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

H. S. Meena¹*, A. Kumar¹, B. Ram¹, V. V. Singh¹, P. D. Meena¹, B. K. Singh¹, and D. Singh¹

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 F₁ hybrids were evaluated in RCBD with 3 replications. Line×tester analysis involving nine breeder 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).

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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 F₁ 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 linextester fashion to generate 36 F₁ 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.

<table>
<thead>
<tr>
<th>Lines</th>
<th>Pedigree</th>
</tr>
</thead>
<tbody>
<tr>
<td>DRMR 2178</td>
<td>(RH 819/BPKR 13)/(RH 819/MDOC 3)</td>
</tr>
<tr>
<td>DRMR 2243</td>
<td>GSL 1/Bio 902</td>
</tr>
<tr>
<td>DRMR 2269</td>
<td>(GSL 1/Bio 902)/(PYSR 2/Brassica nigra)</td>
</tr>
<tr>
<td>DRMR 2326</td>
<td>(RH 819/BPKR 13)/(PYSR 2/PBR 181)</td>
</tr>
<tr>
<td>DRMR 2341</td>
<td>(RH 819/BPKR 13)/(NBPG 272/RK 9903)</td>
</tr>
<tr>
<td>DRMR 2398</td>
<td>(PYSR 2/Brassica nigra)/(Kranti/GSL 1)</td>
</tr>
<tr>
<td>DRMR 2448</td>
<td>(RH 819/Kranti)/(GSL 1/PYSR 2)</td>
</tr>
<tr>
<td>DRMR 2486</td>
<td>GSL 1/Bio 902</td>
</tr>
<tr>
<td>DRMR 2613</td>
<td>(IC 199733/Sinapis alba)/(BEC 107/NRCG 411)</td>
</tr>
<tr>
<td>Testers</td>
<td></td>
</tr>
<tr>
<td>NRC DR 2</td>
<td>MDOC 43/NBPGR 36</td>
</tr>
<tr>
<td>NRCHB 101</td>
<td>BL 4/Pusa bold</td>
</tr>
<tr>
<td>Rohini Selection from natural population of Varuna</td>
<td></td>
</tr>
<tr>
<td>Ashirwab</td>
<td>Krishna/Vardan</td>
</tr>
</tbody>
</table>

Combining Ability and Heterosis in Indian Mustard

The analysis of variance (Table 2) for combining ability revealed that the mean squares due to lines, testers, and line x testers were highly significant for all the traits, and were tested for their significance using a $t$-test:

$$S.E. \text{ (gca for line)} = \left( \frac{MSE}{r} \right)^{\frac{1}{2}}$$ (5)

$$S.E. \text{ (gca for tester)} = \left( \frac{MSE}{t} \right)^{\frac{1}{2}}$$ (6)

$$S.E. \text{ (sca effects)} = \left( \frac{MSE}{r} \right)^{\frac{1}{2}} \times g_0 = \frac{g - 0}{S.E.g}$$ (7)

Where, $S.E.$ 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:

$$BP = \frac{F_1 - BP}{BP} \times 100 \ t = \frac{F_1 - BP}{\sqrt{var(F_1 - BP)}}$$ (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 x testers were highly significant for all the traits.
except for the number of primary branches in testers and plant height, number of silique on main shoot, and number of primary branches in linextesters. 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 silique (cm), silique length (cm), number of seeds per silique, 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 F2 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, NRCDDR 2, and Ashirwad exhibited significant desirable GCA effects for 1,000-seed weight; DRMR 2243, DRMR 2398, DRMR 2486, DRMR 2613, NRCDDR 2 and Rohini for oil content; DRMR 2269, DRMR 2448 and NRCDDR 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, NRCDDR 2 and Rohini for point to first silique; DRMR 2178, DRMR 2341, DRMR 2398, DRMR 2613 and Ashirwad for number of silique on main shoot; DRMR 2243, DRMR 2398, DRMR 2448, NRCDDR 2 and NRCHB 101 for silique length. Similarly, for number of seeds per silique 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.

