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Estimation of combining ability and heterosis for yield and yield attributing traits in Indian mustard (*Brassica juncea*)

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ABSTRACT

Indian mustard [*Brassica juncea* (L) Czern. and Coss.] is an important oilseed crop which occupies leading position in oilseed sector of Indian agriculture. Development of high yielding genotypes with high oil content in Indian mustard has been a major breeding objective owing to high edible oil import in India. Present study was conducted with a set of 53 genotypes, that included 40 crosses and 13 parents evaluated for pooled estimation of combining ability and heterosis for yield and yield attributing traits during *rabi* 2014-15 under timely sown, late sown and extra late sown environmental conditions. The crosses were developed in line × tester design involving 8 lines and 5 testers during *rabi* 2013-14. The genotype × environment interaction was significant for almost all the traits studied indicating differential response of genotypes to the change in environments. The pooled analysis of variance over environments revealed sufficient differences among environments, parents, hybrids and parent vs. hybrids for most of the traits studied. Importance of both additive and non-additive types of gene actions was observed for seed yield and yield attributing traits. Estimates of GCA effects indicated that NRCHB-101, Pusa Bold and RGN-73 were good general combiners for seed yield/plant and yield attributing traits, i.e. 1000-seed weight, siliqua length, number of primary branches and number of secondary branches. The parent, Pusa Mustard-25 showed good combining ability for dwarfness and early maturity. The hybrids, viz. NRCHB-101 × EC552577, NRCHB-101 × BPR543-2, Pusa Mustard-25 × EC552577, BAUM-2007 × EC552577 and BAUSM 92-1-1 × RGN-73 had significantly high SCA effects, >15% heterobeltiosis and high *per se* performances for seed yield per plant. The parents showing good combining ability would be identified as promising genotypes and the hybrids having high SCA effects with high heterobeltiosis could give transgressive segregants for seed yield and yield attributing traits under different sowing conditions.

Key words: General combining ability, Heterobeltiosis, Indian mustard, Pooled analysis, Seed yield, Specific combining ability

Currently, Indian mustard [*Brassica juncea* (L.) Czern and Coss] is the 2nd most important oilseed crop in India after soybean in terms of production, while, it ranks 1st in terms of oil yield among all oilseeds crops due to more oil content ranging from 35-45% (Anonymous 2015a). In India, rapeseed–mustard is grown in diverse agro-climatic conditions ranging from north-eastern/north-western hills to down south under irrigated/rainfed, timely/late sown and mixed cropping. Indian mustard accounts for about 75-80% of the 5.79 million ha under these crops in the country during 2014-15. It is an important edible oil yielding crop in India. The major mustard producing states include Rajasthan, Uttar Pradesh and Haryana contributing about 70% of total production with productivity of 1243 kg/ha, 1162 kg/ha and 1639 kg/ha, respectively. However, productivity of rapeseed-mustard in minor mustard producing state like Jharkhand is 690 kg/ha only (Anonymous 2014). This poor productivity or yield loss to the tune of 30-40 percent is linked to the poor crop management practices, mainly due to delayed sowing of the crop, deficit of time after harvesting of long-duration previous rice crop. In the present era of high edible oil import of 7.95 mt worth ₹ 440 billion in the year 2013-2014 (Anonymous 2015b) in India, there is an urgent need to increase productivity of crop in the minor mustard producing states also. Improvement of Indian mustard for both productivity and oil quality are essential to meet the demands of the national as well as the international markets. Seed yield of Indian mustard is a quantitative trait that is largely influenced by the different environmental factors and hence in most of the cases it has low heritability (Rameeh 2010). Under such a situation, heterosis breeding approach

