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Estimation of Genetic Parameters for Yield, Yield Components and Glucosinolate in Rapeseed (*Brassica napus* L.)

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ABSTRACT

Eight genotypes of rapeseed (*Brassica napus* L.), including six cultivars and two breeding lines, were used to determine the genetic parameters for number of pods per main axis (NPM), number of pods per plant (NPP), length of pod (LOP), number of seeds per pods (NSP), 1000-seed weight , seed yield, and total glucosinolate. Analysis of variance based on Hayman's method revealed significant general *(a)* and specific *(b)* combining ability mean squares for all traits except for 1000-seed weight, which indicated the importance of additive and non-additive genetic effects. For 1000-seed weight, only the general combining ability mean square was statistically significant. Significant ratios of *a* to *b* mean squares and high narrow-sense heritability estimates were observed for 1000-seed weight and total glucosinolate, which indicated the importance of additive genetic effects for these traits. Therefore, the efficiency of selection for improving these traits will be high. The significant *b*1 (mean deviation of F_1's from their mid-parental values) mean squares for all of the studied traits except LOP and 1000-seed weight, exhibited directional dominance and subsequently significant average heterosis. Significant maternal *(c)* mean squares were observed for all of traits, except LOP. Among yield components, NPM and NPP had a significant correlation with seed yield and can therefore be used as good criteria for improving seed yield. The correlation between seed yield and total glucosinolate was not significant, and so reducing this antiquality trait without any considerable changes in seed yield is possible. In general, the parents PF7045/91 and BL1 were good combiners and the crosses BL1×PF7045/91, BL1×BL2 and PF7045/91×Shiralee were good combinations for improving seed yield and total glucosinolate, simultaneously.

Keywords: Genetic parameters, Glucosinolate, Rapeseed, Yield components.

INTRODUCTION

Both yield and quality related characters have important roles for increasing the expansion of rapeseed cultivation [3,17]. Besides oil quality, the meal quality also is important, and this mainly depends on the contents of glucosinolates [3]. Glucosinolates are a family of secondary plant metabolites particulary abundant in the seed and green tissues of the family Brassicae [4, 13, 16, 18, 23, 24].

Glucosinolates and their hydrolysis products have presented a major obstacle to the utilization of rapeseed meal in animal or human nutrition. They are considered as antinutritional factors and have been implicated in several physiological disorders in animals, including goiter and hemorrhagic liver syndrome [18].

Because of their detrimental effects, plant breeders have focused on a drastic reduction of seed glucosinolates contents in the major oil crops of the family of Brassica, i.e. *B. napus*, *B. campestris* and *B. juncea* [23].

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Significant general combining ability (*gca*) and sepecific combining ability (*sca*) effects of glucosinolates have been reported in *B. napus* [11]. Partial dominance and high narrow-sense heritability were reported for total glucosinolate [8, 11, 16]. Love *et al*. [14] reported multiple additive alleles on more than one locus for allyl glucosinolate and 3-butenyl glucosinolate in mustard *(B. juncea)*.

Although the improved nutritional quality of the oil and meal has been a major breeding objective of Brassica oilseed, seed yield must be maintained and improved if these crops are to remain competitive [3]. Because seed yield is probably the most difficult and costly trait to measure accurately, numerous attempts have been made to identify the most important yield components [3, 6, 7]. For this reason, the estimation of genetic parameters for yield components can be important for indirect selection for seed yield. Significant *gca* and *sca* effects were reported for the number of pods per main axis (NPM), number of pods per plant (NPP), length of pod (LOP), number of seeds per pods (NSP), 1000-seed weight and seed yield in *B. napus* [13,19, 22]. However in another study [21], the importance of additive genetic effects for NPP and 1000-seed weight was emphasized.

Significant levels of heterosis for agronomic and quality related traits have been obtained in F_1 hybrids of both spring and winter forms of *B. napus* [3]. Heterosis effects varied for each yield component, depending on the environmental and/or genotypic effects [1, 6, 12, 13, 15]. Thakur and Sagwal [22] reported significant high parent heterosis for NPP, NSP and seed yield. Reciprocal effects due to cytoplasmic organels such as mitochondria, and/or choloroplast DNA or mother genes have been reported for both quantity [2, 19] and also quality [17,20] characters in *B. napus* and other Brassica species.

The objective of the present study was to determine the importance of genetic parameters for yield components, seed yield and total glucosinolate in order to select a suitable breeding program for rapeseed breeding lines and cultivars.

