International Journal of Agriculture Sciences
ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 12, Issue 3, 2020, pp.-9537-9541.
Available online at https://www.bioinfopublication.org/jouarchive.php?opt=&jouid=BPJ0000217

Research Article

HETEROSIS AND INBREEDING DEPRESSION STUDY IN INDIAN MUSTARD [*Brassica juncea* (L.) Czern & Coss]

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Received: February 02, 2020; Revised: February 12, 2020; Accepted: February 13, 2020; Published: February 15, 2020

Abstract: *Brassica juncea* (L.) commonly known as Indian mustard is globally used as oilseed, vegetable and condiments. The analysis of variance for the experimental design indicated to significant differences among the genotypes for all the traits studied. Partitioning of genetic variance indicated to highly significant differences among the parents as well as hybrids for all the traits under study. This indicated that materials used for present investigation had adequate variability for different traits. The highly significant mean sum of squares for parents *vs*. hybrids indicated to existence of heterosis for all the characters studied. The performance of hybrids revealed that crosses RH-749 x RH-406 and NRCDR-02 x RGN-73 were among best performing hybrids. The *gca* and *sca* mean squares were significant for all the traits indicating importance of both additive and dominant gene actions controlling the expression of characters.

Keywords: *Heterosis, Inbreeding*

Citation: Singh B., *et al*., (2020) Heterosis and Inbreeding Depression Study in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 12, Issue 3, pp.- 9537-9541.

Academic Editor / Reviewer: Dr Vijayachandra Reddy S, B Arunkumar, P. T. Patel, Namrata Dwivedi, P. K. Singh

Introduction

Indian mustard (*Brassica juncea* L.) is a natural amphidiploid (2n=36) of B. compastris (2n=20) and *B. nigra* (2n=16). Indian mustard (*B. juncea* L.) popularly known as rai or raya is one of the most important oilseed crops of the country and it occupies considerably large acreage among the Brassica group of oil seed crops. By exploiting heterosis in the F1 hybrids, production cost could be reduced by increasing yield level and enhancing input use efficiency. Indian mustard being a self-pollinated crop, diallel mating system for combing ability analysis is very important for screening of lines with rapidity. Combining ability analysis provides a guideline for the assessment of relative breeding potential of parental material which can be utilized in pursuing a systematic breeding programme [1]. This possibility was explored in the present investigation and the combining ability of the desirable lines was studied. Selection of parents is an important step for planning an appropriate hybridization programme. The combining ability analysis furnishes useful information of this aspect. Knowledge of the relative importance of additive and non additive gene action is essential to a plant breeder. The per se performance, *gca* and *sca* effects determine the potentiality of parents/crosses for mobilizing them in an efficient breeding programme. Identifying parental material with strong heterosis for yield and obtain genetic parameters are the important steps in the development of new cultivars. It is important to have information about the desirable parental combinations which can represent a high degree of heterotic response [2,3]. By exploiting heterosis in the F1 hybrids, production cost could be reduced by increasing yield level and enhancing input use efficiency by Pingali (1997) [4]. Indian mustard being a self-pollinated crop, diallel mating system for combing ability analysis is very important for screening of lines with rapidity

Materials and Methods

A set of 36 genotypes comprising 8 parents and their 28 F1 hybrids were sown in a Randomized Block Design with three replications during Rabi 2016-17, 2017-18 and 2018-19 at Nana Ji Deshmukh New Agricultural Campus, MGCGV, Chitrakoot, Satna, Madhya Pradesh, India. Each genotype was sown in single row of 5meter length. The distance between rows and plants was 30 cm and 20 cm, respectively. Other recommended agronomic practices and plant protection measures were adopted throughout the crop period.

