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Thippesh KS
Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Kartikeya Srivastava
Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Karthik R
Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Corresponding Author:
Thippesh KS
Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Harnessing mutagenesis-derived lines for the development of heterotic hybrids for yield and component traits in Indian mustard (*Brassica juncea* L. Czern & Coss)

Thippesh KS, Kartikeya Srivastava and Karthik R

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Abstract
Heterosis breeding approach is one of the most successful technological options being employed for the improvement of brassica variety for quality and quantity of seed yield and other yield related parameter. The present investigation was undertaken at Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during 2020-21 using line × tester analysis to study the heterosis in Indian mustard. Ten lines and 3 testers and their 30 F_1 s were planted in a randomized complete block design with three replications. Significant differences indicated the presence of adequate genetic variability among the parents as well as crosses. The most heterotic cross combinations were RH-749 × TM-117, RH-749 × TM-130, RH-749 × TM-143, RH-749 × TM-217 and HUJM-10-6 × TM-263-3 showed the high *per se* performance coupled with high, better parent heterosis, mid-parent and standard heterosis over the national check Kranti for seed yield per plant, seed yield per hectare and other yield associated traits. So, these cross combinations can be utilized for improving seed yield through improvement in yield related traits in Indian mustard.

Keywords: *Brassica juncea*, line × tester, heterosis, Indian mustard, seed yield

Introduction

Indian mustard is an important oil seed crop of the world. It plays a major role in catering edible oil demand of the country. The genus Brassica, belongs to Cruciferae or Brassicaceae family. Indian mustard is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). It was introduced in India from China and from where it spread to Afghanistan and other countries. It is generally self-pollinated crop yet certain percentage (5-18%) of cross fertilization may happen [Labana and Banga, 1984] [10]. Rai (*B. juncea*) is a popular rapeseed and mustard variety among farmers because of its excellent yield and resistance to lodging, shattering, drought, heat, and disease, as well as saline sodic environments (Karthik *et al.*, 2024) [8]. Mustard is generally cultivated in temperate climates, but it can also grow successfully as a winter crop in some tropical and subtropical regions. Indian mustard adapts well to diverse environmental conditions, thriving with annual rainfall between 500 and 4,200 mm, temperatures ranging from 6 to 27°C, and soil pH levels from 4.3 to 8.3 (Karthik *et al.*, 2024) [8]. India ranks second in terms of cultivation area, covering 6.70 million hectares, following China, and ranks third in production, with 8.50 million tonnes, after China and Canada (USDA, 2020-21). It covers an area of 6.23 million hectares with 9.34 million tonnes production and 1499 kg/ha productivity in India during 2018-19 [Anonymous, 2020] [1]. Rajasthan is the largest producer of rapeseed-mustard followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat and Assam. In the year 2020-21, Rajasthan led mustard production with 4.51 million tonnes cultivated over 2.72 million hectares, followed by Madhya Pradesh, which produced 1.31 million tonnes from an area of 0.77 million hectares (Anonymous, 2021) [2]. Productivity of Indian mustard is very low in India as compared with Germany, France and UK. Therefore; it is need to increase the seed yield of mustard for getting self-sufficiency in edible oils [Yadava *et al.*, 2012] [16]. The productivity of mustard is constrained by several prevalent and newly emerging biotic and abiotic stresses.

Hybridization is an important role in overcoming such challenges and increasing agricultural production and productivity. Heterosis breeding on the other hand is a very effective option to break the yield barriers which is realized as increased vigour, size, fruitfulness, development speed, resistance to disease and insect pests or climatic vigour, manifested by cross-bred organisms as compared with corresponding inbreds. it could be a potential alternative for substantially increasing the production of Indian mustard. Successful exploitation of heterosis would depend upon the identification of hybrids that are more productive than either of the parents and standard check cultivars. In oilseed Brassicas heterosis was first reported in brown sarson by Singh and Mehta (1954). Subsequently many studies have reported the extent of heterosis for seed yield. Significant level of heterosis was reported in *B. juncea* (13 to 91%) by Yadava *et al.*, (2012) [16] and Meena *et al.*, (2015) [11], Chourasiya *et al.*, (2018) [3], Tirkey *et al.*, (2020) [14]

Materials and methods

The experimental material for present study comprised of 30 F_1 cross combinations of Indian mustard (*Brassica juncea* L.) obtained by crossing 10 mutant lines (TM-143, TM-258, TM-130, TM-108, TPM-1, TM-217, TM-108-1, TM-117, TM-52, and TM-263-3) with the 3 testers (RH-749, Giriraj and HUJM-10-6) in a line × tester design during *Rabi* 2019-20. These 30 F_1 crosses along with 13 parents and national checks (Kranti) were evaluated in randomized block design with three replications during *Rabi* 2020-21 at Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The observations were recorded on randomly selected five competitive plants for each genotype in each replication for character *viz*., days to 50% flowering, days to maturity, plant height, Number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, test weight, biological yield per plant, harvest index, seed yield per plant and seed yield per hectare. Heterosis expressed as percent increase (+) or decrease (-) of F_1 over mid-parent (MP), better parent (BP) and standard check (SH) is referred as mid-parent/average heterosis, heterobeltiosis and standard heterosis, respectively.