<table>
<thead>
<tr>
<th>Characters Source of variation</th>
<th>D.F.</th>
<th>Plant height (cm)</th>
<th>Point to first branch (cm)</th>
<th>Number of primary branches</th>
<th>Main shoot length (cm)</th>
<th>Point to first silique (cm)</th>
<th>Number of siliques on main shoot</th>
<th>Silique length (cm)</th>
<th>Number of seeds/ Silique</th>
<th>1000-seed weight (g)</th>
<th>Seed yield / Plant (g)</th>
<th>Oil content (%)</th>
<th>Days to maturity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>2</td>
<td>4.07</td>
<td>16.58**</td>
<td>0.10</td>
<td>2.2</td>
<td>0.05</td>
<td>0.083</td>
<td>0.33**</td>
<td>0.09</td>
<td>0.0006</td>
<td>3.86*</td>
<td>0.06**</td>
<td>0.52</td>
</tr>
<tr>
<td>Treatments</td>
<td>48</td>
<td>35.04**</td>
<td>98.51**</td>
<td>0.23**</td>
<td>17694**</td>
<td>7.10**</td>
<td>93.71**</td>
<td>0.70**</td>
<td>5.41**</td>
<td>0.75**</td>
<td>131.15**</td>
<td>1.76**</td>
<td>18.21**</td>
</tr>
<tr>
<td>Parents</td>
<td>12</td>
<td>39.33**</td>
<td>90.75**</td>
<td>0.25**</td>
<td>29404**</td>
<td>10.23**</td>
<td>101.91**</td>
<td>0.72**</td>
<td>3.82**</td>
<td>1.43**</td>
<td>50.74**</td>
<td>1.26**</td>
<td>12.67**</td>
</tr>
<tr>
<td>Parents (Lines)</td>
<td>8</td>
<td>34.64**</td>
<td>86.72**</td>
<td>0.28**</td>
<td>23478**</td>
<td>5.98**</td>
<td>144.22**</td>
<td>0.49**</td>
<td>1.90**</td>
<td>0.66**</td>
<td>57.86**</td>
<td>0.49**</td>
<td>4.70**</td>
</tr>
<tr>
<td>Parents (testers)</td>
<td>3</td>
<td>60.99**</td>
<td>31.36**</td>
<td>0.15</td>
<td>28066**</td>
<td>6.76**</td>
<td>22.80**</td>
<td>0.65**</td>
<td>7.94**</td>
<td>0.27**</td>
<td>55.52**</td>
<td>2.66**</td>
<td>23.56**</td>
</tr>
<tr>
<td>Parents (LxT)</td>
<td>1</td>
<td>11.89</td>
<td>301.11**</td>
<td>0.23</td>
<td>80831**</td>
<td>54.73**</td>
<td>114.34**</td>
<td>0.73**</td>
<td>2.34</td>
<td>3.30**</td>
<td>449.85**</td>
<td>2.82**</td>
<td>327.82**</td>
</tr>
<tr>
<td>Parents x crosses</td>
<td>1</td>
<td>83.21**</td>
<td>1137.37**</td>
<td>1.54**</td>
<td>1143.34**</td>
<td>5.41**</td>
<td>23.4**</td>
<td>0.30**</td>
<td>28.84**</td>
<td>0.02**</td>
<td>141.19**</td>
<td>1.89**</td>
<td>11.26**</td>
</tr>
<tr>
<td>Crosses</td>
<td>55</td>
<td>32.19**</td>
<td>71.49**</td>
<td>0.19**</td>
<td>10909**</td>
<td>6.08**</td>
<td>93.51**</td>
<td>0.62**</td>
<td>5.28**</td>
<td>0.54**</td>
<td>141.19**</td>
<td>1.89**</td>
<td>11.26**</td>
</tr>
<tr>
<td>Line effects</td>
<td>8</td>
<td>14.81</td>
<td>48.36**</td>
<td>0.18</td>
<td>88.59</td>
<td>5.92**</td>
<td>183.54**</td>
<td>0.59**</td>
<td>2.52</td>
<td>0.83**</td>
<td>121.11**</td>
<td>3.35**</td>
<td>21.52**</td>
</tr>
<tr>
<td>Tester effects</td>
<td>3</td>
<td>109.47**</td>
<td>291.88**</td>
<td>0.27</td>
<td>294.57**</td>
<td>11.20**</td>
<td>52.36**</td>
<td>2.08**</td>
<td>14.35**</td>
<td>1.59**</td>
<td>245.91**</td>
<td>5.49**</td>
<td>13.59**</td>
</tr>
<tr>
<td>L x T effects</td>
<td>24</td>
<td>28.31**</td>
<td>51.65**</td>
<td>0.19**</td>
<td>92.63**</td>
<td>5.49**</td>
<td>68.65**</td>
<td>0.44**</td>
<td>5.07**</td>
<td>0.31**</td>
<td>142.09**</td>
<td>0.96**</td>
<td>7.55**</td>
</tr>
<tr>
<td>Error</td>
<td>96</td>
<td>4.12</td>
<td>2.94**</td>
<td>0.09</td>
<td>2.56</td>
<td>0.42</td>
<td>1.90**</td>
<td>0.07**</td>
<td>0.11</td>
<td>0.0024</td>
<td>9.85**</td>
<td>0.010</td>
<td>0.42</td>
</tr>
<tr>
<td>Total</td>
<td>146</td>
<td>14.28</td>
<td>34.55**</td>
<td>0.14</td>
<td>59.88</td>
<td>2.61</td>
<td>32.06**</td>
<td>0.28**</td>
<td>1.85</td>
<td>0.25</td>
<td>43.73**</td>
<td>0.58</td>
<td>6.27</td>
</tr>
</tbody>
</table>

