Study of combining ability for yield and yield attributing traits in *Brassica rapa* ssp. Brown Sarson

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Abstract

The present investigation on *Brassica rapa* ssp. *Brown Sarson* genotypes is an attempt to study variations and to generate variability through hybridization and also to obtain genetic information on some yield attributes for selection in segregating generations. Seven promising parents *viz.* KBS-33, KBS-38, KBS-49, KBS-57, KBS-81, Shalimar Sarson-1 and Gulchin were selected and crossed in a half diallel mating during rabi 2011-12 at MRCFC, Khudwani, SKUAST-Kashmir. Twenty one F_1's generated along with seven parents were evaluated during *rabi* 2012-13 for various quantitative traits. Analysis of variance for combining ability revealed highly significant differences for all the traits. Parent KBS-49 was identified as best combiner for yield and yield contributing traits on the basis of significant gca effects. KBS-49 x KBS- 57, KBS-49 x KBS-81 and KBS-49 x Gulchin were the best cross combinations for yield and other traits. Based on the results obtained in the present study, it is advocated that the parents and crosses identified should be exploited through heterosis breeding and should be used in recombination programme for tapping desirable trangressive segregants in segregating generations. The inter-mating between selected segregants in advanced generations would help to accumulate favorable alleles for further improvement in seed yield and its component traits in Brown Sarson.

Introduction

The Brassicaceae family consists of many important field crops and vegetables including rapeseed. Rapeseed is the world's second leading source of protein meals. The main rapeseed-producing regions of the world are China, Canada, India and Northern Europe. Brown Sarson (*Brassica rapa* L. spp Brown Sarson) occupies an important position in temperate conditions of Kashmir valley as it is the only oilseed crop cultivated. 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 (Dar *et al*., 2013). Genetic improvement approaches in this crop are limited and based mainly on selection methods. 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).

Therefore, breeding methods for improvement should be based on the nature and magnitude of genetic variance (combining ability) governing the inheritance of quantitative trait (Joshi and Dhawan, 1966).

The concept of good combining ability refers to the potential of a parent to produce by its crossing with another parent a superior offspring for the breeding process and it is widely used in the breeding of cross-pollinated plants. Information and exact study of combining ability can be useful in regard to selection of breeding methods and selection of lines for hybrid combination. For Brown Sarson improvement, breeding methods like inter-varietal hybridization and inter-specific hybridization have potential to broaden the genetic base either through creation of variability or introgression of desirable genes from wild species (Dar *et al*., 2011). The choice of the parents is an important step in

hybridization program to create variation for selection of useful recombinants. Advancement in the yield of *Brassica* requires certain information regarding the nature of combining ability of parents available for use in the hybridization program (Shiva, 2011). Therefore, the present study was undertaken to examine the combining ability patterns of selected lines in a diallel cross for various quantitative traits and to identify candidates for promising cross combinations.

Materials and Methods

The present investigation was undertaken to study the gene action and combining ability for yield and yield attributing traits in *B. rapa* spp. Brown Sarson under temperate conditions of Kashmir valley. Seven promising genotypes of *B. rapa* spp Brown Sarson viz KBS-33, KBS-38, KBS-49, KBS-57, KBS-81, Shalimar Sarson-1 and Gulchin were selected and involved a 7x7 half diallel mating design of Griffing (1956) during rabi 2011-12 at MRCFC, Khudwani, SKUAST-Kashmir. The set of 21 F_1'S along with seven parents were evaluated

at MRCFC, Khudwani, SKUAST-Kashmir during *rabi* 2012-13 for various quantitative traits *viz.*, No. primary branches plant^{-1}, No. of secondary branches plant^{-1}, No. of pods plant^{-1}, 1000 grain weight (g) and seed yield ha^{-1} in a completely randomized block design. Each genotype was replicated thrice and grown in a 3m row length with the crop geometry of 30x10cm. Data recorded were subjected to biometrical analysis. All the recommended practices were adopted to raise a good crop.