(a) Average/mid-parent heterosis (%): Average heterosis/mid-parent heterosis was calculated as per procedure suggested by Shull (1908).

$$\text{Average heterosis/mid-parent heterosis (\%)} = \frac{\overline{F1} - \overline{MP}}{\overline{MP}} \times 100$$

Where,
Mean value of two parents of corresponding $\overline{F1}$ i.e. (P_1 + P_2)/2,
$\overline{F1}$= Mean performance of cross

(b) Heterobeltiosis/better parent heterosis (%)

Heterobeltiosis/better parent heterosis was calculated as per procedure suggested by Fonesca and Patterson (1968).

$$\text{Heterobeltiosis/better parent heterosis (\%)} = \frac{\overline{F1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,
$\overline{BP}$ = Mean performance of better parent in desired direction,
$\overline{F1}$ = Mean performance of F_1 cross

c) Economic heterosis/standard heterosis (%)

Economic heterosis/standard heterosis was calculated as per procedure suggested by Meredith and Bridge (1972).

$$\text{Economic/standard heterosis (\%)} = \frac{\overline{F1} - \overline{SC}}{\overline{SC}} \times 100$$

Where,
$\overline{S\ C}$ = Mean performance of standard check in desired direction
F_1 = Mean performance of F_1 cross,
P_1 = Mean value of first parent,
P_2 = Mean value of second parent.

Results and Discussion

Analysis of variance (ANOVA) was performed and the result are presented in (Table 1). Mean sum of squares due to genotypes were significant for all the characters studied. This indicated the presence of substantial genetic variability for these characters. Genetic variability in the mutant lines used in this study was also reported by Karthik *et al.* (2025) [7]. Further partitioning of treatment variance into components namely, parents, crosses and parent's *vs* crosses revealed that mean sum of squares due to parents were highly significant for all the characters. This indicates that parents significantly differed among themselves for all the characters. Mean sum of square due to crosses were significant for all the characters. The mean sum of square due to parents versus crosses were significant for all the character except days to maturity, number of primary branches, siliquae length, test weight and biological yield. This indicates the presence of an appreciable amount of variability in the parents as well as in the material generated i.e. F_1 hybrids. Similarly, significant difference among parents, crosses and parents vs crosses was reported previously by many researchers (Patel *et al.*, 2013; Kaur *et al.*, 2019) [12, 9].

Estimates of Heterosis

The estimates of mid-parent heterosis, better parent heterosis for seed yield are presented in Table 2. Positive heterosis was considered desirable for all the traits whereas negative values for days to 50 percent flowering, days to maturity and plant height. Heterosis over mid-parent, better parent for days to 50% flowering was estimated over earlier flowering parent of the hybrids. Hence, crosses with negative heterosis were considered as desirable. Manifestation of heterosis was found in both positive and negative directions. Seven crosses showed the desirable negative mid parent heterosis with value ranging from-11.85 to-5.88 whereas eight crosses showed the negative better parent heterosis and cross combination Giriraj × TM-143 (-6.73), and RH-749 × TPM-1 (-10.58) showed desirable economic heterosis over the check for days to flowering (Table 2). The cross combinations namely, HUJM-10-6 × TPM-1 (-3.45), Giriraj × TPM-1 (-3.66) and Giriraj × TM-52 (-3.40) showed the negative and desirable significant mid parent heterosis for days to maturity (Table 2). RH-749 × TM-143 (-2.60), HUJM-10-6 × TM-258(-2.88) and Giriraj × TM-52(-3.76) showed the negative and significant for heterobeltiosis.

Table 1: Analysis of variance for different traits in Indian mustard

	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Canopy temperature deficit	Chlorophyll content	No. of primary branches	No. of secondary branches	No. of siliquae raceme	Length of main raceme (cm)	Total siliquae per plant	Siliquae length (cm)	No. of seeds per siliquae	Test weight (gm)	Seed yield per plant (gm)	Biological yield per plant (gm)	Harvest index (%)	Yield (Kg/ha)
Replicates	2	3.930	37.209**	751.39**	0.023	1.640	0.893**	0.768*	73.975**	7.745	18973.501**	0.1141	2.0768*	0.023	3.810**	171.001**	7.754	79790.72***
Treatments	42	87.981**	45.954**	1047.534**	1.885**	40.669**	0.714**	10.325**	99.498**	218.784**	6585.190**	0.254**	2.971**	0.728**	9.430**	212.059**	25.569**	205725.16**
Parents	12	84.769**	32.355**	1520.102**	1.039**	45.443**	0.879**	10.54**	130.619**	278.303**	7596.677**	0.241**	3.089**	0.783**	5.400**	171.889**	26.421**	112763.45**
Parents vs Crosses	1	105.376**	3.212	2247.110**	46.410**	199.24**	0.010	29.147**	277.619**	296.263**	29042.412**	0.149	3.102*	0.044	9.272**	8.207	61.494**	219753.96**
Crosses	29	88.711**	53.055**	810.62**	0.700**	33.226**	0.669**	9.587**	80.479**	191.484**	5392.256**	0.263**	2.918**	0.729**	11.103**	235.711**	23.978**	243708.32**
Error	84	4.287	4.578	58.118	0.178	0.822	0.129	0.231	9.116	4.851	499.306	0.047	0.516	0.052	0.260	9.315	2.633	5575.489
Total	128	31.744	18.664	393.602	0.736	13.909	0.332	3.551	39.786	75.093	2784.896	0.116	1.346	0.273	3.325	78.367	10.239	72409.213