MATERIALS AND METHODS

The materials under study consisted of two breeding lines (Yanter ×Tower (BL1), Cobra ×A.W (BL2)) and six cultivars (Shiralee, Regent, Ceres, PF7045/91, Darmor, and Falcon), which were selected on the basis of their different glucosinolate contents and other agronomic characters. Genotypes were crossed in all possible combinations, including reciprocals. The eight parents and 56 F_1's were grown in a lattice design with two replications at the Research Farm of Isfahan University of Technology (51˚, 32′ E longitude and 32˚ 32′ N latitude, 1630 m above sea level) during November 2000. Each plot consisted of three two meter rows. Between and within row were 60 and 5cm, spacings respectively. Fertilizer was applied at a concentration of 150 kg N, 60 kg P2O5 and 75 kg K2O / hectare. Two thirds of the fertilizer was applied at the time of planting and one third of it was applied at the beginning of the reproductive stage. The NPM and NPP were recorded on the basis of ten randomly selected plants from each plot. The LOP and NSP were recorded on the basis of five randomly selected pods on the main axis of five plants in each plot. Seed yield was recorded on the basis of one meter from the middle row of each plot. Total glucosinolate was measured by an economical and efficient high performance liquid chromatography (HPLC) method which was revised by Kaushik and Agnihorti [10]. This method involves a single step extraction of glucosinolates in boiling water. The separation of glucosinolate was achieved on a Novapack RP-18 column (3.99 × 150mm), using 0.2M ammonium sulphates as mobile phase and peaks were monitored at 229 nm.

The studied traits were analyzed on the basis of a lattice design, and the results revealed that its relative efficiency compared to a randomized complete block design for 1000-seed weight was more than one. Therefore, this trait was adjusted for incomplete block effects and then all of the traits were analyzed based on Hayman's method [8]. In Hayman's analysis, the *a* and *b* mean squares refer to additive and dominant genetic effects, respectively. The mean squares of *b1*, *b2* and *b3* refere to mean deviation of F_1's from their mid-parental values (average heterosis), differences in the mean deviaton of F_1 from their parents over arrays and dominance deviaton that is uniqe to each F_1, respectively. Whereas the *c* (maternal) mean square in Hayman's method was significant, other genetic parameters were calculated based on Griffing's method [5].

RESULTS AND DISCUSSION

Yield and Yield Components

Significant *a* and *b* mean squares were observed for NPM, NPP, LOP, NSP, and seed yield, indicating the importance of additive and dominance genetic effects for these traits (Table 1). For 1000-seed weight, only *a* mean square was significant which indicated the importance of additive genetic effects. A significant ratio of *a* to *b* mean square, a high narrow-sense heritability and a low degree of dominance were observed for 1000-seed weight, again indicating the importance of additive genetic effects for this trait. Therefore, it can be concluded that breeding programs based on the selection method will be efficient for 1000-seed weight. The degree of dominances greater than one, and low narrow-sense heritability estimates for NPP, NSP and seed yield revealed the higher importance of non-additive genetic effects for these traits. Thus they may be improved by a hybridization method mainly using cytoplasmic male sterility. The importance of additive and non-additive genetic effects for yield and yield components was emphasized by Thakur and Sagwal [22], but in another study [1] additive genetic effects was reported to be more important.

Significant positive correlations were observed between seed yield and NPM and also NPP (0.56^{**} and 0.47^{**}, respectively), suggesting these traits can be considered as good criteria for improving seed yield. Therefore, PF7045/91 and Shiralee with positive *gca* effects for NPM and NPP and also significant positive *gca* effects for seed yield were considered as good combiners for having these traits, simultaneously (Table 2). Thakur and Sagwal [22] also reported similar *gca* effects for NPP and seed yield. The

Table 1. Analysis of variance based on the Hayman (1954) method for yield components, yield and total glucosinolate in rapeseed.

		MS						
S.O.V^a	Df	No. of pods on main axis	No. of pods per Plant	Length of pod	No. of Seeds per Pod	1000-Seed Weight	Yield	Total glucosinolate
Rep.	1	430.75**	507.75**	4.09**	50.52**	2.44**	3559.00*	306.75*
a	7	29.9*	1006.86**	1.08**	33.15**	1.26**	8934.29**	33642.48**
b	28	87.34**	464.63**	0.30**	13.07**	0.10	7656.66**	1853.00**
b1	1	820.67**	4896.96**	0.13	78.39**	0.01	62481.23**	4087.16**
b2	7	59.17**	617.31**	0.58	4.14	0.11	2443.63**	2141.87**
b3	20	60.45**	189.57**	0.21	12.93**	0.11	6740.00**	1640.18**
c	7	71.53**	1038.17**	0.01	10.11**	0.22*	18703.94**	1141.63**
d	21	59.93**	421.40**	0.15	19.21*	0.11	5696.47**	1200.24**
Error	63	12.68	49.17	0.14	3.23	0.09	587.11	64.52
MS*gca* / Ms*sca*		0.34	2.17	3.60**	2.53*	12.6**	1.17	18.16**
Degree dominance		8.47	2.63	1.63	2.29	0.38	3.36	0.92
Narrow-sense heritability		0.02	0.20	0.28	0.22	0.61	0.12	0.69

*, ** Significant at p< 0.05 and 0.01 probability levels, respectively.
^{a} S.O.V are defined in the text

Table 2. Estimates of *gca* effects for yield components, yield and total glucosinolate in eight parents of *B. napus*.

