Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2020; 9(1): 1766-1773
Received: 25-11-2019
Accepted: 27-12-2019

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Estimation of heterosis for yield related traits for single cross hybrids of *Brassica* species

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Abstract
The genetic investigation was carried out line x tester design for heterosis analysis studies the experimental material comprised with line x tester (4 x 23) and their parents. Several hybrids exhibited heterobeltiosis and standard heterosis for seed yield per plant and other characters. The hybrids viz., GDM-4 x EC-766443, GDM-4 x EC-766060 and GDM-4 x EC-766558 were found promising for commercial exploitation of heterosis as they showed maximum standard heterosis. Multilocation evaluation is required before commercial cultivation. On the basis of estimates of heterobeltiosis and standard heterosis hybrids *viz.*, GDM-4 x EC-766043 and GDM-4 x EC-766434 respectively, found to be most promising for seed yield per plant and other desirable traits, hence could be further evaluated to exploit the heterosis or utilized in future breeding programme to obtain desirable segregants for the development of superior genotypes.

Keywords: Mustard, heterobeltiosis, standard heterosis, *Brassica* Spp

Introduction
Oilseeds occupy prime importance in India as well as the world, which is evident from the impact created by yellow revolution. The major rapeseed-mustard producing countries are Canada, China, Germany and France. Rapeseed-mustard group of crops is the third most important oilseed crop after soybean and groundnut, contributing nearly 20-25% of the total oilseed production in the country. India with an area of 6.32 million hectares, 7.91 million metric tonnes production and 1183 kg/ha productivity ranks second in area and third in production in rapeseed-mustard scenario of the world in 2017 (Anonymous, 2016-17) [2]. They are next to cereals in production of agricultural commodities in India. The genus *Brassica* belongs to *Cruciferae* or *Brassicaceae* family and includes six cultivated species. Among those, *Brassica nigra* (n=8), *B. oleraceae* (n=9), *B. rapa* (n=10) are diploids. Rest of the three, namely *B. carinata* (n=17), *B. napus* (n=19) and *B. juncea* (n=18) are amphidiploids (Nagaheru U, 1935). Indian mustard is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). It originated in Asia with its major center of diversity in China (Vaughan, 1977) [31]. It was introduced in India from China and from where it spread to Afghanistan and other countries. It is largely self-pollinated crop (85-90%). However, owing to insects, especially the honeybees, the extent of cross-pollination varies from 4.0 to 16.6% (Rambhajan *et al.*, 1991) [23]. Mustard is a *Rabi* season crop of temperate region, which requires relatively cool temperature. Mustard seed is largely crushed for edible oil, which is perhaps the cheapest source of oil in our daily diet. Mustard seeds contain about 38-42% oil, which is golden yellow, fragrant and considered among the healthiest and most nutritional cooking medium. It is also utilized as a condiment, for medicinal uses and has industrial applications. Mustard meal or cake is also nutritious and contains about 12% oil and 38 to 42% protein (Nagraj, 1995) [17].

Material & Methods
The experimental material comprised of four females, twenty three male parents and their 92 F_{1S} developed by crossing four females (lines) with twenty three males (testers) in a Line x tester mating system. The seeds of 92 F_1 hybrids and 27 parents were produced by hand emasculation-hand pollination and selfing, respectively from Agronomy farm, B. A. College of Agriculture, Anand Agricultural University, Anand during *rabi* 2015-16. The hybrids along with parents were evaluated in a randomized block design with three replications during *rabi*, 2016-17. Each genotype was represented by a single row plot of 3m length. Inter and intra row spacing was kept 45 cm and 15 cm, respectively. All the recommended package of practices was adopted to raise a good crop. Observations were recorded on five randomly selected competitive plants in each parents and hybrids every replication for collection of various

characters as described below. The phenological characters *viz.*, days to 50% flowering and days to maturity were recorded on plot/row basis. The replication wise mean values were used in statistical analysis.

List of genotypes along with their species

Sr. No.	Name of Genotypes	Species	Sources
Females			
1	GM-1, GM-2, GM-3 & GDM-4	*Brassica juncea* L.	Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand-388 110
Males			
2	EC-766043, EC-766060, EC-766242 EC-766378, EC-766434, EC-766437 EC-766495, EC-766558, EC-766590 & EC-766632	*Brassica juncea* L.	National Bureau of Plant Genetic Resources, Pusa campus, New Delhi - 110 012
3	RH-119, RH-406, RH-749, NRCHB-101, NRCDR-02 & DRMR-IJ-31		Directorate of Rapeseed-Mustard Research, Bharatpur (Rajasthan) - 321 303
4	IC-399790 IC-399819 NRCM-120	*Brassica juncea* L.	Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand-388 110
5	NRCY-05-02	*Brassica rapa* L.	
6	Neelam	*Brassica napus* L.	
7	Kiran	*Brassica carinata* L.	
	Pusa Swarnim		