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studied in pooled over environments created by sowing of parents and crosses on different dates can be one of the suitable options for breaking the present yield barrier. The heterosis breeding needs testing of the genetic value of parental lines for production of superior recombinants. The line × tester mating design (Kempthorne 1957) has been extensively used in Indian mustard to analyze the combining ability effects and to provide information regarding genetic mechanisms controlling seed yield and yield attributing traits (Parmar *et al.* 2011, Yadava *et al.* 2012, Singh *et al.* 2013, Meena *et al.* 2015). Knowledge of gene action and estimation of general and specific combining ability effects (GCA and SCA) are important parameters, as they provide an essential tool to the breeders in selection of better parental combinations for further improvement in rapeseed-mustard crops. Therefore it becomes imperative to study combining ability of locally grown cultivars along with nationally grown varieties, so that suitable parental lines can be developed and specific combiners if any can be identified. Further, it would be more informative, if level of heterosis between nationally recommended and locally grown genotypes can be accessed.

MATERIALS AND METHODS

The experimental materials used in the present study comprised 13 diverse parents of Indian mustard including 8 lines, viz. NRCHB-101 (BL-4 × Pusa Bold), NRCDR-02 (MDOC-43 × NBPGR-36), Kranti (Selection from Varuna), Pusa Bold (Varuna × BIC-1780), Shivani (Derived from local selection), Pusa Mustard-25 (SEJ-8 × Pusa Jagannath), BAUSM-92-1-1 (Pusa Barani × RCC-4), BAUM 2007 (Bio-902 × Laxmi) and 5 testers, viz. Pusa Mustard-21 (Pusa Bold × Zem-2), Heera (ZYR-4 × BJ-1058), EC552577 (Exotic line from Australia), RGN-73 (RGN-8 × Pusa Bold) and BPR 543-2 (TM-2 × PCR-9202) crossed in line × tester mating design at Birsa Agricultural University, Ranchi during *rabi* 2013-14. The 40 crosses along with 13 parents were evaluated during *rabi* 2014-15 in randomized block design with two replications under three different dates of sowing, viz. 21 October (timely sown condition), 6 November (late sown condition) and 21 November (extra late sown condition) in order to maximize the yield in different sowing conditions. Each treatment was raised in a single row of 5 m length kept at a distance of 30 cm between rows and 15 cm between plants. Standard agronomic practices were followed to raise the crop (N:P:K:S::80:40:40:40 kg/ha; four irrigations including pre sowing). Observations were recorded on randomly selected five competitive plants for thirteen quantitative traits, i.e. seed yield/plant (g), plant height (cm), point to first branch (cm), point to first siliqua (cm), main shoot length (cm), number of primary branches, number of secondary branches, number of siliquae on main shoot, siliqua length (cm), number of seeds/siliqua, 1000-seed weight (g), days to 50% flowering and days to maturity. The mean values were used for the analysis of variance. Data were first subjected to the usual analysis followed for a randomized block design for individual environment as suggested by Panse and Sukhatme (1967). The combining ability analysis was carried out as per Kempthorne (1957). The per cent heterosis over better parent (heterobeltiosis) was calculated as deviation of F_1 value from better parent.

RESULTS AND DISCUSSION

The present study was, thus, undertaken to determine type of gene action, general and specific combining ability of parental lines and heterobeltiosis of the cross combinations as some of the lines taken for conducting this study are locally recommended genotypes and their crosses, sown under three dates of sowing, i.e. timely, late and extra late conditions. The genotype × environment interactions was significant for most of the traits studied, indicating differential response of genotypes to the change in environments. The pooled analysis over the environments (Table 1) revealed significant differences between genotypes, the parents and crosses interacted differentially for the traits under study in different environments. The crosses interacted more markedly with environments, thereby, suggesting that hybrids did not have the same relative performance across different sowing times. The mean squares due to lines, testers and line × tester were significant for all the traits under study suggesting that the experimental material possessed considerable variability. Similar observations had also been recorded by Tomar *et al*. (2017). The significant mean square due to parents and their crosses, revealed that both *GCA* and *SCA* were involved in genetic expression of the traits under study. Moreover, the significant variance due to hybrids indicated that sufficient amount of genetic variability was generated during recombination in the crosses. The variation due to parents vs. hybrids was also significant for all the traits studied indicating that the hybrids differed from the parents up to considerable extent for these traits. The interaction due to line × tester were significant for all the traits studied, suggesting significant contribution due to *SCA* effects towards the variation among crosses. The results were in accordance with the studies conducted by Parmar *et al*. (2011) and Yadava *et al*. (2012) in Indian mustard with different set of materials.

