



Combining ability and heterobeltiosis for yield and yield-attributing traits in Indian mustard (*Brassica juncea* L.)

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Abstract

A line (7) x tester (3) analysis was made to estimate combining ability effects and heterosis over better parent in Indian mustard (*Brassica juncea* L.) during *Rabi* season 2014-15. There was significant variation among the parents and crosses and the average heterosis was exhibited for seed yield plant⁻¹ and component traits. Combining ability effects revealed that DRMR-150-35, RH-932 and TM-2 were good general combiners among the parents whereas DRMR 150-35 x Pusa Bold, GM-3 x SEJ-2 and MCP 802 x SEJ-2 were the best specific combiners. Greater SCA variance than GCA was observed for all the characters indicating greater role of non-additive gene action. Heterosis over better parent (heterobeltiosis) was high in DRMR-15 x SEJ-2, DRMR 150-35 x Pusa Bold, RH-932 x TM-2 and GM-3 x SEJ-2. Therefore, based on mean performance and GCA effects, the most promising parents were DRMR 150-35, TM-2 and RH-932 and based on SCA effects and heterosis, DRMR 150-35 x Pusa Bold, MCP 802 x SEJ-2, RH 932 x TM-2 and GM-3 x SEJ-2 were the most potential crosses.

Key words: *Combining ability, heterobeltiosis, Indian mustard*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is mainly used as vegetables, fodder and condiments but its most important economic use is as the source of edible oils. With 78.2 million tonnes production, India is the third largest producer of rapeseed-mustard after China and Canada, and it accounts for 19.29% of world acreage and 11.12% of production. Rapeseed-mustard is the second most important oilseed crop after soybean which plays a significant role in the Indian oilseed economy by contributing 24.2% to the total oilseeds production during 2013-14. The demand for edible oil is going up day-by-day and India has only 50% self-sufficiency. So the country is laying emphasis to meet the challenge of bridging the widening gap of demand and production of edible oil. One of the considerations is development of short duration and high yielding Indian mustard varieties. Rapeseed-mustard can be grown under diverse agro-climatic conditions and has gained momentum among the annual oilseed crops. Development of superior varieties of Indian mustard therefore assumes enormous importance to enhance production. It is realized that in addition to improvement through conventional breeding approaches hybrids offer an opportunity for utilizing greater amount of genetic variability and high heterotic response in Indian mustard. Presently, there is about 15 percent yield increase by use of hybrids (Yadava *et al.*, 2012). A high yielding genotype may or may not transmit

its superiority to its progeny. Hence, development of superior variety could be done by utilizing combining ability of suitable parents through hybridization. Moreover, it is also necessary to know about the nature and magnitude of gene action responsible for controlling the inheritance of various yield attribute along with combining ability of parents and crosses. Combining ability analysis helps in choosing suitable parents for hybridization and provides valuable information regarding cross combinations to be exploited for commercial varieties and hybrids. Therefore, the present investigation was undertaken to evaluate combining ability effects of parents and F₁'s and estimate the better parent heterosis of the hybrids.

Materials and Methods

The study was conducted at Assam Agricultural University, Jorhat, India during *Rabi* 2013-14 and 2014-15. During 2013-14, parents were grown in crossing block and hybridization was carried out among the 7 lines and 3 testers following Line x Tester method (Kempthorne, 1957). In the year 2014-2015, parents and hybrids were evaluated in an experiment laid out in randomized block design with 2 replications. Each treatment was sown in 3 rows per plot with a plot size of 4m x 0.9 m. Recommended package of practices for Indian mustard were followed to raise a healthy crop. The observations were recorded on five randomly selected plants for fourteen characters *viz.*,

days to 50% flowering, days to maturity, plant height (cm), foot length (cm), number of primary branches per plant, number of secondary branches per plant, length of main shoot (cm), number of siliquae on main shoot, length of siliqua (cm), number of seeds per siliqua, thousand seed weight (g), maximum root length (cm), seed yield per plant (g) and stem hollowness. The combining ability analysis was carried out according to Kempthorne (1957). The percent heterosis over the better parent (heterobeltiosis) was calculated as deviation of F_1 value from the better parent. Genotypes utilized for generation of 21 crosses and their F_1 s were DRMR-15, DRMR-150-35, GM-3, TM 106 (ICAR-DRMR, Bharatpur), Pusa Kranti (ICAR-IARI, New Delhi), MCP 802, RH 932 (RARS, Shillongani) and testers viz., Pusa Bold (ICAR-IARI, New Delhi), TM-2, SEJ-2 (RARS, Shillongani).

