Combining Ability and Heterosis for Seed Yield and Its Components in Indian Mustard (*Brassica juncea* L.)

H. S. Meena[1*], A. Kumar[1], B. Ram[1], V. V. Singh[1], P. D. Meena[1], B. K. Singh[1], and D. Singh[1]

ABSTRACT

Brassica juncea L. is an important oilseed crop which occupies premier position in Indian agriculture. Developing high yielding genotypes has been a major breeding objective in Indian mustard. Present study was conducted at Directorate of Rapeseed-Mustard Research, India, during 2010-2013 to determine General combining ability (GCA) and Specific combining ability (SCA) of parental lines and better parent heterosis of 36 crosses of Indian mustard. Parents and F_1 hybrids were evaluated in RCBD with 3 replications. Line×tester analysis involving nine breeding lines and four testers revealed the operation of both additive and non-additive gene actions with predominance of non-additive gene action in controlling yield and contributing traits. Four lines, namely, DRMR 2243, DRMR 2341, DRMR 2486, DRMR 2613, and one tester, NRCHB 101, were adjudged the best general combiner possessing highly significant positive GCA effects for seed yield and yield contributing traits. Significant SCA effects for seed yield, 1000-seed weight, oil content, and other attributing traits in desirable direction were recorded in a series of hybrids and a close association between SCA effects and heterosis was observed amongst the best hybrids identified on the basis of SCA effects. Hybrids DRMR 2243/NRCHB 101, DRMR 2269/NRCHB 101, DRMR 2326/NRCHB 101, DRMR 2341/NRCDR 2, DRMR 2398/NRCHB 101, DRMR 2486/Ashirwad and DRMR 2613/NRCDR 2 exhibited highest magnitude of better parent heterosis with highly significant SCA effects and higher per se performance for seed yield. The high yielding crosses may be exploited for developing superior genotypes and the parents involved may be converted to well adapted cytoplasmic male sterile or restorer lines.

Keywords: Additive gene actions, High yielding genotypes, Restorer lines, Specific combining ability.

INTRODUCTION

Oilseed *Brassicas,* also known as rapeseed-mustard, have a significant role in Indian agriculture since almost each part of the plant is consumed either by human beings or animals depending upon the crop and its growth stage. Rapeseed-mustard crops in India include toria (*Brassica campestris* L. var. toria), brown sarson (*B. campestris* L. brown sarson), yellow sarson (*B. campestris* L. var. yellow sarson), Indian mustard (*B. juncea* L. Czernj and cosson), black mustard (*B. nigra*) and taramira (*Eruca sativa/vesicara* Mill.)

species. These species have been grown traditionally since about 3,500 BC along with non-traditional species like gobhi saraon (*B. napus* L.) and karan rai (*B. carinata* A. Braun). Among them, Indian mustard is an important oilseed crop of the Indian subcontinent and contributes more than 80% of the total rapeseed-mustard production of the country. It is the second important oilseed crop at national level and contributes nearly 27% of edible oil pool of the country (Singh *et al*., 2013).

There is wider yield gaps when productivity of India is compared with countries like Germany (4.3 tons ha^{-1}), France (3.8 tons ha^{-1}) and UK (3.4 tons ha^{-1}) (Yadava *et al*., 2012).

[1] Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur (Rajasthan), PIN Code: 321303, India.

*Corresponding author; e-mail: singh_hari2006@yahoo.co.in

There is compelling need to increase and stabilize the productivity of Indian mustard. This can be achieved through effective utilization of germplasm resources and integration of genomic tools to impart efficiency and pace of breeding processes (Banga, 2012).

Exploitation of heterosis may play a very significant role in boosting up the production and productivity of Indian mustard. Heterosis breeding can be one of the most viable options for breaking the present yield barrier. Comprehensive analysis of the combining ability involved in the inheritance of quantitative traits and in the phenomenon of heterosis is necessary for evaluation of various breeding procedures (Allard, 1960). Combining ability analysis is one of the powerful tools to test the value of parental lines to produce superior hybrids and valuable recombinants (Singh *et al.,* 2013). Further, for developing better genotypes through hybridization, the choice of suitable parents is of great concern.

Combining ability studies emphasized the predominant effect of GCA on yield and most of the yield components indicating the importance of additive gene action (McGee and Brown, 1995; Wos *et al.,* 1999; Gupta *et al.,* 2006). Pandey *et al.* (1999) reviewed the evidences for the presence of significant SCA effects for seed yield and its components indicating importance of non-additive gene action. Availability of effective means of hybrid seed production led to the development of few commercial hybrids in India during last decade (Kumar *et al.,* 2012); however, the level of yield gain achieved from these hybrids is marginal.

Yadava *et al.* (1974) reported heterosis over better parent up to 239 per cent for seed yield per plant in Indian mustard. A wide range of positive heterosis for number of primary branches and secondary branches per plant, plant height, and number of seeds per siliqua was reported by Rawat (1975). Similarly, significant positive heterosis for seed yield and component traits in Indian mustard were reported by many workers (Ram *et al.,* 1976; Banga and Labana, 1984; Hirve and Tiwari,

1992; Verma, 2000; Aher *et al.*, 2009; Verma *et al.,* 2011) using different sets of materials. It clearly demonstrates the scope of improving the productivity of Indian mustard through genetic manipulations.