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

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

<table>
<thead>
<tr>
<th>Characters Component of variance</th>
<th>Plant height (cm)</th>
<th>Point to first branch (cm)</th>
<th>Number of primary branches</th>
<th>Main shoot length (cm)</th>
<th>Point to first silique (cm)</th>
<th>Number of siliques on shoot</th>
<th>Silique length (cm)</th>
<th>Number of seeds/ Silique</th>
<th>1000-seed weight (g)</th>
<th>Seed yield / Plant (g)</th>
<th>Oil content (%)</th>
<th>Days to maturity</th>
</tr>
</thead>
<tbody>
<tr>
<td>σ² lines</td>
<td>0.891</td>
<td>3.784</td>
<td>0.007</td>
<td>7.195</td>
<td>0.458</td>
<td>15.137**</td>
<td>0.044</td>
<td>0.200</td>
<td>0.069**</td>
<td>10.021</td>
<td>0.278**</td>
<td>1.758**</td>
</tr>
<tr>
<td>σ² testers</td>
<td>3.902**</td>
<td>10.701**</td>
<td>0.007</td>
<td>10.815**</td>
<td>0.399</td>
<td>1.869</td>
<td>0.057**</td>
<td>0.528</td>
<td>0.059**</td>
<td>9.067</td>
<td>0.203**</td>
<td>0.488</td>
</tr>
<tr>
<td>σ² GCA</td>
<td>2.975**</td>
<td>8.573**</td>
<td>0.007</td>
<td>9.701**</td>
<td>0.417**</td>
<td>5.051**</td>
<td>0.065**</td>
<td>0.427**</td>
<td>0.062**</td>
<td>9.367**</td>
<td>0.226**</td>
<td>0.878**</td>
</tr>
<tr>
<td>σ² SCA</td>
<td>0.868**</td>
<td>16.237**</td>
<td>0.032**</td>
<td>30.026**</td>
<td>1.690**</td>
<td>22.248**</td>
<td>0.126**</td>
<td>1.654**</td>
<td>0.102**</td>
<td>47.078**</td>
<td>0.317**</td>
<td>2.376**</td>
</tr>
<tr>
<td>σ² GCA / σ² SCA</td>
<td>0.369</td>
<td>0.528</td>
<td>0.219</td>
<td>0.323</td>
<td>0.247</td>
<td>0.267</td>
<td>0.516</td>
<td>0.258</td>
<td>0.608</td>
<td>0.159</td>
<td>0.713</td>
<td>0.370</td>
</tr>
</tbody>
</table>