Results and Discussion

Highly significant differences among parents and crosses except thousand seed weight were observed as was also reported by Singh *et al.* (2011). The variation due to parents vs. crosses was significant for foot length, number of primary branches per plant, number of secondary branches per plant, length of main shoot, siliqua length, maximum root length, thousand seed weight and seed yield per plant indicating the presence of average heterosis for these traits. Further, the combining ability variances for line x tester was significant for all the characters except thousand seed weight. Similar finding was obtained by Kang *et al.*, 2013.

The combining ability variance revealed that SCA variances were higher than GCA variances for all the traits studied reflecting the predominance of non-additive gene action for these traits. The dominance genetic variance (σ^2_D) was greater than additive genetic variance (σ^2_A) for all the characters except days to maturity and foot length indicating non-additive gene action playing greater role in the inheritance of these traits as shown in Table 2. Therefore, heterosis breeding and postponement of selection to later generations will be effective for all the traits except for days to maturity and foot length where simple selection could be done. Recurrent selection procedures would also be effective for improvement of these traits.

The estimates of GCA and SCA are presented in table 3 and table 4 respectively. Among the parents, DRMR-150-35 was a good general combiner for days to 50% flowering, days to maturity, plant height, foot length and number of seeds per siliqua. RH 932 also showed good GCA for number of secondary branches, length of main shoot, number of siliquae on main shoot, maximum root length

and seed yield per plant. TM-2 exhibited good GCA for days to 50% flowering, days to maturity, foot length, number of secondary branches, length of main shoot, number of siliquae on main shoot, number of seeds per siliqua and seed yield per plant. Therefore, these three parents viz. DRMR-150-35, RH-932 and TM-2 appeared to be good general combiners.

Among the crosses, DRMR 150-35 x Pusa Bold exhibited good SCA for 50% flowering, number of secondary branches, siliqua length and seed yield per plant. MCP 802 x SEJ-2 showed good SCA for number of seeds per siliqua and seed yield per plant. RH-932 x TM-2 was a good specific combiner for foot length, number of secondary branches, siliqua length, maximum root length and seed yield per plant. GM-3 x SEJ-2 was a good specific combiner for foot length, number of secondary branches, length of main shoot, number of seeds per siliqua and seed yield. Hence, DRMR 150-35 x Pusa Bold, MCP 802 x SEJ-2, RH 932 x TM-2 and GM-3 x SEJ-2 were the best specific combiners.

Most of the studies showed significant GCA and SCA effects for yield and its components, indicating both additive and non-additive gene actions were important in the inheritance of the traits. Similar observations were made by Singh *et al.* (2006), Sabaghnia *et al.* (2010), Turi *et al.* (2010), Parmar *et al.* (2011), Verma *et al.* (2011), Maurya *et al.* (2012), Yadava *et al.* (2012), Gami *et al.* (2013), Kang *et al.* (2013), Kumar *et al.* (2013), Meena *et al.* (2013), Singh *et al.* (2013) and Iqbal *et al.* (2014) with different experimental materials.

Significant negative heterosis is desirable for early flowering, early maturing, short and medium stature plant and reduced foot length in mustard. In the present study, negative better parent heterotic values for these traits were noted for two crosses viz. DRMR-15 x SEJ-2 and DRMR 150-35 x Pusa Bold as shown in table 5. The present findings are similar to the earlier report of Pourdad and Sachan (2003) who reported significant negative heterosis for days to 50% flowering and maturity and high negative heterosis for plant height in *Brassica napus*. Similarly, Nassimi *et al.* (2006) also obtained significant negative better-parent heterosis for maturity and plant height. Engquist and Becker (1991) found that rapeseed hybrids with earlier flowering and higher yields were slightly late maturing. Their report is similar to the present study for three crosses viz. MCP 802 x SEJ-2, RH 932 x TM-2 and GM-3 x SEJ-2 which showed significant positive heterosis for seed yield per plant but they exhibited positive heterosis for days to maturity. However, positive heterosis is desirable for remaining yield related traits