Keeping these points in view, the present investigation was undertaken to determine general combining ability and specific combining ability of parental lines and better parent heterosis of different cross combinations in *B. juncea*.

MATERIALS AND METHODS

The study was conducted at Directorate of Rapeseed-Mustard Research, Bharatpur during 2010-11 and 2012-13. The experimental material consisted of 36 F_1 hybrids of Indian mustard (*B. juncea*) involving 9 advanced breeding lines and 4 released high yielding varieties (Table 1) that were utilized as lines and testers, respectively. The parental genotypes were crossed in line×tester fashion to generate 36 F_1 hybrids (crosses) during 2010–2011. The crosses along with their parents were planted in randomized complete block design with three replications during *rabi* 2012–2013. The treatments were raised in rows of 3 m length with a distance of 30 cm between rows and 15 cm between plants, where each treatment was represented by a single row.

Standard agronomic practices were followed to raise the good crop. Recommended doses of fertilizers *viz.,* 80:40:40:40 kg ha^{-1} of N:P:K:S, respectively, were applied and irrigated thrice including pre-sowing irrigation. Observations were recorded on randomly selected five competitive plants for twelve quantitative traits, *viz.,* seed yield/plant (g), plant height (cm), point to first branch (cm), number of primary branches, main shoot length (cm), point to first siliqua (cm), number of siliquae on main shoot, siliqua length (cm), number of seeds per siliqua, 1,000-seed weight (g), oil content (%) and days to maturity. The combining ability analysis was carried out as per Kempthorne (1957) and better parent heterosis (heterobeltiosis) was calculated as

Table 1. Parental genotypes (lines and testers) and their pedigree.

Parental genotype	Pedigree
Lines	
DRMR 2178	(RH 819/BPKR 13)/(RH 819/MDOC 3)
DRMR 2243	GSL 1/Bio 902
DRMR 2269	(GSL 1/Bio 902)/(PYSR 2/*Brassica nigra*)
DRMR 2326	(RH 819/BPKR 13)/(PYSR 2/PBR 181)
DRMR 2341	(RH 819/BPKR 13)/(NBPGR 272/RK 9903)
DRMR 2398	(PYSR 2/*Brassica nigra*)/(Kranti/GSL 1)
DRMR 2448	(RH 819/Kranti)/(GSL 1/PYSR 2)
DRMR 2486	GSL 1/Bio 902
DRMR 2613	(IC 199733/*Sinapis alba*)/(BEC 107/NRCG 411)
Testers	
NRCDR 2	MDOC 43/NBPGR 36
NRCHB101	BL 4/Pusa bold
Rohini	Selection from natural population of Varuna
Ashirwab	Krishna/Vardan

deviation of F_1 value from the better parent through a computer generated program WINDOW STAT version 8.6 from INDOSTAT Services, Hyderabad, India.

Analyses Of Variance (ANOVA) for the crosses for each trait were done assuming the following model for L×T analysis (Dabholkar, 1999; Singh and Chaudhary, 2004):

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk} \qquad (1)$$

Where, Y_{ijk} is the mean value of a character measured on cross $i \times j$ in the kth replication, μ is the population mean effect, g_i is the GCA effect of the ith line, g_j is the GCA effect of the jth tester, s_{ij} is the SCA effect of the cross between the ith line and the jth tester, r_k is the replication effect and e_{ijk} is the environmental error associated with each observation.

The GCA effects for the lines and testers and SCA $i \times j$th cross were calculated using the procedures by Dabholkar (1999) and Singh and Chaudhary (2004) as follows:

GCA effects (lines) $g_i = \frac{y_{i..}}{t\,r} - \frac{y_{...}}{l\,t\,r} \qquad (2)$

GCA effects (testers) $g_j = \frac{y_{.j.}}{l\,r} - \frac{y_{...}}{l\,t\,r} \qquad (3)$

SCA effects $g = \frac{y_{ij.}}{r} - \frac{y_{i..}}{t\,r} - \frac{y_{.j.}}{l\,r} + \frac{y_{...}}{l\,t\,r} \qquad (4)$

Where, l= Number of lines, t= Number of testers and r= Number of replications.

The standard error for combining ability effects were estimated by Equations (5-7)

and were tested for their significance using a t-test:

$$S.E.(gca\ for\ line) = \left(\frac{MSe}{r\,t}\right)^{\frac{1}{2}} \qquad (5)$$

$$S.E.(gca\ for\ tester) = \left(\frac{MSe}{r\,l}\right)^{\frac{1}{2}} \qquad (6)$$

$$S.E.(sca\ effects) = \left(\frac{MSe}{r}\right)^{\frac{1}{2}} \quad tg = \frac{g-0}{S.E.g} \qquad (7)$$

Where, SE and MSe are the standard error and error mean square in the analysis of variance.

Better Parent heterosis (BP) was calculated (Falconer and Mackay, 1996) as Equation (9) by deviation of F_1 value from the better parent and the level of heterosis was tested using the student's "t" test:

$$BP = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100 \quad t = \frac{\overline{F_1} - \overline{BP}}{\sqrt{var(\overline{F_1} - \overline{BP})}} \qquad (8)$$

Where, $\overline{F_1}$ and $\overline{BP}$ are the mean of F_1 progenies and better parent in all replications.

