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Rohit
S.G. College of Agriculture & Research Station Kumhrawand, Jagdalpur, IGKV, Raipur, Chhattisgarh, India

Ravikant Chandravanshi
Department of Agro Meteorology, IGKV, Raipur, Chhattisgarh, India

Lilesh Sahu
S.G. College of Agriculture & Research Station Kumhrawand, Jagdalpur, IGKV, Raipur, Chhattisgarh, India

Parshottam Kumar Sinha
Krishi Vigyan Kendra Kawardha, Newari, Chhattisgarh, India

Vinod Chandravanshi
Department of Agro Meteorology, IGKV, Raipur, Chhattisgarh, India

Corresponding Author:
Rohit
S.G. College of Agriculture & Research Station Kumhrawand, Jagdalpur, IGKV, Raipur, Chhattisgarh, India

Heterosis analysis of yield and its components for parents and F1's in *Brassica juncea* L.

Rohit, Ravikant Chandravanshi, Lilesh Sahu, Parshottam Kumar Sinha and Vinod Chandravanshi

Abstract

The present study entitled "Heterosis analysis of yield and its components for parents and F1'S in *Brassica juncea* L." was carried out at the Research and Instructional Farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur (C.G.), Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh) during Rabi 2016-17. Experimental materials comprised 10 F1 from a half diallel cross of five parents was grown in Randomized Complete Block Design with three replications with the objectives to estimate the heterosis is estimated for average, heterobeltiosis and standard genotype results. Days taken to 50% flowering, days taken to 50% maturity, plant height, number of primary branches, number of secondary branches, number of siliquae per plant, number of seeds per siliquae, 1000 seed weight and seed yield per plant exhibited significant ($p \geq 0.01$-0.05) differences among all the entries.

The relative heterosis (Mid) RH-406 x NRCHB -101 (65.75) trait hybrids showed exhibited positive significant followed by RH-119 x DRMRIJ-31 (58.06), RH-749 x RH-406 (35.26), DRMRIJ-31 x NRCHB-101 (29.44), RH-119 x RH-406 (24.72)

The heterobeltiosis (Better parent) Out of ten hybrids four hybrids showed positive significant heterobeltiosis RH-119 x DRMRIJ-31 (48.21) followed by RH-406 x NRCHB-10 (44.94), RH-749 x RH-406 (27.53) and RH-749 x RH-119, The heterosis over check (Best parent) for this traits ranged from -32.89 (RH-749 x DRMRIJ-31) to 46.00 (RH-119 x DRMRIJ-31). Out of ten hybrids three hybrids showed exhibited positive standard heterosis RH-119 x DRMRIJ-31 (46.00) followed by RH-406 x NRCHB-10 (44.94) and RH-749 x RH-406 (27.53). Improved seed yield is a primary objective in a crop breeding program and therefore, positive heterosis for seed yield is of prime importance to develop high yielding genotypes.

Keywords: Average, better parents and best parents, seed yield, *Brassica juncea* L.

Introduction

Mustard (*Brassica juncea* L.) common name-Indian mustard, Family- Brassicaceae or Cruciferae and Chromosome number (2n = 36). India is one of the largest producers of mustard in the world. Crop Brassicaceae are important sources of edible oil with lowest amount of saturated fats and leafy vegetables rich in minerals, antioxidants and tasteful condiments crops. Rapeseed mustard is an important group of oilseed crops accounting about one-fourth of the total oilseeds production in the country. These crops are predominantly grown on varied soils of diverse agroclimatic regions in India. Rapeseed-mustard is mainly grown as oilseed crop. The oil obtained from the seed is edible and contains several important nutritional components. The cake obtained from oil extraction is used as cattle feed and improves the quality of milk and other animal produce. The oil content of seeds ranges from 40-50 per cent. The oil obtained is the main cooking medium and excellent source of chemical industry such as lubricants, and in the manufacture of a variety of products like rubber, soap, plastic, nylon. The seed and oil are used as a condiment in the preparation of pickles and for flavouring curries and vegetables. In India, area, production and productivity of mustard crop was 6.70 million hectare (7.96) million tons and 1188 kg per hectare, respectively but in Chhattisgarh in area, production and productivity is 1.07 lakh hectare, 0.94 lakh tons and 879 kg per hectare respectively (Anonymous, 2015) [2].

The term heterosis was first used by Shull in (1914). Heterosis breeding has played a pivotal role in crop improvement programme for obtaining higher production. The pre-requisite is to know the magnitude and direction of heterosis so, that it can be effectively exploited in crop improvement. The hybrid vigour has so far not been extensively exploited in self pollinated crop in comparison to cross pollinated ones. However, heterosis as a means of increasing productivity has been an object of considerable study in Indian mustard.

In Chhattisgarh, great scope to extension of early maturing rapeseed and mustard crop in rabi season due to low water requirement as compare to other crops. Therefore mustard crop can grow in rice based cropping system; it can act as a source of income for the marginal and small farmers in rainfed area. Hence, looking to above facts present investigation entitled "Heterosis analysis of yield and its components for parents and F1'S in *Brassica juncea* L." is being carried out with the objective of genetic variability parameters.

