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Analysis of combining ability in brown sarson (*Brassica rapa* L.) under temperate conditions

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A study was undertaken to estimate the combining ability in brown sarson through diallel analysis involving ten diverse genotypes. The combining ability analysis revealed significant mean squares for general and specific combining ability for all the traits studied. The estimates of variance due to dominance deviation ($\sigma^2{}_D$) were much higher than the corresponding additive genetic variance ($\sigma^2{}_A$) for all the traits. The predictability ratio was less than unity for all the traits which indicated that performance on general combining ability of parents alone would not be advisable to select materials in segregating generations, but a combination involving both general and specific combining ability of the parents and particular crosses along with their *per se* performance would be more useful in selecting materials in the segregating generations. None of the parents revealed significant and desirable general combining ability effects for all the traits. The study of specific combining ability effects revealed that none of the crosses was a desirable specific combiner for all the traits under study. However, several cross combinations were observed to have highest desirable significant sca effects for these traits.

Key words: Combining ability, general combining ability (gca), specific combining ability (sca), brown sarson.

INTRODUCTION

In most breeding programs, the common approach of selecting the parents on the basis of *per se* performance has 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 due to its fitness in the cropping sequences. However, the yields are disappointingly low and hover around 0.8 to 1.0 tonnes/hectare. There is a dire need of developing high yielding genotypes of brown sarson to make its cultivation profitable. Breeding methods for crop improvement are organised based on the nature and magnitude of genetic variance and effective combination of parental lines for deriving desirable segregants based on combining ability analysis (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.

MATERIALS AND METHODS

The experimental material for the present investigation comprised

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Table 1. Analysis of variance for combining ability and estimates of components of variance for yield and yield attributing traits in Brown sarson (*Brassica rapa* L.) Pooled over environments.

Source of variation	d.f.	Plant height (cm)	Primary branches/ plant	Number of siliquae on main raceme	Number of siliquae plant^{-1}	Number of seeds siliqua^{-1}	1000-seed weight (g)	Seed yield plant^{-1} (g)
Environments	1	42.90**	0.41**	88.25**	42.50**	4.41**	1.07**	1.61**
gca	9	551.34**	7.80**	58.14**	3051.88**	30.71**	1.11**	10.52**
sca	45	60.49	1.46**	28.37**	584.37**	2.85**	0.17**	1.61**
gca × environments	9	15.40**	0.05**	30.11**	5.80	0.01**	0.04**	0.02**
sca × environments	45	9.19**	0.03**	14.51**	20.18**	0.02**	0.02*	0.03**
Pooled	108	0.34	0.002	0.15	7.03	0.005	0.01	0.002
$\hat{\sigma}^2 g$	-	22.95	0.32	2.41	126.86	1.22	0.06	0.43
$\hat{\sigma}^2 s$	-	30.07	0.73	14.10	288.67	1.46	0.08	0.61
$\hat{\sigma}^2 A$	-	91.80	1.28	9.64	507.44	4.88	0.24	1.72
$\hat{\sigma}^2 D$	-	120.28	2.92	56.40	1154.68	5.84	0.32	2.44
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.76	0.44	0.17	0.43	0.83	0.75	0.70
$2\hat{\sigma}^2 g / 2\hat{\sigma}^2 g + \hat{\sigma}^2 s$	-	0.53	-0.45	0.32	0.46	0.62	0.60	0.58
$[\hat{\sigma}^2 D / \hat{\sigma}^2 A]^{½}$	-	1.14	1.51	2.41	1.50	1.09	1.33	1.19

*,** = significant at 5% and 1% level of significance.

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 and RS), Khudwani. CR-1485, CR-1630, CR-1607, CR-1480, CR-2871, CR-2638, CR-1617, CR-2677 are the germplasm accessions received from various gene banks (IPKGermany, Nordic gene bank) whereas KOS-1 and KS-101 are the varieties developed by SKUAST-K. Forty five F$_1$ crosses (excluding reciprocals) were generated through a 10 × 10 diallel mating design during *rabi* (winter) 2008 to 2009. The field experiment was laid out in a completely randomized block design with two replications at RR and RS, Khudwani, Anantnag (E$_1$) and Experimental Farm of the Division of Plant Breeding and Genetics, SKUAST-K, Shalimar, Srinagar (E$_2$) during *rabi* 2010 to 2011. The experimental plot comprised 3 rows each of 1 m length. Row to row and plant to plant spacing was maintained at 30 and 10 cm. From each parent and F$_1$'s five plants were randomly taken from each replication and observations were recorded for plant height, number of primary branches plant-^{1}, number of siliquae on main raceme, number of seeds siliquae-^{1}, number of siliquae plant-^{1}, 1000-seed weight and seed yield plant-^{1}. The estimates of variance for general combining ability (gca) and specific combining ability (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) using WINDOSTAT software.

