parents and F1s were grown in single row of five meter length spaced 45 cm apart. The distance of 20 cm between the

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plants in a row was maintained by thinning. All the recommended agronomic practices were followed for raising the good crop. The following observations were recorded on 5 randomly taken plants in parents and F1s in each replication namely, Days to 50% flowering, Days to maturity, plant height, no. of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, no. of seed per siliqua, 1000- seed weight, biological yield per plant, harvest index, oil content and seed yield per plant. Diallel numerical approach was suggested by Griffings in 1956. Oil content is estimated by using NMR Spectro 4000**.**

Results & Discussion

The analysis of variance was carried out for twelve characters for testing the significance of Differences amongst the genotypes are presented in table-1.

Highly significant differences were recorded among the treatments for all the characters namely, Days to 50% flowering, Days to maturity, plant height, no. of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, no. of seed per siliqua, 1000-seed weight, biological yield per plant, harvest index, oil content and seed yield per plant. Analysis of variance further indicated highly significant differences among the parents except biological yield. Highly significant differences were also found among F1s for all the characters except no. of secondary branches per plant, no. of seeds per siliqua and biological yield per plant, parent vs. F1s revealed highly significant differences for all the characters, plant height, and number of siliquae per plant. These findings were also similar as Arunachalam (1976) [2] and Yadav et al. (1993) [12]. Analysis of components was carried out for all the twelve characters in F1 generations are presented in table-2. Regression coefficient 'b1' deviated from unity for only length 1000-seed weight. Such significant deviation of regression coefficient from unity indicates non-allelic gene interaction (epistasis), while the regression coefficient did not deviate significantly from unity for Days to 50% flowering, Days to maturity, plant height, no. of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, no. of seed per siliqua, biological yield per plant, harvest index, oil content and seed yield per plant, indicating the involvement of additive gene action. The finding were also suggested by Kumar and Srivastava (2000) [9], Ghosh and Gulati (2001) [4], Ghosh et al. (2002) [5], Singh and Sachan (2003) [22], Sheikh and Singh (2004) [10], Goswami and Behl (2005) [6], Singh et al. (2007) [17].

The estimates of all genetic components viz., Dˆ, Hˆ1,H ˆ2, Fˆ, h2ˆ a n d Eˆ along with their standard errors were calculated. These estimates are presented in table-3. The estimates of additive components were highly significant for all the characters except seed yield per plant. The estimated dominance components (H_1^ and H_2^) was highly significant for all characters except days to maturity and plant height. The estimates of H_1^ were higher than that of the estimates of H_2^ for majority of characters except days to 50% flowering, days to maturity, plant height and biological yield per plant. It indicates unequal distribution of positive and negative alleles. The dominant components exhibited the prevalence of non-additive gene action for controlling these attributes. All the estimates of Fˆ (mean of Fr value, where Fr is the proportion of negatives effects of Genes in rth parents) were positive and significant only for number of secondary branches per plant. Indicating the excess of dominant, positive Genes for controlling the characters. The estimates of h2ˆ were positive and highly significant for all the characters. Exhibiting that mean direction of dominance was positive. The values of Eˆ Component were highly significant for days to 50% flowering, days to maturity, plant height, no. of primary branches per plant, no. of secondary branches per plant, no. of seeds per siliqua, biological yield per plant and harvest index. The Eˆ Values of other traits did not show significance, indicating that these characters were less stable than other characters having environmental inferences and vice-versa. The estimates of mean degree of dominance (H_1ˆ / Dˆ) 0.5 were more than unity for number of secondary branches per plant, no. of seeds per siliqua, 1000-seed weight, biological yield, harvest index, oil content and seed yield per plant indicating over dominance in these traits. The proportion of genes with positive and negative effects (H_2ˆ/4 H_1ˆ) were near or equal to theoretical value (0.25) for majority of characters except seed yield per plant, indicating that positive and negative genes were symmetrically distributed among the parents for these attributes. The ratio ˆh2 / H_2ˆ which measures the group of genes showing over dominance was more than unity for all the characters except plant height (negative). In which more than one gene groups were responsible for the expression of these traits. The coefficient of correlation (r) between parental order of dominance and parental measurements were found positive for all characters. These findings were also similar to Chauhan et al. (2008) [16], Upadhyay et al. (2009) [20], Sohan Ram and Nutan Verma (2010) [18], Lal et al. (2011) [19], Yadav et al. (2012) [15], Singh et al. (2013) [13] and Shekhawat et al. (2014) [14].

Table 1: ANOVA of parents vs F1's for 12 characters in a 7 x 7 parental diallel cross of Indian mustard (*Brassica juncea* L. Czern & Coss): mean sum of squares.