Materials and Methods

The present investigation "Determination of the combining ability analysis of parents and F1'S in Indian Mustard (Brassica juncea L.)'' carried out at Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Kumhrawand Jagdalpur, Chhattisgarh, Indira Gandhi Krishi Vishwavidyalaya Raipur Chhattisgarh during rabi 2016-17. Jagdalpur is located within 17° 45' to 20° 34'N, and 80° 15' to 820 15; E longitude with an altitude ranging from 530 to 850 meters above mean sea level (MSL) with an annual rainfall 1200 to 1600 mm

Experimental materials comprised ten F1 'S from a half diallel crosses involving five of mustard genotype (RH- 749, RH119, RH-406, DRMRIJ-31, and NRCHB-101) with a check variety of Chhattisgarh sarson 1. The experiment was grown in randomized complete block design with three replication. Soil of the experimental site was vertisol and uniform in topography. Each parent and F1'S with check Chhattisgarh Sarson was represented by three row 5 meter long and 90 cm apart. Each row accommodating present in approximately 49 plants. 80 kg N2, 40kg P2O5, and 40 kg K2O per hectare applied at time of sowing to provide the nutrient through Urea, DAP and Murate of potash (MOP). From each plot five plants will be tagged to observations recorded and for seed yield and yield attributing traits except for days to 50% flowering and days to maturity. Data taken from the five plants were averaged, replication wise and the mean data was used for statistical analysis. The laboratory worked done after the harvest of the crop. Observations on thirteen important traits viz. days to 50% flowering, days to maturity, plant height (cm), number of siliqua per plant, number of seed per siliqua, Siliqua length (cm), number of primary branches per plant, number of secondary branches per plant, test weight (g), Seed oil content (%), biological yield (g), harvest index (%) and seed yield per plant were recorded on five competitive plants randomly selected from each plot while flowering was recorded on row basis.

The exploitation of heterosis is considered an outstanding application of the principles of the science of genetics to Agriculture. Heterosis breeding had led to a breakthrough in yield in several crop plants. For the exploitation of heterosis, it is imperative to study the magnitude of heterosis. The experiment of heterosis is greatly influenced by the magnitude of genetic differences among parents involved in the crosses. The parents with optimal to intermediate genetic diversity will show maximum heterosis (Moll and Stuber, 1974) [8].

Estimation of heterosis

Heterosis is estimated in three different ways, viz. (1) over mid parent (2) over better parent, and (3) over commercial cultivar/ hybrid. Thus the basis of estimation, heterosis is of three types as given bellow:

Average heterosis (Mid)

When the heterosis is estimated over the mid parent, i.e, mean or average of the two parents, which is estimated as follow:

$$\text{Average heterosis} = [F_1 - MP) / MP] / 100$$

Where, F_1 is the mean value F_1 and MP (Mid parent) is the mean of two parents involved in the cross.

Heterobeltiosis (Better)

When the heterosis is estimated over the superior or better parents. It is worked out as follows:

$$\text{Heterobeltiosis} = [F_1 - BP) / BP] /100$$

Where, BP is the mean value (over replication) of the better parent of the particular cross.

Useful heterosis or Standard heterosis (Best)

The term useful heterosis was used by Meredith and Bridge (1972). It refers to the superiority of F1 over the standard commercial check variety. This type of heterosis is of direct practical value in plant breeding. It is estimated as follows:

$$\text{Useful heterosis} = [F_1 - CC/CC] /100$$

Where, CC is the mean value over replication of the local commercial cultivar.

Analysis of variance (ANOVA) with parents and crosses

The data obtained for each character in F_1's and parents were analyzed for each statistical procedure given by Ponse and Sukhatme (1967) [10] 'F' test and 't' test were worked out the analysis of variance to test the significance. It was carried out according to the procedure of RBD analysis for each character as per methodology of Fisher and Yates (1938). The total variance and degree of freedom were portioned into three components namely, replications, genotypes and error. Significance of variance was determined by F-test. Analysis of variance for experiment design was performed to test the significant differences between genotypes for all the character with fixed effect model. The statistical method for randomized block design is:

$$Yij = \mu + gi + rj + eij$$

Where,

Yij = Phenotypic observation in the ith treatment and jth

μ = overall mean

Gi = effect of the i^{th} treatment

Rj = effect of j^{th} replication

Eij = random errors associated the i^{th} treatment and j^{th} replication

Skelton of analysis of variance for heterosis

Source of variation	Degree of Freedom	Sum of Squares	Mean Sum of Squares	F values (calculated)
Replication	r-1	SSr	MSr	SSr/MSr
Genotype	g-1	SSg	MSg	SSg/MSg
Parent	p-1	SSp	MSp	SSp/MSp
Cross	F_1-1	SSF_1	MSF_1	SSF_1/MSF_1
Parent vs Cross	1	SS_{PH}	MS_{PH}	SS_{PH}/MS_{PH}
Error	(r-1)(g-1)	SSE	MSe	

The sum of square was arranged in the following manner to test the significance of different between treatments. The skelton of analysis of variance is presented in the Here, I = 1, 2, 3, 4 --------------- 15
J = 1, 2, 3 ------------- n
Ho = g1 = g2 --------- g15

Where,
r = Number of replications
g = Number of genotypes
p = Number of parents
F_1 = Number of hybrids
SSr = Sum of square due to replications
SSg = Sum of square due to genotypes
SSF_1 = Sum of square due to hybrids
SS_{PH} = Sum of square due to parents Vs hybrids
SSe = Sum of square due to error
MSr = Mean sum of square due to replication
MSg = Mean sum of square due to genotype
MSp = Mean sum of square due to parents.
MSh = Mean sum of square due to hybrid
TSS = Total sum of square
MSe = Mean sum of square due to error

Standard error of mean
Standard error of mean of was calculated by the following formulae:

$$SEm = \frac{\sqrt{EMS}}{r}$$

Critical difference (CD)
The minimum difference required for any two treatment means to differ significantly is called critical difference or least significant difference.

$$CD = \frac{\sqrt{2EMS}}{r} xtedfat\ 5\%$$

Where,
r = number of replication
t = table value of at 5% level of significance corresponding to the D.F. for EMS = mean sum of square due to error.