Result and Discussion

GCA and *SCA* variances and effects

Early flowering is considered desirable. Therefore, genotypes with negative *gca* and *sca* values are to be considered for this trait. Among the parents viz., NRCDR-02 (-0.14), KRANTI (-0.56), GM-2 (-1.18) and RGN-73 (-1.78) exhibited non significant negative *gca* effects for this trait. The significant *gca* values were associated with two parents namely RH-749 (1.32) and RH-406 (1.21) but in positive direction. Significant positive *sca* effects were exhibited only three crosses namely RH-749 x KRANTI (3.33), RH-406 x KRANTI (2.07) and NRC HB-101 x RGN-73 (2.48). Although 24 crosses showed the negative direction but none was significant. The estimates of *gca* effects revealed that out of 8 parents, 4 parents NRC HB-101 (-0.12), KRANTI (-0.32), GM-2 (-3.14) and RGN-73 (-1.02) exhibited non significant negative *gca* effects for this trait. On other hand, two parents RH-749 (0.83) and RH-406 (0.64) recorded significant and positive *gca* effects.

The significant positive *sca* effects were exhibited by 5 crosses namely RH-749 x KRANTI (2.17), RH-406 x KRANTI (2.73), NRC HB-101 x NRCDR-02 (2.94), NRC HB-101 x GM-2 (0.72) and NRCDR-02 x GM-2 (2.83). Remaining 18 crosses showing negative *sca* effects were non significant. The estimates of *gca* effects revealed that out of 8 parents only NRCDR-02 (1.16) and GM-2 (2.31) exhibited positive significant effect therefore was considered to be good combiners for this trait. Remaining parents may be considered poor general combiners as their *gca* values were not significant. The significant positive *sca* effects were exhibited only five crosses namely RH-749 x NRC HB -101 (4.23), RH-749 x DRMR-IJ-31 (3.48), RH-749 x GM-2 (5.86), NRC HB -101 x DRMR-IJ-31 (5.80) and NRCDR-02 x DRMR-IJ-31 (5.07). These hybrids were considered as good combiners for seed yield per plant.

Table-1 *Estimate of general combining ability (GCA) and specific combining ability (SCA) effects*

