GENETIC STUDY OF YIELD, GLUCOSINOLATES, OIL AND PROTEIN CONTENTS IN OILSEED RAPE (*BRASSICA NAPUS* L.)

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ABSTRACT

A complete diallele crosses derived from eight oilseed rape (*Brassica napus* L.) genotypes was used to estimate the genetic parameters for seed yield, 2-propenyl (allyl), 3-butenyl, total glucosinolate, oil and protein contents. Analysis of variance based on Griffing's Method one with Mixed–B Model revealed the presence of significant mean squares for general and specific combining abilities and reciprocal effects, indicating additive, non-additive and maternal effects, contributed to genetic control of the studied characters. High narrow-sense heritability estimates for the three types of glucosinolates indicated the prime importance of additive genetic effects. However, the degree of dominance greater than one for seed yield, oil and protein contents showed the importance of non-additive genetic effects for these traits. Significant heterosis over better parent was detected for allyl, 3-butenyl and total glucosinolate contents, seed yield, oil and protein percentages. Non-significant correlation between studied traits and seed yield suggested the possibility of improving these traits without any considerable changes in the seed yield. In general, PF7045/91 and BL1 (breeding lines) were good combiner parental lines for seed yield and low glucosinolates. The crosses PF7045/91 × Shiralee and BL1 × PF7045/91 had the highest positive and negative heterosis for seed yield and glucosinolates, respectively.

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تحقیقات کشاورزی ایران

مطالعه ژنتیکی عملکرد، گلوکوزینولات‌هـا و درصـدهای روغـن و پروتئین در کلزا (*Brassica napus* L.)

ولی‌اله رامئه، عبدالمجید رضائی و قدرت‌اله سعیدی

به ترتیب، دانشجوی دکتری، استاد و استادیار گروه زراعت و اصـلاح نباتـات دانشـکده کشـاورزی دانشگاه صنعتی اصفهان، اصفهان، جمهوری اسلامی ایران.

چکیده

تلاقی‌های دای‌آلـل کامـل ۸ ژنوتیـپ کلـزا بـرای بـرآورد پارامترهـای ژنتیکـی عملکـرد دانـه، گلوکوزینولات‌ها شامل آلیل، ۳- بوتنیل و گلوکوزینولات کل، و درصـدهای روغـن و پروتئین مـورد استفاده قرار گرفت. تجزیه واریانس براساس روش یک مـدل مخـتلط– B گریفینـگ حـاکی از وجود میانگین مربعات معنی دار برای قابلیت‌های ترکیب‌پذیری عمومی و خصوصی و اثرهـای متقابـل بـود که نشان دهنده اهمیت اثرهای افزایشی، غیر افزایشی و مادری در کنترل ژنتیکی ویژگی هـای مـورد مطالعه است. برآورد قابلیت توارث خصوصی بالا برای سه نوع گلوکوزینولات نمایانگر اهمیـت زیـاد اثرهای افزایشی ژن ها در کنترل آن ها بود. با وجود این برآورد، درجـه غالبیت بیش از یـک بـرای

عملکرد دانه و درصدهایی روغن و پروتئین، نشانگر اهمیت بیشــتر اثرهـای غیــر افزایشـی ژن هــا در

کنترل آن ها بود. هتروزیس معنی‌داری نسبت به والد برتـر بـرای عملکـرد دانـه، آلیـل، ۲- بوتنیـل و

گلوکوزینولات کل و برای درصدهای روغن و پروتئین مشاهده شـد. نبـود همبسـتگی معنی‌دار بـین

عملکرد دانه و دیگر ویژگی های مورد مطالعه امکان بهبود آن ها را بدون تغییـر قابـل ملاحظـه‌ای در

عملکرد دانه ممکن مـی سـازد. بـه طـور کلـی رقـم PF7045/91 و لایـن اصـلاحی BL1 از ترکیـب

شــونده‌هـای مناسـب بـرای عملکـرد دانـه و مقـدار پـایین گلوکوزینـولات‌هـا هسـتند. تلاقـی‌هـای

PF7045/91×Shiralee و BL1×PF7045/91 دارای هتـروزیس مثبـت بـرای عملکـرد دانـه و

هتروزیس منفی برای گلوکوزینولات‌ها بودند.

