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Research Article

Genetic analysis of seed yield and yield attributes in Indian mustard (*Brassica juncea* (L.) Czern and Coss.)

H. Manjunath, D.S. Phogat, Pummy Kumari and Dhiraj Singh
Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, India
E-mail: manjunathh@gmail.com

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Abstract
An experiment was conducted during winter seasons of 2005-06 and 2006-07 to study the nature and magnitude of gene effects involved in the genetic control of seed yield and yield attributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] through generation mean analysis. Two crosses namely; RH 0115 x EC 126745 and RH 0120 x EC 126745 were grown in a randomized block design under normal and late sown conditions. In six parameter model additive gene effects were significant for days to maturity, number of primary and secondary branches per plant, number of seeds per siliqua and oil content. Both additive and non-additive gene effects were found to be significant for main raceme length, number of siliquae on main raceme, seed yield per plant and 1000-seed weight. Thus on the basis of above study it is advocated that the breeding methods which exploit both the components of genetic variation may be useful for further genetic amelioration. For the improvement of seed yield and its component characters; reciprocal recurrent selection or diallel selective mating would be helpful.

Key words
Indian mustard, generation means, gene effects, yield components

Introduction

In India, oilseed *Brassica juncea* (L.) Czern and Coss. occupy a prominent position as rabi oilseed crops in terms of area and production. Among different oilseed *Brassica* species, Indian mustard (*B. juncea)* is a predominantly grown oilseed *Brassica* species of Indian sub continent for edible oil purpose. In spite of the fact that India ranks second in area and production of rapeseed-mustard in the world, in terms of productivity it is far below the world average. Consequently, large quantities of edible oil have to be imported for making up the short fall.

For the success of any breeding programme there is an urgent need to investigate genetic variability engraved in the breeding material. The assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a pre-requisite for making effective selection. Yield is a complex trait, polygenic in inheritance, more prone to environmental fluctuations than ancillary traits such as branches/ plant, seeds/siliqua, main shoot length, and 1000-seed weight. Understanding the association between yield and its components is of paramount importance for making the best use of these relationships in selection (Sarawgi *et al.* 1997).

The important economic character which is prime importance is yield and is an outcome of multiplicative interaction of component characters. For breeding high yielding varieties of crop plants, breeders usually face problem of selection of desirable parents. In general, parents are selected on basis of their *per se* performance, but many times high yielding genotype may/may not transmit its superiority to progeny. Hence, critical choice of parents is of utmost importance, particularly for improvement of complex quantitative characters such as yield. Different mating designs have been used by different workers as an aid in the choice of parents, and to understand their genetic nature. The most commonly used mating designs diallel and Line × Tester; provide estimates of additive and dominance/ non-additive components of gene effect in relation to whole population studied. However, partitioning of genetic variance into its all the probable components i.e. additive, dominance and all types of epistasis can be detected by generation mean analysis using the scale test, which measures epistasis accurately whether it is complimentary (Additive x Additive) or duplicate (Additive x Dominance) and (Dominance x Dominance) at the digenic level. For this purpose there is a need to augment its productivity through the development of high yielding varieties.

Thus the present study was undertaken to understand the gene effects involved in inheritance of various quantitative and qualitative traits in Indian mustard to provide a basis for an evaluation of selection methods for the improvement of population. Therefore, sincere efforts are needed to increase the yield levels and to achieve self-sufficiency. It is very difficult to evolve long lasting and stable high yielding varieties without the prior knowledge of mode of inheritance of yield attributing traits. Hence, the present investigation has been made to find out the

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inheritance of seed yield and yield attributing traits for further utilization in the breeding programme.

Materials and methods

An experiment was conducted over two seasons (i.e. Rabi 2005-2006 and 2006-2007) under normal and late sown conditions at the research area of Department of Plant Breeding CCS, Haryana Agricultural University, Hisar. Six generations namely, P_1, P_2, F_1, F_2, B_1 and B_2 each of the two crosses *viz*. RH 0115 x EC 126745 (Cross I) and RH 0120 x EC 126745 (Cross II) were raised in a randomized block design with three replications in 5 m long rows spaced 30 cm. apart with plant to plant distance of 15 cm. There were two rows each for P_1, P_2 and F_1's; four rows each for back crosses (B1 and B2) and ten rows for F_2 in each replication for both the crosses in E1 and E2. Five plants from each of the non-segregating generations (P_1, P_2 and F_1), 20 plants from each of the back cross generations (B_1 and B_2) and 60 plants from F_2 generation in each replication were randomly selected in both the environments. These selected plants were tagged before flowering. The observations on these plants were recorded for days to maturity, number of primary branches per plant, number of secondary branches per plant, main raceme length, and number of siliquae on main raceme, number of seeds per siliqua, seed yield per plant, 1000-seed weight and oil content. The individual plant data of three replications were pooled to calculate the mean of generation. The data were subjected to scaling tests as per Mather (1949) to detect the presence of epistasis. In case of significance of scaling tests, data was then subjected to the estimation of various genetic components as per Hayman (1958). In the case of scaling tests being non-significant, the three parameter model of Cavalli (1952) which is based on least square estimates (joint scaling test) was used to estimate main effects, m, d and h. The adequacy of three parameter model was tested by χ^2 test (3df).