GCA	DF	DM	PH	PB	SL	SPP	SS	SYP	1000-SW	OC (%)
RH-749	1.32**	0.83*	3.12**	0.01	0.05	-0.84	0.13	0.05	-0.02	-0.06
RH-406	1.21**	0.64*	2.46*	-0.05	-0.32	10.23	-0.41	-0.54	0.07	-0.01
NRC HB -101	0.23	-0.12	1.45	0.14	1.12**	12.06	-0.36	0.05	-0.14	0.11
NRCDR-02	-0.14	0.31	-3.16	-0.36	-1.47	31.72**	-0.21	1.16**	0.18**	0.19**
DRMR-IJ-31	0.16	0.12	5.24**	0.11	-0.54	-3.18	0.63**	-0.26	0.15**	-0.10
KRANTI	-0.56	-0.32	-1.18	0.25**	0.31	8.17	-0.03	-021	-0.24	0.01
GM-2	-1.18	-3.14	-9.62	0.38**	2.16**	46.45**	0.16	2.31**	-0.15	0.17
RGN-73	-1.78	-1.02	0.53	-0.22	-0.35	15.42	0.41*	-0.08	0.35**	0.31**
SCA	DF	DM	PH	PB	SL	SPP	SS	SYP	1000-SW	OC (%)
RH-749 x RH-406	-2.56	-1.86	8.45**	0.46**	-0.86	-2.45	0.04	-2.65	0.05	0.16
RH-749 x NRC HB -101	-0.21	1.51	-0.62	0.21	1.78	21.56	-0.02	4.23**	0.04	0.51**
RH-749 x NRCDR-02	0.32	-0.64	-6.12	-0.04	-2.19	-41.58	-0.35	-2.45	-0.16	-0.05
RH-749 x DRMR-IJ-31	-1.52	-2.84	-8.38	0.43**	1.63	52.44**	-0.94	3.48**	0.74**	0.28
RH-749 x KRANTI	3.33**	2.17**	-0.68	-0.12	-0.04	12.89	0.84	1.71	0.18	0.24
RH-749 x GM-2	-1.82	-1.84	12.27**	1.32**	4.96**	79.64**	1.84**	5.86**	0.12	0.03
RH-749 x RGN-73	-1.54	-1.82	-3.12	0.13	0.85	35.12	-0.18	2.23	0.97**	-0.49
RH-406 x NRC HB -101	-1.68	-0.62	-6.12	0.38	1.18	2.78	-0.68	-0.17	0.54**	-0.31
RH-406 x NRCDR-02	-2.29	-2.97	-3.21	-0.51	-0.48	25.89	-0.59	-0.62	-0.39	0.78
RH-406 x DRMR-IJ-31	-0.99	-3.03	-2.01	-0.79	-1.76	-44.81	0.24	-1.74	-0.75	-0.64
RH-406 x KRANTI	2.07**	2.73*	-0.79	-0.31	2.03	15.44	0.86	-0.90	-0.78	-0.86
RH-406 x GM-2	-1.85	-1.73	-0.22	-0.23	-1.71	-5.74	-0.63	-1.17	0.39**	0.53**
RH-406 x RGN-73	-0.96	1.47	-1.21	0.21	-1.71	-21.65	0.77	0.38	-0.04	0.61**
NRC HB -101 x NRCDR-02	0.15	2.94**	-0.08	0.38	2.52	-31.01	0.19	-1.04	0.19	0.24
NRC HB -101 x DRMR-IJ-31	-2.46	-0.51	-0.49	0.99	1.44	31.61	1.12	5.80**	-0.28	-0.45
NRC HB -101 x KRANTI	-0.46	1.13	10.01**	0.27	0.49	-51.10	-0.11	-3.12	-0.12	-0.14
NRC HB -101 x GM-2	-3.07	0.72**	-5.34	-0.62	1.93	20.44	0.39	-0.03	-0.08	-0.75
NRC HB -101 x RGN-73	2.48**	5.41	-4.99	0.16	-0.04	-6.19	0.53	-1.25	0.28	-0.54
NRCDR-02 x DRMR-IJ-31	0.84	0.05	7.79**	0.69**	4.85**	74.24**	1.26**	5.07**	-0.92	-0.69
NRCDR-02 x KRANTI	0.63	-0.56	-0.21	0.71	-0.37	-21.71	0.52	-1.13	0.41	0.86**
NRCDR-02 x GM-2	0.36	2.83**	-6.32	-0.05	-1.26	-33.03	-0.23	-1.59	0.58**	0.69**
NRCDR-02 x RGN-73	-1.74	-0.28	-0.48	-0.29	-1.04	-41.78	1.98**	-0.26	-0.69	0.47**
DRMR-IJ-31 x KRANTI	-0.18	-0.88	10.45**	-0.18	-1.04	7.47	1.35**	-0.92	-0.56	-0.97
DRMR-IJ-31 x GM-2	-0.09	-0.51	-5.12	-0.73	1.19	12.11	-0.74	1.13	-0.16	-0.56
DRMR-IJ-31 x RGN-73	-0.68	-0.08	-8.78	-0.23	-2.17	-41.33	0.98	-1.95	-0.56	-0.53
KRANTI x GM-2	-0.18	2.27	-1.57	0.49**	1.66	41.18	0.19	1.45	-0.57	0.64
KRANTI x RGN-73	-2.32	-4.65	-3.79	0.01	1.26	24.33	-1.55	-0.48	0.42**	-0.64
GM-2 x RGN-73	-0.96	-2.06	14.23**	0.25	0.67	-1.06	0.37	2.79	0.03**	0.62**