Results & Discussion

Analysis of variance for experimental design

The analysis of variance was carried out to test the differences amongst parents and hybrids for all the fourteen characters and is presented in Table 1 and 2. The results revealed that mean squares due to genotypes were highly significant for all the characters. This indicated that sufficient genetic variability was present in the materials for all the characters under study. The mean squares due to genotypes were further partitioned into parents, hybrids and parents *vs* hybrids. The analysis revealed significant differences among parents for all the characters except primary branches per plant, length of siliqua and 1000 seed weight. Among parents, mean squares due to females differed significantly for all the characters except primary branches per plant, secondary branches per plant, seeds per siliqua and 1000 seed weight. Mean squares due to males were significant for all the characters. This revealed the presence of great deal of diversity among the parents with respect to most of the characters under study. The mean squares due to females *vs* males also differed significantly for all the characters except days to 50% flowering, primary branches per plant and length of siliqua which indicated that male and female parents differed significantly with respect to majority of characters studied in the present investigation. From the Anova, it was observed that mean squares due to males were higher in magnitude than females for most of the characters indicating greater diversity existing in males than females for these characters.

Table 1: Analysis of variance (mean squares) for parents and hybrids for days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, effective length of main branch and siliquae per main branch

Source	d. f.	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ plant	Secondary branches / plant	Effective length of main branch	Siliquae/main branch
Replications	2	83.95**	168.85**	5517.00**	0.42	459.34**	5278.53**	2163.19**
Genotypes (G)	118	9.17**	6.40**	94.17**	7.21**	23.68**	100.34**	80.17**
Parents (P)	26	6.55**	5.13**	101.19**	0.80	5.95**	43.66**	15.03**
Females (F)	3	29.77**	38.78**	350.36**	0.45	0.76	5.51**	7.10**
Males (M)	22	137.72**	79.04**	2269.75**	16.88**	112.32**	433.04**	277.83**
F *vs* M	1	2.70**	15.64**	10.94**	3.51	41.51**	696.64**	105.84**
Hybrids (H)	91	4.56**	2.42**	93.04**	4.06**	6.60	20.14**	13.52**
Parents *vs* Hybrids	1	496.61**	400.94**	14.38**	460.77**	2039.55**	8872.41**	7838.41**
Error	236	1.17	0.76	46.45	0.27	2.26	12.06	4.57

*, ** Significant at 5% and 1% levels, respectively

Table 2: Analysis of variance (mean squares) for parents and hybrids for siliquae per plant, length of silique, seeds per silique, oil content, protein content, 1000 seed weight and seed yield per plant

Source	d. f.	Siliquae/plant	Length of siliqua	Seeds/siliqua	Oil content	Protein content	1000 seed weight	Seed yield/plant
Replications	2	59472.36**	0.87	31.95**	202.59**	43.38**	25.73**	383.86**
Genotypes (G)	118	3677.36**	6.50**	11.58**	45.47**	11.83**	5.45**	30.67**
Parents (P)	26	2743.78**	0.98	2.44**	2.64**	2.83**	0.76**	22.11**
Females (F)	3	8867.46**	11.45**	1.71	3.91**	7.94**	0.63**	5.99**
Males (M)	22	61153.95**	13.98**	34.39**	26.60**	16.67**	13.76**	181.69**
F *vs* M	1	1316.94**	0.06	27.37**	38.20**	49.06**	5.30**	387.18**
Hybrids (H)	91	3320.46**	0.71	4.14**	4.48**	3.94**	2.23**	10.85**
Parents *vs* Hybrids	1	60428.07**	677.21**	926.04**	4888.99**	964.61**	420.68**	2057.06**
Error	236	1419.62	0.06	0.63	0.73	0.93	0.23	4.32

*, ** Significant at 5% and 1% levels, respectively

Estimation of Heterosis

The magnitude of heterosis, measured as per cent increase or decrease of F_1 value over better parent (heterobeltiosis) and over standard check, GDM-4 (standard heterosis) for 14 characters. For the characters such as days to 50 per cent flowering, days to maturity and plant height, the low scoring values were considered as better parent for estimation of heterosis and remaining all the characters were considered as higher value as desirable heterosis. The character wise results are summarized in the following.