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

Source of Variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Foot length (cm)	Number of primary branches	Number of secondary branches	Length of main shoot (cm)	Number of Siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Maximum root length (cm)	Thousand seed weight (g)	Seed yield per plant (g)
Replication	1	7.81*	5.82	93.55	72.94	0.00	1.06	27.26	23.75	0.00	0.40*	0.18	0.25	3.44
Genotypes	30	18.29**	58.26**	586.35**	412.69**	1.29**	11.54**	175.10**	65.67**	0.22**	0.94**	23.02**	1.11**	24.90**
Parents	9	24.83**	74.8**	571.69**	404.72**	0.99**	6.55**	97.88**	24.63**	0.34**	0.49**	22.03**	2.52**	9.85**
Crosses	20	16.24**	53.46**	620.16**	425.47**	1.37**	13.57**	206.08**	87.28**	0.16**	1.19**	22.59**	0.43	28.77**
Parents vs crosses	1	0.38	5.35	42.01	229.08**	2.37**	15.84**	250.43**	2.74	0.26**	0.01	40.47**	2.07**	82.92**
Lines	6	21.65*	75.60**	886.13**	373.35**	2.29**	21.77**	348.83**	91.45**	0.11**	0.61**	56.57**	0.57*	37.82**
Testers	2	55.74**	262.78**	561.76**	170.11**	0.03	20.60**	309.74**	270.61**	0.49**	1.32**	12.36*	1.13**	44.14**
Lines x testers	12	6.96**	7.51*	496.90**	494.09**	1.14**	8.30**	117.43**	54.64**	0.13**	1.46**	7.30*	0.25	21.69**
Error	30	1.51	3.42	79.00	21.71	0.13	0.66	9.88	7.99	0.02	0.06	2.71	0.23	3.42

* Significant at P = 0.05; ** Significant at P = 0.01

Table 2: Estimates of components of variance for different characters in Indian mustard

Source of Variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Foot length (cm)	Number of primary branches	Number of secondary branches	Length of main shoot (cm)	Number of Siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Maximum root length (cm)	Thousand seed weight (g)	Seed yield per plant (g)
σ^2 GCA	0.36	1.79	4.81	-2.68	0.01	0.20	3.46	1.27	0.00	-0.01	0.60	0.01	0.29
σ^2 SCA	2.73	2.04	208.95	236.19	0.50	3.82	53.78	23.32	0.06	0.70	2.29	0.37	10.70
σ^2 A	0.72	3.59	9.63	-5.36	0.02	0.41	6.92	2.55	0.00	-0.02	1.19	0.03	0.58
σ^2 D	2.73	2.04	208.95	236.19	0.50	3.82	53.78	23.32	0.06	0.07	0.29	0.37	10.70
σ^2 A/ σ^2 D	0.26	1.76	0.05	-0.02	0.04	0.11	0.13	0.11	0.00	-0.03	4.1	0.08	0.05