Test of significance
If the variance ratio (F- calculated) is greater than the 'F' tabulated value at 1% & 5% level of significance, the difference between characters were considered to the significant and vice-versa.
If the variance ratio (Vi/Ve) degree of freedom was greater than the 'F' at 5% or 1% level of significance the difference between treatments are considered to be significant and if it was lower than the table value the difference was considered to be non – significant.
Mean value of each character was worked out by dividing the sum of the value, by the number of observation.

Mean = ∑x/N
∑x = sum of all the observation for each character in each replication
N = total number of observations.

Results and Discussion
Carried out triple test cross analysis in Indian mustard using twelve's Indian mustard strains and 3 testers to study the heterosis for seed yield, oil content, silique on main raceme, seeds per siliqua, seed yield per plant, 1000-seed weight and harvest index exhibited significant ($p \geq 0.01$-0.05) differences among all the entries (Table 1, 2 and 3). These results revealed that genetic variability existed in the breeding material that allowed analyzing the data further for heterosis..
A wide range of variation in the estimates of standard heterosis in positive and negative direction was observed for seed yield per plant. Improved seed yield is a primary objective in a crop breeding program and therefore, positive heterosis for seed yield is of prime importance to develop high yielding genotypes. Similar results were reported by Nair *et al.* (2005), Aher (2009), Malviya *et al.* (2012) [9, 1, 5].
The average, heterobeltiosis and standard (best parents) results are furnished in Table 1, 2, and 3.

Table 1: Average heterosis for yield and yield attributes of Indian mustard

Crosses	DFF	DM	PH	SPP	SPS	SL	PBPP	SBPP	TW	SOP	BY	HI	SYPP
RH-749XRH-119	-6.83**	-3.39**	-0.88	2.22	17.14**	-5.90	-4.27	2.22	-0.14	-3.63**	-6.94	33.18**	22.57**
RH-749XRH-406	-2.50	-1.64	6.50	37.36**	9.59	-8.35	20.37	15.45*	-2.87	3.12**	-1.72	35.48**	**35.26****
RH-749xDRMRIJ-31	-13.86**	-3.27**	-10.78**	-31.73**	8.33	9.51	-20.26*	-15.42**	-5.42	-2.85**	-12.93	-16.97	-28.26**
RH749xNRCHB-101	-4.10	-2.53*	-0.80	-3.49	5.5 6	0.23	7.14	9.28	4.55	-1.30*	23.35**	-4.87	12.19
RH-119xRH-406	-1.94	-2.38*	2.62	10.45**	1.33	-14.51**	18.10	15.70*	16.01**	0.34	-2.96	31.70**	24.72**
RH-119xDRMRIJ-31	9.32**	1.63	-2.00	35.89**	2.70	9.69	9.68	0.00	10.78	-0.30	27.42**	29.32**	58.06**
RH-119xNRCHB-101	-0.33	-1.49	-3.39	28.57**	-10.81*	-3.91	19.27	9.97	2.99	2.01**	53.62**	26.21*	18.40
RH-406xDRMRIJ-31	-4.37*	-2.26	-10.88**	-13.59**	1.30	2.13	-11.30	-2.72	-12.16*	-1.60*	-17.00**	-11.68	-26.63**
RH-406xNRCHB-101	-2.95	-2.41*	10.16*	52.83**	6.49	2.21	38.00**	19.47**	6.39	2.69**	31.49**	27.88**	65.75**
DRMRIJ-31xNRCHB-101	-0.32	-2.56*	-4.11	18.39**	-5.26	2.90	9.24	6.54	11.10	-0.34	9.91	17.27	29.44**
CD at 5% level	2.22	2.63	11.20	8.04	1.23	0.57	0.86	0.80	0.54	0.51	3.61	6.51	1.22
CD at 1% level	2.71	3.21	13.68	9.81	1.51	0.70	1.05	0.98	0.66	0.63	4.41	7.96	1.48

*&**, Significant $P<0.05$ and $P<0.01$, respectively.
Where, DFF = Days to flowering, DM= Days to maturity, PH = Plant height, SPP =Siliqua per plant, SPS =Seed per siliqua, SL = Siliqua length, PBPP = Primary branches per plant, SBPP = Secondary branches per plant, TW = Test weight, SOP = Seed oil percent, BY = Biological yield, HI = Harvest index, SYPP = Seed yield per plant.