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

Table 2: Extent of heterosis for *d*ays to 50% flowering, days to maturity, plant height, No.of primary branches, No.of secondary branches.

Sl. No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height			No.of primary branches per plant			No.of secondary branches per plant		
		MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH
1	RH-749 × TM-143	6.48*	-3.36	10.58**	-1.32	-2.6*	3.97**	3.39	-8.35 *	2.25	3.3	2.17	-14.55	29.13 **	-1.2	-19.61**
2	RH-749 × TM-258	1.22	-1.59	19.23**	0.91	-0.72	9.52**	9.88 **	8.16 *	24.55**	-3.61	-11.11	-27.27**	-13.56**	-31.08**	-50.00**
3	RH-749 × TM-130	6.38*	5.04	20.19**	2.77*	2.21	10.32**	14.15**	4.99	17.13**	-2	-10.91*	-10.91	0.00	-6	-53.92**
4	RH-749 × TM-108	3.7	1.61	21.15**	2.94*	1.82	11.11**	1.03	-2.66	8.59 *	-22.58**	-25.00**	-34.55**	-42.31 **	-50.00**	-70.59**
5	RH-749 × TPM-1	-11.85**	-21.85**	-10.58**	-1.53	-4.46**	1.98	4.98	-15.73 **	-5.99	19.32**	16.67	-4.55	-7.81	-29.76**	-42.16**
6	RH-749 × TM-217	2.98	1.68	16.35**	-0.19	-0.37	6.35**	-8.49 **	-10.95 **	-0.66	-2.33	-6.67	-23.64*	-13.27**	-28.99**	-51.96**
7	RH-749 × TM-108-1	2.5	1.65	18.27**	-1.11	-1.83	6.35**	-3.81	-4.45	8.02 *	9.3	4.44	-14.55	8.57	-6.56	-44.12**
8	RH-749 × TM-117	10.91*	2.52	17.31**	1.69	0.37	7.14**	6.18 *	4.83	16.95**	-4.76	-9.09	-18.18	-5.71	-31.25**	-35.29**
9	RH-749 × TM-52	1.35	-5.04	8.65*	-0.56	-1.49	5.16**	-16.40**	-25.87 **	-17.31**	14.61*	13.33*	-7.27	-1.05	-7.84	-53.92**
10	RH-749 × TM-263-3	7.42**	3.36	18.27**	0.37	0.00	7.54**	-0.6	-6.39	4.43	-7.37	-12*	-20.00*	-27.13 **	-44.71**	-53.92**
11	Giriraj × TM-143	-8.92**	-16.38**	-6.73*	-2.27	-3.01*	2.38	2.88	-1.71	-6.95	3.45	-2.17	-18.18	-17.99 *	-31.33**	-44.12**
12	Giriraj × TM-258	4.13	0.00	21.15**	2.94*	0.72	11.11**	12.61**	2.6	18.14**	-3.8	-7.32	-30.91**	-35.38 **	-43.24**	-58.82**
13	Giriraj × TM-130	9.48 **	9.48	22.12**	3.35**	2.21	10.32**	18.86**	18.22 **	11.92 **	-2.08	-14.55**	-14.55	28.30 **	21.43**	-33.33**
14	Giriraj × TM-108	7.5**	4.03	24.04**	2.03	0.36	9.52**	-5.26	-9.26 *	-6.17	-7.87	-14.58**	-25.45*	12.07	8.33	-36.27**
15	Giriraj × TPM-1	-2.88	-12.93**	-2.88	-3.66**	-6.02**	-0.79	14.80**	-1.64	-6.89	16.67	13.95*	-10.91	28.57 **	7.14	-11.76**
16	Giriraj × TM-217	7.76**	7.76*	20.19**	2.25	1.87	8.33**	1.79	-3.46	1.92	-14.63	-14.63*	-36.36**	-55.20 **	-59.42**	-72.55**
17	Giriraj × TM-108-1	6.33*	4.13	21.15**	2.04	0.73	9.13**	4.41	-4.08	8.44 *	7.32	7.32	-20.00*	-14.53	-18.03**	-50.98**
18	Giriraj × TM-117	16.13**	8.62**	21.15**	4.55 **	3.76**	9.52**	14.71 **	7.3 *	16.65**	-0.55	-9.09	-18.18	-28.95 **	-43.75**	-47.06**
19	Giriraj × TM-52	-10.00*	-14.66**	-4.81	-3.4**	-3.76**	1.59	2.38	-2.15	-7.37	8.24	4.55	-16.36	33.64 **	27.68**	-29.90**
20	Giriraj × TM 263-3	7.96**	5.17	17.31**	1.3	0.37	7.94**	8.71 *	6.56	5.03	5.49	-4	-12.73	-3.55	-20.00*	-33.33**
21	HUJM-10-6 × TM-143	-5.61*	-13.68**	-2.88	-0.56	-1.86	4.76**	1.34	-8.04 *	-2.69	6.17	-6.52	-21.82*	-51.30 **	-66.27**	-72.55**
22	HUJM-10-6 × TM-258	-9.47**	-12.70**	5.77	-1.28	-2.88*	7.14**	-4.34	-8.22 *	5.69	9.59	5.26	-27.27**	-15.09	-39.19**	-55.88**
23	HUJM-10-6 × TM-130	-7.3**	-7.69*	3.85	-1.66	-2.21	5.56*	16.06 **	9.39 **	15.75**	11.11	-9.09	-9.09	36.59 **	12	-45.10**
24	HUJM-10-6 × TM-108	2.9	0.00	19.23**	1.1	0.00	9.13**	0.00	-1.13	4.61	-3.61	-16.67**	-27.27**	2.17	-21.67**	-53.92**
25	HUJM-10-6 × TPM-1	-6.22*	-16.24**	-5.77	-3.45**	-6.32**	0.00	8.05 *	-11.49 **	-6.35	30.77*	18.6**	-7.27	67.24 **	15.48**	-4.9
26	HUJM-10-6 × TM-217	3	2.56	15.38**	2.42*	2.23	9.13**	7.14 *	7.02	13.23**	-2.63	-9.76	-32.73**	-48.51 **	-62.32**	-74.51**
27	HUJM-10-6 × TM-108-1	-0.84	-2.48	13.46**	-0.37	-1.1	7.14**	-0.41	-3.6	8.98*	18.42	9.76	-18.18	1.08	-22.95**	-53.92**
28	HUJM-10-6 × TM-117	11.01**	3.42	16.35**	2.45*	1.12	7.94**	-1.63	-2.95	5.51	-0.59	-15.15*	-23.64*	-50.00 **	-66.67**	-68.63**
29	HUJM-10-6 × TM-52	-5.88*	-11.11*	0.00	-3.94**	-4.83**	1.59	-1.93	-10.98 **	-5.81	18.99	6.82	-14.55	30.12 **	5.88	-47.06**
30	HUJM-10-6 × TM-263-3	3.96	0.85	13.46**	-1.11	-1.48	5.95**	6.71 *	3.06	9.04 *	-10.59	-24.00**	-30.91**	35.04 **	-7.06	-22.55**
SE diff		1.4641	1.6906	1.6906	1.5130	1.7471	1.7471	5.3906	6.2246	6.2246	0.2540	0.2933	0.2933	0.3402	0.3929	0.3929