The significant interaction of parents and crosses with environments for most of the traits revealed that the alleles controlling the *GCA* and *SCA* behaved differently in the environments tested. The interaction effects of crosses × environments were significant for all the traits studied except point to first siliqua, main shoot length, number of siliquae on main shoot and siliqua length indicated that the *SCA* effects of hybrids were interacted with the environments. Similar interactions over the environments had also been reported by Mahto and Haider (2004), Sabaghnia *et al.* (2010) and Parmar *et al.* (2011) in Indian mustard. The relative estimates of variances due to *SCA* were higher than *GCA* variances in pooled over environments for seed yield/plant, number of primary branches, number of secondary branches, number of seeds/siliqua, days to 50% flowering and days to maturity, reflecting the predominance of non-additive gene action for these traits. On the other hand, *GCA*

Table 1 Pooled ANOVA for parents and hybrids for thirteen characters of seed yield and its components traits in Indian mustard genotypes

Sources	DF	Seed yield/plant (g)	Plant height (cm)	Point to first branch (cm)	Point to first siliqua (cm)	Main shoot length (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds/ siliqua	1000 – seed weight (g)	Days to 50% flowering	Days to maturity
Replicates	1	0.65	0.01	0.00	253.81*	134.23	0.00	0.59	0.35	0.01	0.26	0.01	4.08	0.11
Environments	2	71.87**	868.40**	1268.54**	1351.83**	173.42*	5.41**	3.99**	1317.08**	0.11	17.09**	10.76**	600.46**	6599.45**
Rep. × Env.	2	0.04	209.44	2.79	32.38	64.20	0.03	0.15	8.03	0.00	0.44	0.02	2.29	0.58
Genotypes	52	3.49**	634.79**	171.41**	206.51**	181.46**	1.16**	7.18**	194.45**	0.47**	1.26**	1.88**	29.56**	21.40**
Parents	12	4.44**	353.45**	185.44**	207.46**	118.79*	1.15**	6.82**	123.06**	0.93**	3.20**	3.58**	57.59**	71.43**
Parents vs Crosses	1	20.66**	6162.17**	67.75	643.32**	1712.96**	14.07**	47.62**	1795.25**	0.02	2.76**	2.07**	5.48	44.09**
Crosses	39	2.76**	579.63**	169.76**	195.02**	161.47**	0.83**	6.26**	175.37**	0.34**	0.63**	1.35**	21.55**	5.42**
Line	7	2.27*	265.57**	84.99**	120.97*	122.88*	0.67**	4.75**	98.62*	0.58**	3.40**	2.61**	60.78**	62.97**
Tester	4	7.80**	420.66**	227.91**	215.94**	117.63	1.23**	10.11**	95.71*	0.98**	3.36**	2.37**	12.38	14.22**
L × T	1	6.23**	699.78**	718.66**	779.00**	94.85	4.27**	8.18**	403.49**	3.15**	1.13	15.17**	216.04**	359.45**
Env. × Gen.	104	2.31**	149.96**	74.73**	63.14	56.94	0.38**	3.24**	59.09**	0.07	0.58**	0.29**	7.32*	7.58**
Env. × Parents	24	1.23	170.31*	107.89**	69.01	49.94	0.38	2.47**	99.83**	0.09	0.89**	0.42**	6.18	14.26**
Env. × P vs C	2	1.17	169.91	12.25	20.63	32.01	0.47	3.96**	60.37	0.00	0.18	0.55**	5.95	12.40**
Env. × Crosses	78	2.67**	143.19*	66.13**	62.42	59.73	0.38**	3.46**	46.52	0.07	0.49*	0.25**	7.70*	5.41**
Env. × Lines	14	0.87	104.47	91.85**	49.81	47.94	0.22	1.62**	43.25	0.08	1.02**	0.31**	7.77	7.78**
Env. × Testers	8	1.38	206.14*	120.47**	106.94*	47.18	0.57*	2.83**	181.60**	0.11	0.68	0.62**	4.78	3.87*
Env. × L × T	56	2.26**	117.77	64.69**	51.80	51.57	0.38*	3.37**	38.39	0.07	0.50*	0.22**	5.64	4.24**
Error	156	0.90	95.63	24.34	53.38	52.21	0.24	0.35	36.44	0.10	0.35	0.02	5.29	1.58
Total	317	2.23	207.19	72.64	90.39	76.06	0.47	2.44	77.58	0.15	0.68	0.48	13.67	48.41
σ^2 GCA		0.07	50.14	13.81	14.85	11.36	0.03	0.17	15.41	0.03	0.02	0.13	0.99	0.15
σ^2 SCA		0.19	12.65	6.99	3.48	4.87	0.04	0.85	2.69	-0.01	0.04	0.04	1.49	0.62
σ^2 GCA/σ^2 SCA		0.37	3.96	1.98	4.27	2.33	0.75	0.2	5.73	3	0.5	3.25	3	0.5