Table 2: Heterobeltiosis for yield and yield attributes of Indian mustard

Crosses	DFF	DM	PH	SPP	SPS	SL	PBPP	SBPP	TW	SOP	BY	HI	SYPP
RH-749xRH-119	-9.64**	-3.53**	-1.14	-5.38	13.89*	-8.01	-6.67	0.55	-4.36	-5.39**	-8.70	32.45**	20.95*
RH-749xRH-406	-6.02**	-2.65	-3.50	28.21**	2.56	-8.89	8.33	14.52	-3.74	1.24	-9.51	34.41**	27.53**
RH-749xDRMRIJ-31	-13.86**	-4.13**	-11.31**	-32.41**	2.63	3.62	-25.37*	-22.37**	-5.49	-5.39**	-17.95*	-17.24	-31.88**
RH-749xNRCHB-101	-8.43**	-3.54**	-6.39	-14.87**	0.00	-3.40	0.00	6.19	2.79	-2.40**	11.01	-6.82	3.53
RH-119xRH-406	-2.56	-3.53**	-6.80	9.47*	-2.56	-16.92**	8.77	12.90	12.08	0.34	-12.20	29.95*	16.14

RH-119xDRMRIJ-31	6.02**	0.59	-2.33	24.62**	0.00	6.09	1.49	-9.59	6.17	-1.12	17.95*	28.18*	48.21**
RH-119xNRCHB-101	-1.92	-2.65	-8.61	21.99**	-13.16*	-5.29	14.04	5.15	-2.95	1.27	40.66**	24.30	10.61
RH-406xDRMRIJ-31	-7.83**	-2.40	-18.82**	-20.10**	0.00	-3.90	-23.88*	-10.05	-12.89	-2.41**	-19.02**	-12.09	-27.18**
RH-406xNRCHB-101	-3.90	-2.41	5.49	43.79**	5.13	-2.06	32.69*	17.01*	3.67	1.95**	10.00	24.30	44.94**
DRMRIJ-31xNRCHB-101	-4.82	-2.70	_	3.52	-5.26	0.95	-2.99	0.46	9.15	-1.86**	-6.15	14.49	13.93
CD at 5% level	2.56	3.04	12.93	9.27	1.42	0.66	1.00	0.92	0.62	0.59	4.17	7.52	1.40
CD at 1% level	3.13	3.71	15.79	11.33	1.74	0.81	1.22	1.13	0.76	0.73	5.09	9.19	1.71

*&**, Significant *P*<0.05 and *P*<0.01, respectively.
Where, DFF = Days to flowering, DM = Days to maturity, PH = Plant height, SPP = Siliqua per plant, SPS = Seed per siliqua, SL = Siliqua length, PBPP = Primary branches per plant, SBPP = Secondary branches per plant, TW = Test weight, SOP = Seed oil percent, BY = Biological yield, HI = Harvest index, SYPP = Seed yield per plant.

Table 4.12: Standard heterosis for yield and yield attributes of Indian mustard

Crosses	DFF	DM2	PH	SPP	SPS	SL	PBPP	SBPP	TW	SOP	BY	HI	SYPP
RH-749xRH-119	-9.64**	-3.53**	-1.14	-7.29*	5.13	-9.11	-16.42	-15.98**	-4.36	-5.39**	-23.17**	28.44*	7.12
RH-749xRH-406	-6.02**	-2.94*	-3.50	25.63**	2.56	-8.89	-2.99	-2.74	-10.27	1.24	-9.51	28.91*	27.53**
RH-749xDRMRIJ-31	-13.86**	-4.41**	-11.31**	-32.41**	0.00	2.39	-25.37*	-22.37**	-13.36*	-5.39**	-21.95**	-20.63	-32.89**
RH-749xNRCHB-101	-8.43**	-3.82**	-6.39	-16.58**	-2.56	-4.56	-10.45	-5.94	-5.91	-2.40**	-6.59	-6.82	-8.31
RH-119xRH-406	-8.43**	-3.53**	-7.29	-7.04*	-2.56	-16.92**	-7.46	-4.11	12.08	-3.31**	-12.20	26.01*	16.14
RH-119xDRMRIJ-31	6.02**	0.59	-2.84	24.62**	-2.56	0.11	1.49	-9.59	6.17	-4.72**	12.20	24.30	46.00**
RH-119xNRCHB-101	-7.83**	-2.65	-9.09	1.76	-15.38**	-10.63	-2.99	-6.85	-2.95	-0.99	13.90	24.30	-4.62
RH-406xDRMRIJ-31	-7.83**	-4.41**	-19.78**	-20.10**	0.00	-3.90	-23.88*	-10.05	-18.79**	-5.97**	-19.02**	-16.25	-27.18**
RH-406xNRCHB-101	-10.84**	-4.71**	-6.39	22.11**	5.13	-2.06	2.99	3.65	-3.36	-0.33	10.00	24.30	44.94**
DRMRIJ-31xNRCHB-101	-4.82*	-4.71**	-10.08*	3.52	-7.69	-7.48	-2.99	0.46	0.07	-4.06**	-10.73	14.49	12.23
CD at 5% level	2.56	3.04	12.93	9.27	1.42	0.66	0.99	0.92	0.62	0.59	4.17	7.52	1.40
CD at 1% level	3.13	3.71	15.79	11.33	1.74	0.80	1.22	1.13	0.76	0.73	5.09	9.19	1.71

*&**, Significant *P*<0.05 and *P*<0.01, respectively.
Where, DFF = Days to flowering, DM= Days to maturity, PH = Plant height, SPP = Siliqua per plant, SPS =Seed per siliqua, SL = Siliqua length, PBPP = Primary branches per plant, SBPP = Secondary branches per plant, TW = Test weight, SOP = Seed oil percent, BY = Biological yield, HI = Harvest index, SYPP = Seed yield per plants

Heterosis estimation for average, heterobeltiosis and standard or better parents

Days to 50% flowering

The relative heterosis for this trait ranged from -13.86% (RH-749 x DRMRIJ-31) to 9.32% (RH-119 x DRMRIJ-31). Out of ten hybrids only one hybrid showed significant positive relative heterosis RH-119 x DRMRIJ-31, while, three hybrids showed negetive relative heterosis this trait were RH-749 x DRMRIJ-31 (-13.86%), RH-749 x RH-119 (-6.83) and RH-406 x DRMRIJ -31 (-4.37).