Days to 50% flowering estimates of heterobeltiosis revealed that out of 92 hybrids, 49 hybrids exhibited significant heterobeltiosis, of which 23 hybrids depicted significant and negative heterobeltiosis, which is desirable for earliness. The extent of heterobeltiosis ranged from -10.82 (GM-1 x EC-766632) to 3.11% (GM-2 x EC-766495). The hybrid GM-1 x EC-766632 (-10.82%) showed maximum significant negative heterobeltiosis over better parent followed by GM-1 x DRMR-IJ-31 (-10.75%) and GM-1 x Kiran (-10.68%) in desirable direction. The estimates of standard heterosis over the check GDM-4 varied from -12.94 (GM-3 x EC-766437) to -4.28% (GM-3 x EC-766558). In all, 3 hybrids exhibited significant negative standard heterosis over GDM-4. Maximum estimates were observed for the hybrid GM-3 x EC-766437(-12.94%) followed by GM-1 x EC-766632 (-11.81%) and GM-1 x DRMR-IJ-31 (-11.74). Out of 92 hybrids, 80 hybrids were significant, whereas 44 hybrids showed significant and negative standard heterosis in desirable direction. The similar results were also obtained by Khulbe *et al.* (1998) [10], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Kumbhalkar *et al.* (2000) [12], Sheikh and Singh (2001) [25], Ghosh *et al.* (2002) [6], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24] and Barupal *et al.* (2015) [3] for heterobeltiosis. While, Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] for standard heterosis (Table 3&4).

Days to maturity estimates of heterobeltiosis revealed that out of total 62 significant hybrids, 25 hybrids depicted significant and negative heterobeltiosis, which are desirable for earliness. The extent of heterobeltiosis ranged from -4.35% (GM-3 x Pusa Swarnim) to 1.92% (GM-1 x Neelam, GM-1 x EC-766437 and GM-1 x RH-406). The hybrid GM-3 x Pusa Swarnim (-4.35%) showed maximum significant and negative heterosis over better parent followed by GDM-4 x Kiran (-4.25%) and GDM-4 x EC-766043 (-4.20%). Out of 80 hybrids, 44 hybrids exhibited significant negative standard heterosis over GDM-4. The estimates of standard heterosis over the check GDM-4 varied from -5.76 (GM-3 x Kiran) to -2.36 (GDM-4 x IC-399819) per cent. The hybrids GM-3 x Kiran (-5.76%) showed maximum negative heterosis over standard check followed by GDM-4 x EC-766043 (-4.71%) and GM-2 x NRCY-05-02 (-4.70%). The results are in agreement with the findings of Khulbe *et al.* (1998) [10], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Hirve and Tiwari (1991) [8], Kumbhalkar *et al.* (2000) [12], Ghosh *et al.* (2002) [6], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24] and Barupal *et al.* (2015) [3] for heterobeltiosis. While, Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] for standard heterosis (Table 3&4).

For plant height, the estimates of negative heterosis over better parent ranged from -3.56 (GDM-4 x RH-406) to 8.53 (GM-2 x IC-399819) per cent. None of the hybrids depicted significant and negative heterobeltiosis for plant height. The hybrids *viz.*, GDM-4 x EC-766437 (-3.42) and GM-1 x RH-406 (-3.40) also shoed negative heterobrltiosis. The estimates of standard heterosis over check GDM-4 revealed that out of 54 hybrids, 21 hybrids exhibited significant negative standard heterosis. The range of standard heterosis was from -5.82 (GM-2 x NRCY-05-02, GM-2 x Pusa Swarnim, GDM-4 x EC-766043 and GDM-4 x RH-406) to 2.50 (GM-3 x NRCHB-101). This results was also similar to findings of Khulbe *et al.* (1998) [10], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Kumbhalkar *et al.* (2000) [12], Sheikh and Singh (2001) [25], Ghosh *et al.* (2002) [6], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) for heterobeltiosis. The result were akin to Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] for standard heterosis (Table 3&4).

Heterobeltiosis for primary branches per plant were all hybrids showed significant and positive heterosis over better parent. The magnitude of heterobeltiosis varied from 4.30 (GM-1 x EC-766043) to 68.12 (GDM-4 x RH-116) per cent. Maximum heterobeltiosis for this trait was depicted by hybrid GDM-4 x RH-116 (68.12%) followed by GDM-4 x EC-766060 (65.56%) and GDM-4 x EC-766434 (62.32%). The range of standard heterosis was from 14.77 (GM-3 × EC-766558) to 74.98 per cent (GDM-4 x EC-766434). Total 80 hybrids expressed significant positive heterosis over standard check GDM-4. The hybrid GDM-4 x EC-766434 (74.98%) showed maximum positive heterosis over standard check GDM-4, followed by GDM-4 × EC-766043 (72.31%) and GDM-4 × RH-116 (64.51%). This results were similar to those obtained by Khulbe *et al.* (1998) [10], Katiyar *et al.* (2000) [9], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Thakur and Bhteria (1993) [30], Kumbhalkar *et al.* (2000) [12], Sheikh and Singh (2001) [25], Ghosh *et al.* (2002) [6], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) for heterobeltiosis. Agrawal and Badwal (1998) [1], Parmar *et al.* (2004) [20], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] reported same results for standard heterosis (Table 3&4).