**, * 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.

<table>
<thead>
<tr>
<th>Parents</th>
<th>Plant height (cm)</th>
<th>Point to first branch (cm)</th>
<th>Number of primary branches</th>
<th>Main shoot length (cm)</th>
<th>Point to first siliqua (cm)</th>
<th>Number of siliqua on main shoot</th>
<th>Siliqua length (cm)</th>
<th>Number of seeds / siliqua</th>
<th>1000-seed weight (g)</th>
<th>Seed yield / plant (g)</th>
<th>Oil content (%)</th>
<th>Days to maturity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lines</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>DRMR 2178</td>
<td>1.659**</td>
<td>1.598**</td>
<td>0.037</td>
<td>3.320**</td>
<td>-0.449*</td>
<td>7.336**</td>
<td>0.038</td>
<td>0.458**</td>
<td>0.026</td>
<td>-1.471**</td>
<td>-0.891**</td>
<td>-0.028</td>
</tr>
<tr>
<td>DRMR 2243</td>
<td>0.909</td>
<td>-1.784**</td>
<td>0.120</td>
<td>1.029*</td>
<td>-1.174</td>
<td>-1.581**</td>
<td>0.296**</td>
<td>0.025</td>
<td>0.026</td>
<td>0.901**</td>
<td>0.244**</td>
<td>2.306**</td>
</tr>
<tr>
<td>DRMR 2269</td>
<td>0.726</td>
<td>0.35*</td>
<td>-0.013</td>
<td>-3.021*</td>
<td>-0.032</td>
<td>-2.097**</td>
<td>-0.058</td>
<td>0.042</td>
<td>0.003</td>
<td>0.419</td>
<td>-0.381**</td>
<td>-1.028**</td>
</tr>
<tr>
<td>DRMR 2326</td>
<td>0.226</td>
<td>2.599**</td>
<td>-0.180*</td>
<td>0.495</td>
<td>1.301**</td>
<td>0.319</td>
<td>0.158**</td>
<td>0.208*</td>
<td>0.152**</td>
<td>-1.940**</td>
<td>-0.523**</td>
<td>-0.019</td>
</tr>
<tr>
<td>DRMR 2341</td>
<td>-0.307</td>
<td>-3.001**</td>
<td>0.070</td>
<td>1.629**</td>
<td>0.666**</td>
<td>3.278**</td>
<td>0.100</td>
<td>0.542**</td>
<td>0.294**</td>
<td>2.321**</td>
<td>-0.026</td>
<td>-0.028</td>
</tr>
<tr>
<td>DRMR 2398</td>
<td>-2.274**</td>
<td>1.966**</td>
<td>0.070</td>
<td>-5.055**</td>
<td>-0.345</td>
<td>1.386**</td>
<td>0.184**</td>
<td>0.167</td>
<td>0.008</td>
<td>-2.391**</td>
<td>0.439**</td>
<td>1.222**</td>
</tr>
<tr>
<td>DRMR 2448</td>
<td>-0.491</td>
<td>1.340**</td>
<td>-0.230*</td>
<td>1.329**</td>
<td>0.551**</td>
<td>-5.506**</td>
<td>0.200**</td>
<td>0.375**</td>
<td>-0.290**</td>
<td>-5.327**</td>
<td>0.005</td>
<td>-2.528**</td>
</tr>
<tr>
<td>DRMR 2486</td>
<td>-0.457</td>
<td>-1.901**</td>
<td>0.054</td>
<td>-1.838**</td>
<td>-0.837**</td>
<td>-4.181**</td>
<td>-0.233**</td>
<td>-0.500**</td>
<td>-0.312**</td>
<td>5.521**</td>
<td>0.817**</td>
<td>0.222</td>
</tr>
<tr>
<td>DRMR 2613</td>
<td>0.009</td>