Results and discussion

Analysis of Variance: It is evident from analysis of variance between family comparisons depicted significant differences for all growth attributes except number of secondary branches. The estimates of gene effects and interactions for the best fit model with respect to different yield attributing traits in two crosses of Indian mustard are given in Table 1. The inheritance pattern varied with cross, yield component and environment. However, both additive and non-additive gene effects were observed for different traits. Similar results were reported by Rahman *et al.* (2011) that proportion of positive and negative effects as indicated by F value was significant for all the characters. Positive F value for days to maturity, primary branches plant, length of siliqua, siliquae plant, seeds siliqua, seed yield and oil content indicates great frequency of dominant alleles governing these characters in *Brassica juncea*.

Rahman *et al.* (2011) also reported that the environmental component "E" exhibited significant values for all the traits, indicating the influence of environmental factors in the expression of those traits. Chowdhury *et al.* (2004) obtained significant E value for plant height, primary branches plant, seeds siliqua, seed yield plant and oil content in Turnip rape indicating that the characters were influenced less by the environment. These traits can be improved through simple selection as they were under the control of additive gene effect which is heritable and fixable variation.

Contrary to this the additive-dominance model was inadequate hence indicating the role of gene interaction or linkage or both for the control of characters like main raceme length, siliquae on main raceme, seed yield per plant and 1000-seed weight which can be exploited through reciprocal recurrent selection, diallele selective mating and simple pedigree method (Table 1). Both duplicate and complementary type of epitasis were present but not frequent.

Scaling Tests and Estimation of Gene Effects: Significant values for all scaling tests (Table 1) indicated the presence of non-allelic interactions. Hence six parameter model was used to explain the nature of gene action and types of epistasis for the expression of characters. The existence of inadequacy of additive-dominance model suggested possibility for existence of interallelic interactions in the most of characters.

Significant additive gene effects for days to maturity, number of primary branches, number of secondary branches, number of seeds per siliqua and oil content in Indian mustard were reported by Kant and Gulati (2001), Kumar and Thakral (2003) and Gami *et al.* (2012). Similarly, Singh and Srivastava (1999), Katiyar *et al.* (2000), Sachan *et al.* (2004), Goswami (2005) Prajapati *et al.* (2008) and Meena *et al.* (2013) reported the significance of both additive and non- additive gene effects for main raceme length, number of siliquae on main raceme, seed yield per plant and 1000-seed weight in Indian mustard.

Therefore, these finding suggested the presence of additive and non additive type of gene action for inheritance of characters. Considering the significance of dominance and dominance × dominance, duplicate epistasis as observed in most of the crosses for majority of the characters may result in decreased variation in F_2 and subsequent generations and may decrease heterosis and also hinder the pace of progress through selection. The present study demonstrates the importance of

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additive, dominance and epistatic gene effects in the inheritance of seed yield and yield attributing traits. The system of breeding that can be employed for improvement of character depends upon the type of gene action involved for its expression. In general, the character governed or preponded by fixable additive gene effect could be improved through pedigree selection method. For the characters, which are controlled by non-additive gene action (dominance or epistasis) heterosis breeding would be most effective; however, mode of reproduction of crop and lack of workable CGMS system would restrict it; therefore selection in later generation would be remunerative as by that time dominance could be reduced by selfing and/or inbreeding. The characters governed by both additive and non-additive gene effects, population improvement through inter se/bi-parental mating and cyclic selection such as reciprocal recurrent selection or diallel selective meeting would help in improving the seed yield and its component characters.

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Table 1. Estimates of additive and non-additive gene effects of generation means on three/six parameters model for yield attributing traits in Indian mustard