RESULTS AND DISCUSSION

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 trangressive 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^{-1}; 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^{-1}; 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^{-1}. These parents may therefore be used in crop breeding program aimed

Table 2. General combining ability effects for yield and yield attributing traits in Brown sarson (*Brassica rapa* L.) Pooled over environments.

S/N	Parent	Plant height (cm)	Primary branches/ plant	Number of siliquae on main raceme	Number of siliquae plant^{-1}	Number of seeds siliqua^{-1}	1000-seed weight (g)	Seed yield plant^{-1} (g)
1.	CR-1485	-4.812**	-0.097**	0.313**	-16.259**	1.054**	-0.165**	-0.585**
2.	CR-1630	-9.151**	-0.696**	-3.658**	-12.582	-0.318**	-0.238**	-0.923**
3.	CR-1607	-3.198**	0.041**	-0.410**	1.887**	-0.578**	0.036**	-0.011
4.	CR-1480	-0.065	-0.139**	1.572**	-8.786**	-0.726**	0.246**	-0.200**
5.	CR-2871	-0.712**	1.338**	0.392**	6.343**	0.524**	0.428**	1.325**
6.	CR-2638	0.941**	0.175**	0.330**	23.512**	-0.817**	-0.087**	0.555**
7.	CR-1617	6.222**	0.001	1.852**	2.637**	-0.141**	0.148**	0.335**
8.	CR-2677	4.314**	0.347**	0.945**	-3.127**	2.966**	-0.182**	0.381**
9.	KOS-1	0.992**	-0.483**	-0.343**	6.024**	-1.055**	-0.165**	-0.498**
10.	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

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 per 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 × CR-1607 was exceptionally good combiner for seed yield per plant. While as cross combination CR-1617 × KOS-1,CR-1630 × KS-101 and CR-1617 × KS-101 were desirable for plant height; CR-1485 × CR-1607, CR-1485 × CR-2871, CR-1607 × CR-2638 for primary branches plant^{-1}; CR-1630 × CR-1607, CR-1607 × KOS-1, CR-1480 × CR-1617 for number of siliqua on main raceme,CR-2638 × KS-107, CR-1630 × CR-2871, Cr-1485 × CR-2871 for number of siliqua plant^{-1} ; CR-1485 × CR-2638, CR-1485 × CR-1607,CR-2677 × KOS-1 for number of seeds siliqua^{-1} and CR-1485 × CR-1607, CR-2871 × CR-2638, CR-2871 × CR-2677 for 1000 seed weight.

In all these best combinations, parents involved were of low × low or low x 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 × high sca effects. Such high × high gca combinations indicates addictive type of interaction between parents for the expression of the characters. In view of the importance of additive × 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 × CR-2638 for primary branches plant^{-1}, CR- 1485 × CR-1480 and CR- 1480 × CR-1617 for number of siliquae on main raceme, CR- 2638 × KOS-1 and CR-1607 × CR-1617 for number of siliquae plant^{-1} and CR- 1630 × KOS-1 for days to maturity showed low sca effects though the parents showed high × high gca effects. Thus, it revealed that high × high type of combinations not necessary results into high sca effects. This is probably due to internal cancellation of gene effects in these parents. 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 × CR-2638, CR-1485 × CR-1607, CR- 2871 × CR-1617, CR- 1485 × CR-2871 and CR- 2871 × KOS-1 should be exploited through heterosis breeding should be used in recombination programme for tapping desirable trangressive segregants in segregating generations. The inter-mating between selected segregants in advanced

Table 3. Specific combining ability effects for yield and yield attributing traits in Brown sarson (*Brassica rapa* L.) pooled over environments.

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

generations would help to accumulate favorable, desirable alleles for further improvement in seed yield

Table 4. Top ranking specific cross combinations for different traits on the basis of sca, *per se* performance and gca of parents involved in brown sarson (pooled analysis).