A perusal data of secondary branches per plant indicated that out of 92 hybrids, 82 hybrids showed significant positive heterosis over better parent. The extent of heterobeltiosis ranged from -2.02% (GM-1 x Pusa Swarnim) to 64.51% (GDM-4 x RH-116) per cent. The hybrids GDM-4 x RH-116 (64.51%) showed maximum positive heterosis over better parent followed by GDM-4 x EC-766434 (60.71%) and GM-3 x DRMR-IJ-31 (51.80%). The standard heterosis over the best check GDM-4 for secondary branches per plant was positive and significant for 80 hybrids. The magnitude of standard heterosis among hybrids ranged from 27.02 (GM-3 × EC-766558) to 69.18 (GDM-4 × EC-766434) per cent. Maximum standard heterosis was depicted by hybrid GDM-4 × EC-

766434 (69.18%), followed by GDM-4 × EC-766043 (66.56%) and GDM-4 × RH-116 (65.47%). The results were also supported by Khulbe *et al.* (1998) [10], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Thakur and Bhateria (1993) [30], Sheikh and Singh (2001) [25], Macwana (2008) [13], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) for heterobeltiosis. While, Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] recorded similar result for standard heterosis (Table 3&4).

Total 92 hybrids evaluated for effective length of main branch, none of the hybrids recorded significant and positive heterobeltiosis for effective length of main branch. Heterobeltiosis varied from 3.52 (GM-1 × EC-766378) to 27.80 (GDM-4 x EC-766060) per cent. Maximum estimates for heterobeltiosis were observed for the hybrid GDM-4 x EC-766060 (27.80%), followed by GDM-4 × EC-766558 (27.74%) and GM-3 × NRCHB-101 (26.34%). Here also none of the hybrids were found significantly superior for standard heterosis over check (GDM-4) for effective length of main branch. The estimates of standard heterosis varied from 21.94 (GM-2 × NRCY-05-02) to 38.90 (GM-3 × NRCM-120) per cent. Numerically maximum estimate for standard heterosis was observed for the hybrid GM-3 × NRCM-120 (38.90%), followed by GDM-4 × EC-766590 (37.78%) and GDM-4 × EC-766590 and GDM-4 x NRCDR-02 (35.73%). Similar result were also obtained by Khulbe *et al.* (1998) [10], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5] and Niranjana *et al.* (2014) [19] for heterobeltiosis and standard heterosis. However Ghosh *et al.* (2002) [6], Macwana (2008) [13] and Gupta *et al.* (2011) [7] recorded same result for only heterobeltiosis, while, Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] for only standard heterosis (Table 3&4).

Estimates of heterobeltiosis for siliquae per main branch revealed that 83 hybrids were observed significant positive heterosis over better parent. The extent of heterobeltiosis ranged from 5.88 (GM-1 x EC-766378) to 30.60 (GDM-4 x EC-766060) per cent. The magnitude of heterobeltiosis showed maximum positive heterobeltiosis for siliquae on main branch of GDM-4 x EC-766060 (30.60%) followed by GM-3 x NRCHB-101 (30.38%) and GDM-4 x EC-766558 (30.28%). The range of standard heterosis was from -16.70 (GM-2 x NRCY-05-2) to 33.46 (GDM-4 x EC-766590) per cent. The data also revealed that 80 hybrids showed significant positive heterosis over check GDM-4. Highest top three significant positive standard heterosis observed for siliquae on main branch were hybrids GDM-4 x EC-766590 (33.46%), GDM-4 x EC-766434 (32.96%) and GDM-4 x EC-766242 (32.21%). These findings were akin to the results of Khulbe *et al.* (1998) [10], Katiyar *et al.* (2000) [9] and Rai and Verma (2005) [22] for heterobeltiosis and standard heterosis. Whereas Gupta *et al.* (2011) [7] and Rai *et al.* (2017) for heterobeltiosis. Whereas, Chaurasiya *et al.* (2018) [4] reported similar results for standard heterosis (Table 3&4).