Crosses	Environments	Gene effects							
		m	(d)	(h)	(i)	(j)	(l)	Type of Epistasis	Joint scaling test (χ^2)
Days to maturity									
RH 0115 x EC 126745	E_1	151.06±0.23	3.04*±0.28	0.31±0.41	-	-	-	-	2.24
	E_2	131.35±2.72	1.97*±0.28	-3.45±6.09	-	-	-	-	7.32
RH 0120 x EC 126745	E_1	151.97±3.27	12.73*±0.21	-1.33±7.03	2.87±3.26	-2.92*±1.20	3.60±3.86	-	37.85*
	E_2	134.45±2.87	2.13*±0.21	-0.35±6.45	1.14±2.86	5.12*±1.34	2.10±3.72	-	19.28*
Number of primary branches per plant									
RH 0115 x EC 126745	E_1	5.22±0.10	0.13±0.21	-0.53±0.60	-	-	-	-	4.26
	E_2	4.03±0.08	0.77*±0.16	-0.07±0.47	-0.70±0.44	0.67±0.38	1.63*±0.79	-	10.33*
RH 0120 x EC 126745	E_1	4.96±0.07	0.40*±0.19	0.60±0.49	-	-	-	-	7.58
	E_2	4.10±0.08	0.73*±0.16	-0.20±0.48	-0.97*±0.46	1.00*±0.40	1.57*±0.80	-	14.39*
Number of secondary branches per plant									
RH 0115 x EC 126745	E_1	16.25±0.21	1.80*±0.44	0.47±1.27	-	-	-	-	0.48
	E_2	12.06±0.22	2.17*±0.39	3.37*±1.20	-	-	-	-	5.73
RH 0120 x EC 126745	E_1	14.99±.24	3.17*±0.47	5.27*±1.37	5.43*±1.34	2.40*±0.98	-6.77*±2.18	D	25.38*
	E_2	13.09±0.20	1.93*±0.41	-1.97±1.19	-3.83*±1.15	0.53±0.93	6.50*±1.93	-	13.19*
Number of seeds per siliqua									
RH 0115 x EC 126745	E_1	12.17±0.11	0.35±0.28	0.05±0.70	-	-	-	-	7.70
	E_2	11.17±0.12	0.79*±0.19	0.49±0.63	0.03±0.62	0.95*±0.40	2.46*±0.92	-	86.24*
RH 0120 x EC 126745	E_1	12.19±0.09	-0.16±0.24	-0.10±0.60	-	-	-	-	5.59
	E_2	11.25±0.12	0.90*±0.15	0.80±0.55	0.20±0.55	1.29*±0.31	1.52*±0.76	-	110.12*

* Significant at 5% level ; D – Duplicate type of epistasis

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Table 1. Contd.,

Crosses	Environments	Gene effects							
		m	(d)	(h)	(i)	(j)	(l)	Type of Epistasis	Joint scaling test (χ^2)
Oil content									
RH 0115 x EC 126745	E_1	40.47±2.03	1.76*±0.16	-1.64±4.77	-0.24±2.02	3.37*±1.15	2.23±2.85	-	10.84*
	E_2	37.88±0.16	0.14±0.17	0.80*±0.30	-	-	-	-	5.05
RH 0120 x EC 126745	E_1	40.62±0.17	1.01*±0.17	1.64*±0.36	-	-	-	-	6.52
	E_2	37.19±0.15	0.38*±0.15	2.23*±0.24	-	-	-	-	1.65
Main raceme length									
RH 0115 x EC 126745	E_1	70.76±0.68	9.27*±0.97	16.47*±3.43	11.37*±3.32	6.33*±2.07	-3.70±5.02	-	44.04*
	E_2	63.44±0.64	2.60±1.41	0.17±3.83	-2.70±3.81	-3.33±2.88	20.57*±6.32	-	53.31*
RH 0120 x EC 126745	E_1	70.94±0.70	8.33*±0.87	11.80*±3.35	6.23±3.29	5.40*±1.83	1.67±4.63	-	35.24*
	E_2	61.23±0.65	2.37*±1.09	3.53±3.45	-3.13±3.38	-7.00*±2.38	19.20*±5.25	-	49.15*
Number of siliquae on main raceme									
RH 0115 x EC 126745	E_1	53.18±0.57	8.67*±1.21	7.43*±3.37	2.37±3.32	16.40*±2.51	4.17±5.47	-	56.37*
	E_2	46.78±0.53	2.83*±1.16	3.27±3.18	-	-	-	-	7.45
RH 0120 x EC 126745	E_1	54.26±0.51	1.50±0.98	6.53*±2.88	1.57±2.81	5.20*±2.08	0.57±4.56	-	9.16*
	E_2	47.54±047	4.43*±0.91	-6.13*±2.65	-9.83*±2.67	3.87*±1.91	21.03*±4.19	D	30.28*
Seed yield per plant									
RH 0115 x EC 126745	E_1	24.69±0.39	5.47*±0.52	2.42±1.87	-1.77±1.86	4.01*±1.04	-0.84±2.62	-	25.68*
	E_2	14.68±0.20	4.58*±0.30	2.57*±0.99	-0.45±0.99	4.87*±0.61	4.59*±1.45	C	188.72*
RH 0120 x EC 126745	E_1	22.60±0.29	4.11*±0.41	3.64*±1.43	0.35±1.42	2.35*±0.83	3.83±2.02	-	58.82*
	E_2	4.73±0.19	4.31*±0.24	3.00*±0.90	0.04±0.90	4.39*±0.50	3.02*±1.24	C	175.82*
1000 seed weight									
RH 0115 x EC 126745	E_1	4.04±0.06	0.68*±0.14	1.42*±0.37	-	-	-	-	2.34
	E_2	3.43±0.04	0.75*±0.09	-0.57*±0.25	-1.20*±0.24	0.52*±0.18	1.12*±0.40	D	56.31*
RH 0120 x EC 126745	E_1	3.66±0.06	0.10±0.10	1.43*±0.31	0.41±0.31	0.87*±0.21	0.71±0.48	-	73.57*
	E_2	3.38±0.04	0.98*±0.08	-0.32±0.24	-0.80*±0.22	0.87*±0.17	0.11±0.41	-	61.60*

* Significant at 5% level; D – Duplicate type of epistasis; C – Complimentary type of epistasis