INTRODUCTION

Brassica species especially *B. napus* have important role in oilseed production because of their wide adaptation to different climatic conditions (3). In breeding programs for oilseed rape, the improvement of both agronomic and quality characters is important. Glucosinolate content of the meal and erucic acid content of the oil are major quality characters in *Brassica* species, especially in *B. napus* (10, 19, 21). Glucosinolates are sulfur-containing glycosides which occur in the seed and green tissues of the Cruciferae and related families in other Caparales (6). They consist of a common aglycone moiety and a variable aglycone side chain which are derived from α-amino acids. More than 100 different glucosinolates, showing different side chain structure, have been identified in the plant kingdom, mainly in *Brassica* species (6, 28). Both the glucosinolates and their degradation products are associated with antinutritive and toxic effects, limiting the usefulness of seeds and seed meals for human and animal feed (14, 28). Therefore, breeding for low glucosinolate content of oilseeds such as *B. napus*, *B. rapa* and *B. juncea* has been the subject of intensive research during recent decades (27).

Significant general combining ability (GCA) and specific combining ability (SCA) mean squares have been reported for total glucosinolate (14,

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17). The importance of partial dominance and the presence of multiple alleles for glucosinolates in *B. napus* have also been emphasized (18). Sodhi *et al.* (23) investigated the inheritance of total glucosinolates using double haploid populations of *B. juncea*, and on the basis of the frequency of the low glucosinolate individuals, concluded that seven genes were involved in the inheritance of total glucosinolate.

The marketability of oilseed rape depends on the high content and quality of oil and protein. Therefore, improvement of these quality characters will increase the economic value of the seed for the producers and consumers. Oil content within and among *Brassica* oilseed crops varies from 35 to 44%, depending on the variety and environmental conditions (3). Previous studies have shown the importance of non-additive genetic effects for seed yield, oil and protein contents (20, 21, 26), whereas other researchers emphasized on the importance of additive gene effects for oil and seed yields (1, 22).

Although, *B. napus* is usually classified as a highly self-pollinated species, significant levels of heterosis for seed yield and its components have been observed in F_1 hybrids of both the spring and winter types (8, 9, 16, 26). Reciprocal effects due to cytoplasmic factors such as mitochondria or choloroplast DNA and/or maternal genes can be important in controlling the traits in some of the plants (8) and have been reported for agronomic and quality characters in *B. napus* (19, 21) and other *Brassica* species (15, 20).

This study was performed to obtain information on the genetic parameters of seed yield and some important quality characters for eight breeding lines and cultivars of *B. napus* in order to plan a suitable breeding program for improving these characters.

MATERIALS AND METHODS

Eight diverse genotypes including two breeding lines (BL_1 and BL_2 derived from crosses Yanter × Tower and Cobra × A.W., respectively) and six cultivars (Shiralee, Regent, Ceres, PF7045/91, Darmor and Falcon) were hand crossed in a complete diallele design to produce 56 cross combinations. Parental lines were hand-selfed at the same time. The F_1 families and eight parents were evaluated in a lattice design with two

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replications in Research Farm of Isfahan University of Technology (51°, 32 E longitude and 32° 32′ N latitude, 1630 m above sea level), in November 2000. Each plot consisted of three rows of two meters length. The distance between and within rows was 0.6 and 0.05 m, respectively. Fertilizer was applied at the rate of 150 kg N+ 60 kg P_2O_5+ 75 kg K_2O ha^{-1}. Two-thirds of nitrogen fertilizer was applied at the planting time and one-third after the rosette stage. Seed yield was recorded from 1 m sample of the middle row of each plot. Glucosinolates including allyl, 3-butenyl and total glucosinolate were estimated by high performance liquid chromatography (HPLC) equipment which consisted of a Novapack RP-18 (3.99 × 150mm) column, an ultraviolet detector at a wavelength setting of 229 nm and mobile phase ammonium sulfate 0.2M on the basis of Clausen *et al.* (2) method which was developed by Kaushik and Agnihorti (11). Oil and protein contents were estimated using nuclear magnetic resonance (NMR) and Kjeldahl analysis, respectively. Parental and cross means were derived from analysis according to simple lattice design and for estimating the genetic parameters, data were analyzed based on Griffing's (7) Method 1 with Mixed-B Model.