<td>-1.168*</td>
<td>0.070</td>
<td>2.112**</td>
<td>-0.678**</td>
<td>1.044**</td>
<td>-0.370**</td>
<td>-0.833**</td>
<td>-0.295**</td>
<td>1.967**</td>
<td>0.316**</td>
<td>0.056</td>
</tr>
<tr>
<td>SE ±</td>
<td>0.586</td>
<td>0.495</td>
<td>0.087</td>
<td>0.461</td>
<td>0.187</td>
<td>0.398</td>
<td>0.0741</td>
<td>0.095</td>
<td>0.014</td>
<td>0.266</td>
<td>0.028</td>
<td>0.188</td>
</tr>
<tr>
<td>CD (P=0.05)</td>
<td>1.168</td>
<td>0.987</td>
<td>0.174</td>
<td>0.920</td>
<td>0.373</td>
<td>0.794</td>
<td>0.147</td>
<td>0.191</td>
<td>0.028</td>
<td>0.531</td>
<td>0.057</td>
<td>0.376</td>
</tr>
<tr>
<td>CD (P=0.01)</td>
<td>1.551</td>
<td>1.311</td>
<td>0.231</td>
<td>1.221</td>
<td>0.496</td>
<td>1.054</td>
<td>0.196</td>
<td>0.253</td>
<td>0.037</td>
<td>0.705</td>
<td>0.075</td>
<td>0.499</td>
</tr>
<tr>
<td>Testers</td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRCDBR 2</td>
<td>1.287**</td>
<td>4.070**</td>
<td>-0.144*</td>
<td>-4.708**</td>
<td>-0.324*</td>
<td>-1.847**</td>
<td>0.210**</td>
<td>-0.375**</td>
<td>0.146**</td>
<td>-0.663**</td>
<td>0.143**</td>
<td>-0.731**</td>
</tr>
<tr>
<td>NRCDBR 101</td>
<td>0.339</td>
<td>-2.436**</td>
<td>0.056</td>
<td>0.318</td>
<td>0.681**</td>
<td>0.123</td>
<td>0.265**</td>
<td>1.014**</td>
<td>-0.072**</td>
<td>4.320**</td>
<td>-0.287**</td>
<td>0.972**</td>
</tr>
<tr>
<td>Rohini</td>
<td>1.317**</td>
<td>1.242**</td>
<td>0.078</td>
<td>2.836**</td>
<td>-0.731**</td>
<td>0.190</td>
<td>-0.192**</td>
<td>0.014</td>
<td>-0.308**</td>
<td>-0.954**</td>
<td>0.571**</td>
<td>-0.102</td>
</tr>
<tr>
<td>Ashirwad</td>
<td>-2.943**</td>
<td>-2.884**</td>
<td>0.011</td>
<td>1.555**</td>
<td>0.374**</td>
<td>1.534**</td>
<td>-0.283**</td>
<td>-0.653**</td>
<td>0.235**</td>
<td>-2.703**</td>
<td>-0.426**</td>
<td>-0.139</td>
</tr>
<tr>
<td>SE ±</td>
<td>0.391</td>
<td>0.330</td>
<td>0.058</td>
<td>0.307</td>
<td>0.125</td>
<td>0.265</td>
<td>0.049</td>
<td>0.063</td>
<td>0.009</td>
<td>0.177</td>
<td>0.019</td>
<td>0.125</td>
</tr>
<tr>
<td>CD (P=0.05)</td>
<td>0.779</td>
<td>0.658</td>
<td>0.116</td>
<td>0.613</td>
<td>0.249</td>
<td>0.529</td>
<td>0.098</td>
<td>0.127</td>
<td>0.018</td>
<td>0.354</td>
<td>0.038</td>
<td>0.250</td>
</tr>
<tr>
<td>CD (P=0.01)</td>
<td>1.034</td>
<td>0.878</td>
<td>0.154</td>
<td>0.814</td>
<td>0.331</td>
<td>0.703</td>
<td>0.130</td>
<td>0.169</td>
<td>0.024</td>
<td>0.470</td>
<td>0.050</td>
<td>0.332</td>
</tr>
</tbody>
</table>