* and ** Significant at 5% and 1% level of significance, respectively.

Table 3: Extent of heterosis for No.of siliquae on main raceme, length of main raceme, siliquae length, siliquae per plant & seeds/siliqua

Sl. No.	Genotypes	No. of siliquae on main raceme			Length of main raceme			Siliquae length			No. of Siliquae per plant				No. Seeds per siliquae	
		MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH
1	RH-749 × TM-143	5.58	2.52	-9.76	12.18 **	11.80**	13.53 **	14.34 **	10.18**	30.32 **	14.83*	2.02	-11.79*	9.02 *	5.56	4.72
2	RH-749 × TM-258	7.4	-4.42	7.87	15.52 **	1.54	35.10 **	0.83	-4.55	17.20 **	-20.03**	-32.65 **	-33.91 **	7.09	6.25	7.09
3	RH-749 × TM-130	31.48**	30.98**	15.3**	28.08 **	26.99 **	28.08 **	4.65	1.47	18.49 **	9.36	6.22	-24.31 **	11.3 *	5.56	4.72
4	RH-749 × TM-108	-0.51	-1.51	-13.3*	-3.45	-6.38	0.51	7.65*	6.27	16.56 **	-26.88**	-34.57 **	-44.35 **	9.09 *	4.76	3.94
5	RH-749 × TPM-1	16.32**	5.04	-7.54	13.56**	-1.87	-1.03	-2	-4.12	5.16	2.54	-5.09	-25.11 **	11.74 **	9.52 *	8.66
6	RH-749 × TM-217	-3.97	-16.42**	-0.67	12.31**	-0.26	29.62 **	-2.29	-4.66	9.89*	-5.5	-20.66 **	-21.54 **	2.11	-3.97	-4.72
7	RH-749 × TM-108-1	10.35	6.84	0.44	3.21	-4.35	13.01 **	5.16	0.9	20.43 **	1.03	-11.31	-21.18 **	3.37	-2.13	8.66
8	RH-749 × TM-117	13.07*	9.28	3.1	7.4**	-2.03	19.86 **	-7.54*	-8.78*	2.8	3.28	-13.62 **	-13.76 **	-1.43	-3.97	-4.72
9	RH-749 × TM-52	-9.83	-19.14**	-28.82**	-17.76**	-21.39 **	-20.72 **	7.04*	4.31	14.41**	-2.05	-2.68	-34.63**	3.59	3.17	2.36
10	RH-749 × TM-263-3	10.51	8.5	-0.89	-9.32 **	-13.89 **	-3.42	-1.96	-1.96	7.53	4.25	-10.98*	-15.52**	-5.26	-7.14	-7.87
11	Giriraj × TM-143	-7.56	-15.02**	-15.96**	-6.33*	-7.41*	-3.77	1.83	1.27	19.78 **	-16.96**	-20.14 **	-30.95 **	-8.4 *	-16.67 **	-5.51
12	Giriraj × TM-258	-1.36	-7.47	4.43	-2.46	-13.13 **	15.58 **	-5.65*	-7.88*	13.12	-30.80 **	-37.25 **	-38.43 **	3.68	-2.08	11.02 *
13	Giriraj × TM-130	16.43*	9.64	8.43	17.54 **	14.83 **	19.35 **	-0.83	-0.92	15.91**	14**	7.87	-13.87**	3.5	-7.64	4.72
14	Giriraj × TM-108	4.67	-2.02	-3.1	7.46	5.74*	13.53 **	1.25	-3.13	13.33**	-13.43**	-16.08 **	-28.63 **	12.31 **	1.39	14.96 **
