

Diallel in brown sarson (*Brassica rapa*)

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In any breeding program, the common approach of selecting the parents on the basis of *per se* performance does not necessarily lead to fruitful results (Allard 1960). The information on genetic architecture and genetic parameters such as combining ability of parents and nature and extent of gene action for yield and its component traits has been found to be a useful tool in selection of parents which when used meticulously in a hybridization programme are likely to yield successful results. Brown sarson (*Brassica rapa* L.) occupies an important position in temperate conditions of Kashmir valley as it is the only oilseed crop cultivated. Breeding methods for improvement should be based on the nature and magnitude of genetic variance (combining ability)

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governing the inheritance of quantitative trait (Joshi and Dhawan 1966). Therefore, the present investigation was carried out to study the combining ability in respect of yield and yield attributes in brown sarson.

The experimental material for the present investigation comprised of ten diverse genotypes of brown sarson (*Brassica rapa* L.), viz. CR 1485, CR 1630, CR 1607, CR 1480, CR 2871, CR 2638, CR 1617, CR 2677, KOS 1 and KS 101 selected from the germplasm collection maintained at Regional Rice and Research Station (RR & RS) Khudwani. Forty five F₁ crosses (excluding reciprocals) were generated through a 10 × 10 diallel mating design during *rabi* 2007-08. The experiment was laid out in a completely randomized block design with two replications at Regional Rice and Research Station (RR & RS), Khudwani, Anantnag (E₁) and Experimental Farm of the Division of Plant Breeding & Genetics, SKUAST-K, Shalimar, Srinagar (E₂) during *rabi* 2008-09. The experimental plot comprised 3 rows each of 1 meter length. Row to row and plant to plant spacing was maintained at 30 and 10 cm. From each parent and F₁'s five plants were randomly taken from each replication and

Table 1 General combining ability effects for yield and yield attributing traits in Brown sarson (*Brassica rapa*) [Pooled over environments]

Parent	Plant height (cm)	Primary branches/plant	Number of siliquae on main raceme	Number of siliquae/plant	Number of seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
CR 1485	-4.812**	-0.097**	0.313**	-16.259**	1.054**	-0.165**	-0.585**
CR 1630	-9.151**	-0.696**	-3.658**	-12.582	-0.318**	-0.238**	-0.923**
CR 1607	-3.198**	0.041**	-0.410**	1.887**	-0.578**	0.036**	-0.011
CR 1480	-0.065	-0.139**	1.572**	-8.786**	-0.726**	0.246**	-0.200**
CR 2871	-0.712**	1.338**	0.392**	6.343**	0.524**	0.428**	1.325**
CR 2638	0.941**	0.175**	0.330**	23.512**	-0.817**	-0.087**	0.555**
CR 1617	6.222**	0.001	1.852**	2.637**	-0.141**	0.148**	0.335**
CR 2677	4.314**	0.347**	0.945**	-3.127**	2.966**	-0.182**	0.381**
KOS 1	0.992**	-0.483**	-0.343**	6.024**	-1.055**	-0.165**	-0.498**
KS 101	5.469**	-0.487**	-0.993**	0.351	-0.909**	-0.021	-0.379**
SE ± (g)	0.11	0.02	0.07	0.21	0.01	0.01	0.01
SE ± (g _i -g _j)	0.16	0.03	0.11	0.32	0.03	0.04	0.02

Table 2 Specific combining ability effects for yield and yield attributing traits in brown sarson (*Brassica rapa*) [pooled over environments]