The estimates of heterobeltiosis for siliquae per plant varied from -15.03 (GM-2 x NRCHB-101) to 23.99 (GM-3 x NRCM-120) per cent. Among all the hybrids none of the cross exhibited significant or positive heterobeltiosis. Numerically maximum estimate for heterobeltiosis was observed for the hybrid GM-3 x NRCM-120 (23.99%) followed by GDM-4 x NRCHB-101 (22.03%) and GDM-4 x EC-766060 (20.99%). With regard to standard heterosis, out of the 92 hybrids, total 78 hybrids exhibited significant positive heterosis over the standard check GDM-4. The magnitude of standard heterosis varied from -3.59 (GM-3 x Neelam) to 39.12 (GM-3 x EC-766242) per cent. The maximum significant and positive estimates of standard heterosis were observed in hybrid GM-3 x EC-766242 (39.12%) followed by GM-3 x NRCM-120 (37.33%) and GDM-4 x EC-766437 (36.88%). Similar results were also obtained by Khulbe *et al.* (1998) [10], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Hirve and Tiwari (1991) [8], Thakur and Bhateria (1993) [30], Kumbhalkar *et al.* (2000) [12], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Saeed *et al.* (2013) [24], Meena *et al.* (2013) [14] and Barupal *et al.* (2015) [3] reported only for heterobeltiosis. While, Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] reported solely for standard heterosis only (Table 3&4).

The extent of heterosis over better parent for length of siliqua ranged from 11.28 (GDM-4 x Pusa Swarnim) to 104.41 (GM-1 x IC-399819) per cent. A perusal of data indicated that all the 92 hybrids exhibited significant positive heterobeltiosis. The highest estimate was observed for the hybrid GM-1 x IC-399819 (104.41%) followed by GM-2 x EC-766437 (102.15%) and GM-1 x NRCHB-101 (87.02%). The data revealed that significant positive standard heterosis over the check GDM-4 for length of siliqua was recorded by 80 hybrids. The estimates of standard heterosis ranged from 11.28 (GDM-4 ×Pusa Swarnim) to 42.37 (GM-1 × IC-399819) per cent. The maximum estimate of positive and significant standard heterosis was exhibited by hybrid GM-1 × IC-399819 (42.37%) followed by GM-1 x EC-766434 (40.89%) and GM-3 × EC-766434 (40.36%). These results are in agreement with the findings of Khulbe *et al.* (1998) [10], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Hirve and Tiwari (1991) [8], Kumbhalkar *et al.* (2000) [12], Macwana (2008) [13], Mishra (2010) [15], Nasrin *et al.* (2011) [18] and Rai *et al.* (2017) reported same only for heterobeltiosis. Agrawal and Badwal (1998) [1] also similar reported for standard heterosis only (Table 3&4).

Total 92 hybrids were evaluated for seeds per siliqua and 90 hybrids depicted positive significant heterobeltiosis for seed per siliquae. The heterobeltiosis ranged from 15.89 (GM-2 x EC-766434) to 62.39 (GDM-4 x EC-766060) per cent. Hybrid GDM-4 x EC-766060 (62.39%) showed maximum heterosis over better parent followed by GDM-4 x EC-766558 (62.36%) and GM-3 x NRCDR-02 (52.48%). The standard heterosis for seeds per siliqua varied from 36.11 (GM-2 x NRCY-05-02 and GM-3 x Pusa Swarnim) to 71.51 (GDM-4 x EC-766043 and GDM-4 x EC-766434) per cent. The estimates of standard heterosis over the best check GDM-4 revealed that out of 92 hybrids, 80 hybrids exhibited significant and positive standard heterosis. The results are supported by Khulbe *et al.* (1998) [10], Katiyar *et al.* (2000) [9], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Thakur and Bhateria (1993) [30], Kumbhalkar *et al.* (2000) [12], Sheikh and Singh (2001) [25], Sohan Ram (2009) [27], Mishra (2010) [15], Saeed *et al.* (2013) [24], Meena *et al.* (2013) [14], Dholu *et al.* (2014) [5], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) reported for heterobeltiosis only, whereas Agrawal and Badwal (1998) [1] reported for standard heterosis only (Table 3&4).

A perusal data of oil content indicated that all the hybrids showed positive significant heterobeltiosis for oil content in seed. The heterobeltiosis for oil content ranged from -13.61 (GM-3 x EC-766378) to 34.91 (GDM-4 x EC-766043) per cent. The hybrid GDM-4 x EC-766043 (34.91%) exhibited maximum heterobeltiosis followed by GDM-4 x EC-766060 (33.03%) and GDM-4 x EC-766437 (32.54%). The standard heterosis for oil content ranged from 22.83 (GDM-4 x Pusa Swarnim) to 42.17 (GDM-4 x EC-766043) per cent. Out of 92 hybrids, 80 hybrids showed positive significant heterosis over standard check GDM-4. The hybrid GDM-4 x EC-766043 (42.17%) exhibited maximum relative heterosis followed by GDM-4 x EC-766590 (39.81%) and GDM-4 x EC-766060 (38.82%). Similar results have been reported by Khulbe *et al.* (1998) [10], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Kumbhalkar *et al.* (2000) [12], Makwana *et al.* (2008), Sohan Ram (2009) [27] and Mishra (2010) [15] recorded the same for only heterobeltiosis. While, Agrawal and Badwal (1998) [1] and Kumar *et al.* (2013) [11] also reported similar result for standard heterosis (Table 3&4).