**,*Significant at P=0.01 and P=0.05, respectively.

variances were higher than the *SCA* variances in pooled over environments, for plant height, point to first branch, point to first siliqua, main shoot length, number of siliquae on main shoot, siliqua length and 1000-seed weight, thereby, indicating that these traits are governed by the additive gene action. Since yield attributing traits are governed by both additive and non-additive gene actions, therefore, genetic improvement for these traits can be achieved by hybridization followed by selection. Importance of both additive and non-additive gene action in controlling yield attributing traits in Indian mustard had also been reported by Yadava *et al.* (2012) and Patel *et al*. (2012). The magnitude and direction of combining ability effects are known to be useful in selecting parent plants in crop improvement programs (Mather and Jinks 1971). The pooled estimates of *GCA* effects (Table 2) of the parents revealed that the lines NRCHB-101 and Pusa Bold were good general combiners exhibiting significant positive *GCA* effects for seed yield/plant and yield contributing traits like 1000-seed weight, siliqua length, number of primary branches and number of secondary branches. The line, NRCHB-101 also possessed favorable allele for short plant height and point to first branching by recording significant *GCA* effects in negative direction. The line, Pusa Mustard-25 showed negative significant *GCA* effects for days to 50% flowering and days to maturity along with plant height, point to first branch and point to first siliqua indicating its usefulness in breeding for early maturing dwarf type hybrids. Among the testers, RGN-73 was the best general combiner exhibiting significant positive *GCA* effects for seed yield/plant and 1000-seed weight. It also possessed favorable genes for early flowering and dwarf plant type by recording highly significant negative *gca* effects for days to 50% flowering, plant height, point to first branch and point to first siliqua. Negative GCA values for these characters were also observed by Gupta *et al*. (2011) in Indian mustard. The tester, Heera possessed highly significant positive *GCA* effects for main shoot length, number of primary branches and number of secondary branches and number of siliquae on main shoot, however, it showed highly significant negative *GCA* effects for 1000-seed weight resulting into reduced seed size in the hybrids. All the testers except Heera showed highly significant and positive *GCA* effects for 1000-seed weight, which is reflected in the hybrids developed using these genotypes as one of the parents. Thus, NRCHB-101 and RGN-73 were proved to be good general combiners under study, complimenting good traits like high seed yield/plant, reduced plant height, reduced point to first branch and improved 1000-seed weight in the hybrids. These parents can be included in breeding progamme for yield improvement. Similar findings had also been reported by Singh *et al.* (2005), Singh *et al*. (2013) and Meena *et al.* (2015) in Indian mustard with different set of materials.