In case of heterobeltiosis (Better parent) for days to 50% flowering among the hybrids ranged from -13.86% (RH-749 x DRMRIJ-31) to 6.02% (RH-119 x DRMRIJ-31). Out of ten hybrids only one hybrid showed significant positive better parent heterosis 6.02% (RH-119 x DRMRIJ-31), while, five hybrids showed negetive heterobeltiosis *viz.*, RH-749 x DRMRIJ-31 (-13.86), RH-749 x RH-119 (-9.64), RH-749 x NRCHB-101 (-8.43), RH-406 x DRMRIJ-31 (-7.83) and RH-749 x RH-406 (-6.02).

The heterosis over check (Best parent) genotypes ranged from -13.86% (RH-749 x DRMRIJ-31) to 6.02% (RH-119 x DRMRIJ-31). Out of ten hybrids none of hybrids exhibited showed significant positive heterosis over check for this trait. Whereas, seven hybrids showed negetive heterosis over check, *viz.*, RH-749 x DRMRIJ-31(-13.86), RH-406 x NRCHB-101(-10.84), RH-749 x RH-119 (-9.64), RH-119 x RH-406 (-8.43), RH-749 x NRCHB-101 (-8.43), RH-119 x NRCHB-101 (-7.83) and RH-406 x DRMRIJ-31 (-7.83).

Negative heterosis is preferred for days to flowering to develop early maturing genotypes. These genotypes will be used in cropping sequence after *Kharif* crop under rainfed condition. Majority of the crosses showing significant negative heterosis for days to flowering involved early maturing parents. The present findings are in agreement with those of Mahto and Haider (2004), Gupta *et al.* (2011) Sabaghnia *et al.* (2010) and Sincik *et al.* (2014) [6, 4, 11].

Days to maturity

The relative heterosis for this trait ranged from -3.39% (RH-749 x RH-119) to 1.63% (RH-119 x DRMRIJ-31). Out of ten hybrids six hybrid showed significant negetive relative heterosis RH-749 x RH-119 (-3.39), RH-749 x DRMRIJ-31 (-3.27), DRMRIJ-31 x NRCHB-101 (-2.56), RH-749 x NRCHB-101 (-2.53), RH-406 x NRCHB-101 (-2.56) and RH-119 x RH-406 (-2.38). None of hybrids exhibited significant positive relative heterosis for this trait.

The heterobeltiosis (Better parents) for this traits ranged from -4.13 (RH-749 x DRMRIJ-31) to 0.59 (RH-119 x DRMRIJ-31). Out of ten hybrids four hybrids showed exhibited negetive significant heterobeltiosis *viz.*, RH-749 x DRMRIJ-31(-4.13), RH-749 x NRCHB-101 (-3.53), RH-749 x RH-119 (-3.53) and RH-119 x RH-406 (-3.53). None of hybrids exhibited significant positive relative heterosis for this trait.

The heterosis over check (Best parent) genotypes ranged from -4.71 (RH-406 x NRCHB-101) to 0.59 (RH-119 x DRMRIJ-31). Out of ten hybrids eight hybrids showed negetive high significant heterosis over check namely, RH-406 x NRCHB-101(-4.71), DRMRIJ-31 x NRCHB-101 (-4.71), RH-406 x DRMRIJ-31 (-4.41), RH-749 x DRMRIJ-31(-4.41), RH-749 x NRCHB-101 (-3.82), RH-749 x RH-119 (-3.53) and RH-749 x RH-406 (-2.94). None of hybrids exhibited significant positive relative heterosis for this trait.

Similar result were reported by Turi *et al.* (2006) estimated mid-parent and better-parent heterosis in *Brassica juncea* L. genotypes. Out of 56 hybrids, negative mid-parent and better-parent heterosis for days to 50% emergence, days to 50% flowering, days to physiological maturity and plant height, respectively; whereas positive heterosis for number of primary branches per plant. Better-parent heterosis reduced to 27% for emergence, 3.85% for flowering, 4.08% for maturity and 22.63% for plant height; whereas it reached to 44% for branches per plant. Among parents, four parents proved to be superior when used as parents in most of the hybrid combinations.

Plant height (cm)

The relative heterosis (Mid) for this trait ranged from -10.88 (RH-406 x DRMRIJ-31) to 10.16 (RH-406 x NRCHB-101). Out of ten hybrids only one hybrid showed significant positive relative heterosis (10.16) whereas, two hybrid showed negetive significant relative heterosis, RH-406 x DRMRIJ-31) (-10.88) RH-749 x DRMRIJ-31 (-10.78).

The heterobeltiosis (Better parent) for this traits ranged from -18.82 (RH-406 x DRMRIJ-31) to 5.49 (RH-406 x NRCHB-101). Out of ten hybrids none hybrids showed exhibited positive significant heterobeltiosis whereas, two hybrids RH-406 x DRMRIJ-31(-18.82) and RH-749 x DRMRIJ-31 (-11.31) showed negetive high significant.