Results and Discussion

Combining ability gives useful information for the choice of parents in terms of expected performance of their crosses and progenies (Dhillon, 1975). The said analysis was performed to obtain information on the combining ability effects of parents and their crosses along with nature and magnitude of gene action involved in the expression of various quantitative traits. Analysis of variance for yield & yield attributing traits are presented in Table-1. Perusal of the said Table 1 reveals highly significant differences for all the

Table 1: Analysis of variance for yield and yield attributing traits in *B. rapa* spp. Brown Sarson

Source of variation	df	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	1000 seed weight (g)	Seed yield (Qha^{-1})
Replication	2	0.06	0.01	44.20	0.02	203.58
Treatments	27	0.78**	1.86**	503.02**	0.28**	75713.91**
Parents	6	0.19**	2.39**	397.37**	0.16**	91424.89**
Hybrids	20	0.95**	1.04**	437.07**	0.20**	35518.73**
Parent *vs* hybrids	1	1.06**	15.15**	2455.94**	2..68**	785351.70**
Error	54	0.03	0.05	23.28	0.03	256.30
Total	83	0.28	0.64	179.85	0.11	24801.48

*, ** Significant at 5 and 1 per cent levels, respectively

characters among the parents and crosses, indicating that the material selected was diverse resulting in creation of substantial variability in the crosses. Performance of crosses was also highly significant when compared with the parents for all the traits. Analysis of variance for general and specific combining ability (Table 2) revealed that mean squares were highly significant indicating importance of both additive and non-additive components in the inheritance of these characters. Similar results for yield and yield attributing traits

have also reported by Dar *et al*. (2013) in B. *rapa* and Farshadfar *et al.* (2013) in B. *napus*. Larik and Rajput (2000); and Yadav *et al*., (2005) also reported additive gene action in controlling number of primary branches which contradict the results of present study.

Variances due to sca ($\hat{\sigma}^2 s$) was higher in magnitude than their corresponding gca variances ($\hat{\sigma}^2 g$) for all the traits. The estimates of additive genetic

Table 2: Analysis of variance for combining ability and estimates of components of variance for yield and yield attributing traits in *B. rapa* spp. Brown Sarson

Source of variation	df	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	1000 seed weight (g)	Seed yield (Qha^{-1})
GCA	6	0.25**	1.42**	314.73**	0.08**	25339.03**
SCA	21	0.26**	0.40**	125.66**	0.10**	25209.10**
Error	54	0.01	0.01	7.76	0.01	85.43
$\hat{\sigma}^2 g$		0.02	0.15	34.10	0.01	2805.95
$\hat{\sigma}^2 s$		0.25	0.37	117.90	0.08	25123.66
$\hat{\sigma}^2 A$		0.05	0.31	68.21	0.01	5611.91
$\hat{\sigma}^2 D$		0.25	0.37	117.89	0.08	25123.66
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$		0.20	0.83	0.57	0.12	0.22
$[\hat{\sigma}^2 D / \hat{\sigma}^2 A]^{1/2}$		2.23	1.09	1.31	2.82	2.11

*, ** Significant at 5 and 1 per cent levels, respectively

variance and dominance variance revealed that the magnitude of dominance variance was higher in range, indicating preponderance of non-additive gene action. The ratio of additive genetic variance to dominance variance ($\acute{o}^2A/\acute{o}^2D$) was less than unity for all the traits, whereas estimates of average degree of dominance revealed preponderance of over dominance for all yield and yield attributing traits.

The gca effects estimated through combining ability analysis (Griffing, 1956) provide a measure to identify potent parents that would on an average nick well in forecasting the behavior of crosses and also help in obtaining homozygous lines from heterozygous hybrid populations for improving a particular trait. General combining ability of parents (Table 3) has revealed that none of the parents showed significant combining ability for all the traits.