Crosses	Plant height (cm)	Primary branches/plant	Number of siliquae on main raceme	Number of siliquae/plant	Number of seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
CR 1485 × CR 1630	5.203**	0.486**	2.533*	4.145*	0.289**	0.084**	0.056
CR 1485 × CR 1607	7.396**	1.592**	0.018	-4.850*	1.711**	0.600**	1.551**
CR 1485 × CR 1480	4.687**	0.927**	3.620**	-0.851	0.177**	0.285**	0.343**
CR 1485 × CR 2871	-4.302**	1.355**	0.216	39.720**	-0.879**	-0.302**	0.940**
CR 1485 × CR 2638	0.437	-0.612**	2.188**	-16.699**	1.978**	0.053	0.206**
CR 1485 × CR 1617	-2.341**	0.494**	-2.952**	-5.824**	0.059	0.150**	0.020
CR 1485 × CR 2677	-3.921**	-0.272**	0.128	16.365**	-0.992*	-0.197**	-0.028
CR 1485 × KOS 1	-3.944**	-0.134**	2.027**	-16.413**	0.612**	0.123**	-0.345**
CR 1485 × KS 101	0.782*	0.280**	1.233**	-22.288**	1.235**	0.127**	-0.476**
CR 1630 × CR 1607	-11.108**	-0.095**	3.996**	-9.702**	-0.259**	0.178**	-0.306**
CR 1630 × CR 1480	-6.673**	0.053	2.093**	-5.053*	0.544**	0.280**	0.311**
CR 1630 × CR 2871	6.526**	0.818**	-0.178	42.393**	-1.154**	-0.252**	0.816**
CR 1630 × CR 2638	-8.735**	0.299*	3.108**	6.174**	-0.035	-0.297**	0.248**
CR 1630 × CR 1617	5.529**	0.223**	-1.411**	6.349**	0.234**	0.155**	0.696**
CR 1630 × CR 2677	0.273	0.704**	-0.782**	-7.987**	1.127**	0.075*	-0.278**
CR 1630 × KOS 1	1.044*	0.282*	3.056**	-4.915*	0.996**	-0.094**	0.086*
CR 1630 × KS 101	7.948**	-0.116**	-0.643*	-10.840**	0.332**	0.352**	-0.042
CR 1607 × CR 1480	3.134**	0.708**	0.083	15.728**	-0.859**	-0.013	0.334**
CR 1607 × CR 2871	3.356**	0.211**	2.126**	0.573	1.461**	0.082*	0.337**
CR 1607 × CR 2638	2.205**	0.942**	0.743**	8.380**	1.002**	-0.181**	0.501**
CR 1607 × CR 1617	-5.208**	0.975**	3.118**	18.830**	0.169**	-0.013	0.883**
CR 1607 × CR 2677	2.390**	0.307**	0.555**	-2.222	1.389**	0.044	0.553**
CR 1607 × KOS 1	1.109**	-0.377*	1.125**	-4.735*	-0.486**	-0.058	-0.574**
CR 1607 × KS 101	1.040*	-0.353**	3.854**	-7.360**	-1.038**	0.023	-0.577**
CR 1480 × CR 2871	1.273**	-0.003	-1.212**	12.797**	0.713**	-0.405**	0.008
CR 1480 × CR 2638	5.282**	0.052	1.765**	-20.972**	0.120**	0.267**	-0.089*
CR 1480 × CR 1617	-5.273**	-0.122**	3.543**	-0.822	0.504**	-0.088*	0.233**
CR 1480 × CR 2677	2.197**	-0.408**	-2.035**	-8.808**	1.147**	0.197**	0.474**
CR 1480 × KOS 1	-0.423	-0.105*	1.360**	-1.336**	-0.358**	0.070*	-0.085*
CR 1480 × KS 101	4.230**	-0.201**	2.666**	-2.086	-0.040	0.078*	-0.088*
CR 2871 × CR 2638	6.584**	0.047	1.789**	-36.851**	0.767**	0.595**	0.126**
CR 2871 × CR 1617	2.574**	0.019	1.154**	0.499	0.336**	-0.215**	-0.210**
CR 2871 × CR 2677	3.072**	0.155**	0.398	-19.587**	-0.016	0.479**	0.012
CR 2871 × KOS 1	-2.917**	0.691**	1.376**	-8.265**	0.441**	0.445**	0.893**
CR 2871 × KS 101	1.929**	0.320**	2.062**	-7.315**	0.904**	0.349**	0.402**
CR 2638 × CR 1617	-3.109**	-0.086	-0.519**	-13.870**	0.458**	0.254**	-0.168**
CR 2638 × CR 2677	-0.397	0.368*	1.095**	-12.506**	1.511**	0.114**	0.209**
CR 2638 × KOS 1	5.162**	0.846**	8.280**	29.166**	-0.300**	-0.015	1.042**
CR 2638 × KS 101	-0.062	0.503**	-0.341	46.566**	-1.592**	-0.099**	0.724**
CR 1617 × CR 2677	-2.770**	0.547**	1.623**	3.919*	0.057	0.209**	0.161**
CR 1617 × KOS 1	8.877**	-0.340	1.833**	-18.384**	0.082*	0.163**	-0.533**
CR 1617 × KS 101	7.555**	0.759**	3.097**	8.491**	0.737**	0.096**	0.879**
CR 2677 × KOS 1	6.885**	0.334**	2.448**	11.830**	1.737**	-0.115**	0.864**
CR 2677 × KS 101	0.738	0.768**	0.879**	5.730**	0.738**	0.091**	1.036**
KOS 1 × KS 101	1.893**	-0.414*	-4.910**	12.451**	-0.238**	-0.211**	0.144**
SE ± (S _{ij})	0.374	0.036	0.233	1.727	0.042	0.032	0.031
SE ± (S _{ij} - S _{ik})	0.556	0.042	0.370	2.539	0.071	0.048	0.046

observations were recorded for plant height, number of primary branches/plant, number of siliquae on main raceme, number of seeds/siliquae, number of siliquae/plant, 1000-

seed weight and seed yield/plant.