The heterosis over check (Best parent) genotypes out of ten hybrids none positive significant heterosis over check, whereas, three hybrids showed negetive significant heterosis over check namely, (RH-406 x DRMRIJ-31) (-19.78), RH-749 x DRMRIJ-31(-11.31) and DRMRIJ-31 x NRCHB-101(-10.08).

Similar result were reported by Gupta *et al.* (2010) [4].

Number of seed per plant

The relative heterosis (Mid) for this trait ranged from -31.73 (RH-749 x DRMRIJ-31) to 52.83 (RH-406 x NRCHB-10). Out of ten hybrids six hybrids showed significant positive relative heterosis RH-406 x NRCHB-101 (52.83) followed by RH-749 x RH-406 (37.36), RH-119 x DRMRIJ-31 (35.89), RH-119 x NRCHB-101 (28.57), DRMRIJ-31 x NRCHB-101 (18.39) and RH-119 x RH-406 (10.45), whereas, two hybrid showed negetive significant relative heterosis, RH-749 x DRMRIJ-31 (-31.73) and RH-406 x DRMRIJ-31 (-10.88).

The heterobeltiosis (Better parent) for this traits ranged from -32.41 (RH-749 x DRMRIJ-31) to 43.79 (RH-406 x NRCHB-101). Out of ten hybrids five hybrids showed exhibited positive significant heterobeltiosis RH-406 x NRCHB-101 (43.79), followed by RH-749 x RH-406 (28.21), RH-119 x DRMRIJ-31 (24.62), RH-119 x NRCHB-101 and RH-119 x RH-406 (9.47), whereas, three hybrids RH-749 x DRMRIJ-31 (-32.41), RH-406 x DRMRIJ-31(-20.10) and RH-749 x NRCHB-10 (-14.87) showed negetive high significant.

The heterosis over check (Best parent) for this traits ranged from -32.41 (RH-749 x DRMRIJ-31) to 25.63 (RH-749 x RH-406). Out of ten hybrids three hybrids showed exhibited positive significant standard heterosis RH-749 x RH-406 (25.63), followed by RH-119 x DRMRIJ-31 (24.62) and RH-406 x NRCHB-101 (22.11) whereas, five hybrids RH-749 x DRMRIJ-31 (-32.41), RH-406 x DRMRIJ-31(-20.10), and RH-749 x NRCHB-10 (-16.58), RH-749 x RH-119 (-7.29) and RH-119 x RH-406 (-7.04) showed negetive high significant. Similar result were reported by Gupta *et al.* (2010) [4].

Number of seed per siliqua

The relative heterosis (Mid) for this trait ranged from -10.81 (RH-119 x NRCHB-101) to 17.14 (RH-749 x RH-119). Out of ten hybrids only one hybrids showed significant positive relative heterosis RH-749 x RH-119 (17.14), whereas, one RH-119 x NRCHB-101 (-10.81) showed negetive significant relative heterosis.

The heterobeltiosis (Better parent) for this traits ranged from -13.16 (RH-119 x NRCHB-101) to 13.89 (RH-749 x RH-119). Out of ten hybrids only one hybrids showed exhibited positive significant heterobeltiosis RH-749 x RH-119 (13.89) and showed negetive high significant RH-119 x NRCHB-101 (-13.16).

The heterosis over check (Best parent) for this traits ranged from -15.38 (RH-119 x NRCHB-101) to 5.13 (RH-749 x RH-119). Out of ten hybrids only one hybrid showed exhibited negative significant standard heterosis RH-119 x NRCHB-101 (-15.38).

Similar results were reported by Malviya *et al.* (2012) [5] carried out triple test cross analysis in Indian mustard using twelves Indian mustard strains and 3 testers to study the heterosis for seed yield, oil content, silique on main raceme, seeds per siliqua, seed yield per plant, 1000-seed weight and harvest index. A wide range of variation in the estimates of standard heterosis in positive and negative direction was observed for seed yield per plant.

Siliqua length (cm)

The relative heterosis (Mid) for this trait ranged from -14.5 (RH-119 x RH-406) to 9.69 (RH-119 x DRMRIJ-31). Out of ten hybrids only one hybrid showed negetive significant relative heterosis RH-119 x RH-406 (-14.5).

The heterobeltiosis (Better parent) for this traits ranged from -13.14 (RH-119 x NRCHB-101) to 3.62 (RH-749 x DRMRIJ-31). Out of ten hybrids one hybrid showed exhibited negative significant heterobeltiosis RH-119 x NRCHB-101 (-13.14).

The heterosis over check (Best parent) for this traits ranged from -16.92 (RH-119 x RH-406) to 2.39 (RH-749 x DRMRIJ-31). Out of ten hybrids only one hybrid showed exhibited negative significant standard heterosis RH-119 x RH-406 (-16.92).

Number of primary branches per plant

The relative heterosis (Mid) for this trait ranged from -20.26 (RH-749 x DRMRIJ-31) to 38.00 (RH-406 x NRCHB-101). Out of ten hybrids only one hybrid showed positive significant RH-406 x NRCHB-101 (38.00) and negetive significant (RH-749 x DRMRIJ-31) (-20.26) relative heterosis.

The heterobeltiosis (Better parent) for this traits ranged from -25.37 (RH-749 x DRMRIJ-31) to 32.69 (RH-406 x NRCHB-101). Out of ten hybrids one hybrid showed exhibited positive significant heterobeltiosis RH-406 x NRCHB-101(32.69) while, two hybrids RH-749 x DRMRIJ-31(-25.37) and RH-406 x DRMRIJ-31 (-23.88).