and significant at 5% and 1% level of significance, respectively*

Table-2 *Magnitude of heterobeltiosis (HB) for various traits*

Crosses	DF	DM	PH	PB	SL	SPP	SS	SYP	1000-SW	OC (%)
RH-749 x RH-406	-12.59	-5.01	11.02**	11.16**	11.15**	11.12	3.15**	131.95**	11.23**	-0.32
RH-749 x NRC HB -101	-3.92	0.12	4.82	6.06**	21.16**	7.63	3.07**	112.20**	1.41	0.83
RH-749 x NRCDR-02	-8.77	-3.44	-1.99	-2.49	-36.49	-21.69	-5.01	-11.49	-7.98	-1.83
RH-749 x DRMR-IJ-31	1.64	1.00	-4.04	-21.05	-35.08	-23.78	8.56**	-11.57	-0.63	-0.95
RH-749 x KRANTI	-11.22	-4.52	6.73	13.86**	21.91**	31.38	-0.59	29.87**	12.38**	-0.43
RH-749 x GM-2	-12.66	-1.53	3.27	-16.22	-24.43	-12.39	9.11**	31.16**	2.69**	-0.75
RH-749 x RGN-73	-7.22	-1.75	12.70**	21.68**	81.08**	75.15*	-0.52	116.12**	1.52**	4.21**
RH-406 x NRC HB -101	-9.19	-4.71	8.11	1.46**	31.57**	41.23	-7.44	27.87**	7.93**	-2.36
RH-406 x NRCDR-02	-8.84	-2.38	9.85	8.56**	6.01	-3.12	-12.16	29.52**	6.71**	-2.67
RH-406 x DRMR-IJ-31	-11.57	-3.13	-1.11	-22.22	-3.45	34.74	-8.39	30.47**	-4.75	-0.56
RH-406 x KRANTI	-7.32	-3.99	3.59	-17.19	-21.18	-31.98	0.99	-21.96	-7.64	-1.17
RH-406 x GM-2	-15.34	-6.27	-3.21	-10.73	14.91**	-17.34	0.68	-18.44	-4.75	-1.24
RH-406 x RGN-73	-11.02	-3.06	2.99	-3.54	-13.51	-15.18	-11.55	-16.74	6.94**	-0.81
NRC HB -101 x NRCDR-02	-6.65	-0.75	-2.81	-10.71	-34.84	-31.54	5.62**	-17.58	-3.62	1.79**
NRC HB -101 x DRMR-IJ-31	-7.72	-0.94	2.78	3.57**	17.42**	-30.04	-6.35	-11.45	-4.53	1.31**
NRC HB -101 x KRANTI	-14.33	-4.75	-2.34	-0.05	29.57**	1.09	10.38*	9.59	-6.58	2.27**
NRC HB -101 x GM-2	-16.99	-6.07	3.19	-5.99	12.71**	-30.75	-2.79	-25.04	-4.35	-2.08
NRC HB -101 x RGN-73	-16.12	-3.43	3.53	-13.35	35.92**	0.91	3.51**	-13.53	11.63	-2.38
NRCDR-02 x DRMR-IJ-31	-3.74	1.06	-5.03	-8.81	-7.86	-21.08	2.81**	-21.87	4.28**	-3.76
NRCDR-02 x KRANTI	-10.57	-4.82	3.26	5.59**	46.29**	10.96	-2.54	5.43	-5.19	-3.11
NRCDR-02 x GM-2	-9.73	-5.99	-5.56	1.01**	13.14**	-9.22	3.05**	-11.22	5.27**	-0.86
NRCDR-02 x RGN-73	-8.74	0.25	-0.99	-5.32	0.12	-3.74	4.78**	-5.64	1.13**	-2.01
DRMR-IJ-31 x KRANTI	-17.57	-5.71	4.59	-22.30	-18.14	-14.12	8.17**	-2.71	-9.78	-1.73
DRMR-IJ-31 x GM-2	-11.34	-1.77	10.03	-12.39	-18.24	-7.44	9.34**	0.97	-11.74	-3.48
DRMR-IJ-31 x RGN-73	-6.73	-0.51	3.23	-12.22	4.92	0.17	-0.62	7.40	-8.62	-3.13
KRANTI x GM-2	-12.11	-2.49	-0.11	-21.14	-21.23	-11.66	2.11	-15.81	-17.24	-2.98

Table-3a *Estimates of inbreeding depression (ID), narrow sense heritability (h2ns) and expected genetic advance as percent of mean (GA %) for various characters in 28 crosses in Indian mustard*