RESULTS AND DISCUSSION

The analysis of variance (Table 2) for combining ability revealed that the mean squares due to lines, testers, and line×testers were highly significant for all the traits,

except for the number of primary branches in testers and plant height, number of siliqua on main shoot, and number of primary branches in line×testers. This shows that considerable amount of genetic variability was present in the experimental material and both GCA and SCA were involved in the genetic expression of studied traits. The variation due to parents vs. crosses was highly significant for seed yield/plant (g), plant height (cm), point to first branch (cm), number of primary branches, main shoot length (cm), point to first siliqua (cm), siliqua length (cm), number of seeds per siliqua, oil content (%) and days to maturity, suggesting the presence of heterosis for these traits in the series of crosses. Similarly, highly significant variance due to crosses revealed that the sufficient amount of genetic variability was generated in the hybrids. Estimates of GCA and SCA variances were significant for most of the traits suggesting the operation of both additive and non-additive components of gene action in the materials study (Table 3). However, the relative estimation of variance due to general combining ability indicated that the specific combining ability variances were predominant for all traits. The ratio of variance due to general and specific combining ability ranged from 0.199 for seed yield / plant to 0.713 for percent oil content, which was less than unity for all the traits indicating the predominance of non-additive gene action for these traits. In such cases, a breeding strategy which would enable to utilize maximum proportion of fixable genetic variation (additive and additive×additive epistasis) as well as non-additive genetic components (dominance, additive×dominance and dominance×dominance) would be effective. In order to make an effective breeding program, biparental mating among randomly selected plants in F_2 and the subsequent generation would help in pooling the desired genes together to develop pure lines. Further crossing of these lines would help in exploiting non-additive genetic components of variation to develop hybrids. Moreover,

biparental mating, recurrent selection and selective diallel mating might be effective to exploit additive × additive type of epistasis. Furthermore, the combining ability variances for lines, testers and line × tester are significant for almost all the traits indicating the sufficient variation for combining ability in parents as well as in hybrids.

The estimates of GCA effects (Table 4) revealed that the parents DRMR 2243, DRMR 2341, DRMR 2486, and DRMR 2613 among the lines, and NRCHB 101 among the testers possessed highly significant positive GCA effects for seed yield/plant, indicating the presence of additive gene action or additive×additive interaction effects. Spragme (1966) reported that when general combining ability effects are significant, additive or additive×additive gene effects are responsible for the inheritance of that particular trait. Similarly, parents DRMR 2243, DRMR 2326, DRMR 2341, NRCDR 2, and Ashirwad exhibited significant desirable GCA effects for 1,000-seed weight; DRMR 2243, DRMR 2398, DRMR 2486, DRMR 2613, NRCDR 2 and Rohini for oil content; DRMR 2269, DRMR 2448 and NRCDR 2 for days to maturity; DRMR 2398 and Ashirwad for plant height; DRMR 2243, DRMR 2341, DRMR 2486, DRMR 2613, NRCHB 101 and Ashirwad for point to first branch; DRMR 2178, DRMR 2243, DRMR 2341, DRMR 2448, DRMR 2613, Rohini and Ashirwad for main shoot length; DRMR 2178, DRMR 2486, DRMR 2613, NRCDR 2 and Rohini for point to first siliqua; DRMR 2178, DRMR 2341, DRMR 2398, DRMR 2613 and Ashirwad for number of siliqua on main shoot; DRMR 2243, DRMR 2398, DRMR 2448, NRCDR 2 and NRCHB 101 for siliqua length. Similarly, for number of seeds per siliqua significant and positive GCA effects were possessed by DRMR 2178, DRMR 2326, DRMR 2341, DRMR 2448 and NRCHB 101. Among the lines, DRMR 2486 had highest GCA effects and also complemented for point to first branch,

Table 2. Analysis of variance for morphological traits in line x tester analysis in Indian mustard.

Characters Source of variation	D.F.	Plant height (cm)	Point to first branch (cm)	Number of primary branches	Main shoot length (cm)	Point to first siliquae (cm)	Number of siliqua on main shoot	Siliqua length (cm)	Number of seeds/ Siliqua	1000- seed weight (g)	Seed yield / Plant (g)	Oil content (%)	Days to maturity
Replication	2	4.07	16.58**	0.10	2.23	0.05	0.083	0.33**	0.09	0.0006	3.86*	0.06**	0.52
Treatments	48	35.04**	98.51**	0.23**	176.94**	7.10**	93.71**	0.70**	5.41**	0.75**	131.15**	1.76**	18.21**
Parents	12	39.33**	90.75**	0.25**	294.04**	10.23**	101.91**	0.72**	3.82**	1.43**	60.74**	1.26**	12.67**
Parents (Lines)	8	34.64**	86.72**	0.28**	234.78**	5.98**	144.22**	0.49**	1.90**	0.66**	57.86**	0.49**	4.70**
Parents (testers)	3	60.99**	31.36**	0.15	280.66**	6.76**	22.80**	0.65**	7.94**	0.27**	55.52**	2.66**	23.56**
Parents (L×T)	1	11.89	301.11**	0.23	808.31**	54.73**	0.73	2.86**	6.84**	11.06**	99.34**	3.28**	43.81**
Parents × crosses	1	83.21**	1137.37**	1.54**	1146.34**	5.41**	2.34	3.30**	28.84**	0.02*	449.85**	2.82**	327.82**
Crosses	35	32.19**	71.49**	0.19**	109.09**	6.08**	93.51**	0.62**	5.28**	0.54**	141.19**	1.89**	11.26**
Line effects	8	14.81	48.36	0.18	88.89	5.92	183.54*	0.59	2.52	0.83*	121.11	3.35**	21.52*
Tester effects	3	109.47*	291.88**	0.27	294.57*	11.20	52.36	2.08*	14.35	1.59**	245.91	5.49**	13.59
L x T effects	24	28.31**	51.65**	0.19**	92.63**	5.49**	68.65**	0.44**	5.07**	0.31**	142.09**	0.96**	7.55**
Error	96	4.12	2.94	0.09	2.56	0.42	1.90	0.07	0.11	0.0024	0.85	0.010	0.42
Total	146	14.28	34.55	0.14	59.88	2.61	32.06	0.28	1.85	0.25	43.73	0.58	6.27