The estimates of variance for gca and sca and their effects were computed according to model-1 (fixed effect

model) and method-II (parents and crosses, excluding reciprocals) as given by Griffing (1956).

The analysis of variance of combining ability (Table 1) reflected that both the general combining ability (gca) and specific combining ability (sca) mean squares were highly significant. This revealed that additive and non-additive gene effects seemed important in controlling the inheritance of all the traits. The estimates of variance due to dominance deviation (σ^2_D) were much higher than the corresponding additive genetic variance (σ^2_A) for all the traits, indicating preponderance of non-additive gene action as compared to additive gene action (pooled analysis over environments).

Combining ability gives useful information for the choice of parents in terms of expected performance of their crosses and progenies (Dhillon 1975). The gca effect is controlled by fixable additive gene and the cross involving parents with high gca will give better transgressive segregants in later generations. Therefore, selection of parents based on gca effects would have an impact on breeding program. High gca coupled with high *per se* performance is the indication of an outstanding parent with reservoir of superior genes. Hence, both mean performance and gca effects may be taken into account for parental selection (Singh and Dixit 2007, Dar *et al.* 2010).

A perusal of the general combining ability effects for parents (Table 2) indicated that none of the parents were good general combiner for all the traits studied. However, CR 2871, CR 2638, CR 2677 were observed to be good combiners for primary branches/plant; CR 2638, CR 1617, CR 2677, KOS 1 and KS 101 for plant height; CR 1480, CR 2638, CR 1617 and CR 2677 for number of siliquae on main raceme; CR 1607, CR 2871, CR 2638, CR 1617 and KOS 1 for number of siliquae/plant; CR 1607, CR 1480, CR 2871 and CR 1617 for 1000-seed weight; CR 2871, and CR 2638, CR 1617 and CR 2677 for seed yield/plant. These parents may therefore be used in crop breeding program aimed at improvement of the respective traits. Further, consideration of *per se* performance in combination with combining ability estimates was reported to provide a better criteria for choice of superior parents in hybridization program (Khan and Khan 2005). The parents CR 2638, CR 1617, CR 1607 and CR 2871 exhibited significant and desirable gca effects for most of the traits and had also recorded *per se* performance for the traits. Further, these parents also recorded desirable gca effects for seed yield/plant. Hence, these parents may be used in the hybridization program aimed at development of superior genotypes.

A perusal of the Table 3 revealed that among 45 F_1 's, CR 1485 \times CR 1607 was exceptionally good combiner for seed yield/plant. While as cross combination CR 1617 \times KOS 1, CR 1630 \times KS 101 and CR 1617 \times KS 101 were desirable for plant height; CR 1485 \times CR 1607, CR 1485 \times CR 2871, CR 1607 \times CR 2638 for primary branches/plant; CR 1630 \times CR 1607, CR 1607 \times KOS 1, CR 1480 \times CR 1617 for

number of siliqua on main raceme, CR 2638 \times KS 107, CR 1630 \times CR 2871, CR 1485 \times CR 2871 for number of siliqua/plant; CR 1485 \times CR 2638, CR 1485 \times CR 1607, CR 2677 \times KOS 1 for number of seeds/sliqua and CR 1485 \times CR 1607, CR 2871 \times CR 2638, CR 2871 \times CR 2677 for 1000 seed weight.

In all these best combinations, parents involved were of low \times low or low \times average gca effects. This may be due to the presence of genetic diversity in the form of dispersed genes for these characters. Some of the crosses showed significant sca effects (Table 4) which had the combination of high \times high sca effects. Such high \times high gca combinations indicates additive type of interaction between parents for the expression of the characters. In view of the importance of additive \times additive effects and its possibility of fixation, single plant selection could be practiced in further segregating generations to isolates superior pure lines from such combinations.

Cross combinations, viz. CR 1607 \times CR 2638 for primary branches/plant, CR 1485 \times CR 1480 and CR 1480 \times CR 1617 for number of siliquae on main raceme, CR 2638 \times KOS 1 and CR 1607 \times CR 1617 for number of siliquae/plant and CR 1630 \times KOS 1 for days to maturity showed low sca effects though the parents showed high \times high gca effects. Thus, it revealed that high \times high type of combinations not necessary results into high sca effects. This is probably due to internal cancellation of gene effects in these parents.

SUMMARY

Based on the results obtained in the present study, it is advocated that the parents namely CR 2638, CR 1617, CR 1607 and CR 2871 identified as good general combiners and the identified specific cross combinations namely CR 2871 \times CR 2638, CR 1485 \times CR 1607, CR 2871 \times CR 1617, CR 1485 \times CR 2871 and CR 2871 \times KOS 1 should be exploited through heterosis breeding should be used in recombination programme for tapping desirable transgressive segregants in segregating generations. The inter-mating between selected segregants in advanced generations would help to accumulate favorable, desirable alleles for further improvement in seed yield and its component traits in brown sarson.

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