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GENETICAL STUDIES FOR YIELD AND OIL CONTENT IN *BRASSICA JUNCEA* (L.) CZERN & COSS

J. N. Singh, Mahesh C. Yadav and I. A. Sheikh

Division of Genetics, Indian Agricultural Research Institute
New Delhi 110012

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ABSTRACT

Combining ability analysis of eight diverse cultivars for ten characters in *Brassica juncea* (L.) Czern & Coss revealed high magnitude of σ^2_s for most of the characters. However, σ^2_g was high only for plant height, siliqua length and 1000-seed weight for which high estimates of $\hat{h}^2$ was also recorded. The parent variety PR-1108 was the best general combiner for seed yield, oil content, 1000-seed weight, plant height, number of primary and secondary branches and length of siliqua. PR-1108 was also involved in the best cross combinations for seed yield, oil content 1000-seed weight and number of branches. Glossy mutant, an early white flowered parent, showed desirable gca for early flowering, reduced plant height and it was involved in crosses with high sca for seed yield, oil content and seed per siliqua but its per se performance and gca was low. High BP heterosis was recorded in the crosses PR-1108 x BJ-679 (77.6%) and BJ-1257 x Glossy mutant (13.1%) for seed yield and oil content, respectively. Oil content was positively associated with 1000-seed weight and seed yield indicating the possibility of simultaneous improvement for these characters, Yellow colour of corolla was dominant over white and segregated in 15:1 ratio, indicating control of duplicate genes.

Key words: *Brassica juncea*, combining ability, correlation, diallel, flower colour.

Low yield levels of Indian mustard has probably been affected by a number of factors such as past history of selection, environmental conditions and edaphic situations where crop is being cultivated from ancient time [1]. The present study was planned to understand the genetic architecture of diverse parents, their combining abilities and association between oil content and seed yield to facilitate the formulation of future breeding programme. Exploitation of heterosis may also change the yield level, however, it is possible only through an effective cytoplasmic–genetic male sterile system. Mode of inheritance of white colour of corolla against yellow along with above aspects will be dealt in this presentation.

MATERIALS AND METHODS

The experimental material consisted of eight parents of *Brassica juncea* and F_1s of their direct as well as reciprocal crosses. Ten developmental, quantitative and qualitative characters were studied. The material was sown in plots of two 5 m long rows planted at 45 x 15 cm spacing in RBD with three replications. Selected F_2 populations with white coloured flower were grown in the next season in large plots. The data were statistically analysed for combining ability by Method 1, Model I of Griffing [2]. Correlation coefficients among oil content, 1000-seed weight and seed yield were calculated as per [3]. The χ^2 test was used to determine the goodness of fit of segregation ratio as suggested by [4].

RESULTS AND DISCUSSION

Mean sum of squares due to gca and sca were significant for most of the characters. The magnitude of $\hat{\sigma}^2_s$ being higher than $\hat{\sigma}^2_g$ for all the characters except plant height, siliqua length and 1000-seed weight (Table 1). This indicated preponderance of non-additive gene action as was also observed earlier [5, 6]. Higher magnitude of $\hat{\sigma}^2$ for number of primary, secondary

Table 1. ANOVA (mean squares) for combining ability for ten characters in a 8 x 8 diallel cross in *Brassica juncea*

Source	d.f.	Days to flowering	Plant height	No. of primary branches	No. of secondary branches	No. of tertiary branches	Length of siliqua	Seeds per siliqua	1000-seed weight	Seed yield	Oil content
Gca	7	46.9**	1002.7**	22.1**	185.4**	571.0**	2.4**	7.4**	4.5**	139.5**	20.9**
Sca	28	19.7**	120.5**	2.1**	69.0**	84.2**	0.2**	5.2**	0.3	88.0**	4.4**
Reciprocal cross effects	28	11.7**	118.2**	3.1**	43.6**	114.4**	0.5**	1.2*	0.4*	49.5*	3.5*
Error	126	0.3	42.5	0.5	14.6	7.5	0.1	0.6	0.2	28.3	0.8
$\hat{\sigma}^2_g$		1.7	55.2	1.2	7.3	30.5	0.1	0.1	0.3	3.3	1.0
$\hat{\sigma}^2_s$		10.9	43.8	1.3	30.6	43.1	0.1	2.6	0.1	33.5	2.0
$\hat{\sigma}^2_r$		5.7	37.8	1.3	14.2	53.5	0.2	0.3	0.1	10.6	1.4
$\hat{\sigma}^2_g/\hat{\sigma}^2_s$		0.2	1.3	0.9	0.2	0.7	1.7	0.1	13.0	0.1	0.5
$\hat{h}^2$		9.4	30.8	27.7	11.0	22.7	29.2	4.1	44.1	4.3	19.0

*,**Significant at 5% and 1% levels, respectively.

and tertiary branches, siliqua length, seeds per siliqua, seed yield per plant, and oil content indicated the importance of nucleo cytoplasmic interaction in the expression of these characters. Similar results were reported for several characters in this crop [7].