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

Table 3. Estimates of components of variance for morphological traits in Indian mustard.

Characters Component of variance	Plant height (cm)	Point to first branch (cm)	Number of primary branches	Main shoot length (cm)	Point to first siliquae (cm)	Number of siliqua on main shoot	Siliqua length (cm)	Number of seeds / Siliqua	1000- seed weight (g)	Seed yield / Plant (g)	Oil content (%)	Days to maturity
σ^2 lines	0.891	3.784	0.007	7.195	0.458	15.137*	0.044	0.200	0.069*	10.021	0.278**	1.758*
σ^2 testers	3.902*	10.701**	0.007	10.815*	0.399	1.869	0.075*	0.528	0.059**	9.076	0.203**	0.488
σ^2 GCA	2.975**	8.573**	0.007	9.701**	0.417*	5.951**	0.065**	0.427*	0.062**	9.367*	0.226**	0.878**
σ^2 SCA	8.066**	16.237**	0.032*	30.026**	1.690**	22.248**	0.126**	1.654**	0.102**	47.078**	0.317**	2.376**
σ^2 GCA / σ^2 SCA	0.369	0.528	0.219	0.323	0.247	0.267	0.516	0.258	0.608	0.199	0.713	0.370

**, *: significant at *P*=0.01 and *P*=0.05, respectively.

Table 4. Estimates for GCA effects of line and testers for twelve characters in Indian mustard.

Parents	Plant height (cm)	Point to first branch (cm)	Number of primary branches	Main shoot length (cm)	Point to first siliquae (cm)	Number of siliqua on main shoot	Siliqua length (cm)	Number of seeds / siliqua	1000-seed weight (g)	Seed yield / plant (g)	Oil content (%)	Days to maturity
Lines												
DRMR 2178	1.659**	1.598**	0.037	3.320**	-0.449*	7.336**	0.038	0.458**	0.026	-1.471**	-0.891**	-0.028
DRMR 2243	0.909	-1.784***	0.120	1.029*	-0.174	-1.581**	0.296**	-0.125	0.420**	0.901**	0.244**	2.306**
DRMR 2269	0.726	0.357	-0.013	-3.021**	-0.032	-2.097**	-0.058	0.042	-0.003	0.419	-0.381**	-1.028**
DRMR 2326	0.226	2.599**	-0.180*	0.495	1.301**	0.319	-0.158*	0.208*	0.152**	-1.940**	-0.523**	-0.194
DRMR 2341	-0.307	-3.001**	0.070	1.629**	0.663**	3.278**	0.100	0.542**	0.294**	2.321**	-0.026	-0.028
DRMR 2398	-2.274**	1.966**	0.070	-5.055**	-0.345	1.386**	0.184*	-0.167	0.008	-2.391**	0.439**	1.222**
DRMR 2448	-0.491	1.349**	-0.230*	1.329**	0.551**	-5.506**	0.200**	0.375**	-0.290**	-5.327**	0.005	-2.528**
DRMR 2486	-0.457	-1.901**	0.054	-1.838**	-0.837**	-4.181**	-0.233**	-0.500**	-0.312**	5.521**	0.817**	0.222
DRMR 2613	0.009	-1.168*	0.070	2.112**	-0.678**	1.044*	-0.370**	-0.833**	-0.295**	1.967**	0.316**	0.056
SE ±	0.586	0.495	0.087	0.461	0.187	0.398	0.0741	0.095	0.014	0.266	0.028	0.188
CD (P= 0.05)	1.168	0.987	0.174	0.920	0.373	0.794	0.147	0.191	0.028	0.531	0.057	0.376
CD (P= 0.01)	1.551	1.311	0.231	1.221	0.496	1.054	0.196	0.253	0.037	0.705	0.075	0.499
Testers												
NRCDR 2	1.287**	4.079**	-0.144*	-4.708**	-0.324*	-1.847**	0.210**	-0.375**	0.146**	-0.663**	0.143**	-0.731**
NRCHB 101	0.339	-2.436**	0.056	0.318	0.681**	0.123	0.265**	1.014**	-0.072**	4.320**	-0.287**	0.972**
Rohini	1.317**	1.242**	0.078	2.836**	-0.731**	0.190	-0.192**	0.014	-0.308**	-0.954**	0.571**	-0.102
Ashirwad	-2.943**	-2.884**	0.011	1.555**	0.374**	1.534**	-0.283**	-0.653**	0.235**	-2.703**	-0.426**	-0.139
SE ±	0.391	0.330	0.058	0.307	0.125	0.265	0.049	0.063	0.009	0.177	0.019	0.125
CD (P= 0.05)	0.779	0.658	0.116	0.613	0.249	0.529	0.098	0.127	0.018	0.354	0.038	0.250
CD (P= 0.01)	1.034	0.874	0.154	0.814	0.331	0.703	0.130	0.169	0.024	0.470	0.050	0.332