Sources of variance	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of siliquae per plant	No. of seeds per siliqua	1000-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)	Seed yield per plant (g)
Replication	2	0.04	0.74	4.30	0.96	0.87	8.05	0.75	0.01	1.92	2.37	0.44	0.38
Treatments	27	4.08**	2.38**	9.27**	6.82**	2.06**	487.92**	1.87**	1.28**	7.56**	3.88**	3.52**	1.81**
Parents	6	5.41**	2.32*	19.21**	7.94**	2.98**	925.21**	2.41**	1.06**	6.38	2.48*	1.97**	0.71*
F1s	20	2.88**	1.92*	6.13**	4.06**	0.45	303.87 **	0.94	1.17**	2.00	3.06**	2.01**	0.91**
Parents vs F1s	1	20.00**	12.00**	12.44**	55.25**	28.67**	1545.14**	17.29**	4.96**	125.83**	28.91**	43.21**	26.38**
Error	54	0.79	0.92	2.67	0.82	0.82	35.78	0.58	0.02	3.77	0.82	0.43	0.16
Total	83	1.84	1.39	4.85	2.77	1.22	182.19	1.00	0.43	4.96	1.86	1.44	0.70

*, ** significant at 5 and 1 percent level, respectively.

Table 2: Estimates of bi, SE_{bi} (b-0)/SE_{bi}, and t^2 for 12 characters of F_1's in a 7 x 7 parental diallel cross of Indian mustard

Character	bi	SE_{bi}	(b-0)/ SE_{bi}	(1-b) / SE_{bi}	t^2
Days to 50% flowering	0.82	0.08	10.25	2.25	2.87
Days to maturity	0.66	0.14	4.71	2.42	2.63
Plant height (cm)	0.88	0.04	22.00	3.00	7.19
Number of primary branches per plant	0.98	0.09	10.88	2.22	0.00
Number of secondary branches per plant	0.81	0.02	40.50	9.50	34.98
Number of siliquae per plant	0.82	0.16	5.12	1.12	0.32
Number of seeds per siliqua	0.80	0.12	6.66	1.66	1.25
1000-seed weight (g)	1.03	0.09	11.44	-0.33	0.37
Biological yield per plant (g)	0.82	0.08	10.25	2.25	2.89
Harvest index (%)	0.58	0.21	2.76	2.00	1.02
Oil content (%)	0.53	0.14	3.78	3.35	4.41
Seed yield per plant (g)	0.13	0.31	0.41	2.80	0.55

*, ** significant at 5 and 1 percent level, respectively.

Table 3: Estimates of variance components and related for 12 characters in a 7x 7 parental diallel cross of F_1's in Indian mustard.

Characters	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	$\hat{h}^2$	$\hat{E}$	$(\hat{H}_1 / \hat{D})^{0.5}$	$\hat{H}_2 / 4\hat{H}_1$	$\hat{h}^2 / \hat{H}_2$	r
Days to 50% flowering	1.55*	0.96*	1.09*	-0.41	3.61*	0.25*	0.78	0.28	3.31	0.99
SE	0.06	0.14	0.12	0.14	0.08	0.02				
Days to maturity	0.46*	0.26*	0.31*	-0.68	2.09*	0.30**	0.74	0.29	6.66	0.90
SE	0.08	0.19	0.17	0.19	0.11	0.02				
Plant height (cm)	5.49**	-0.98	-0.48	-0.02	1.87*	0.90*	0.41	0.12	-3.90	0.99
SE	0.10	0.26	0.23	0.26	0.15	0.03				
No. of primary branches per plant	2.37**	1.82*	1.82*	-0.70	10.17*	0.27*	0.87	0.25	5.56	0.97
SE	0.14	0.36	0.31	0.35	0.21	0.05				
No. of secondary branches per plant	0.72*	0.99*	0.91*	0.52*	5.21*	0.27*	1.17	0.22	5.709	0.99
SE	0.06	0.14	0.13	0.14	0.08	0.02				
No. of siliquae per plant	296.80**	208.90*	177.09*	122.99*	282.62*	11.59*	0.83	0.21	1.59	0.91
SE	39.13	94.21	83.02	93.88	55.76	13.83				
No. of seeds per siliqua	0.60*	0.85*	0.82*	0.15	3.13*	0.19*	1.18	0.24	3.77	0.94
SE	0.07	0.18	0.16	0.18	0.10	0.02				
1000-seed weight (g)	0.34*	0.46*	0.34*	-0.28	0.92*	0.00	1.16	0.18	2.68	0.98
SE	0.01	0.04	0.03	0.04	0.02	0.00				
Biological yield per plant (g)	0.89*	1.95*	2.65*	-1.05	22.87*	1.23*	1.47	0.33	8.60	0.97
SE	0.17	0.43	0.37	0.42	0.25	0.06				
Harvest index (%)	0.53*	1.34*	1.15*	-0.02	5.25*	0.29*	1.58	0.21	4.52	0.77
SE	0.18	0.45	0.40	0.45	0.26	0.06				
Oil content (%)	0.51*	2.45*	2.37*	-0.27	7.99*	0.14	2.19	0.24	3.36	0.85
SE	0.25	0.60	0.53	0.60	0.36	0.08				
Seed yield per plant (g)	0.18	1.50*	1.50*	-0.11	4.89*	0.05	2.88	2.08	3.25	0.18
SE	0.11	0.27	0.24	0.27	0.16	0.04				

*, ** significant at 5 and 1 percent level, respectively.

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