A perusal of data of protein content indicated that out of 92 hybrids, 88 hybrids showed positive significant heterobeltiosis for protein content of seed. The significant and positive heterobeltiosis for protein content varied from 6.07 (GM-2 x EC-766043) to 30.49 (GDM-4 x EC-766043) per cent. The hybrid GDM-4 x EC-766043 (30.49%) exhibited maximum heterobeltiosis followed by GDM-4 x EC-766060 (27.29%) and GDM-4 x EC-766495 (27.11%). The standard heterosis for protein content over the check GDM-4 was observed positive and significant for 80 hybrids. The magnitude of standard heterosis among hybrids ranged from 12.51 (GM-3 × EC-766558) to 40.76 (GDM-4 × EC-766043) per cent. Maximum standard heterosis was depicted by hybrid GDM-4 × EC-766043 (40.76%) followed by GDM-4 x EC-766434 (37.77%) and GDM-4 x RH-116 (34.75%). Similar results were also obtained by Singh *et al.* (2003) [26], Dholu *et al.* (2014) [5] and Niranjana *et al.* (2014) [19] for heterobeltiosis and standard heterosis (Table 3&4).

With regard to heterobeltiosis for 1000 seed weight out of the 92 hybrids, total 91 hybrids exhibited significant positive heterosis over the respective better parent for 1000 seed weight. The 1000 seed weight of seed ranged from 4.54 (GM-3 × EC-766378) to 97.03 (GDM-4 × RH-749). Whereas maximum heterobeltiosis for 1000 seed weight observed were hybrids GDM-4 × RH-749 (97.03) followed by GDM-4 × RH-116 (89.99) and GDM-4 × NRCDR-02 (88.06). The range of standard heterosis was from 28.90 (GDM-4 x Pusa Swarnim) to 106.22 (GDM-4 x EC-766378) per cent. The data also revealed that total 80 hybrids showed significant and positive heterosis over check GDM-4. It was maximum for the cross GDM-4 x EC-766378 (106.22) followed by GDM-4 x EC-766434 (105.23) and GDM-4 x EC-766242 (99.36). These results were related to Khulbe *et al.* (1998) [10], Singh *et al.* (2003) [26], Rai and Verma (2005) [22], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heteriobeltiosis and standard heterosis. Whereas, Kumbhalkar *et al.* (2000) [12], Sheikh and Singh (2001) [25], Macwana (2008) [13], Sohan Ram (2009) [27], Mishra (2010) [15], Gupta *et al.* (2011) [7], Saeed *et al.* (2013) [24], Meena *et al.* (2013) [14], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) reported similar results for only heteriobeltiosis, while Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] reported the same for standard heterosis only (Table 3&4).

Significant positive estimates of heterobeltiosis for seed yield per plant were observed in 37 hybrids out of 92 hybrids. The magnitude of heterobeltiosis ranged from -1.69 (GM-1 x EC-766242) to 27.64 (GdM-4 x EC-766043) per cent. The maximum positive significant estimate was observed in GDM-4 x EC-766043 (27.64%) followed by GdM-4 x RH-749 (25.49%) and GM-3 x RH-749 (24.98%). With regard to standard heterosis, out of the 92 hybrids, total 80 hybrids exhibited significant positive heterosis over the standard check GDM-4 for seed yield per plant. The extent of standard heterosis varied from 17.81 (GM-2 x DRMR-IJ-31) to 41.03 (GDM-4 x EC-766434) per cent. The maximum standard heterosis was observed in hybrid GDM-4 x EC-766434 (41.03%) followed by GDM-4 x EC-766060 (40.91%) and GDM-4 x IC-766558 (40.44%). Similar results were also obtained by Khulbe *et al.* (1998) [10], Katiyar *et al.* (2000) [9], Singh *et al.* (2003) [26], Dholu *et al.* (2014) [5], Niranjana *et al.* (2014) [19] and Surin *et al.* (2018) [29] for heterobeltiosis and standard heterosis. Whereas Hirve and Tiwari (1991) [8], Patel *et al.* (1993) [21], Kumbhalkar *et al.* (2000) [12], Sood *et al.* (2000), Sheikh and Singh (2001) [25], Macwana (2008) [13], Gupta *et al.* (2011) [7], Nasrin *et al.* (2011) [18], Yadava *et al.* (2012) and Saeed *et al.* (2013) [24], Meena *et al.* (2013) [14], Barupal *et al.* (2015) [3] and Rai *et al.* (2017) reported similar results for heterobeltiosis only. However, Agrawal and Badwal (1998) [1], Kumar *et al.* (2013) [11] and Chaurasiya *et al.* (2018) [4] recorded the same trend for standard heterosis only (Table 3&4).