Table 3: General combining ability of parents for yield and yield attributing traits in *B. rapa* spp. *Brown Sarson*

Parents	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	1000 seed weight (g)	Seed yield (Qha^{-1})
KBS-33	-0.17**	-0.09**	-4.22**	-0.15**	-48.53**
KBS-38	-0.12**	-0.18**	-0.17	0.04	0.91
KBS-49	0.30**	0.84**	11.75**	0.13**	87.57**
KBS-57	-0.07*	-0.07	-1.30	-0.04	-72.79**
KBS-81	0.02	0.08	2.50**	0.05	39.24**
Shalimar Sarson-1	-0.08*	-0.40**	-6.43**	-0.06**	-5.09
Gulchin	0.13**	-0.17**	-2.10*	0.04	-1.31
SE± (g)	0.06	0.08	1.72	0.06	5.71
SE± (g$_i$-g$_j$)	0.10	0.12	2.63	0.10	8.73

*, ** Significant at 5 and 1 per cent levels, respectively

Table 4: Top ranking cross combinations for yield and yield attributing characters *in B. rapa* spp. Brown Sarson

Trait	Cross combination	SCA effects	GCA effects of parents
Primary branches plant^{-1}	KBS-49 x KBS-57	0.68	High x Low
	KBS-49 x Gulchin	0.68	High x High
	KBS-33 x KBS-38	0.38	Low x Low
Secondary branches plant^{-1}	KBS-33 x Gulchin	0.78	Low x Low
	KBS-38 x KBS-81	0.62	Low x Average
	KBS-33 x KBS-38	0.59	Low x Low
No. of pods plant^{-1}	KBS-81 x Shalimar Sarson-1	18.40	High x Low
	KBS-38 x KBS-81	15.14	Average x High
	KBS-49 x KBS-81	12.88	High x High
1000 seed weight (g)	KBS-38 x KBS-81	0.46	Average x Average
	KBS-33 x Gulchin	0.40	Low x Average
	KBS-81 x Shalimar Sarson-1	0.37	Average x Low
Seed yield (Qha^{-1})	KBS-49 x KBS-57	218.74	High x Low
	KBS-49 x Gulchin	173.92	High x Average
	KBS-38 x KBS-81	163.37	Average x High

However only one parent, KBS-49, observed significant positive gca effect revealing high combining ability of this genotype for No. primary branches plant^{-1}, No. of secondary branches plant^{-1}, No. of pods plant^{-1}, 1000 grain weight (g) and seed yield ha^{-1}, whereas, it was observed that KBS-81 showed significant gca effect for No. of primary branches plant^{-1} and seed yield ha^{-1}. Contrarily, KBS-33 showed significant negative gca effect for all the traits. From the results of this study, it can be concluded that genotype KBS-49 possesses desirable alleles.

None of the cross combinations showed significant sca effect for all the traits. Cross combination KBS-33 x Gulchin observed high significant sca effect for No. of secondary branches plant^{-1} and 1000 grain weight (g). KBS-49 x KBS-57 and KBS-49 x Gulchin showed positive significant combining ability for No. of primary branches plant^{-1} and seed yield ha^{-1}. Top ranking cross combination involved HxH, HxL, LxH and LxL combiners (Table 4). The cross combinations involving either both or one parent with high gca effect indicated additive gene action in controlling the expression of respective trait. These cross combinations would give rise to transgressive segregants in later generations (Singh *et al.*, 2010) which matched with the results

obtained by Yogeshwar and Sachan, (2003). 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 isolate superior pure lines from such combinations. While cross combinations involving L x L combiners reflected non-additive gene action, which is non- fixable in nature and could be exploited only through heterosis breeding for further improvement of the respective trait. Similar findings were also reported by Srivastava *et al.* (2009) and Singh *et al.* (2009). Thus it is revealed that high × high type of combinations not necessarily 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 KBS-49 and KBS-81 were identified as good general combiners and the identified specific cross combinations namely KBS-49 x KBS-57, KBS-49 x Gulchin and KBS-38 x KBS-81 should be exploited through heterosis breeding; these specific cross combinants should also be used in recombination programme for tapping desirable trangressive 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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