The heterosis over check (Best parent) for this traits ranged from -25.37 (RH-749 x DRMRIJ-31) to 2.99 (RH-406 x NRCHB-101). Out of ten hybrids two hybrids showed exhibited negative significant standard heterosis RH-749 x DRMRIJ-31 (-25.37) and RH-406 x DRMRIJ-31(-23.88).

Similar result were reported by Synrem *et al.* (2015) reported hybrid RL-1359 x JM-2 exhibited superior performance for seed yield and its component traits as reflected by significant positive estimates for relative heterosis, heterobeltiosis and economic heterosis.

Secondary branches per plant

The relative heterosis (Mid) for this trait ranged from -15.42 (RH-749 x DRMRIJ-31) to 19.47 (RH-406 x NRCHB-101). Out of ten hybrids three hybrids showed positive significant RH-406 x NRCHB-101 (19.47) followed by RH-119 x RH-406 (15.70) and RH-749 x RH-406 (15.45) while, negetive significant relative heterosis (RH-749 x DRMRIJ-31) (-15.42).

The heterobeltiosis (Better parent) for this traits ranged from -22.37 (RH-749 x DRMRIJ-31) to 17.01 (RH-406 x NRCHB-101). Out of ten hybrids one hybrid showed exhibited positive significant RH-406 x NRCHB-101 (17.01) and negative significant heterobeltiosis RH-749 x DRMRIJ-31(-22.37).
The heterosis over check (Best parent) for this traits ranged from -22.37 (RH-749 x DRMRIJ-31) to 3.65 (RH-406 x NRCHB-101). Out of ten hybrids two hybrids showed exhibited negative significant standard heterosis RH-749 x DRMRIJ-31 (-22.37) and RH-749 x RH-119 (-15.98).

Test weight (g)
The relative heterosis (Mid) for this trait ranged from -12.16 (RH-406 x DRMRIJ-31) to 16.01 (RH-119 x RH-406). Out of ten hybrids one hybrid showed positive RH-119 x RH-406 (16.01) and negetive RH-406 x DRMRIJ-31 (-12.16) significant relative heterosis.
The heterobeltiosis (Better parent) for this traits ranged from -12.89 (RH-406 x DRMRIJ-31) to 12.08 (RH-119 x RH-406). Out of ten hybrids none hybrids showed exhibited positive and negative significant heterobeltiosis.
The heterosis over check (Best parent) for this traits ranged from -18.79 (RH-406 x DRMRIJ-31) to 12.08 (RH-119 x RH-406). Out of ten hybrids two hybrids showed exhibited negative significant standard heterosis RH-406 x DRMRIJ-31 (-18.79) and RH-749 x DRMRIJ-31 (-13.36).

Seed oil content (%)
The relative heterosis (Mid) for this trait ranged from -3.63% (RH-749 x RH-119) to 3.12% (RH-749 x RH-406). Out of ten hybrids three hybrids showed positive significant relative heterosis RH-749 x RH-406 (3.12%), RH-406 x NRCHB-101 (2.69%) and RH-119 x NRCHB-101 (2.01%) whereas, four hybrids showed negetive significant relative heterosis was RH-749 x RH-119 (-3.63) followed by RH-749 x DRMRIJ-31 (-2.85), RH-406 x DRMRIJ-31 (-1.60) and RH-749 x NRCHB-101 (-1.30) respectively.
The heterobeltiosis (Better parent) for this traits ranged from -5.39% (RH-749 x RH-119) to 1.95% (RH-406 x NRCHB-101). Out of ten hybrids only one hybrid none showed positive significant heterobeltiosis RH-406 x NRCHB-101 (1.95) whereas, five hybrids showed exhibited negative significant heterobeltiosis. Namely, RH-749 x RH-119 (-5.39) DRMRIJ-31 (-5.39), RH-406 x DRMRIJ-31 (-2.41), RH-749 x NRCHB-101 (-2.40) and DRMRIJ-31 x NRCHB-101 (-1.86) respectively.
The heterosis over check (Best parent) for this traits ranged from -5.97 (RH-406 x DRMRIJ-31) to 1.24 (RH-749 x RH-406). Out of ten hybrids none hybrids showed exhibited positive heterosis whereas, seven hybrids showed negative significant standard heterosis RH-406 x DRMRIJ-31 (-5.97) followed by RH-749 x RH-119 (-5.39), RH-749 x DRMRIJ-31 (-5.39), RH-119 x DRMRIJ-31 (-4.72), DRMRIJ-31 x NRCHB-101 (-4.06), RH-119 x RH-406 (-3.31) and RH-749 x NRCHB-101 (-2.40) respectively.