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

point to first siliqua, and oil content followed by DRMR 2341 desirably complemented for point to first branch, main shoot length, number of siliqua on main shoot, number of seeds per siliqua and seed size. Similarly, among the testers, only NRCHB 101 had significant positive GCA effects for seed yield and complemented for other attributing traits like point to first branch, siliqua length, number of seeds/siliqua and earliness. These parents can be used in further breeding programs in Indian mustard. Verma (2000), Singh *et al.* (2005), Yadava *et al.* (2012) and Singh *et al.* (2013) reported similar results in Indian mustard with a different set of material. These results clearly indicated that there was a scope for improving combining ability of parents for attributing traits, as good combiners for seed yield traits were not good for various other yield-contributing traits, therefore, one should breed to improve the combining ability of yield-contributing traits which would ultimately improve the GCA of seed yield directly. Parents, *viz.* DRMR 2243, DRMR 2341, DRMR 2486, DRMR 2613, and NRCHB 101 adjudged the best general combiner possessing high GCA for seed yield and yield contributing traits like reduced point to first branch, reduced point to first siliqua, higher main shoot length, higher siliqua length, more number of siliqua on main shoot, more number of seeds / siliqua, improved 1,000 seed weight, higher oil content and earliness shall be included in the breeding program for accumulation of favorable alleles in a single genetic background.

The estimates of SCA are presented in Table 5. For plant height, four crosses *viz.* DRMR 2243/Ashirwad, DRMR 2326/Rohini, DRMR 2341/NRCDR 2, and DRMR 2398/NRCDR 2 recorded highly significant, but negative SCA effects. Similar effects were observed for point to first branch, point to first siliqua, and days to maturity in seven crosses each. This indicates that the reduction in plant height, point to first branch, point to first siliqua,

and days to maturity may be due to negative heterosis in these crosses for these traits, which is desirable. The results are in accordance with Yadava *et al.* (2012). Highly significant and positive SCA effects were observed for seed yield in 12 hybrids, 1,000-seed weight in 14 hybrids, oil content in 12 hybrids, main shoot length in 12 hybrids, number of siliqua on main shoot in 11 hybrids, number of seeds/siliqua in 11 hybrids, siliqua length in 5 hybrids, and number of primary branches in 1 hybrid. The outcomes clearly indicate that the parents involved in these crosses were good specific combiners; however, the relative contribution of the parents to specific combining ability effect for seed yield was through various yield attributing traits in different hybrids. Again, the results indicate that there is no direct relationship between SCA effects and heterobeltiosis/better parent heterosis.

The estimates of better parent heterosis for seed yield are presented in Table 6. Out of 36 hybrids, 13 hybrids exhibited highly significant and positive better parent heterosis and from them 11 hybrids showed > 15% better parent heterosis and seven hybrids *viz.* DRMR 2243/NRCHB 101 (67.62%), DRMR 2269/NRCHB 101 (46.32%), DRMR 2326/NRCHB 101 (23.20%), DRMR 2341/NRCDR 2 (35.37%), DRMR 2398/NRCHB 101 (23.31%), DRMR 2486/Ashirwad (129.22%) and DRMR 2613/NRCDR 2 (31.85%) possessed >15% better parent heterosis, highly significant SCA effects and higher *per se* performance. Yadava *et al.* (2012) reported 54.38% heterobeltiosis in hybrid Pusa Mustard 25/RGN 145 and Vaghela *et al.* (2011) reported 44.8% heterobeltiosis in the hybrid RSK 28/RH(0E)0103 with highly significant SCA effects and higher *per se* performance. Similarly, Hirve and Tiwari (1992) reported 161% better parent heterosis in hybrid RAU RP 4/PR 18, Dhillon *et al.* (1990) reported 113.6% in RLM 198/RK 2, Duhoom and Basu (1981) reported 102.7% in YS 51/YS 9, and Yadava *et al.*

Table 5. Highly significant (positive except for plant height, point to first branch, point to first siliqua and days to maturity) SCA effects for twelve yield and yield attributing characters in crosses of Indian mustard genotypes.