The per se performance and gca effects of parents showed that PR-1108 was the best general combiner for most of the characters including oil content, followed by BJ-679 and BJ-1235, while BJ-1257 had desirable gca for oil content and 1000-seed weight (Table 2). The estimates for different strains showed that desirable gca effects for different traits were dispersed among different parents.

Table 2. Estimates of gca effects of parents for ten characters in a 8 x 8 diallel cross of *Brassica juncea*

Source	Days to flowering	Plant height	No. of primary branches	No. of secondary branches	No. of tertiary branches	Length of siliqua	Seed per siliqua	1000-seed weight	Seed yield	Oil content
BJ 679	1.3^{**}	6.4^{**}	0.3^{*}	1.6	-2.7^{**}	0.6^{**}	1.0^{**}	0.3^{**}	1.6	1.0^{**}
PR-1108	1.1^{**}	6.3^{**}	0.6^{**}	1.3	3.5^{**}	0.3^{**}	-0.0	0.7^{**}	3.3^{**}	1.0^{**}
B-55	-1.8^{**}	-7.9^{**}	-1.2^{**}	-1.6	0.5	-0.5^{**}	0.1	-0.4^{**}	0.4	-1.8^{**}
RW-4/86	0.4^{**}	2.0	0.5^{**}	-0.6	-4.5^{**}	-0.1^{**}	0.7^{**}	-0.2^{**}	-3.7^{**}	0.9^{**}
Poorbijaya	0.2^{**}	-2.2	0.5^{*}	1.0	1.4^{*}	-0.2^{**}	-0.1	-0.2	2.0	0.4
Glossy mutant	-2.9^{**}	-15.1^{**}	-2.0^{**}	-5.5^{**}	-6.0^{**}	-0.3^{**}	0.2	-0.7^{**}	-4.4^{**}	-1.0^{**}
BJ-1257	-1.0^{**}	3.5^{*}	-0.5^{**}	-2.4^{**}	-4.5^{**}	-0.1	-0.9^{**}	0.8^{**}	-1.8	0.8^{**}
BJ-1235	2.0^{**}	7.0^{**}	1.7^{**}	6.1^{**}	12.3^{*}	0.3^{**}	-0.9^{**}	-0.2^{*}	2.7^{*}	-1.2^{**}
SE (gi)	0.1	1.5	0.2	0.9	0.6	0.1	0.2	0.1	1.2	0.2
CD at 5%	0.2	3.0	0.3	1.7	1.2	0.1	0.4	0.2	0.4	0.4
CD at 1%	0.3	3.9	0.4	2.3	1.6	0.1	0.5	0.3	3.2	0.5

*,**Significant at 5% and 1% levels, respectively.

Six crosses showed significant sca for desirable characters (Table 3). The sca of the cross BJ-679 x PR-1108 was significant for seed yield and 1000-seed weight and both of parents of this cross showed good per se performance and high gca effects. Therefore, transgressive segregation for these characters is expected in this cross. A similar situation was observed in the cross PR-1108 x BJ-1235 for primary, secondary and tertiary branches, and oil content. The sca effect of the crosses B-55 x Poorbijaya, RW-4/86 x BJ-1257 and Glossy mutant x

Table 3. Estimates of sca effects for ten characters in a 8 X 8 diallel crosses in *Brassica juncea*