Table 3: Range of heterobeltiosis and standard heterosis

Sr. No.	Traits	S.Em. ±	Range of heterosis	
			Heterobeltiosis	Standard heterosis
1.	Days to 50% flowering	0.88	-10.82 to 3.11	-12.94 to -4.28
2.	Days to maturity	0.71	-4.35 to 1.92	-5.76 to -2.36
3.	Plant height	5.56	-3.56 to 8.53	-5.82 to 2.50
4.	Primary branches/ plant	0.43	4.30 to 68.12	14.77 to 74.98
5.	Secondary branches / plant	1.23	-2.02 to 64.51	27.02 to 69.18
6.	Effective length of main branch	28.30	3.52 to 27.80	21.94 to 38.90
7.	Siliquae/ main branch	1.74	5.88 to 30.60	16.70 to 33.46
8.	Siliquae/plant	30.76	-15.03 to 23.99	-3.59 to 39.12
9.	Length of siliqua	0.19	11.28 to 104.41	11.28 to 42.37
10.	Seeds/siliqua	0.65	4.07 to 48.71	21.95 to 57.35
11.	Oil content	0.69	13.61 to 34.91	22.83 to 42.17
12.	Protein content	0.78	6.07 to 30.49	12.51 to 40.76
13.	1000 seed weight	0.39	4.51 to 97.03	28.90 to 106.22
14.	Seed yield/plant	1.69	-1.69 to 27.64	17.81 to 41.03

Table 4: Best three performing hybrids to their magnitude of heterosis for various traits

Traits	Rank	Magnitude of heterosis			
		Heterobeltiosis		Standard heterosis	
Days to 50% flowering	1st	GM-1 x EC-766632	-10.82**	GM-3 x EC-766437	-12.94**
	2nd	GM-1 x DRMD-IJ-31	-10.75**	GM-1 x EC-766632	-11.81**
	3rd	GM-1 x Kiran	-10.68**	GM-1 x EC-DRMR-IJ-31	-11.75**
Days to maturity	1st	GM-3 x Kiran	-4.35**	GM-3 x Kiran	-5.76**
	2nd	GM-4 x Kiran	-4.25**	GM-1 x EC-766378	-5.06**
	3rd	GDM-4 x EC-766043	-4.20**	GDM-4 x IC399790	-4.80**
Plant height	1st	GDM-4 x RH-406	-3.56**	GM-2 x NRCY-05-02	-5.82**
	2nd	GDM-4 x EC-766437	-3.42**	GM-1 x EC-766378	-5.78**
	3rd	GM-1 x RH-406	-3.40**	GM-2 x RH-116 & EC-766434	-5.64**
Primary branches/ plant	1st	GDM-4 x RH-116	68.12**	GDM-4 x EC-766434	74.78**
	2nd	GDM-4 x EC-766060	65.56**	GDM-4 x EC-766043	72.31**
	3rd	GDM-4 x EC-766558	65.13**	GDM-4 x RH-116	68.12**
Secondary branches / plant	1st	GDM-4 x RH-116	64.51**	GDM-4 x EC-766434	69.18**
	2nd	GDM-4 x EC-766434	60.71**	GDM-4 x EC-766043	66.65**
	3rd	GM-3 x DRMR-IJ-31	51.80**	GDM-4 x RH-116	64.51**
Effective length of main branch	1st	GDM-4 x EC-766060	27.80**	GM-3 Xnrcm-120	38.90**
	2nd	GDM-4 x EC-766558	27.74**	GDM-4 x EC-766590	37.78**
	3rd	GM-3 x NRCHB-101	26.34**	GDM-4 x ec-766242	36.70**
Siliquae/ main branch	1st	GDM-4 x EC-766060	30.60**	GDM-4 x EC-766590	33.66**
	2nd	GM-3 x NERCHB-101	30.38**	GDM-4 x EC-766434	32.96**
	3rd	GM-3 x EC-766558	30.28**	GDM-4 x EC-766242	32.21**
Siliquae/ plant	1st	GM-3 x NRCM-120	23.99**	GM-3 x EC-766242	39.12**
	2nd	GDM-4 x NRCHB-101	22.03**	GM-3 x NRCM-120	37.33**
	3rd	GDM-4 x EC-766060	20.99**	GDM-4 x EC-766437	36.88**
Length of siliqua	1st	GM-1 x IC-399819	10.41**	GM-1 x IC-399819	42.37**
	2nd	GM-2 x EC-766437	102.15**	GM-1 x EC-766434	40.89**
	3rd	GM-2 x NRCDR-02	95.50**	GM-3 x EC-766434	40.36**
Seeds/ siliqua	1st	GDM-4 x EC-766060	62.39**	GDM-4 x EC-766043	71.51**
	2nd	GDM-4 x EC-766558	62.36**	GDM-4 x EC-766434	71.51**
	3rd	GDM-4 x EC-766043	52.89**	GDM-4 x EC-766378	70.17**
Oil content	1st	GDM-4 x EC-766043	34.91**	GDM-4 x EC-766043	30.49**
	2nd	GDM-4 x EC-766060	33.03**	GDM-4 x EC-766060	27.29**
	3rd	GDM-4 x EC-766437	32.54**	GDM-4 x EC-766558	27.11**
Protein content	1st	GDM-4 x EC-766043	40.76**	GDM-4 x EC-766043	42.17**
	2nd	GDM-4 x EC-766437	37.77**	GDM-4 x EC-766590	39.80**
	3rd	GDM-4 x RH-116	34.75**	GDM-4 x EC-766060	38.82**
1000 seed weight	1st	GDM-4 x RH-749	97.03**	GDM-4 x EC-766378	106.22**
	2nd	GDM-4 x RH-116	89.99**	GDM-4 x EC-766434	105.23**
	3rd	GDM-4 x NRCDR-02	88.06**	GDM-4 x EC-766242	99.36**
Seed yield/plant	1st	GDM-4 x EC-766043	27.64**	GDM-4 x EC-766443	41.03**
	2nd	GDM-4 x RH-749	25.49**	GDM-4 x EC-766060	40.91**
	3rd	GM-3 x RH-749	24.98**	GDM-4 x EC-766558	40.44**