RESULTS AND DISCUSSION

Seed Yield

Non-significant ratio of GCA to SCA mean square, degree of dominance greater than one, and low heritability were observed for seed yield (Table 1), suggesting critical impact of non-additive genetic effects on this trait. Therefore, selection based on seed yield would not be efficient and presumably, it must be conducted based on correlated and highly heritable yield components. The results of other studies in oilseed rape (20, 21, 26) also indicated the importance of non-additive genetic effects for seed yield. Significant and positive GCA effects for BL1, PF7045/91 and Shiralee indicated that these are good combiner cultivars (Table 2). In crosses with high significant SCA effects for seed yield (nearly 54% of the crosses), at least one of the parents had significant and positive GCA effects for this trait (Table 3). Therefore, GCA effect of parents can be considered as a good criterion for predicting seed yield of their crosses. Thakur and Sagwal (26) also reported similar results for oilseed rape.

The magnitudes of heterosis over the better parent were significant in 64% of the crosses (Table 4). Many crosses, such as Falcon × Regent, Falcon × Ceres, Falcon × PF7045/91, BL1 × Falcon and Regent × Darmor showed high significant heterosis effects.

Table 1. Analysis of variance for yield, glucosinolates, oil and protein contents based on Griffing's Method one with Mixed-B Model

S.O.V.	DF	MS					
		Yield	Allyl	3-Butenyl	Total glucosinolates	Oil %	Protein %
Replication	1	4689.72**	101.03	70.97**	306.11*	99.67**	8.17*
Cross	63	8505.42**	3 356.80**	220.16**	5088.15**	7.83**	4.93**
GCA	7	8799.89**	21872.71**	1271.36**	33640.52**	17.95**	3.58**
SCA	28	7829.68**	26.82**	127.40**	1853.13**	6.01*	3.99**
Reciprocal	28	9107.52**	57.80**	50.12**	1185.08**	7.12*	6.02*
Error	63	442.59	44.42	9.08	64.53	2.83	1.66
MS(GCA)/MS(SCA)		1.12	7.83**	9.98**	18.15**	2.99*	0.89
Degree of dominance		3.36	0.93	1.22	0.92	1.83	4.41
Narrow-sense heritability		0.12	0.69	0.55	0.69	0.24	0.06
Average heterosis (%)		30.84	34.09	16.43	28.63	1.59	-1.03

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

Table 2. Estimates of GCA effects for yield, glucosinolates, oil and protein contents in eight parents of *B. napus*.

Parents	Yield	Allyl	3-Butenyl	Total glucosinolate	Oil%	Protein%
BL1	12.23**	-25.32**	-7.47**	-32.69**	-0.57	0.35
Falcon	2.22	42.79**	10.81**	53.69**	0.22	0.38
PF7045/91	13.56**	-28.87**	-5.81**	-34.94**	1.13*	-0.17
Bl2	-15.91**	-8.69**	-2.85**	-11.46**	0.04	-0.57*
Ceres	-20.99**	36.15**	7.75**	43.98**	-1.04**	-0.28
Regent	4.19	-7.51**	0.23	-7.54**	0.89*	0.24
Darmor	-19.15**	-5.62**	-1.17*	-6.71**	-0.64	0.13
Shiralee	23.17**	-2.93*	-1.49*	-4.32*	-0.02	-0.08

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

Table 3. Estimates of SCA effects for yield, glucosinolates, oil and protein
contents in the diallele crosses of eight parents of *B. napus*.