15	Giriraj × TPM-1	-0.52	-14.57**	-15.52**	12.16 **	-4.28	-0.51	-4.07	-9.01**	6.45	8.79	8.15	-13.65**	-1.13	-9.03 *	3.15
16	Giriraj × TM-217	-13.03**	-20.34*	-5.32	0.15	-9.88 **	17.12 **	1.85	1.1	18.28 **	-41.39 **	-47.03 **	-47.62 **	5.1	-6.94	5.51
17	Giriraj × TM-108-1	6.9	4.26	3.1	0.54	-5.51*	11.64 **	-5	-5.95	12.26**	-26.81 **	-30.53 **	-38.26 **	-7.37 *	-8.33 *	3.94
18	Giriraj × TM-117	20.02**	17.26**	15.96**	5.18*	-2.73	19.01 **	-10.49**	-12.13**	2.8	-11.31*	-20.19 **	-20.32 **	-2.09	-10.42 *	1.57
19	Giriraj × TM-52	-3.29	-17.49**	-18.4**	-1.92	-7.58*	-3.94	0.58	-4.96	11.18**	-5.1	-13.14	-30.65 **	-6.32	-12.5 **	-0.79
20	Giriraj × TM 263-3	6.76	2.69	1.55	-1.43	-5.04	6.51	-9.68**	-12.50 **	2.37	-7.35	-14.7**	-19.05 **	8.68 *	0.00	13.39 **
21	HUJM-10-6 × TM-143	0.28	-5.08	-21.29**	3.95	-0.17	1.37	-2.71	-3.41	15.91 **	-15.64*	-30.07 **	-39.53 **	-10.32 *	-15.67 **	-11.02 *
22	HUJM-10-6 × TM-258	-3.2	-19.84**	-9.53	7.33**	-8.62 **	21.58 **	-7.71**	-8.76**	12.04**	-21.63 **	-38.09 **	-39.26 **	-12.98 **	-14.93**	-10.24 *
23	HUJM-10-6 × TM-130	32.69**	22.59**	7.1	25.51 **	21.93 **	20.89 **	-4.81	-6.09	12.69**	23.27 **	10.84	-21.01 **	-10.12 *	-17.16 **	-12.6 **
24	HUJM-10-6 × TM-108	44.67**	34.45**	15.96**	32.48 **	23.92 **	33.05 **	-2.18	-7.53*	10.97**	5.71	-11.78	-24.97 **	-7.2	-13.43 **	-8.66
25	HUJM-10-6 × TPM-1	33.64**	30.84**	-3.1	31.90 **	17.77 **	10.1**	2.29	-4.12	15.05 **	49.64 **	28.77 **	1.61	-4.31	-8.96 *	-3.94
26	HUJM-10-6 × TM-217	9.2	-11.38	5.32	21.23 **	4.22	35.45 **	-5.67*	-7.53*	10.97**	-17.9 **	-35.33 **	-36.05 **	-1.22	-9.7 *	-4.72
27	HUJM-10-6 × TM-108-1	25.86**	12.5*	5.76	11.81 **	0.14	18.32 **	-9.25**	-9.5**	8.6*	5.91	-13.15*	-22.81 **	-7.64 *	-9.93 *	0.00
28	HUJM-10-6 × TM-117	9.81	-2	-7.54	6.94**	-5.67*	15.41 **	-13.22**	-15.86 **	0.97	-14.33 **	-32.75 **	-32.86 **	0.2	-5.22	0.00
29	HUJM-10-6 × TM-52	10.94	7.78	-20.18**	-2.68	-3.48	-9.76**	-4.61	-10.93**	6.88	-7.33	-13.9	-42.91 **	-15.06 **	-17.91 **	-13.39 **
30	HUJM-10-6 × TM-263-3	19.03*	7.77	-1.55	12.57**	3.21	15.75 **	-4.87	-8.96**	9.25*	17.27 **	-6.21	-10.99*	8.24	2.99	8.66
SE differ		0.3929	2.4653	2.4653	1.5575	1.7984	1.7984	0.1538	0.1776	0.1776	15.8004	18.2447	18.2447	0.5081	0.5867	0.5867