Traits	DFF	DM	PH	PB	SL	SPP	SS	SYP	1000-SW	Oil (%)
1	RH-749 x RH-406									
ID	6.17**	1.05**	6.10**	0.14	3.41	10.46**	8.11**	2.25	12.01**	5.02**
h2ns	96.12	95.46	98.15	22.12	68.78	39.15	80.78	16.12	72.19	97.72
GA	11.14	3.15	17.14	3.15	2.15	8.12 **	14.73	3.18	2.87	12.96
2	RH-749 x NRC HB -101									
ID	3.12**	0.95**	5.46**	12.45**	10.75**	-6.23	0.12	-2.43	1.13	-5.48**
h2ns	99.12	97.19	82.15	36.44	46.47	19.17	95.72	45.15	86.12	92.25
GA	19.18	9.12	3.12	4.16	1.23	1.66	16.56	12.16	12.10	16.45
3	RH-749 x NRCDR-02									
ID	3.77**	2.09**	13.22**	0.26	9.64**	0.52	3.48	3.25	12.59**	3.21
h2ns	98.12	96.46	48.47	48.12	36.17	71.72	99.11	17.16	91.49	46.71
GA	14.27	3.16	4.78	14.19	1.02	21.16	26.18	3.19	2.16	11.49
4	RH-749 x DRMR-IJ-31									
ID	3.12*	1.46*	11.49**	5.45**	3.19*	3.45	1.14	-3.56	-11.40**	-12.31**
h2ns	77.16	81.16	38.17	62.43	44.88	44.61	25.12	41.49	34.12	98.17
GA	6.46	7.14	3.46	20.72	5.49	17.61	2.67	9.12	3.49	14.91
5	RH-749 x KRANTI									
ID	3.19**	1.25**	15.56**	3.43	8.56**	6.37	0.62	-8.92**	12.07	6.01**
h2ns	45.16	53.78	12.49	69.47	94.56	66.15	25.12	56.72	92.65	16.84
GA	1.26	2.46	0.28	11.95	19.07	12.07	5.55	11.54	51.63	2.65
6	RH-749 x GM-2									
ID	3.91**	1.03**	12.18**	0.21	-4.97**	-4.90**	3.57**	-5.23**	-12.80**	7.68**
h2ns	62.4	61.4	60.04	71.05	56.42	71.52	11.94	78.98	54.68	90.53
GA	6.56	2.86	4.63	9.12	15.51	16.87	0.87	15.07	15.34	11.71
7	RH-749 x RGN-73									
ID	2.77**	1.09**	11.22**	0.12	8.64**	0.62	3.18	3.15	10.59**	2.21
h2ns	80.12	88.19	58.47	38.12	31.17	48.72	69.11	57.16	31.49	36.72
GA	11.27	2.16	1.78	12.19	1.08	11.16	13.18	1.19	1.16	10.41
8	RH-406 x NRC HB -101									
ID	3.17**	2.05**	7.10**	2.14	1.41	5.46**	6.11**	3.25*	10.01**	2.02
h2ns	86.12	85.46	78.15	42.12	78.55	39.15	90.78	26.12	12.19	87.72
GA	9.14	13.15	11.14	9.15	8.15	6.12	17.73	2.18	6.87	21.96
9	RH-406 x NRCDR-02									
ID	3.57**	3.09**	10.22**	1.46	8.64**	5.78	2.48	1.25*	11.59**	1.21
h2ns	95.46	90.45	52.47	61.49	48.79	40.19	98.79	59.41	21.49	26.71
GA	10.78	5.78	7.45	11.45	2.73	12.48	20.68	5.44	3.43	8.77
10	RH-406 x DRMR-IJ-31									
ID	5.46**	3.03**	12.18**	1.21	24.97**	-5.96**	5.57	8.23**	8.80**	7.56**
h2ns	90.12	88.46	60.03	51.05	86.42	31.52	41.94	65.22	84.68	46.53
GA	5.56	3.86	7.63	11.12	12.51	12.87	8.87	17.55	18.34	8.71
11	RH-406 x KRANTI									
ID	5.17**	2.05**	8.10**	1.47	5.41	9.77**	8.11**	6.25	12.01**	5.02
h2ns	86.12	89.46	88.15	21.12	58.78	39.15	80.78	16.12	8.19	77.72
GA	11.14	2.15	11.17	3.85	8.15	6.12	12.73	8.18	6.87	12.96
12	RH-406 x GM-2									
ID	2.45**	3.25**	15.56**	3.43	3.56**	4.37	5.62	6.92**	12.07	8.01**
h2ns	67.56	88.78	84.45	45.48	94.47	42.79	31.49	49.78	88.12	12.84
GA	8.26	16.46	11.28	8.95	29.07	11.07	7.55	5.54	8.63	7.65
13	RH-406 x RGN-73									
ID	5.46**	3.48**	11.78**	1.23	8.16**	3.12	3.78	6.71	16.17**	3.68
h2ns	72.40	81.45	70.04	61.05	46.45	78.18	41.94	68.98	64.68	80.23
GA	3.46	5.49	7.46	9.44	7.46	12.45	6.87	3.07	8.34	9.71
14	NRC HB -101 x NRCDR-02									
ID	6.12**	1.95**	8.46**	9.45**	12.75**	7.23	1.12	3.43	6.13	3.48
h2ns	96.12	91.19	80.15	42.44	59.47	44.17	42.72	25.15	19.12	48.25
GA	7.18	9.12	3.12	4.16	1.29	3.66	16.56	12.16	12.10	16.45