Crosses	Yield	Allyl	3-Butenyl	Total glucosinolates	Oil %	Protein %
BL1 × Falcon	48.79**	18.94**	4.51**	23.36**	-0.91	1.03
BL1 × PF7045/91	28.00**	0.76	1.58	2.59	-0.89	1.21*
BL1 × BL2	27.03**	-14.79**	-2.31	-17.19**	0.46	-0.79
BL1 × Ceres	-34.16**	-7.24*	-3.06*	-10.39**	-1.19	0.63
BL1 × Regent	30.72**	-5.49	-2.10	-7.33*	0.41	-1.13*
BL1 × Darmor	21.14*	7.97*	-0.03	7.83*	-1.41	0.65
BL1 × Shiralee	-59.03**	2.70	-0.32	2.30	2.13**	-1.14*
Falcon × PF7045/91	28.74**	-1.33	4.18**	3.10	0.17	0.04
Falcon × BL2	-1.27	-5.94	1.63	-4.39	1.12	0.02
Falcon × Ceres	63.59**	3.26	5.37**	8.54*	2.35**	-1.29*
Falcon × Regent	49.09**	22.89**	12.02**	35.17**	-0.60	0.11
Falcon × Darmor	-53.01**	0.62	4.62**	5.15	-0.89	0.08
Falcon × Shiralee	-55.28**	5.99	-7.32**	-1.42	-0.73	0.47
PF7045/91 × BL2	34.05**	1.53	0.49	2.27	0.57	0.21
PF7045/91 × Ceres	-5.03	-32.26**	-4.81**	-36.81**	0.69	-1.47**
PF7045/91 × Regent	-26.41**	16.56**	0.55	14.96**	-1.69*	1.23*
PF7045/91 × Darmor	19.87*	13.95**	1.79	16.02**	1.18	-1.74**
PF7045/91 × Shiralee	7.82	-3.28	-2.77*	-5.79	-0.42	0.58
BL2 × Ceres	-49.83**	48.03**	0.94	48.88**	-0.71	1.12*
BL2 × Regent	-16.77	-7.82*	-2.38	-9.94**	0.64	-0.79
BL2 × Darmor	-18.34	1.96	0.86	2.74	-1.58*	1.09*
BL2 × Shiralee	27.89**	5.95	2.55	8.41*	0.92	-1.28*
Ceres × Regent	0.64	6.86*	0.39	7.51*	0.35	0.88
Ceres × Darmor	-2.19	-1.15	-2.89*	-4.12	1.33	-1.02*
Ceres × Shiralee	68.14**	12.32**	8.39**	20.63**	-1.44	0.66
Regent × Darmor	31.98**	-29.72**	-9.37**	-38.84**	0.49	0.28
Regent × Shiralee	23.35*	-14.69**	-4.21**	-18.64**	0.21	0.62
Darmor × Shiralee	47.27**	3.29	1.98	5.19	1.79*	-1.19*

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

Table 4. Estimates of high parent heterosis for yield, glucosinolates, oil and protein contents in the diallele crosses of eight parents of *B. napus.*