Table 4: Extent of heterosis test weight, seed yield per plant, biological yield, harvest index and seed yield per hectare

Sl. No.	Genotypes	Test weight			Seed yield per plant			Biological yield			Harvest index			Seed yield per hectare		
		MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH	MPH	BPH	SH
1	RH-749 × TM-143	18.99 **	11.9**	4.44	40.54 **	35.61 **	25.64 **	20.30 **	19.40 **	19.27 **	16.82 **	11.89 *	5.32	44.88 **	39.28 **	28.07 **
2	RH-749 × TM-258	6.49	-2.38	-8.89*	18.39 **	11.7 **	16.67 **	20.46 **	10.97 *	29.60 **	-1.92	-4.45	-10.06	20.16 **	12.76 **	18.25 **
3	RH-749 × TM-130	11.63**	9.09*	6.67	26.68 **	18.71 **	25.81 **	21.64 **	19.91 **	17.98 **	3.74	-4.3	6.59	29.22 **	20.37 **	28.26 **
4	RH-749 × TM-108	-7.14	-7.14	-13.33**	-13.65 *	-17.13 **	-16.50 *	-25.10 **	-28.26 **	-22.93 **	14.71 **	14.44 **	8.22	-15.00 *	-18.74 **	-18.06 **
5	RH-749 × TPM-1	-14.63 **	-16.67 **	-22.22 **	13.00 *	3.41	-4.19	-0.86	-12.04 *	-13.46**	14.54 **	10.78 *	11.61 *	14.48 *	3.76	-4.58
6	RH-749 × TM-217	-4.26	-13.46 **	0.00	33.40 **	31.73 **	22.05 **	3.4	3.28	1.61	29.24 **	28.07 **	20.54 **	36.88 **	35.00 **	24.14 **
7	RH-749 × TM-108-1	0.00	-4.76	-11.11**	20.10 **	14.12 **	17.44 **	15.94 **	8.14	22.93 **	3.67	2.21	-3.79	22.06 **	15.42 **	19.09 **
8	RH-749 × TM-117	8.24**	6.98	2.22	33.33 **	21.52 **	36.84 **	24.50 **	15.03 **	33.48 **	6.16	3.25	2.82	38.27 **	26.40 **	40.33 **
9	RH-749 × TM-52	9.09*	0.00	-6.67	-3.34	-9.32 *	-15.98 **	-18.12**	-29.32 **	-30.46 **	17.39 **	6.91	22.49 **	-3.71	-10.28 *	-17.50 **
10	RH-749 × TM-263-3	4.88	2.38	-4.44	14.76 *	12.04 **	8.97 *	-3.39	-13.24 **	7.21	18.54 **	9	2.6	16.24 **	13.21 **	9.82*
11	Giriraj × TM-143	-5.75	-18.00 **	-8.89*	-9.8 **	-20.41 **	-10.34 **	-12.88**	-14.01 *	-14.1 *	3.62	-9.84 *	4.98	-10.74 **	-22.11 **	-11.32 **
12	Giriraj × TM-258	-29.41 **	-40.00 **	-33.33 **	-12.36 **	-15.55 **	-4.87	-7.49	-15.21 **	-0.97	-6.61	-17.51 **	-3.95	-13.43 *	-16.85 **	-5.33
13	Giriraj × TM-130	-17.02 **	-22.00 **	-13.33 **	-2.66	-5.54	6.41	33.04 **	31.86 **	28.31 **	-27.09 **	-28.67 **	-16.95 **	-2.89	-6	7.02
14	Giriraj × TM-108	-19.57 **	-26.00 **	-17.78 *	-24.07 **	-28.07 **	-18.97 **	-11.46 *	-15.63 **	-9.36	-14.92 **	-22.91 **	-10.24	-26.19 **	-30.41 **	-20.77 **