*, ** Significant at 0.05 and 0.01 levels, respectively

Conclusion

The analysis of variance was performed to test the difference amongst parents and hybrids for all the fourteen characters. The results revealed that mean squares due to genotypes were highly significant for all the characters. This indicated that sufficient genetic variability was present in the material for all the characters under study. The mean squares due to genotypes were further partitioned into parents, hybrids and parents *vs*. hybrids. The analysis revealed significant differences among parents for all the characters except primary branches per plant, length of siliqua and 1000 seed weight. Among parents, mean squares due to females differed significantly for all the characters except primary branches per plant, secondary branches per plant, seeds per siliqua and 1000 seed weight. Mean squares due to males were significant for all the characters. This revealed the presence of great deal of diversity among the parents with respect to most of the characters under study. The mean squares due to females *vs.* males also differed significantly for all the characters except days to 50% flowering, primary branches per plant and length of siliqua which indicated that male and female parents differed significantly with respect to majority of characters studied in the present investigation. From the ANOVA, it was observed that mean squares due to males were higher in magnitude than females for most of the characters indicating greater diversity existing in males than females for these characters.

The analysis of variance further revealed that hybrids differed significantly for all the characters except length of siliqua as their mean square values were highly significant. Therefore existence of considerable genetic variability among the hybrids was confirmed for all the characters. Mean squares due to parent *vs* hybrids were significant for all the characters. This suggested the presence of heterosis for these characters. Out of 92 hybrids, total 80 hybrids exhibited significant standard heterosis in positive direction for seed yield per plant against the check GDM-4. The hybrid GDM-4 x EC-766443 exhibited maximum estimates of significant positive standard heterosis for seed yield and yield contributing characters followed by GDM-4 x EC-766060 and GDM-4 x EC-766558.

The hybrids GM-3 x EC-766437 followed by GM-1 x EC-766632 and GM-1 x DRMR-IJ-31 exhibited the highest estimates of significant negative standard heterosis for days to 50 per cent flowering and the hybrids GM-3 x Kiran followed by GM-1 x EC-766378 and GDM-4 x IC-399790 days to maturity. While hybrids GDM-4 x EC-766043 and GDM-4 x EC-766043 exhibited maximum estimates of significant positive standard heterosis for oil and protein content, respectively. Out of the 92 hybrids, total 82 hybrids exhibited significantly positive heterobeltiosis for seed yield per plant. The maximum estimate of positive significant heterobeltiosis for seed yield per plant was exhibited by hybrid GDM-4 x EC-766043 followed by GDM-4 x RH-749 and GM-3 x RH-749. The hybrids GM-1 x EC-766632 and GM-3 x Kiran exhibited significant negative heterobeltiosis for days to per cent flowering and days to maturity respectively. While hybrids GDM-4 x EC-766043 and GDM-4 x EC-766043 exhibited maximum estimates of significant positive heterobeltiosis for oil and protein content, respectively.

Acknowledgment
I gratefully acknowledge the whole support received from the vice-chancellor and Directorate of Research and Dean Post-Graduate Studies, Anand Agriculture University, Anand (Gujarat) for carrying out this study. I also thankful to my guide and other faculty members of department of Genetics & Plant Breeding for providing fully guidance during study and research facilities of laboratory.

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