* Significant at P0.05; ** Significant at P = 0.01

Table 3: Estimates of GCA effects for different characters in Indian mustard

Parents	Days to 50% flowering	Days to maturity	Plant height (cm)	Foot length (cm)	Number of primary branches	Number of secondary branches	Length of main shoot (cm)	Number of Siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Maximum root length (cm)	Thousand seed weight (g)	Seed yield per plant (g)
LinesDRMR-15	-0.45	0.57	-10.57**	0.44	-0.62**	-2.31**	3.02*	-0.55	-0.18**	-0.46**	1.80*	0.02	1.03
DRMR 150-35	-3.45**	-6.76**	-14.49**	-8.62**	-0.16	-0.23	-9.65**	-0.75	0.10	0.42**	-5.64**	0.21	0.92
Pusa Kranti	-0.29	-0.76	0.01	4.53*	-0.67**	-0.53	10.55**	0.08	0.08	0.20	1.92**	-0.32	-3.29**
MCP 802	-0.45	1.74*	-4.61	5.41**	-0.25	-1.84**	-7.91**	-4.44**	-0.09	-0.31**	-2.73**	-0.47*	-0.17
TM 106	0.88	-1.59*	-1.83	-13.23**	0.98**	3.39**	-1.63	0.80	0.18**	-0.13	1.60*	0.40**	-3.27**
RH932	1.05*	3.74**	20.42**	3.73	0.08	0.68*	8.01**	7.83**	0.04	0.02	2.77**	-0.01	3.73**
GM-3	2.71**	3.07**	11.08**	7.74**	0.64**	0.84*	-2.39	-2.97*	-0.13*	0.26*	0.29	0.39	0.71
SE±	0.50	0.75	3.63	1.90	0.14	0.33	1.28	1.15	0.05	0.10	0.67	0.20	0.76
CD(P=0.05)	1.02	1.53	7.41	3.88	0.28	0.67	2.61	2.35	0.10	2.14	1.37	0.41	1.55
CD(P=0.01)	1.37	2.06	9.98	5.22	0.38	0.91	3.52	3.16	0.14	0.27	1.84	0.55	2.09
Testers													
Pusa Bold	2.17**	5.00**	7.19**	3.2*	-0.02	-1.18**	-5.35**	-5.08**	0.21**	-0.03	0.81	0.27**	-1.76**
TM - 2	-1.76**	-2.36**	-4.77	-3.71**	0.05	1.24**	1.85*	2.55**	-0.07	0.32**	0.22	-0.29**	1.78**
SEJ-2	-0.40	-2.64**	-2.42	0.51	-0.03	-0.07	3.50**	2.52**	-0.14**	-0.29**	-1.03*	-0.07	0.15
SE±	0.33	0.49	2.37	1.24	0.09	0.22	0.84	0.75	0.03	0.07	0.44	0.13	-0.02
CD(P=0.05)	0.01	0.02	0.99	0.05	0.00	0.00	0.03	0.03	0.00	0.00	0.02	0.00	0.02
CD(P=0.01)	0.91	1.35	6.52	3.41	0.25	0.60	2.31	2.06	0.08	0.19	1.21	0.36	1.35

* Significant at P0.05; ** Significant at P = 0.01

Table 4: Estimates of SCA effects for different characters in Indian mustard

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Foot length (cm)	Number of primary branches	Number of secondary branches	Length of main shoot (cm)	Siliqua on main shoot	Number of Siliqua length (cm)	Number of seeds per siliqua	Maximum root length (cm)	Thousand seed weight (g)	Seed yield per plant (g)
DRMR-15 x Pusa Bold	2.67**	3.00*	11.71	-19.18**	0.34	0.73	5.21*	1.79	-0.01	0.02	0.76	0.05	0.99