* &** *significant at 5% and 1% level of significance, respectively*

On the basis of estimates of *gca* effects only 2 parents, NRCDR-02 (0.19) and RGN-73 (0.31) were found good general combiners as there exhibited positive significant effect for this trait. Remaining parents may be considered poor general combiners as their *gca* values were not significant. The significant positive *sca* effects were exhibited by six crosses namely RH-749 x NRC HB -101 (0.51), RH-406 x GM-2 (0.53), RH-406 x RGN-73 (0.61), NRCDR-02 x KRANTI (0.86), NRCDR-02 x GM-2 (0.69) NRCDR-02 x RGN-73 (0.47) and GM-2 x RGN-73 (0.62), hence were considered as good combiners for oil percentage.

Heterosis and Inbreeding depression

Heterosis or hybrid vigour is the increase in size, vigour or productivity of a hybrid plant over the average or mean of its parents. The heterosis measured over the better parent and standard checks is of much practical importance. The commercial exploitation of heterosis is considered to be an outstanding application of principles of genetics into the field of plant breeding. In the present study a number of hybrids exhibiting significant heterobeltiosis were obtained [Table-2]. The heterosis has been estimated over better parent for the traits under study. Thus, the aim of heterosis analysis in the present study was to identify promising hybrids which may be of commercial use. An examination of performance of hybrids over better parent revealed that 8 hybrids manifested significant positive heterosis for seed yield per plant. The maximum heterobeltiosis for seed yield per plant was exhibited by the hybrid RH-749 x RGN-73.

Table-3b *Estimates of inbreeding depression (ID), narrow sense heritability (h2ns) and expected genetic advance as percent of mean (GA %) for various characters in 28 crosses in Indian mustard [Conti..]*