Character	Crosses
Plant height (cm	DRMR 2243/Ashirwad (-4.724), DRMR 2326/Rohini (-5.70), DRMR 2341/NRCDR 2 (-3.404), DRMR 2398/NRCDR 2 (-3.237)
Point to first branch (cm)	DRMR 2178/NRCDR 2 (-4.212), DRMR 2243/NRCHB 101 (-2.831), DRMR 2269/Ashirwad (-3.157), DRMR 2326/Ashirwad (-6.266), DRMR 2341/NRCDR 2 (-9.229), DRMR 2398/NRCHB 101 (-2.681), DRMR 2486/NRCHB 101 (-3.081)
Number of primary branches	DRMR 2398/Rohini (0.589)
Main shoot length (cm)	DRMR 2178/Rohini (4.806), DRMR 2243/NRCDR 2 (4.042), DRMR 2243/NRCHB 101 (3.749), DRMR 2269/Rohini (4.014), DRMR 2326/NRCHB 101 (3.282), DRMR 2326/Ashirwad (4.379), DRMR 2341/NRCDR 2 (9.042), DRMR 2341/NRCHB 101 (3.082), DRMR 2398/NRCHB 101 (6.566), DRMR 2448/Rohini (5.997), DRMR 2448/Ashirwad (6.812), DRMR 2613/NRCDR 2 (6.758)
Point to first siliquae (cm)	DRMR 2178/NRCHB 101 (-2.306), DRMR 2243/Rohini (-1.469), DRMR 2243/Ashirwad (-1.057), DRMR 2269/Ashirwad (-2.466), DRMR 2326/NRCHB 101 (-1.34), DRMR 2341/Rohini (-1.273), DRMR 2448/NRCDR 2 (-1.668)
Number of siliqua on main shoot	DRMR 2178/Rohini (3.394), DRMR 2243/Rohini (3.310), DRMR 2269/Rohini (3.894), DRMR 2326/Ashirwad (2.799), DRMR 2341/NRCHB 101 (5.285), DRMR 2341/Ashirwad (4.907), DRMR 2398/NRCHB 101 (4.610), DRMR 2398/Rohini (6.210), DRMR 2448/NRCDR 2 (3.039), DRMR 2486/Ashirwad (4.099), DRMR 2613/NRCDR 2 (8.122)
Siliqua length (cm)	DRMR 2269/NRCHB 101 (0.560), DRMR 2341/Rohini (0.409), DRMR 2341/Ashirwad (0.516), DRMR 2398/Rohini (0.492), DRMR 2448/NRCDR 2 (0.590)
Number of seeds / siliqua	DRMR 2178/NRCDR 2 (1.042), DRMR 2243/NRCHB 101 (1.569), DRMR 2269/NRCHB 101 (2.069), DRMR 2326/NRCDR 2 (1.792), DRMR 2341/Rohini (1.403), DRMR 2341/Ashirwad (0.569), DRMR 2398/Rohini (0.611), DRMR 2448/Ashirwad (1.903), DRMR 2486/NRCDR 2 (1.00), DRMR 2486/Rohini (0.944), DRMR 2613/NRCHB 101 (1.278)
1000-seed weight (g)	DRMR 2178/NRCDR 2 (0.249), DRMR 2178/NRCHB 101 (0.228), DRMR 2243/NRCDR 2 (0.649), DRMR 2243/NRCHB 101 (0.137), DRMR 2269/NRCHB 101 (0.077), DRMR 2326/Rohini (0.077), DRMR 2326/Ashirwad (0.311), DRMR 2341/Rohini (0.319), DRMR 2398/Ashirwad (0.228), DRMR 2448/NRCDR 2 (0.125), DRMR 2486/Rohini (0.395), DRMR 2486/Ashirwad (0.285), DRMR 2613/NRCHB 101 (0.079), DRMR 2613/Ashirwad (0.188)
Seed yield/Plant (g)	DRMR 2178/Rohini (1.542), DRMR 2178/Ashirwad (4.281), DRMR 2243/NRCHB 101 (12.172), DRMR 2269/NRCHB 101 (7.212), DRMR 2326/NRCHB 101 (3.676), DRMR 2341/NRCDR 2 (11.232), DRMR 2398/NRCHB 101 (4.154), DRMR 2398/Rohini (2.395), DRMR 2448/Rohini (4.851), DRMR 2448/Ashirwad (3.360), DRMR 2486/Ashirwad (13.316), DRMR 2613/NRCDR 2 (10.590)
Oil content (%)	DRMR 2178/NRCDR 2 (0.502), DRMR 2178/Rohini (1.058), DRMR 2243/Rohini (0.210), DRMR 2243/Rohini (0.176), DRMR 2269/Ashirwad (0.744), DRMR 2326/NRCDR 2 (0.194), DRMR 2341/Ashirwad (0.853), DRMR 2398/NRCHB 101 (0.305), DRMR 2448/NRCHB 101 (0.589), DRMR 2448/Ashirwad (0.458), DRMR 2613/NRCDR 2 (0.608), DRMR 2613/NRCHB 101 (0.445)
Days to maturity	DRMR 2243/NRCHB 101 (-1.972), DRMR 2326/NRCHB 101 (-1.139), DRMR 2326/Ashirwad (-1.361), DRMR 2341/Ashirwad (-1.194), DRMR 2398/NRCDR 2 (-2.852), DRMR 2486/Rohini (-1.148), DRMR 2486/Ashirwad (-1.778),

1868

Table 6. Mean performance and estimates of better parent heterosis for seed yield in *Brassica juncea* genotypes.[a]