A total of six crosses, viz. NRCHB-101 × BPR 543-2, NRCHB-101 × EC552577, NRCHB-101 × RGN-73, BAUSM 92-1-1 × RGN-73, Pusa Mustard-25 × EC552577, BAUM-2007 × EC552577 were identified as good specific combiners for seed yield/plant (Table 3). The crosses with positive *SCA* effect for seed yield/plant also showed significant positive *SCA* effects for other yield contributing traits like, number of primary branches, number of secondary branches, number of siliquae on main shoot, siliqua length and 1000-seed weight. High *SCA* effects for seed yield/plant using line × tester analysis had also been reported earlier (Yadava *et al*. 2012, Singh *et al*. 2013 and Singh *et al*. 2015).

The crosses, viz. NRCHB-101 × RGN-73, NRCHB-101 × EC552577, NRCHB-101 × BPR 543-2 and Pusa Bold × RGN-73 involved parents with high × high *GCA* effects for 1000-seed weight indicating additive × additive type of gene action. This indicated that selection could be effective in F_2 generation that could be utilized in transgressive breeding. The cross, Pusa Bold × RGN-73 showed significant negative *SCA* effect, which is desirable for plant height, point to first branch and point to first siliqua, involving low × high combination of parental *GCA* effects, indicating possibility of interaction between favourable alleles from good combiner and unfavorable alleles from poor combiner. The crosses, Pusa Bold × BPR 543-2, Shivani × Heera, BAUSM 92-1-1 × EC552577, BAUM-2007 × Pusa Mustard-21, BAUM-2007 × RGN-73 and BAUSM 92-1-1 × Heera exhibited significant negative *SCA* effect for earliness, involving poor general combiner parents, indicating over dominance and epistatic interaction. A number of hybrids, viz. 4 hybrids for number of primary branches, 10 hybrids for number of secondary branches, 9 hybrids for 1000-seed weight, 2 hybrids for number of siliquae on main shoot and number of seeds/siliqua showed significant positive *SCA* effects. The outcomes clearly indicated that parents involved in these crosses were good specific combiners and also the relative contribution of parents to *SCA* effect for seed yield/plant is through various yield contributing traits. Similar findings had also been reported by Swarankar *et al.* (2002), Yadava *et al.* (2012) and Gami and Chuahan (2013).

The pooled estimates of heterobeltiosis along with mean seed yield/plant indicated that out of 40 hybrids evaluated in this study, 5 hybrids, viz. Pusa Mustard-25 × EC552577 (30.18%), BAUM-2007 × EC552577 (29.47%), NRCHB-101 × BPR 543-2 (28.83%), NRCHB-101 × EC552577 (28.68%) and BAUSM 92-1-1 × RGN-73 (25.86%) exhibited > 15 % heterobeltiosis, highly significant *SCA* effects and higher *per se* performance (Table 4). Yadava *et al*. (2012) reported heterobeltiosis for seed yield/plant to the extent of 15.91 to 54.38% in 10 crosses. Heterobeltiosis of >15% for seed yield/plant with highly significant SCA effects and higher *per se* performance was also reported by Singh *et al.* (2015). These cross combinations can be exploited through heterosis breeding or these can be advanced in generation to find desirable transgressive segregants in segregating generations. The intermating between the selected segregants in advanced generation can accumulate favourable and desirable alleles for further improvement in seed yield and yield contributing traits.The parents showing good combining ability and the hybrids having high SCA effects with high heterobeltiosis in pooled analysis would be

Table 2 Estimates for *GCA* effects (pooled) of line and testers for thirteen seed yield and its components traits in Indian mustard