Traits	DFF	DM	PH	PB	SL	SPP	SS	SYP	1000-SW	Oil (%)
15	NRC HB -101 x DRMR-IJ-31									
ID	4.46**	3.05**	6.10**	2.47	3.42	8.15**	6.46**	5.48*	11.48**	6.02**
h2ns	82.47	91.12	72.46	32.19	51.49	49.15	42.16	22.17	12.11	45.72
GA	6.14	8.15	7.17	11.85	5.15	9.12	7.73	3.18	5.87	11.96
16	NRC HB -101 x KRANTI									
ID	5.45**	3.19*	3.45*	3.12*	1.46*	11.49	5.45	3.19	2.45*	12.31
h2ns	71.16	75.16	58.17	37.43	64.88	44.631	45.12	45.49	74.12	91.17
GA	5.46	8.14	11.46	2.72	13.49	11.61	8.67	7.12	6.49	15.91
17	NRC HB -101 x GM-2									
ID	3.46**	4.03**	11.18**	5.21	14.97**	3.96	7.57	6.23	9.80**	2.68
h2ns	78.12	68.46	61.03	63.05	81.4 2	41.52	44.94	45.98	74.68	41.53
GA	3.56	8.86	9.63	12.12	9.51	8.87	9.49	12.07	16.34	5.21
18	NRC HB -101 x RGN-73									
ID	3.46**	4.48**	12.78**	2.23	6.16**	5.12	8.78	5.71	12.17**	8.68
h2ns	81.46	78.45	79.04	68.05	76.45	48.18	31.94	77.48	61.68	40.23
GA	2.46	6.49	9.46	8.44	6.46	11.45	8.87	6.07	6.34	10.71
19	NRCDR-02 x DRMR-IJ-31									
ID	7.45**	4.19*	4.45*	8.12*	3.46*	16.49**	9.45**	7.19	6.45*	10.31
h2ns	78.12	72.16	66.16	57.19	88.78	31.82	42.19	31.49	22.16	30.76
GA	5.17	10.15	8.55	7.96	8.43	5.76	5.47	7.49	9.73	6.49
20	NRCDR-02 x KRANTI									
ID	8.46**	3.47**	2.66**	1.26	6.16**	5.12	1.78	-10.45**	3.17**	4.68
h2ns	90.46	96.88	92.86	81.79	81.73	71.63	91.82	81.22	38.79	91.44
GA	13.77	10.42	12.49	20.12	2.13	12.47	6.86	11.45	3.34	7.01
21	NRCDR-02 x GM-2									
ID	3.17**	2.05**	4.10**	4.14	7.41	4.19	10.11**	3.25*	8.01**	6.02
h2ns	95.13	81.48	88.16	48.16	78.19	42.78	82.79	32.47	82.82	96.30
GA	7.13	10.77	6.78	2.85	13.88	3.16	12.77	1.44	0.46	15.33
22	NRCDR-02 x RGN-73									
ID	7.11**	2.44*	4.19*	7.16*	5.46*	6.45	3.44	2.19	4.11*	4.44
h2ns	71.55	61.45	48.77	58.99	71.82	41.44	49.48	40.45	39.41	48.19
GA	7.13	5.13	6.19	5.77	6.75	13.18	1.45	6.19	2.52	6.76
23	DRMR-IJ-31 x KRANTI									
ID	3.12**	4.55*	7.19*	6.17*	-2.16*	-1.86**	6.19	1.56	3.16*	6.44
h2ns	90.16	88.77	66.46	44.16	77.96	44.85	41.66	50.47	82.43	89.46
GA	12.46	7.46	6.46	3.79	8.76	10.46	3.79	6.95	3.18	6.49
24	DRMR-IJ-31 x GM-2									
ID	3.71**	2.45**	6.78**	2.44	-12.78**	-3.79	4.79**	0.78	-7.64**	3.11
h2ns	78.16	68.19	79.18	71.22	66.4 2	41.52	41.94	67.55	74.58	46.53
GA	3.56	2.86	4.63	12.14	8.51	8.87	5.46	3.48	9.46	3.46
25	DRMR-IJ-31 x RGN-73									
ID	6.46*	2.16*	8.79**	3.18**	1.44*	2.49	5.46	7.79	2.13	8.44
h2ns	87.49	78.49	57.44	42.63	32.49	44.79	35.49	22.79	43.46	30.41
GA	3.46	2.14	3.41	5.72	2.49	7.61	2.67	2.12	1.49	4.91
26	KRANTI x GM-2									
ID	5.86**	3.44**	4.77**	2.13	5.44**	6.44**	1.79	4.83	7.44**	1.44
h2ns	71.89	88.45	83.78	61.12	42.88	78.79	47.48	71.46	64.55	80.53
GA	8.79	5.79	9.79	5.75	3.16	4.79	3.81	5.07	5.34	10.71
27	KRANTI x RGN-73									
ID	4.55	2.77	6.44**	3.23	3.16**	4.17	5.42	4.92	2.07	8.70**
h2ns	77.56	78.78	84.45	55.48	84.47	56.79	31.49	49.78	78.12	72.84
GA	5.26	6.46	12.28	7.95	9.07	5.07	3.55	2.54	5.63	13.65
28	GM-2 x RGN-73									
ID	5.11**	1.44*	3.90*	5.16*	6.46*	-5.45**	-2.44**	5.19	3.11	2.44
h2ns	72.55	81.45	68.77	58.99	61.82	51.44	49.48	48.45	49.69	48.19
GA	5.13	6.13	3.19	4.77	4.75	3.18	10.45	5.19	2.51	5.76