Biological yield (g)
The relative heterosis (Mid) for this trait ranged from -17.00 (RH-406 x DRMRIJ-31) to 53.62 (RH-119 x NRCHB-101). Out of ten hybrids four hybrids showed positive significant relative heterosis RH-119 x NRCHB-101(53.62) followed by RH-406 x NRCHB-101 (31.49) RH-119 x DRMRIJ-31 (27.42) and RH- 749 x NRCHB-101 (23.35), whereas, only one hybrid showed negetive significant relative heterosis was RH-406 x DRMRIJ-31 (-17.00) respectively.
The heterobeltiosis (Better parent) for this traits ranged from -19.02 (RH-406 x DRMRIJ-31) to 40.66 (RH-119 x NRCHB-101). Out of ten hybrids two hybrids showed positive significant heterobeltiosis RH-119 x NRCHB-101 (40.66) and RH-119 x DRMRIJ-31 (17.95), whereas, two hybrids showed exhibited negative significant heterobeltiosis namely, RH-406 x DRMRIJ-31 (-19.02) and RH-749 x DRMRIJ-31 (-17.24) respectively.
The heterosis over check (Best parent) for this traits ranged from -23.17 (RH-749 x RH-119) to 13.90 (RH-119 x NRCHB-101). Out of ten hybrids none hybrids showed exhibited positive heterosis whereas, three hybrids showed negative significant standard heterosis RH-749 x RH-119 (-23.17) followed by RH-749 x DRMRIJ-31 (-21.95) and RH-406 x DRMRIJ-31 (-19.02) respectively.

Harvest index (%)
The relative heterosis (Mid) for this trait ranged from -16.97 (RH-749 x DRMRIJ-31) to 35.48 (RH-749 x RH-406). Out of ten hybrids six hybrids showed positive significant relative heterosis namely, RH-749 x RH-406 (35.48) followed by RH-749 x RH-119 (33.18), RH-119 x RH-406 (31.70), RH- 119 x DRMRIJ-31 (29.32), RH-406 x NRCHB-101 (27.88) and RH-119 x NRCHB-101. None hybrids showed negetive significant relative heterosis respectively.
The heterobeltiosis (Better parent) for this traits ranged from -17.24 (RH-749 x DRMRIJ-31) to 34.41 (RH-749 x RH-406). Out of ten hybrids four hybrids showed positive significant heterobeltiosis RH-749 x RH-406 (34.41) followed by RH-749 x RH-119 (32.45), RH-119 x RH-406 (29.95) and RH-119 x DRMRIJ-31. None hybrids showed exhibited negative significant heterobeltiosis respectively.
The heterosis over check (Best parent) for this traits ranged from -20.63 (RH-749 x DRMRIJ-31) to 28.91 (RH-749 x RH-406). Out of ten hybrids three hybrids showed exhibited positive standard heterosis RH-749 x RH-406 (28.91) followed by RH-749 x RH-119 (28.44) and RH-119 x RH-406 (26.01). None hybrids showed negetive significant heterosis respectively.

Seed yield per plant (g)
The relative heterosis (Mid) for this trait ranged from -28.26 (RH-749 x DRMRIJ-31) to 65.75 (RH-406 x NRCHB-101). Out of ten hybrids six hybrids showed exhibited positive significant relative heterosis namely, RH-406 x NRCHB -101 (65.75) followed by RH-119 x DRMRIJ-31 (58.06), RH-749 x RH-406 (35.26), DRMRIJ-31 x NRCHB-101 (29.44), RH-119 x RH-406 (24.72) whereas, RH-749 x DRMRIJ-31 (-28.26) and RH-406 x DRMRIJ-31 (-26.63) hybrids showed negetive significant relative heterosis respectively.
The heterobeltiosis (Better parent) for this traits ranged from -31.88 (RH-749 x DRMRIJ-31) to 48.21 (RH-119x DRMRIJ-31). Out of ten hybrids four hybrids showed positive significant heterobeltiosis RH-119 x DRMRIJ-31 (48.21) followed by RH-406 x NRCHB-10 (44.94), RH-749 x RH-406 (27.53) and RH-749 x RH-119, while, two hybrids showed exhibited negative significant heterobeltiosis RH-749 x DRMRIJ-31 (-31.88) and RH-406 x DRMRIJ-31 (27.18) respectively.
The heterosis over check (Best parent) for this traits ranged from -32.89 (RH-749 x DRMRIJ-31) to 46.00 (RH-119 x DRMRIJ-31). Out of ten hybrids three hybrids showed exhibited positive standard heterosis RH-119 x DRMRIJ-31 (46.00) followed by RH-406 x NRCHB-10 (44.94) and RH-749 x RH-406 (27.53) whereas, RH-749 x DRMRIJ-31 (-

32.89) and RH-406 x DRMRIJ-31 (-27.18) hybrids showed negetive significant standard heterosis respectively.
Improved seed yield is a primary objective in a crop breeding program and therefore, positive heterosis for seed yield is of prime importance to develop high yielding genotypes. Similar result were reported by Nair *et al.* (2005), Aher (2009), Malviya *et al.* (2012) [9, 1, 5] Tomar *et al*. (2014) carried out triple test cross analysis in Indian mustard using twelves Indian mustard strains and 3 testers to study the heterosis for seed yield, oil content, silique on main raceme, seeds per siliqua, seed yield per plant, 1000-seed weight and harvest index. A wide range of variation in the estimates of standard heterosis in positive and negative direction was observed for seed yield per plant.

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Conclusions
The relative heterosis (Mid) RH-406 x NRCHB -101 (65.75) trait hybrids showed exhibited positive significant, the heterobeltiosis (Better parent) Out of ten hybrids four hybrids showed positive significant heterobeltiosis RH-119 x DRMRIJ-31 (48.21) and heterosis over check (Best parent) Out of ten hybrids three hybrids showed exhibited positive standard heterosis RH-119 x DRMRIJ-31 (46.00) Improved seed yield is a primary objective in a crop breeding program and therefore, positive heterosis for seed yield is of prime importance to develop high yielding genotypes with further improvement of plant breeding programmes.

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