Parents	Seed yield/ plant (g)	Plant height (cm)	Point to first branch (cm)	Point to first siliqua (cm)	Main shoot length (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds/ siliqua	1000 – seed weight (g)	Days to 50% flowering	Days to maturity
Lines													
NRCHB-101	0.46*	-4.85**	-2.24*	-2.35	0.58	0.47**	0.85**	-1.09	0.25**	0.10	0.22**	-0.63	-0.02
NRCDR-02	-0.60**	-0.39	2.56**	2.46	-2.80*	-0.02	-0.84**	-2.54*	0.09	0.01	0.26**	0.17	0.72**
Pusa Bold	0.74**	6.14**	0.63	2.98*	-0.58	0.35**	0.77**	-0.99	0.11*	0.11	0.33**	1.00*	0.58**
Shivani	0.01	3.04	1.32	0.98	1.15	0.14	0.66**	2.39*	-0.10	-0.01	-0.37**	0.77	-0.22
Pusa M-25	-0.15	-5.57**	-2.50**	-4.11**	0.13	0.00	-0.03	-0.65	-0.10	0.04	-0.01	-1.43**	-0.48*
KRANTI	-0.21	1.19	1.06	-0.47	0.04	0.15	-0.17	2.05	-0.15**	0.14	-0.14**	0.67	-0.18
BAUSM-92-1-1	-0.30	1.68	0.54	0.99	-0.22	-0.08	0.00	-0.93	-0.01	-0.18	-0.07*	0.17	-0.35
BAUM-2007	0.05	-1.24	-1.38	-0.49	1.70	-0.07	0.46**	1.76	-0.10	-0.21*	-0.22**	-0.70	-0.05
S E ±	0.19	1.79	0.88	1.32	1.28	0.08	0.11	1.09	0.05	0.10	0.03	0.45	0.20
CD (*P*=0.05)	0.37	3.54	1.74	2.61	2.53	0.17	0.22	2.16	0.11	0.20	0.06	0.88	0.40
CD (*P*=0.01)	0.49	4.68	2.31	3.45	3.35	0.22	0.30	2.85	0.14	0.27	0.07	1.17	0.53
Testers													
Pusa M-21	-0.15	2.34	3.44**	3.43**	-2.74**	0.16*	-0.08	-3.58**	0.19**	-0.06	0.20**	0.40	-0.31
Heera	-0.09	13.57**	5.99**	6.66**	6.26**	0.24**	0.24**	8.49**	-0.27**	0.21*	-0.71**	1.75**	0.63**
RGN-73	0.34*	-5.65**	-2.99**	-2.74**	-3.08**	-0.03	0.07	-2.58**	0.05	0.12	0.06**	-1.31**	-0.27
BPR 543-2	-0.15	-8.97**	-1.21	-3.21**	-3.46**	-0.22**	-0.35**	-2.52**	0.15**	-0.03	0.35**	-0.83*	-0.29
EC552577	0.05	-1.29	-5.23**	-4.13**	3.03**	-0.14*	0.12	0.19	-0.13**	-0.24**	0.10**	-0.02	0.25
S E ±	0.15	1.41	0.70	1.04	1.01	0.07	0.09	0.86	0.04	0.08	0.02	0.35	0.16
CD (*P*=0.05)	0.29	2.80	1.38	2.06	2.00	0.13	0.18	1.71	0.09	0.16	0.04	0.70	0.32
CD (*P*=0.01)	0.38	3.70	1.82	2.73	2.65	0.17	0.23	2.26	0.11	0.21	0.06	0.93	0.42

**,*Significant at *P*=0.01 and *P*=0.05, respectively.

Table 3 Crosses of Indian mustard genotypes with significant *SCA* effects for thirteen seed yield and its components traits