Crosses	Yield	Allyl	3-Butenyl	Total glucosinolates	Oil %	Protein %
BL1 × Falcon	01.55**	-4.75	11.24**	6.48	-1.52	1.45
BL1 × PF7045/91	92.10**	0.05	0.95	1.18	-2.98	1.17
BL1 × BL2	58.49**	-2.49	-5.14	-7.63	-0.34	-1.25
BL1 × Ceres	-3.93	-38.89**	-13.93**	-52.82**	-3.08	0.47
BL1 × Regent	85.45**	-34.69**	-14.88**	-49.58**	-1.24	-0.76
BL1 × Darmor	52.53*	-14.80	-9.35**	-24.17**	-2.89	-0.93
BL1 × Shiralee	-9.86	-7.40	-7.98**	-15.39	1.27	-1.99
Falcon × PF7045/91	104.45**	-28.57**	12.55**	-16.02*	-1.13	-0.05
Falcon × BL2	19.91	-13.01	12.96**	-0.05	1.45	-0.47
Falcon × Ceres	121.66**	39.73**	12.77**	52.49**	1.61	-1.49
Falcon × Regent	131.64**	17.01*	17.50**	43.44**	-1.46	0.43
Falcon × Darmor	6,11	-3.37	13.56**	14.26	-1.24	-1.48
Falcon × Shiralee	-16.13	4.68	3.28	10.07	-0.45	-0.35
PF7045/91 × BL2	66.58**	10.29	-0.70	9.60	-0.91	-0.14
PF7045/91 × Ceres	48.16*	-67.45**	-14.04**	-81.49**	-1.87	-1.84
PF7045/91 × Regent	51.26*	-16.19*	-10.59**	-29.54**	-2.33	1.69
PF7045/91 × Darmor	74.20**	-12.35	-5.88*	-18.23*	-0.98	-3.85**
PF7045/91 × Shiralee	58.32**	-16.93	-8.79**	-25.72**	-1.96	-0.79
BL2 × Ceres	-51.16*	33.01**	-5.33	27.68**	-0.39	0.33
BL2 × Regent	6.37	-20.40**	-10.57**	-30.97**	-0.40	-0.42
BL2 × Darmor	-18.35	-4.17	-3.86	-8.04	-0.87	-1.43
BL2 × Shiralee	48.91*	12.47	-0.53	11.94	2.27	-3.05**
Ceres × Regent	66.29**	-6.97	-2.80	-9.77	-1.77	0.91
Ceres × Darmor	40.12	-13.09	-7.47*	-20.56*	1.85	-3.25**
Ceres × Shiralee	84.78**	3.07	3.49	6.56	0.01	-0.82
Regent × Darmor	101.25**	-39.23**	-15.87**	-55.10**	-1.23	-1.42
Regent × Shiralee	64.47**	-21.51**	-11.03**	-32.53**	-0.89	-0.34
Darmor × Shiralee	64.99**	2.91	-1.37	1.55	3.34*	-3.22**

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

Reciprocal effects were significant in most crosses, indicating the maternal and probably cytoplasmic effects for the studied lines and cultivars (Table 5). The importance of maternal effects has been emphasized by earlier

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researcher for *B. napus* (15) and *B. campesteris* (20). For crosses such as BL1 × Falcon, Falcon × BL2 and Ceres × Darmor, the reciprocal effects were high, negative and significant, suggesting that their reciprocal crosses should be used in breeding programs.

Table 5. Estimates of reciprocal effects for yield, glucosinolates, oil and protein contents.in diallele crosses of eight parents of *B. napus*.

Crosses	Yield	Allyl	3-Butenyl	Total glucosinolate	Oil %	Protein %
BL1 × Falcon	-55.93**	0.07	-1.30	-1.22	-0.35	-0.63
BL1 × PF7045/91	-20.98	0.08	1.95	2.03	-0.17	0.18
BL1 × BL2	20.16	-4.69	-0.93	-5.62	-2.09*	2.13**
BL1 × Ceres	-18.76	-4.59	-0.44	-5.03	-0.13	-0.78
BL1 × Regent	-15.61	12.94**	-2.33	-15.27**	0.45	-1.83**
BL1 × Darmor	-1.10	-1.52	-4.17*	-5.67	1.51	0.51
BL1 × Shiralee	22.63*	4.94	-1.67	3.26	-1.13	0.99
Falcon × PF7045/91	-45.90**	-21.85**	-0.24	-22.08**	0.67	-1.06
Falcon × BL2	-91.42**	-3.06	5.13**	2.06	0.68	-0.35
Falcon × Ceres	37.96**	-4.15	-6.28**	-10.42*	0.99	-0.51
Falcon × Regent	-28.93**	-23.28**	-2.28	-25.56**	2.85**	-1.82**
Falcon × Darmor	-33.17**	-5.13	5.67**	0.54	0.18	0.15
Falcon × Shiralee	70.30**	-21.28**	-4.25**	-25.53**	-1.31	2.63**
PF7045/91 × BL2	34.88**	-17.81**	-2.26	-20.07**	0.68	-1.17*
PF7045/91 × Ceres	-47.34**	2.39	-1.52	0.87	1.09	-1.39*
PF7045/91 × Regent	61.82**	-17.95**	-2.62	-23.32**	2.87**	-2.95**
PF7045/91 × Darmor	-22.31*	33.21**	8.55**	41.76**	0.72	0.55
PF7045/91 × Shiralee	72.79**	-4.22	1.37	-2.84	-0.11	0.02
BL2 × Ceres	49.07**	18.21**	1.19	19.39**	-0.61	0.91
BL2 × Regent	-24.92*	-19.32**	-3.61*	-22.94**	-1.11	0.48
BL2 × Darmor	-32.48**	13.28**	5.04**	18.32**	1.83*	0.29
BL2 × Shiralee	58.54**	-16.78**	-1.12	-17.90**	0.83	-1.02
Ceres × Regent	-5.84	20.60**	2.76	23.37**	1.23	-0.09
Ceres × Darmor	-95.21**	-18.20**	-1.83	-20.03**	-1.94*	1.29*
Ceres × Shiralee	-3.06	-7.33*	3.69*	-3.64	-0.88	0.73
Regent × Darmor	-50.16**	-3.26	-2.21	-5.47	1.15	-0.99
Regent × Shiralee	61.91**	21.78**	5.93**	27.71**	-2.17*	1.32*
Darmor × Shiralee	61.99**	4.33	1.57	5.89	-1.28	1.35*