**, *: 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 o first siliqua and days to maturity) SCA effects for twelve yield and yield attributing characters in crosses of Indian mustard genotypes.

<table>
<thead>
<tr>
<th>Character</th>
<th>Crosses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plant height (cm)</td>
<td>DRMR 2243/Ashirwad (-4.724), DRMR 2326/Rohini (-5.70), DRMR 2341/NRCRD 2 (-3.404), DRMR 2398/NRCRD 2 (-3.237)</td>
</tr>
<tr>
<td>Point to first branch (cm)</td>
<td>DRMR 2178/NRCRD 2 (-4.212), DRMR 2243/NRCBH 101 (-2.831), DRMR 2269/Ashirwad (-3.157), DRMR 2326/Ashirwad (-6.266), DRMR 2341/NRCRD 2 (-9.229), DRMR 2398/NRCBH 101 (-2.681), DRMR 2486/NRCBH 101 (-3.081)</td>
</tr>
<tr>
<td>Number of primary branches</td>
<td>DRMR 2398/Rohini (0.589)</td>
</tr>
<tr>
<td>Point to first siliqua (cm)</td>
<td>DRMR 2178/NRCBH 101 (-2.306), DRMR 2243/Rohini (-1.469), DRMR 2243/Ashirwad (-1.057), DRMR 2269/Ashirwad (-2.466), DRMR 2326/NRCBH 101 (-1.34), DRMR 2341/Rohini (-1.273), DRMR 2448/NRCRD 2 (-1.668)</td>
</tr>
<tr>
<td>Siliqua length (cm)</td>
<td>DRMR 2269/NRCBH 101 (0.560), DRMR 2341/Rohini (0.409), DRMR 2341/Ashirwad (0.516), DRMR 2398/Rohini (0.492), DRMR 2448/NRCRD 2 (0.590)</td>
</tr>
<tr>
<td>Number of seeds / siliqua</td>
<td>DRMR 2178/NRCRD 2 (1.042), DRMR 2243/NRCBH 101 (1.569), DRMR 2269/NRCBH 101 (2.069), DRMR 2326/NRCRD 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/NRCRD 2 (1.00), DRMR 2486/Rohini (0.944), DRMR 2613/NRCBH 101 (1.278)</td>
</tr>
<tr>
<td>1000-seed weight (g)</td>
<td>DRMR 2178/NRCRD 2 (0.249), DRMR 2178/NRCBH 101 (0.228), DRMR 2243/NRCRD 2 (0.649), DRMR 2243/NRCBH 101 (0.137), DRMR 2269/NRCBH 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/NRCRD 2 (0.125), DRMR 2486/Rohini (0.395), DRMR 2486/Ashirwad (0.285), DRMR 2613/NRCBH 101 (0.059), DRMR 2613/Ashirwad (0.088)</td>
</tr>
<tr>
<td>Oil content (%)</td>
<td>DRMR 2178/NRCRD 2 (0.502), DRMR 2178/Rohini (1.058), DRMR 2243/NRCRD 2 (0.210), DRMR 2243/Rohini (0.176), DRMR 2269/Ashirwad (0.744), DRMR 2326/NRCRD 2 (0.194), DRMR 2341/Ashirwad (0.853), DRMR 2398/NRCBH 101 (0.305), DRMR 2448/NRCBH 101 (0.589), DRMR 2448/Ashirwad (0.458), DRMR 2613/NRCRD 2 (0.608), DRMR 2613/NRCBH 101 (0.445)</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>DRMR 2243/NRCBH 101 (-1.972), DRMR 2326/NRCBH 101 (-1.139), DRMR 2326/Ashirwad (-1.361), DRMR 2341/Ashirwad (-1.194), DRMR 2398/NRCRD 2 (-2.852), DRMR 2486/Rohini (-1.148), DRMR 2486/Ashirwad (-1.778),</td>
</tr>
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</table>
Table 6. Mean performance and estimates of better parent heterosis for seed yield in *Brassica juncea* genotypes.