Character	Crosses
Seed yield/plant (g)	NRCHB-101 × BPR 543-2 (1.29**), NRCHB-101 × EC552577 (1.08*), NRCHB-101 × RGN-73 (0.86*), BAUSM 92-1-1 × RGN-73 (0.84*), Pusa Mustard-25 × EC552577 (1.27**), BAUM-2007 × EC552577 (1.26**)
Plant height (cm)	Pusa Bold × RGN-73 (-5.39*)
Point to first branch (cm)	NRCHB-101 × EC552577 (-6.07**), Pusa Bold × RGN-73 (-5.18**)
Point to first siliqua (cm)	Pusa Bold × RGN-73 (-5.03*)
Main shoot length (cm)	BAUSM92-1-1 × EC552577 (8.56**)
Number of primary branches	NRCHB-101 × EC552577 (0.37*), NRCDR-02 × BPR 543-2 (0.37*), Pusa Mustard-25 × Heera (0.40*), BAUM-2007 × RGN-73 (0.59**)
Number of secondary branches	NRCHB-101 × BPR 543-2 (1.55**), NRCHB-101 × EC552577 (0.71**), NRCDR-02 × Pusa Mustard-21 (0.72**), Pusa Bold × Pusa Mustard-21 (1.50**), Shivani × EC552577 (0.76**), Pusa Mustard-25 × Heera (1.75**), Kranti × Pusa Mustard-21 (1.18**), BAUSM 92-1-1 × Pusa Mustard-21 (0.64*), BAUM-2007 × RGN-73 (0.98**), BAUM-2007 × EC552577 (1.11**)
Number of siliquae on main shoot	Kranti × BPR 543-2 (6.22*), BAUSM 92-1-1 × RGN-73 (4.96*)
Siliqua length (cm)	NRCHB-101 × BPR 543-2 (0.53*)
Number of seeds/siliqua	Pusa Bold × Pusa Mustard-21 (0.56*), Kranti × Heera (0.54*)
1000 – seed weight (g)	NRCHB-101 × BPR 543-2 (0.25**), NRCHB-101 × EC552577 (0.20**), Pusa Bold × RGN-73 (0.18**), Shivani × BPR543-2 (0.26**), Pusa Mustard-25 × Pusa Mustard-21 (0.37**), Pusa Mustard-25 × RGN-73 (0.16*), Kranti × RGN-73 (0.19*), BAUSM 92-1-1 × RGN-73 (0.13*), BAUM-2007 × RGN-73 (0.13*)
Days to 50% flowering	Pusa Mustard-25 × RGN-73 (-2.49*), BAUSM 92-1-1 × Heera (-2.02*), BAUM-2007 × RGN-73 (-3.78*)
Days to maturity	Pusa Mustard-25 × RGN-73 (-0.89*), Pusa Mustard-25 × Heera (-1.06*), Pusa Bold × BPR 543-2 (-1.04*), Shivani × Heera (-0.99*), BAUSM 92-1-1 × EC552577 (-1.15*), BAUM-2007 × Pusa Mustard-21 (-1.05*), BAUM-2007 × RGN-73 (-1.76**), BAUSM 92-1-1 × Heera (-0.98*)

**,*Significant at *P*=0.01 and *P*=0.05, respectively.

Table 4 Mean performance and estimates of heterobeltiosis for seed yield/plant in Indian mustard genotypes

Line	Testers					Mean seed yield of lines (g)
	Pusa Mustard-21	Heera	RGN-73	BPR 543-2	EC552577	
NRCHB-101	5.71 (-4.12)	5.56 (-6.30)	5.98 (0.82)	7.64 (28.83**)	7.63 (28.68**)	5.93
NRCDR-02	5.52 (-7.25)	5.24 (-10.61)	5.63 (-3.87)	5.49 (-7.56)	5.36 (-8.51)	5.86
Pusa Bold	7.26 (4.81)	6.73(-2.91)	6.74 (-2.67)	6.70 (-3.23)	6.48 (-6.47)	6.93
Shivani	5.53 (-7.06)	6.33 (8.63)	6.47 (10.83)	6.14 (3.54)	5.80 (-0.57)	5.83
Pusa Mustard-25	5.32 (-10.67)	6.16 (20.90)	6.41 (16.58)	4.93 (-17.00)	6.64 (30.18**)	5.10
Kranti	5.88 (-1.26)	05.98 (11.12)	6.43 (16.97)	5.84 (-1.69)	5.03 (-6.57)	5.38
BAUSM-92-1-1	5.76 (-3.16)	5.85 (9.15)	6.92 (25.86*)	4.86 (-18.07)	5.33 (-0.59)	5.36
BAUM-2007	6.17 (3.64)	5.77 (15.14)	6.46 (17.43)	5.59 (-5.84)	6.49 (29.47*)	5.01
Mean seed yield of testers (g)	5.95	3.21	5.50	5.93	4.87	

Values in parentheses represent heterobeltiosis (better parent heterosis).

identified as promising genotypes for seed yield and yield component traits in different dates of sowing to overcome the yield barrier generated due to delayed sowing of Indian mustard in minor mustard producing state like Jharkhand.