DRMR-15 x TM-2	-0.90	-2.14	-11.43	10.67**	-0.54	0.21	1.66	0.42	0.15	-0.33	0.39	-0.03	-1.82
DRMR-15 x SEJ-2	-1.76	-0.86	-0.28	8.50*	0.20	-0.94	-6.87**	-2.21	-0.15	0.31	-1.16	0.27	0.83
DRMR150-35xPusa Bold	-2.83**	-0.17	8.38	-4.29	0.48	3.06**	-4.35	-1.02	0.31**	-0.06	1.61	-0.04	4.76**
DRMR 150-35 x TM-2	0.59	-0.81	1.81	-0.66	0.24	-1.40*	5.09*	6.97**	-0.13	1.65**	-2.02	0.06	-3.00*
DRMR 150-35 x SEJ-2	2.24*	0.98	-10.19	4.95	-0.72**	-1.65**	-0.74	-5.95**	-0.18	-1.60**	0.41	-0.02	-1.76
Pusa Kranti x Pusa Bold	-1.50	1.83	-32.39**	-8.01*	0.39	0.46	-5.84*	-3.25	0.28**	0.76**	1.06	0.09	0.80
Pusa Kranti x TM-2	1.43	-0.81	26.88**	16.51**	-0.38	-0.27	-0.69	2.90	-0.27**	-0.52**	0.57	0.18	0.90
Pusa Kranti x SEJ-2	0.07	-1.02	5.51	-8.50*	-0.01	-0.19	6.53**	0.35	-0.01	-0.24	-1.63	-0.26	-1.70
MCP 802 x Pusa Bold	1.17	-0.67	2.55	14.93**	0.07	-1.16	-1.78	-2.12	-0.18	-0.39*	-1.50	0.03	-3.65**
MCP 802 x TM-2	-0.90	0.19	-7.87	-8.30*	-0.44	0.34	2.86	1.05	0.04	-0.01	1.64	0.03	-0.81
MCP 802 x SEJ-2	-0.26	0.48	5.33	-6.63	0.37	0.82	-1.08	1.08	0.13	0.40*	-0.13	0.01	4.46**
TM 106 x Pusa bold	1.83*	0.67	-8.47	9.08**	-1.56**	-2.87**	-6.33**	-2.77	-0.41**	0.10	1.48	-0.04	1.60
TM 106 x TM-2	-1.74	0.52	-1.42	-19.51**	1.46**	1.20*	3.12	-5.50**	0.18	0.14	-1.93	0.22	-0.23
TM 106 x SEJ-2	-0.09	-1.19	9.89	10.43**	0.09	1.67**	3.21	8.26**	0.23*	-0.24	0.45	-0.18	-1.37
RH-932 x Pusa Bold	-1.33	-3.17*	10.10	15.95**	-0.13	-0.99	3.80	2.76	-0.02	-0.32	-2.87*	0.72*	-2.11
RH-932 x TM-2	1.59	2.69	2.79	-17.04**	0.06	2.46**	3.28	1.23	0.22*	-0.08	2.56*	-0.46	5.72**
RH-932 x SEJ-2	-0.26	0.48	-12.9	1.09	0.07	-1.47*	-7.09**	-4.00	-0.21*	0.40*	0.30	-0.63	-3.61**
GM-3 x Pusa bold	0.00	-1.50	8.13	-8.49*	0.41	0.78	9.28**	4.60*	0.01	-0.10	-0.54	-0.17	-2.39
GM-3 x TM-2	-0.07	0.36	-10.76	18.32**	-0.40	-2.54**	-15.31**	-7.08**	-0.19	-0.85**	-1.22	-0.50	-0.76
GM-3 x SEJ-2	0.07	1.14	2.63	-9.83**	-0.02	1.77**	6.03**	2.47	0.18	0.96**	1.76	0.03	3.15*
Mean	46.06	112.73	186.07	54.14	4.47	9.11	76.78	46.90	5.11	13.06	20.81	5.24	10.89
S.E. (S _y)	0.87	1.31	6.28	3.29	0.25	0.57	2.22	2.00	0.09	0.18	1.16	0.48	1.31
S.E.(g _i -g _j) line	0.71	1.07	5.13	2.69	0.20	0.47	1.81	1.63	0.08	0.15	0.95	0.28	1.07
S.E.(g _i -g _j) tester	0.46	0.70	3.36	1.76	0.13	0.31	1.19	1.07	0.05	0.10	0.62	0.18	0.70
S.E. (S _{ij} - S _{kl})	1.23	1.85	8.89	4.66	0.35	0.81	3.14	2.83	0.13	0.26	1.65	0.48	1.85