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

Glucosinolates

Significant ratios of GCA to SCA mean square, high narrow-sense heritabilitiy estimates and low degrees of dominance for three kinds of glucosinolates indicated the importance of additive gene actions in their genetic control (Table 1). Earlier researches emphasized the importance of additive gene effects for glucosinolates in *B. napus* (18) and other *Brassica* species (6,17). The two breeding lines (BL1 and BL2) with significant negative GCA (Table 2) and low means for the three kinds of glucosinolates (less than 30 μM g^{-1} dry meal) were considered good parents for breeding purposes. Significant negative SCA effects were observed for all three kinds of glucosinolates in some of the crosses (Table 3) which makes it feasible to obtain hybrids with low contents of glucosinolates. To increase seed yield and simultaneously reduce glucosinolates, the crosses PF7045/91×Ceres, Regent × Darmor and Darmor × BL2 with regard to allyl, Regent × Darmor for butenyl and Regent × Darmor, Regent × Shiralee, BL1 × BL2 and BL1 × Regent for total glucosinolate were considered as good cross combinations.

Significant negative heterosis was observed for all three kinds of glucosinolates (Table 4). The crosses Falcon × PF7045/91 and Regent × Darmor had significant negative and positive heterosis for allyl and seed yield, respectively. Similar results were found in crosses BL1 × Regent, Regent × Darmor and Regent × Shiralee for 3-butenyl and seed yield and also in crosses BL1 × Regent, BL1× Darmor, PF7045/91 × Ceres, PF7045/91 × Shiralee and Regent × Darmor for total glucosinolate and seed yield. Therefore, these combinations may be used to improve both seed yield and glucosinolates, simultaneously.

Significant reciprocal effects were observed for all three kinds of glucosinolates, suggesting the importance of maternal effects for these traits (Table 5). Earlier research also emphasized reciprocal effects for glucosinolates in *Brassica juncea* (17). In the presence of significant and positive reciprocal effects, it is suggested to use the reciprocals of the crosses to obtain combinations with minimum glucosinlate contents. Therefore, instead of Regent × Shiralee for allyl, Falcon× BL2, Falcon× Darmor, PF7045/91× Darmor, BL2 × Darmor and Regent × Shiralee for 3-

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butenyl and also PF7045/91 × Darmor and Regent × Shiralee for total glucosinolates, their reciprocal crosses could be used.

The correlation coefficients between seed yield and allyl, 3-butenyl and total glucosinolates (0.015, 0.013 and 0.012, respectively) were not significant; therefore improvement of these traits is possible without any considerable reduction in seed yield.