Lines	Testers				Mean seed yield of lines (g)
	NRCDR 2	NRCHB 101	Rohini	Ashirwad	
DRMR 2178	22.88 (-19.79**)	22.80 (-20.04**)	24.51 (-14.06**)	25.50 (-10.59**)	28.520
DRMR 2243	19.43 (-31.28**)	42.79 (67.62**)	24.57 (5.10)	18.39 (1.49)	17.727
DRMR 2269	20.14 (-28.78**)	37.35 (46.32**)	23.36 (-0.06)	22.40 (15.17**)	19.447
DRMR 2326	23.22 (-17.89**)	31.45 (23.20**)	21.70 (-7.19*)	17.45 (-4.45)	18.260
DRMR 2341	38.28 (35.37**)	26.64 (-2.66)	26.60 (-2.78)	19.33 (-29.35**)	27.363
DRMR 2398	19.55 (-30.86**)	31.48 (23.31**)	24.44 (4.56)	16.54 (-15.37**)	19.540
DRMR 2448	19.42 (-31.34**)	16.16 (-36.68**)	23.96 (2.51)	20.72 (14.39**)	16.787
DRMR 2486	22.36 (-20.92**)	29.41 (15.23**)	30.35 (29.84**)	41.53 (129.22**)	17.480
DRMR 2613	37.29 (31.85**)	29.34 (14.95**)	20.45 (-12.52**)	22.36 (22.99**)	18.180
Mean seed yield of testers (g)	28.280	25.527	23.377	18.117	

[a] Values in parentheses represent heterobeltiosis (better parent heterosis)

**,*: Heterobeltiosis with SCA effects significant at *P*= 0.01 and *P*= 0.05, respectively.

(1974) reported 204% better parent heterosis in hybrid F 48/ IB 494. Heterosis for seed yield to the extent of 24.36 to 80.97% was also reported by Verma *et al*. (2011) in 15 crosses and moderate level of heterosis for seed yield/plant, number of siliquae/plant, and number of secondary branches/plant was reported by Aher *et al*. (2009).

The high yielding cross combinations can further be exploited for their commercial utilization and the parents involved in developing heterotic hybrids in the present study shall be converted to well adapted cytoplasmic male sterile or restorer lines.

REFERENCES

1. Aher, C. D., Shelke, L. T., Chinchane, V. N., Borgaonkar, S. B. and Gaikwad, A. R. 2009. Heterosis for Yield and Yield Components in Indian Mustard [*Brassica juncea* (L.) Czern and Coss.]. *Int. J. Plant Sci.,* **4**: 30–32.

2. Allard, R. W. 1960. *Principles of Plant Breeding*. John Wiley and Sons. New York.

3. Banga, S. S. 2012. Germplasm Enhancement in Indian Mustard: Some Exiting New Developments. In: "*Souvenir of XIX Annual AICRP Group Meet on Rapeseed-Mustard*", Birsa Agricultural University, Ranchi, India, PP. 29-34.

4. Banga, S. S. and Labana, K. S. 1984. Heterosis in Indian Mustard (*Brassica juncea* L.). *J. Plant Breed.*, **92**: 61-70.

5. Dabholkar, A. R. 1999. *Elements of Biometrical Genetics*. Revised and Enlarged Edition, Concept Publishing. New Delhi

6. Dhillon, S. S., Labana, K. S. and Banga, S. K. 1990. Studies on Heterosis and Combining Ability in Indian Mustard (*Brassica juncea* L. Coss.). PAU, *J. Res.* **27**: 1-8.

7. Duhoom, S. S. and Basu, A. K. 1981. Note on Heterosis in Yellow Seeded Indian Colza. *Indian J. Agri. Sci.,* **51**: 121–124.

8. Falconer, D. S. and Mackey, T. F. C. 1996. *Introduction to Quantitative Genetics.* Pearson Education, Ltd., England.

9. Gupta, S. K., Karuna, N. and Dey, T. 2006. Heterosis and Combining Ability in Rapeseed (*Brassica napus* L.). *J. Res.* Skuast, **5(1)**: 42–47.

10. Hirve, C. D. and Tiwari, A. S. 1992. Heterosis and Inbreeding Depression in Indian Mustard. *Indian J. Genet.,* **51**: 190-193.

11. Kempthorne, O. 1957. *An Introduction to Genetic Statistics.* Wiley, New York, 545 PP.

12. Kumar, A., Kumar, V. and Kandpal, B. K. 2012. Production Barriers and Technological Options for Sustainable Production of Rapeseed Mustard in India. In: "*Souviner of 1st National Brassica Conference*", Society for Rapeseed Mustard Research, Bharatpur, India, PP. 25-32.

13. McGee, K. P. and Brown, J. 1995. Investigation of F_1 Hybrids Performance in Fall and Spring Planted Canola. In: "*Proceeding of 9th International Rapeseed Conference*", July 4–10, Cambridge, UK, PP. 116-118.

14. Pandey, L. D., Singh, B. and Sachan, J. N. 1999. Brassica Hybrid Research in India: Status and Prospects: Paper 263. In: "*Proceeding of 10th International Rapeseed Conference [CD-ROM]*", Canberra, Australia.