Cross	Days to flowering	Plant height	No. of primary branches	No. of secondary branches	No. of tertiary branches	Length of siliqua	Seeds per siliqua	1000-seed weight	Seed yield	Oil content
BJ-679 x PR-1108	- 1.4**	- 2.1	0.1	3.4	3.2	0.4**	0.5	0.8*	13.8**	- 0.2
PR-1108 x BJ-1235	- 1.6**	5.9	1.2**	9.9**	5.9**	0.2	0.8	0.2	- 0.3	1.4*
B-55 x Poorbijaya	1.7**	13.4**	1.1*	3.8	18.2**	- 0.2*	1.0**	0.4	4.9	0.5
RW-4/86 x BJ-1257	- 0.1	5.2	2.2**	5.8*	9.1**	- 0.3**	- 1.8**	1.1**	0.9	- 1.8**
Poorbijaya x BJ-1257	- 1.1**	1.6	- 0.2	3.9	- 9.8**	0.1	0.4	- 0.1	- 0.2	1.5**
Glossy mutant x BJ-1257	2.3**	12.2**	1.3**	5.0*	- 0.7	0.3**	1.4**	- 0.2	7.2*	2.0**
S.E. (sij)	0.4	4.1	0.4	2.3	1.7	0.1	0.5	0.3	3.3	0.6
C.D. at 5%	0.7	8.0	0.8	4.6	3.3	0.1	0.9	0.5	6.5	1.1
C.D. at 1%	0.9	10.5	1.1	6.1	4.4	0.2	1.3	0.7	8.5	1.5

*,**Significant at 5% and 1% levels, respectively.

BJ-1257 did not satisfy the above conditions and nonallelic interactions may disappear in advanced generation [8].

Heterosis over BP was observed in three crosses (Table 4); in BJ-1257 x RW-4/86 for 1000-seed weight in PR-1108 x BJ-679 for seed yield, and in BJ-1257 x Glossy mutant for oil content. However, it can be realised on commercial scale only with suitable cytoplasmic-genetic male sterile system.

An examination of correlations among 1000-seed weight, oil content and seed-yield at phenotypic and genotypic levels (Table 5) revealed that genotypic correlation coefficients were higher than phenotypic, suggesting strong inherent relationship among these characters. Seed

Table 4. Heterosis (%) over better parent for 1000-seed weight, seed yield and oil content in *Brassica juncea*

Cross	1000-seed weight	Seed yield	Oil content
PR-1108 x BJ-679	15.8	77.6**	- 2.9
BJ-1257 x RW-4/86	37.2**	- 47.5	- 16.8**
BJ-1257 x Glossy mutant	- 30.8	65.1	13.1**
S.E. (D)	0.6	5.9	1.1
C.D. at 5%	1.1	11.6	2.1
C.D. at 1%	1.4	15.3	2.8

*,**Significant at 5% and 1% levels, respectively.

yield was positively associated with 1000-seed weight, although the correlation was nonsignificant. Oil content on the other hand had significant positive association with 1000-seed weight and seed yield per plant. This means that selection will be effective for yield improvement through 1000-seed weight and oil content [9].

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlations for three characters in *Brassica juncea*

Characters	1000-seed weight	Seed yield	Oil content
1000-seed weight	—	0.35	0.51
Seed yield	0.12*	—	0.33
Oil content	0.30*	0.28*	—

*,**Significant at 5% level, (d.f. = 62).

The flower colour in F_1 generation of direct and reciprocal crosses between the (white flowered) Glossy-mutant and other yellow flowered strain indicated dominance of yellow over white colour. The F_2 generation of all crosses segregated into 15 yellow : 1 white (Table 6). This shows that flower colour was governed by two dominant genes, designated as Y_1 and Y_2. Thus, observed ratio of 15 yellow, 1 white indicate the digenic control of mustard corolla colour. The χ^2 heterogeneity test [1.838, 6 d.f.] over the crosses also confirmed the above findings. However, different mode of gene control of flower colour in mustard has also been reported [10].

Table 6. Segregation for flower colour in F_2 segregation of *Brassica juncea*

Cross	F_2 plants		Expected ratio	χ^2	P
	yellow flowered	white flowered			
BJ-679 x Glossy mutant	160	10	15 : 1	0.039	0.80–0.90
PR-1108 x Glossy mutant	280	22	15 : 1	0.552	0.30–0.50
B-55 x Glossy mutant	219	13	15 : 1	0.165	0.50–0.70
RW-4/86 x Glossy mutant	268	16	15 : 1	0.184	0.50–0.70
Poorbijaya x Glossy mutant	210	12	15 : 1	0.270	0.50–0.70
BJ-1257 x Glossy mutant	213	11	15 : 1	0.686	0.30–0.50
BJ-1235 x Glossy mutant	292	21	15 : 1	0.113	0.70–0.80
Pooled	1642	105	15 : 1	0.171	0.50–0.70

Note. No differences were observed in the segregation pattern of direct and reciprocal crosses. Hence the value presented here are pooled for each cross combination.

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