Oil and Protein Contents

The estimated degree of dominance over one and low ratios of GCA to SCA mean square (although significant for oil percentage, $p < 0.05$), indicated the greater importance of non-additive genetic effects for oil and protein contents (Table 1). Greater importance of non-additive genetic effects for oil (22) and protein (10) contents has been previously reported. In contrast, the importance of additive genetic effects for oil content has been emphasized (10). The parent PF7045/91 had significant positive GCA effects for oil content and seed yield and the parent BL1 had significant and positive GCA effect for seed yield and positive GCA effect for protein content. Therefore, they were considered as good combiners for these quality traits and seed yield, simultaneously (Table 2). The crosses Falcon × Ceres and Darmor × Shiralee with significant positive SCA effects for oil and seed yield and also BL1 × PF7045/91 with significant positive SCA effects for protein and seed yield were considered as good combinations (Table 3).

The estimated best parent heterosis for oil was not significant in most of the crosses due to inadequate variation among the parents. The estimated heterosis for protein content was negative in most of the crosses and negative and significant in some of them, indicating negative non-additive genetic effects (Table 4). The combination Darmor×Shiralee with significant positive heterosis for oil and seed yield was considered as the best cross for improving these two traits, simultaneously.

The reciprocal effects were significant in some of the crosses for oil and protein contents, indicating that maternal effects were existed for these traits. The reciprocal crosses with significant negative maternal effects could be used for improving these two traits.

CONCLUSIONS

On the basis of GCA to SCA mean squares, degrees of dominance and narrow-sense heritability estimates, it was concluded that, three kinds of glucosinolates were controlled by additive genetic effects and therefore, the efficiency of selection for improvement of these traits may be high. For seed yield, oil and protein contents, the non-additive genetic effects were more important, therefore, it is possible to select superior lines from segregating populations derived from those crosses with high SCA effect. Also, high estimates of SCA variances may be due to presence of repulsion phase linkage and linkage disequilibrium might have resulted in an over estimation of nonadditive component (12). Under these situations population improvement by recurrent selection to accumulate desirable genes and breaking of undesirable linkage would be more appropriate. High SCA estimates could also be due to presence of genetic diversity among the parents and there could be some complementation indicating importance of non-additive effects.

Our results revealed the presence of significant reciprocal effects for all studied traits. This emphasized the need for careful selection of the maternal parent. Test crosses also may be needed to identify favorable reciprocal interactions in breeding for studied traits. However, reciprocal effects appeared to be widespreed. Therefore, they could be the result of differences in seed quality. Seed quality is highly variable and can vary within plants causing reciprocal differences.

Finally, if practical breeding is to be successful, efficient screening methodologies must be developed. Since the improvement of high yielding cultivars through conventional breeding methods is faced with many difficulties, there is a need for rapid alternative approaches to screan a large number of breeding lines. The advent of molecular-marker technology has led to the development of genetic maps that make it possible to identify and locate genes controlling quantitative characters. Determination of the number, location and magnitude of effects through molecular-marker linkage of quantitative trait loci (QTLs) could also elucidate the genetic basis of the trait, leading to improved breeding and selection efficieney.

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Two approaches. have been proposed to determine linkage between marker loci and nearby QTLs. Marker-based analysis (13, 24, 25) is based on differences in the mean value of a quantitative trait among marker genotypes in the F_2 or BC progeny of a cross between inbred lines; these differences are presumably generated by QTLs linked to the marker loci. Trait-based analysis (4, 5) is based on changes in marker allele frequencies in selected lines derived from the F_2 or cross between inbred lines or in the high and low phenotypic classes of an F_2 or BC population.

In general the parents BL_1 and PF7045/91 were found to be good combiners for all of the traits, therefore they could be used for development of CMS lines. The crosses BL1 × PF7045/91, BL1 × Regent and PF7045/91 × Shiralee with high yield (5407.83, 5430.33 and 5387.33 kg ha^{-1}, respectively) and low total glucosinolate (9.61, 27.08 and 29.59 µM g^{-1} dry meal, respectively) were considered as good combinations in this study. These parents and crosses should be given due consideration in developing superior cultivars.

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