* &** *significant at 5% and 1% level of significance, respectively*

The heterotic responses over better parent in Indian mustard were also reported by Patel *et al*. (2010) [5], Qian *et al*. (2007) [6], Macwana (2008) [7], Singh *et al*. (2002) [8], and Dar *et al*. (2012) [10]. Conclusively, these three crosses were also found promising for other desirable traits, hence could be further evaluated in heterosis breeding programme. Simultaneously these hybrids could be selfed to obtain desirable recombinants in segregating generations for the development of superior genotypes.

Heterobeltiosis reveals that the oil content did not vary considerably, both parents and hybrids showed more or less similar mean values for oil content. Hence any of the crosses were of no practical difference from the parents for this important character, and hence, concerted efforts are required to improve oil content. The potentiality of a parent in hybridization may be assessed by its per se performance and *gca* effects. The results revealed that most of the genotypes had relatively high degree of correspondence between per se performance and *gca* effects for the observed characters. This can be ascribed to the predominant role of additive and additive x additive type of gene action for the inheritance of these traits.

The inbreeding depression is an important criterion for crop breeding programme. The character and cross-wise results of inbreeding depression are presented in [Table-3ab]. In which positive and significant inbreeding depression was observed in the all the families for days to 50% flowering, days to maturity and plant height indicating possibilities to get the desirable segregants in the segregating generations.

Seed yield per plant had significant and negative estimates of inbreeding depression in the crosses NRCDR-02 x KRANTI, RH-749 x KRANTI and RH-749 x GM-2, which showed possibilities of desirable segregants in F2 population. These crosses also exhibited significant and negative values of inbreeding depression for yield attributing characters.

However, crosses RH-406 x DRMR-IJ-31and RH-406 x GM-2 showed significant and positive estimates of inbreeding depression for seed yield per plant, average siliquae length, number of seeds per siliquae and 1000 seed weight; hence these crosses would not likely to yield beneficial transgressive segregants. The magnitude of mean performance of F2 populations for seed yield per plant and its related traits showed significant inbreeding depression for various characters in majority of crosses studied. The results revealed that the crosses which depicted significant inbreeding depression for seed yield per plant also exhibited positive inbreeding depression for its related traits also. Overall, high estimates of narrow sense heritability and expected genetic advance in most of crosses for plant height, number of seeds per siliqua, seed yield per plant, and 1000-SW revealed that direct selection would be effective for improvement of character; and an additive gene effect was proponed. While high narrow sense heritability coupled with low to moderate expected genetic advance as per cent of mean for characters *i.e.* number of branches per plant, number of siliquae per plant and oil content percentage, revealed importance of both additive and non-additive gene effect with preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. Therefore, population improvement like recurrent selection and biparental mating is suggested for improvement of the character. However, estimates of heritability were moderate to high with low to moderate expected genetic advance as per cent of mean for days to 50% flowering, day to maturity and siliqua length, which suggested the preponderance of non-additive gene effect, and it would be difficult to improve the character through direct selection. Kumari *et al* (2009) [11] reported that the results in F2 generation provide good ground for further study in segregating generations in cotton [12].

Conclusion: It was suggested that yield of F1 did not predict the yield of bulk in advanced generations and combined performance of hybrids in F1 and F2 generation could be a good indicator to identify most promising populations to be utilized either as F2 hybrids or as a source population for further selection in advanced generations.

Application of research: Study of heterosis and inbreeding depression study in Indian mustard

Research Category: Heterosis and Inbreeding

Acknowledgement / Funding: Authors are thankful to Department of Crop Science, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidhyalaya, Chitrakoot, 485334, Madhya Pradesh, India. Authors are also thankful to Crop Improvement Division, ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, 208024, Uttar Pradesh, India

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Research project name or number: PhD Thesis

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Mahatma Gandhi Chitrakoot Gramodaya Vishwavidhyalaya, Chitrakoot, 485334, Madhya Pradesh

Cultivar / Variety / Breed name: *Brassica juncea* (L.) Czern & Coss
Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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