REFERENCES

Anonymous. 2014. *Agricultural Statistics at a Glance 2014*, Government of India. Oxford University Press, New Delhi.

Anonymous. 2015a. *Vision 2050*. ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan.

Anonymous. 2015b. *Pocket Book of Agricultural Statistics 2015*. Government of India.

Gami A and Chauhan R M. 2013. Heterosis and combining ability analysis for seed yield and its attributes in Indian mustard [*Brassica juncea* (l.) Czern & Coss.]. *Indian Journal of Agricultural Research* **47**(6): 535–9.

Gupta P, Chaudhary H B and Lal S K. 2011. Heterosis and combining ability analysis for yield and its components in Indian mustard (*Brassica juncea* L. Czern. & Coss*.). Academic*

Journal of Plant Sciences **4**(2): 45–52.

Kempthorne O. 1957. *An Introduction to Genetic Statistics*. John Wiley and Sons. Inc, New York.

Mahto J L and Haider Z A. 2004. Heterosis in Indian mustard (*Brassica juncea* L. Czern. & Coss.). *Journal of Tropical Agriculture* **42**(1–2): 39–41.

Mather K and Jinks J L. 1971. *Biometrical Genetics*. Chapman and Hall, London.

Meena H S, Kumar A, Ram Bhagirath, Singh V V, Meena P D, Singh B K and Singh D. 2015. Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassica juncea* L.). *Journal of Agricultural Science and Technology* **17**: 1861–71.

Panse V C and Sukhatme P V. 1967. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi.

Parmar S A, Jaimini S N and Ram B. 2011. Combining ability analysis for seed yield and its components over environments in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica* **2**: 61–6.

Patel A M, Prajapati D B and Patel D G. 2012. Heterosis and combining ability studies in Indian mustard (*Brassica Juncea* L.). *Indian Journal of Scientific Research and Technology* **1**(1): 38–40.

Rameeh V. 2010. Combining ability and factor analysis in F_2 diallel crosses of rapeseed varieties. *Plant Breeding and Seed Science* **62**: 73–83.

Sabaghnia N, Dehghani H, Alizadeh B and Mohghaddam M. 2010. Heterosis and combining ability analysis for oil yield and its components in rapeseed. *Australian Journal of Crop Sciences* **4**(6): 390–7.

Singh A, Avtar R, Singh D, Sangwan O, Thakral N K, Malik V S, Goyat B and Dalal U. 2013. Combining ability analysis for seed yield and component traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Research in Plant Biology* **3**: 26–31.

Singh N, Yadava D K, Vasudev S, Singh R, Giri S C, Das B, Barun S and Prabhu K V. 2015. Combining ability and heterobeltiosis for yield and yield contributing traits in high quality oil Indian mustard (*Brassica juncea*) genotypes. *Indian Journal of Agricultural Sciences* **85**(4): 498–03.

Singh S K, Haider Z A and Ram S. 2005. Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences* **75** (4): 228–9.

Swarankar G B, Singh M, Lalita Prasad, Dixit R K and Singh M. 2002. Combining ability for seed yield and its contributing characters in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Plant Archives* **2**(1): 5–14.

Tomar A, Singh M and Singh S K. 2017. Combining ability (SCA & GCA) and heterotic response analysis in Indian mustard (*Brassica juncea* L. Czern & Coss). *Journal of Pharmacognosy and Phytochemistry* **6**(4): 1999–2004.

Yadava D K, Singh N, Vasudev S, Singh R, Singh S, Giri S C, Dwivedi V K and Prabhu K V. 2012. Combining ability and heterobeltiosis for yield and yield-contributing traits in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences* **82**(7): 563–7.