* Significant at P0.05; ** Significant at P = 0.01

Table 5: Percent heterosis over better parent in Indian mustard

Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Foot length (cm)	Number of primary branches	Number of secondary branches	Length of main shoot (cm)	Number of Siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Maximum root length (cm)	Thousand seed weight (g)	Seed yield per plant (g)
DRMR-15 x Pusa Bold	2.02	0.83	-0.60	-41.89**	9.27	-31.63**	8.35	-12.73*	-8.55**	-5.01*	36.27**	-17.65*	24.73
DRMR-15 x TM-2	-10.41**	-8.79**	-12.52*	6.69	0.00	32.31*	7.08	-0.07	-4.16	-5.50*	42.01**	-12.13	-0.39
DRMR-15 x SEJ-2	-9.37**	-7.95**	-8.47	-6.28	-17.28*	-42.85**	20.13**	-5.45	-11.44**	-4.28*	13.62	4.97	88.67**
DRMR 150-35 x Pusa Bold	-15.15**	-7.88**	-4.30**	-32.80**	24.52*	13.26	-24.51**	-15.06*	1.85	1.02	-23.75**	-16.18*	64.10**
DRMR 150-35 x TM-2	1.22	-0.48	5.63	-29.45**	27.97**	11.91	-4.61	17.93**	0.49	16.58**	-41.47**	-2.40	-10.38
DRMR 150-35 x SEJ-2	3.49	-6.28**	-15.77**	-25.27**	-26.51**	-30.13**	-8.52*	-9.76	-0.90	-10.77**	-36.53**	1.93	36.45
Pusa Kranti x Pusa Bold	-7.92**	-1.24	-17.69**	-25.19**	9.27	-16.33	3.64	-17.62**	0.976	5.54**	9.87	-22.06**	-23.66
Pusa Kranti x TM-2	-9.90**	-1.80**	24.26**	-0.12	0.00	52.31**	13.63**	15.82*	-3.25	-1.51	5.19	54.30**	-12.71
Pusa Kranti x SEJ-2	-9.90**	-2.69	0.17	-29.72**	-22.54**	-19.28*	44.69**	5.26	0.29	-2.04	-9.92	-9.06	-5.67
MCP 802 x Pusa Bold	-1.01	-1.24	-2.92	19.04	-2.22	-48.15**	-20.75**	-28.48**	-10.13**	-7.01**	-12.89	-26.03**	-24.78
MCP 802 x TM-2	-7.53**	3.69*	-14.25**	-18.12*	-11.89	-9.49	-5.89	-6.67	0.19	-1.51	-0.48	-5.27	-8.48
MCP 802 x SEJ-2	-3.22	0.89	-6.38**	-21.57**	-6.65	-22.08**	-8.76*	-6.67	0.49**	5.45*	-15.17	-6.94	35.18*
TM 106 x Pusa bold	3.03	-2.90	-6.43	-19.14*	-14.89	-10.20	-21.7**	-15.07*	-9.34**	-4.41*	39.12**	-16.99	-26.03
TM 106 x TM-2	-2.25	-3.95*	-5.90	-23.96**	51.06**	88.89**	-1.63	3.69	8.45**	-1.47	26.96*	26.47*	-21.29
TM 106 x SEJ-2	4.49	-5.70**	1.29	-23.96**	12.21	34.61**	0.48	23.43**	12.07**	-8.82**	21.26*	6.51	-32.71
RH-932 x Pusa bold	-3.03	-1.66	9.83*	-5.168	-3.51	-18.72**	13.12**	11.60	-4.93*	-6.36**	9.25	-2.11	0.33
RH-932 x TM-2	-1.05	3.08	0.40	-55.16**	2.13	75.13**	15.44**	38.69**	0.472	-1.98	33.23**	-28.73*	79.07**
RH-932x SEJ-2	-2.10	0.88	-6.14**	-27.15**	-5.96	-19.89*	19.49**	12.42*	-9.00**	-2.94	15.83	-10.11	7.15
GM-3 x Pusa bold	3.03	-0.83	5.56	-16.82	10.49	-4.21	0.70	-17.01**	-7.49**	-0.49	-10.60	-16.03**	-15.05
GM-3 x TM-2	-3.09	-3.39*	-9.72**	33.18**	-3.92	-12.92	-21.28**	-24.72**	-8.44**	-3.50	-15.74*	5.66	5.43
GM-3xSEJ-2	00.0	2.69	-1.92	-22.88**	1.96	11.78	7.784	-6.60	-2.69	6.06**	-8.73	3.38	86.90**

* Significant at P = 0.05; ** Significant at P = 0.01

such as number of primary branches per plant, number of secondary branches per plant, length of main shoot, number of seeds per siliqua, siliqua length, number of seeds per siliqua, maximum root length, thousand seed weight and seed yield per plant.

DRMR 150-35 x Pusa bold showed positive better parent heterosis for number of primary branches per plant, number of secondary branches per plant, siliqua length and number of seeds per siliqua while DRMR-15 x SEJ-2 showed positive better parent heterosis for length of main shoot, maximum root length and thousand seed weight. The results of this study are similar to earlier findings of Nassimi *et al.* (2006) who reported significant positive heterosis for number of branches per plant in *Brassica napus* genotypes. Satwinder *et al.* (2000) also reported that F₁ generations expressed significant heterosis for number of primary branches, number of seeds per siliqua. Meena *et al.* (2014) found significant positive heterobeltiosis and standard heterosis for seed yield in Indian mustard for various crosses. Similarly, Jorgensen *et al.* (1995) also found high positive heterosis for primary and secondary branches and other yield contributing traits. Therefore, DRMR-15 x SEJ-2, DRMR 150-35 x Pusa Bold, MCP 802 x SEJ-2, RH-932 x TM-2 and GM-3 x SEJ-2 may be used for developing high yielding genotypes by improving the other component traits related to seed yield.

Conclusion

Based on mean performance and GCA effects, the most promising parents were DRMR 150-35, TM-2 and RH-932 and based on SCA effects and heterosis, DRMR 150-35 x Pusa Bold, MCP 802 x SEJ-2, RH 932 x TM-2 and GM-3 x SEJ-2 were the most potential crosses.

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