<table>
<thead>
<tr>
<th>Lines</th>
<th>Testers</th>
<th></th>
<th></th>
<th></th>
<th>Mean seed yield of lines (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>NRCDR 2</td>
<td>NRCHB 101</td>
<td>Rohini</td>
<td>Ashirwad</td>
<td></td>
</tr>
<tr>
<td>DRMR 2178</td>
<td>22.88</td>
<td>22.80</td>
<td>24.51</td>
<td>25.50</td>
<td>28.520</td>
</tr>
<tr>
<td></td>
<td>(-19.79**)</td>
<td>(-20.04**)</td>
<td>(-14.06**)</td>
<td>(-10.59**)</td>
<td></td>
</tr>
<tr>
<td>DRMR 2243</td>
<td>19.43</td>
<td>42.79</td>
<td>24.57</td>
<td>18.39</td>
<td>17.727</td>
</tr>
<tr>
<td></td>
<td>(-31.28**)</td>
<td>(67.62**)</td>
<td>(5.10)</td>
<td>(1.49)</td>
<td></td>
</tr>
<tr>
<td>DRMR 2269</td>
<td>20.14</td>
<td>37.35</td>
<td>23.36</td>
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<tr>
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<td>(-28.78**)</td>
<td>(46.32**)</td>
<td>(-0.06)</td>
<td>(5.10)</td>
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<tr>
<td>DRMR 2326</td>
<td>23.22</td>
<td>31.45</td>
<td>21.70</td>
<td>17.45</td>
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<td></td>
<td>(-17.89**)</td>
<td>(23.20**)</td>
<td>(-7.19**)</td>
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<tr>
<td>DRMR 2341</td>
<td>38.28</td>
<td>26.64</td>
<td>26.60</td>
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<td>(35.37**)</td>
<td>(-2.66)</td>
<td>(-2.78)</td>
<td>(-29.35**)</td>
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<tr>
<td>DRMR 2398</td>
<td>19.55</td>
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<td>16.54</td>
<td>19.540</td>
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<td>(-30.86**)</td>
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<td>(4.56)</td>
<td>(-15.37**)</td>
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<tr>
<td>DRMR 2448</td>
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<td>(-31.34**)</td>
<td>(-36.68**)</td>
<td>(2.51)</td>
<td>(14.39**)</td>
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<tr>
<td>DRMR 2486</td>
<td>22.36</td>
<td>29.41</td>
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<td>(-20.92**)</td>
<td>(15.23**)</td>
<td>(29.84**)</td>
<td>(129.22**)</td>
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<tr>
<td>DRMR 2613</td>
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<td>18.180</td>
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<tr>
<td></td>
<td>(31.85**)</td>
<td>(14.95**)</td>
<td>(-12.52**)</td>
<td>(22.99**)</td>
<td></td>
</tr>
</tbody>
</table>

Mean seed yield of testers (g) 28.280 25.527 23.377 18.117

*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


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چیکه

گیاه (Brassica juncea) از دانه‌های روغنی مهم است که در کشاورزی هندوستان نقش عمدی ایفا می‌کند. از این رو، تولید ژنتیکی های ارزشمند بالا یکی از اهداف اصلی اصلاح زنبوریکی این گیاه در هندوستان بوده است. پژوهش‌ها نشان‌دهنده که هرکلیک‌ها در طی سال‌ها با هر میلیون کلمای GCA و SCA لاین‌ها ودلار و هتروژنیس بهتر و همچنین کنترل عم‌کرد گیاه و صفات مربوط به آن اشکال شد. چهار لاين نهایی به نام DRMR 2326/NRCHB 101، DRMR 2486، DRMR 2341، DRMR 2243/NRCHB 101، DRMR 2326/NRCHB 101 در کنار SCA و DRMR 2398/NRCHB 101، DRMR 2341/NRCDR 2 در ارگلات نژادی شده‌اند. SCA به عنوان بهترین ژن عمومی (general combiner) در این مطالعه معرفی شده است. DRMR 2326/NRCHB 101 می‌تواند همزمان با این اثبات اصلی داشته و اثبات قرار داشته باشد. در این مطالعه، نتایج نشان دهنده که ژن هریبید داشته و در میان هریبید هایی که بر اساس اثرات SCA به عنوان بهترین ژن عمومی شده DRMR 2613/NRCDR 2 و DRMR 2486/Ashirwad به همراه هریبید مراقبت‌های بازاریابی سیستم سپرایسی کمی با لاین‌های اشکال‌دهده باروری (restorer lines) تبدیل شوند.

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