15. Ram, K., Chauhan, Y. S. and Katiyar, R. P. 1976. Partial Diallel Analysis in F_2 Generation in Indian Mustard. *Indian J. Agri. Sci.,* **46(5)**: 229–232.

16. Rawat, D. S. 1975. Genetical Studies on Yield, Oil Content and Characters Related to Yield in *Brassica juncea*. PhD. Thesis, IARI, New Delhi (India).

17. Singh, R. K. and Chaudhary, B. D. 2004. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi.

18. 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 J. Agri. Sci.,* **75**: 228–229.

19. 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 and Coss.]. *Res. Plant Biol.,* **3(2)**: 26–31.

20. Spragme, G. F. 1966. Quantitative Genetics in Plant Improvement. In: "*Plant Breeding*", (Ed.): Fey, K. J.. Iowa State University Press. Iowa, PP. .315-354.

21. Vaghela, P. O., Thakkar, H. S., Bhadauria, H. S., Sutariya, D. A., Parmar, S. K. and Prajapati, D. V. 2011. Heterosis and Combining Ability for Yield and Its Component Traits in Indian Mustard (*Brassica juncea*). *J. Oilseed Brassica,* **2**: 39–43.

22. Verma, O. P., Yadav, R., Kumar, K., Singh, R., Maurya, K. N. and Ranjana. 2011. Combining Ability and Heterosis for Seed Yield and Its Components in Indian Mustard (*Brassica juncea*). *Plant Archiv.,* **11**: 863–865.

23. Verma, R. R. 2000. Combining Ability Analysis for Yield and Its Components through Diallel Crosses in Indica Coiza [*Brassica juncea* (L.) Czern and Coss.]. *Indian J. Agric. Res.,* **34(2)**: 91–96.

24. Wos, H., Bartkowiak-Broda, I., Budzianowski, G. and Krzymanski, J. 1999. Breeding of Winter and Spring Oilseed Rape Hybrids at Malyszyn: Paper 544. In: "*Proceeding of 10th International Rapeseed Conference [CD-ROM]*", Canberra, Australia.

25. Yadava, T. P., Singh, H., Gupta, V. P. and Rana, R. K. 1974. Heterosis and Combining Ability in Raya for Yield and Its Components. *Indian J. Genet.* **34(A)**: 684-695.

26. 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 J. Agri. Sci.,* **82(7)**: 563–567.

توان ترکیبی و هتروزیس برای عملکرد دانه و اجزای آن در خردل هندی(.Brassica juncea L)

ه. س. منا، ا. کومار، ب. رام، و. و. سینگ، پ. د. منا، ب. ک. سینگ، و د. سینگ

چکیده

گیاه (Brassica juncea) از دانه های روغنی مهمی است که در کشاورزی هندوستان نقش عمده ای دارد.از این رو، تولید ژنوتیپ های دارای عملکرد بالا یکی از اهداف اصلی اصلاح ژنتیکی این گیاه در هندوستان بوده است. پژوهش حاضر در اداره کل تحقیقات کلزا-خردل در هندوستان و در طی سال های ۲۰۱۰-۱۳ و به منظور تعیین GCA و SCAلاین های والد و هتروزیس بهتر والد های ۳۶ تلاقی از خردل هندی انجام شد. در اجرای آزمایش، والد ها و هیبرید های F1 در یک طرح بلوک های کامل تصادفی در سه تکرار مورد ارزیابی قرار گرفتند. با انجام تجزیه لاین x محک زن (tester) شامل ۹ لاین بهنژادی و ۴ محک زن، فعال بودن ژن های جمع پذیر وجمع-ناپذیر (که در آنها عمل ژن جمع-ناپذیر غالب بود) در کنترل عملکرد گیاه و صفات مربوط به آن آشکار شد. چهار لاین به نام های DRMR 2243، DRMR 2341، DRMR 2486، و DRMR 2613 همراه با یک محک زن (NRCHB 101) به عنوان بهترین ترکیب گر عمومی(general combiner) شناسایی شدند که دارای GCAمثبت بسیار معنی دار برای عملکرد دانه و صفات مربوط به عملکرد بودند. نیز، اثر های معنی دار SCAبر عملکرد دانه، وزن هزار دانه، مقدار روغن، و دیگر صفات مطلوب در یک سری هیبرید ثبت شد و در میان هیبرید هایی که بر اساس اثرات SCAبه عنوان بهترین ها شناسایی شده بودند همراهی نزدیکی بین اثرات SCAو هتروزیس مشاهده شد.هیبرید های DRMR 2243/NRCHB 101،DRMR 2269/NRCHB 101،DRMR 2326/NRCHB 101، DRMR 2341/NRCDR 2،DRMR 2398/NRCHB 101،DRMR 2486/Ashirwad و DRMR 2613/NRCDR 2بالاترین امتیاز های مربوط به هتروزیس والدهای بهتر را داشتند و اثرات SCAآنها خیلی معنی دار بود و عملکرد دانه بیشتری داشتند. به این قرار، تلاقی های با عملکرد بالا را می توان برای تولید ژنو تیپ های برتر استفاده کرد و والدهای مربوطه ممکن است به لاین های کاملا سازگار نرعقیمی سیتوپلاسمی یا لاین های برگرداننده باروری(restorer lines) تبدیل شوند.