15	Giriraj × TPM-1	-26.67 **	-34.00 **	-26.67 **	-6.58 *	-21.40 **	-11.45 **	-10.67	-20.35 **	-22.50 **	5.1	-1.98	14.13 **	-7.24 *	-23.18 **	-12.54 **
16	Giriraj × TM-217	-23.53 **	-25.00 **	-13.33 **	-25.73 **	-33.08 **	-24.62 **	-30.84 **	-31.14 **	-32.40 **	7.11	-3.94	11.85 *	-28.12 **	-35.83 **	-26.95 **
17	Giriraj × TM-108-1	-15.91 **	-26.00 **	-17.78 *	-18.08**	-21.62**	-11.71 **	-13.67**	-19.89 **	-8.93	-6.67	-16.67 **	-2.98	-19.66 **	-23.42 **	-12.82 **
18	Giriraj × TM-117	-20.43 **	-26.00**	-17.78 *	-4.23	-4.25	7.86 *	0.71	-7.42	7.43	-6.53	-13.3 *	0.95	-3.4	-4.6	8.61 *
19	Giriraj × TM-52	-5.88	-20.00**	-11.11 **	4.06	-10.47 **	0.85	2.55	-11.06*	-13.46 *	1.79	0.97	17.57**	4.45	-11.34 **	0.94
20	Giriraj × TM 263-3	-4.44	-14.00 **	-4.44	7.49 *	0.15	12.82 **	-4.29	-14.46**	5.71	9.76 *	-7.89	7.24	8.17	0.16	14.04 **
21	HUJM-10-6 × TM-143	13.92**	7.14	0.00	-2.47	-3.63	-14.96 **	-16	-24.78 **	-24.87 **	14.88 **	1.76	13.68 *	-2.75	-4.03	-16.37 **
22	HUJM-10-6 × TM-258	27.27 **	16.67 **	8.89 *	9.2 *	0.74	5.21	-19.08 **	-32.17**	-20.78 **	32.35 **	19.05 **	32.99 **	10.11 **	0.8	5.71
23	HUJM-10-6 × TM-130	18.60 **	15.91 **	13.33 **	18.24 **	8.35 *	14.83 **	28.24**	17.12**	11.95 *	-8.03	-8.17	2.58	20.02 **	9.09 *	16.23 **
24	HUJM-10-6 × TM-108	0.00	0.00	-6.67	-18.79**	-23.83**	-23.25**	-1.39	-14.43 **	-8.07	-18.44 **	-24.70 **	-15.88 **	-20.68 **	-26.07 **	-25.45 **
25	HUJM-10-6 × TPM-1	-12.2**	-14.29**	-20.00**	28.12 **	19.90 **	5.81	37.31**	34.88 **	6.57	-6.35	-10.95	-0.52	31.42 **	22.07 **	6.36
26	HUJM-10-6 × TM-217	2.13	-7.69*	6.67	1.65	0.47	-9.23 *	-1.09	-10.75	-12.38 *	1.91	-6.89	4.01	1.83	0.52	-10.11 **
27	HUJM-10-6 × TM-108-1	-5	-9.52*	-15.56 **	2.12	-5.15	-2.39	9.72 *	-7.01	5.71	-9.04 *	-17.27 **	-7.58	2.34	-5.62	-2.62
28	HUJM-10-6 × TM-117	-8.24**	-9.3*	-13.33 **	-2.98	-13.47 **	-2.56	-7.73	-22.45**	-10.01	2.73	-2.84	8.54	-1.9	-12.46 **	-2.81
29	HUJM-10-6 × TM-52	1.3	-7.14	-13.33 **	-2.85	-6.73	-17.69**	-1.29	-5.99	-25.7 **	-2.19	-3.41	10.66*	-3.17	-7.46	-19.37 **
30	HUJM-10-6 × TM-263-3	9.76**	7.14	0.00	30.15 **	24.12**	20.73 **	20.72 *	-1.05	22.28 **	3.63	-11.55 *	-1.19	33.26 **	26.48 **	22.69 **
SE diff		0.1617	0.1867	0.1867	0.3611	0.4170	0.4170	2.1582	2.4921	2.4921	1.1476	1.3251	1.3251	52.7991	60.9671	60.9671

* and ** Significant at 5% and 1% level of significance, respectively.