S/N	Trait	*Per se* performance	Sca effect	Gca effect of parents
1.	Plant height (cm)	CR- 1617 x KS-101	CR-1617xKOS-1	High x High
		CR- 1617 x KOS-1	CR-1630xKS-101	Low x High
		CR- 2677 x KOS-1	CR-1617xKS-101	High x High
		CR- 2627 x KS-101	CR-1485xCR-1607	Low x Low
		CR- 1480 x KS-101	CR-2677xKOS-1	High x High
2.	Primary branches plant^{-1}	CR- 1485 x CR-2871	CR-1485xCR-1607	Low x High
		CR- 2871 x CR-2677	CR-2871xCR-2871	Low x High
		CR- 1607 x CR-2871	CR-1607xCR-1617	High x Average
		CR- 2871 x CR-2638	CR-1607xCR-2638	High x High
		CR- 2871 x KOS-1	CR-1485xCR-1480	Low x Low
3.	Number of siliquae on main raceme	CR- 2638 x KOS-1	CR-2638xKOS-1	High x Low
		CR- 1480 x CR-1617	CR-1630xCR-1607	Low x Low
		CR- 1485 x CR-1480	CR-1607xKS-101	Low x Low
		CR- 1607 x CR-1617	CR-1485xCR-1480	High x High
		CR- 1617 x CR-2677	CR-1480xCR-1617	High x High
4.	Number of siliquae plant^{-1}	CR- 2638 x KS-101	CR-2638xKS-101	High x Average
		CR- 2638 x KOS-1	CR-1630xCR-2871	Low x High
		CR- 1630 x CR-2871	CR-1485xCR-2871	Low x High
		CR- 1607 x CR-2638	CR-2638xCR-KOS-1	High x High
		CR- 1485 x CR-2871	CR-1607xCR-1617	High x High
5.	Number of seeds siliqua^{-1}	CR- 1607 x CR-2677	CR-1485xCR-2638	High x Low
		CR- 1630 x CR-2677	CR-2677xKOS-1	High x Low
		CR- 2638 x CR-2677	CR-1485xCR-1607	High x Low
		CR- 2677 x KOS-1	CR-2638xCR-2677	Low x High
		CR- 2871 x CR-2677	CR-1607xCR-2871	Low x High
6.	1000-seed weight (g)	CR- 2871 x CR-2638	CR- 1485 x CR-1607	Low x High
		CR- 2871 x KS-101	CR- 2871 x CR-2638	High x Low
		CR- 2871 x CR-2677	CR- 2871 x CR-2677	High x Low
		CR- 2871 x KOS-1	CR- 2871 x KOS-1	High x Low
		CR- 1607 x CR-2871	CR- 1485 x CR-1480	Low x High
7.	Seed yield plant-1 (g)	CR- 2871 x CR-2638	CR- 2871 x CR-2638	Low x Average
		CR- 2871 x KS-101	CR- 2638 x KOS-1	High x Low
		CR- 2871 x CR-2677	CR- 2677 x KS-101	High x Low
		CR- 1485 x CR-2871	CR- 1485 x CR-2871	Low x High
		CR- 1607 x CR-2871	CR- 2871 x KOS-1	High x Low

and its component traits in brown *sarson*.

REFERENCES

Allard RW (1960). Principles of Plant Breeding. John Wiley and Sons, Inc. New York, pp. 463-470.

Dar ZA, Wani,Shafiq A, Ahmad I, GulZaffar (2010). Heterosis and combining ability in brown sarson (*Brassica rapa* L.). Cruciferae Newslett. 29:46-50.

Dhillon BS (1975). The application of partial diallel cross in plant breeding - A Rev. Crop Improv. 2:1-7.

Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Australian J. Biol. Sci. 9:463-493.

Joshi AB, Dhawan NL (1966). Genetic improvement in yield with special reference in self-fertilizing crops. Indian J. Genet. Breed. 26:21-36.

Khan FA, Khan RSA (2005). Inheritance pattern of quantitative characters in *Brassica napus.* Int. J. Agric. Biol. 7(3):420-423.

Singh RK, Dixit P (2007). Heterosis and combining ability studies for seed yield, its attributes and oil content in Indian mustard (*Brassica juncea* (L. Czern and Coss). Crop Improv. 34(2):192-196.