The cross combination *viz*. RH-749 × TM-52 (-3.76) showed the significant and negative economic heterosis and also showed the negative and significant mid-parent (-16.40) and heterobeltiosis (-25.87) for plant height (Table:2). The estimates of economic desirable heterosis for number of primary branches per plant were exhibited by the four crosses, *viz*. HUJM-10-6 × TPM-1 (18.60), RH-749 × TPM-1(16.67), Giriraj × TPM-1 (13.95) and RH-749 × TM-52 (13.33) but, in case of secondary branches per plant none of the cross combinations showed positive and significant heterosis (Table:2). Eleven cross showed positive significant mid-parent heterosis for number of siliquae on main raceme with values ranging from 13.07 to 44.64 whereas for heterobeltiosis its values ranging from 12.50 to 34.45 and the crosses RH-749 × TM-130 (15.30), HUJM-10-6 × TM-108 (15.96) and Giriraj × TM-117 (15.96) exhibited the positive and significant economic or standard heterosis (Table:3). Estimates heterosis for length of main raceme showed that nineteen cross exhibit the positive significant average heterosis with values ranging from 5.18 to 32.48 while six cross showed the heterobeltiosis in positive direction and almost all cross exhibited the economic heterosis (Table:3). Five cross exhibited the mid-parent heterosis with values ranging from 14.00 to 49.64 while for heterobeltiosis one cross HUJM-10-6 × TPM-1 (28.77) had positive significant heterosis and none of the cross combinations showed positive significant heterosis for number of siliquae per plant (Table:3). Estimates of heterosis reported that only one RH-749 × cross TM-143 (14.34) had positive significant mid parent heterosis and better parent heterosis (10.18) and for economic heterosis almost all cross exhibited the positive significant values for siliquae length (Table:3). For test weight (Table:4) seven cross combinations expressed mid parent heterosis in positive direction with value ranging from 8.24 to 27.27 in case of better parent heterosis four cross showed the positive significant values and in standard heterosis only one cross HUJM-10-6 × TM-130 (13.33) exhibited the positive significance. For seed yield per plant, average heterosis thirteen cross combinations showed significant values in positive direction with values ranging from 7.49 to 40.54 whereas ten crosses exhibited the positive significance for heterobeltiosis, its magnitude ranging from 11.70 to 35.61and the crosses *viz*, RH-749 × TM-117 (36.84), RH-749 × TM-130 (25.81), RH-749 × TM-14 (25.64) had the positive and significant standard heterosis for this trait (Table: 4). These result are in similar and accordance with Dixit and Chauhan (2005) [4], Kapadia (2020) [6] and Tirkey *et al.* (2020) [14]. Estimates for biological yield per plant (Table:4) for mid parent heterosis showed that 10 crosses showed the positive significance with values ranging from 9.72 to 37.31 while 8 cross showed the positive better parent heterosis with a magnitude ranging from 10.97 to 34.88 and the crosses namely, RH-749 × TM-117 (33.48), RH-749 × TM-258 (29.60) and Giriraj × TM-130 (28.31) showed the positive significant standard heterosis for this trait. For seeds per siliquae six crosses exhibited the positive significant mid-parent heterosis with a magnitude ranging from 8.24 to 11.74 in case of better parent heterosis one cross RH-749 × TPM-1 (9.52) showed the positive significance and for economic heterosis the crosses, Giriraj × TM-108 (14.96), Giriraj × TM-263-3 (13.39) and Giriraj × TM-258 (11.02) showed the positive significance for this trait (Table:4). Nine crosses showed the positive significant heterosis with a values ranging from 9.76 to 32.34 in case of heterobeltiosis the five crosses showed the positive significant heterosis and for economic heterosis the crosses, HUJM-10-6 × TM-258 (32.99), RH-749 × TM-52(22.49) and RH-749 × TM-217 (20.55) reported the positive significance for harvest index (Table:4). For seed yield per hectare fourteen cross with a values from 8.17 to 44.88 showed the positive significant mid parent heterosis while 10 cross exhibited the better parent heterosis with magnitude ranging from 13.21 to 39.28 and for standard heterosis crosses RH-749 × TM-117 (40.33), RH-749 × TM-130 (28.26), RH-749 × TM-143 (28.07), RH-749 × TM-217 (24.14) and HUJM-10-6 × TM-263-3 (22.69) showed the positive significance for this trait. Kaur *et al.* (2019) [9] worked line × tester using 5 lines and 3 testers in Indian mustard. On the basis of *per se* performance and estimates of heterosis they inferred, the cross IC-597879 × IC-571648 was promising followed by IC-597919 × IC-335852 and IC-589669 × IC-338586 for seed yield/plant. Rout *et al.* (2025) [13] also highlighted hybrid combinations showing significant positive heterosis over both mid-parent and better-parent values while working on 28 crosses derived from half diallel mating design in Indian mustard. Gupta *et al.* (2024) [5] also reported hybrid vigour across 28 crosses for traits like earlier flowering, earlier maturity, and increased seed weight and seed yield per plant. Similar results were reported by many researchers including Meena *et al.*, (2015) [11], Chaurasiya *et al.*, (2018) [3] and Kaur *et al.*, (2019) [9].

Conclusion

The five cross combinations RH-749 × TM-117, RH-749 × TM-130, RH-749 × TM-143, RH-749 × TM-217 and HUJM-10-6 × TM-263-3 proved best heterotic crosses along with the high *per se* performance for seed yield per hectare. The cross combination RH-749 × TM-117 proved best heterotic cross for all types of heterosis. So, these crosses may further be exploited in the development of *B. juncea* varieties which can help to improve seed yield of this important oilseed crop.

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