Parents	No. of pods on main axis	No. of pods per Plant	Length of pod	No. of Seeds per Pod	1000-Seed Weight	Yield	Total glucosenolate
Bl1	-0.79	3.53	0.14	0.68	-0.20 **	12.23 **	-32.69 **
Falcon	0.41	0.76	0.18	0.23	0.27 **	2.22	53.69 **
PF7045/91	1.07	9.73**	-0.23 **	-1.09 **	0.13	13.56 **	-34.94 **
Bl2	-1.67	-7.53 **	0.11	1.36 **	0.11	-15.91 **	-11.46 **
Ceres	0.28	-1.09	0.05	0.73	-0.29 **	-20.29 **	43.98 **
Regent	0.43	-7.21 **	-0.15	-1.40 **	0.11	4.19	-7.54 **
Darmor	-0.68	0.26	0.13	0.49	-0.17 **	-19.15 **	-6.71 **
Shiralee	0.95	1.55	-0.23	-0.98	0.04	23.17 **	-4.33*

*, ** Significant at p<0.05 and 0.01 probability levels, respectively.

parents BL2 and Falcon had significant positive *gca* effects for NSP and 1000-seed weight respectively, so they can be considered as good combiners for each of these traits.

Except for LOP and 1000-seed weight, the mean squares of *b*1 and *b*3 were significant for yield and other yield components, indicating significant heterosis and *sca* for yield and yield components except for LOP and 1000-seed weight. The *b*2 mean square was significant for NPM, NPP and seed yield, indicating significant differences of dominance deviation of the F_1 from the mid parental value among the arrays. The crosses BL1×Ceres, BL1×Darmor, Falcon × BL2 and Falcon × Regent had significant positive *sca* effects for NPP (Table 3). For NPM, the crosses BL1×BL2, BL1 × Regent, Falcon × BL2 and Ceres × Shiralee had high significant positive *sca* effects. For LOP, the best combination with a significant positive *sca* effect was BL2 × Regent. For NSP, the crosses BL1 × Darmor, BL1 × Shiralee, Falcon × Ceres, PF7045/91 × Darmor and BL2 × Regent with significant positive *sca* effects were considered as good combinations. None of the crosses had significant positive *sca* effects for 1000-seed weight. The top five combinations with positive *sca* effects for seed yield were Ceres × Shiralee, Falcon × Ceres, Falcon × Regent, BL1 × Falcon and Darmor × Shiralee, with seed yields of 5828.32, 5403.50, 5569.83, 5698.83 and 5498.67 kg/hectare, respectively. Among these crosses, at least one of their parents had significant positive *gca* effects for seed yield. In a previous study, [22] similar results were reported. Therefore *gca* effects can be considered as a good criterion for predicting *sca* effects on seed yield.

None of the crosses showed significant positive high parent heterosis for yield components simultaneously (Table 4), indicating compensatory effects of yield components. Although a significant positive correlation was observed between NPM and NPP, only one of the crosses (BL1 × Regent) had significant positive high parent heterosis for both traits, simultaneously. LOP and NSP were under non-additive genetic effects, but due to low variability among parents, few crosses showed significant heterosis for these traits. Most of the crosses with high heterosis for NPP, also showed high heterosis for seed yield, therefore NPP can be considered a better criterion than NPM for seed yield heterosis prediction. The crosses Falcon × BL2, BL1 × Darmor, Falcon × Darmor and BL2 × Darmor exhibited significant positive high parent heterosis for NPP. For NSP the crosses BL1 × Darmor, BL1× Shiralee and PF7045/91× Darmor had significant positive high parent heterosis and were considered as good combinations for this trait. In earlier studies, [3,6,12,13,22] significant heterosis for yield components and seed yield in *B. napus* and other Bras-

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Table 3. Estimates of *sca* effects for yields components, yield and total glucosinolate in a diallel crosses of eight parents of *B. napus.*

Crosses	No. of pods on main axis	No. of pods per Plant	Length of pod	No. of Seeds per Pod	1000-Seed Weight	Yield	Total glucosinolate
BL1 × Falcon	-2.12	1.11	0.16	0.11	-0.10	48.79 **	23.36 **
BL1×PF7045/91	3.75*	6.09	-0.23	1.05	0.06	28.00 **	2.59
BL1 1 × BL2	5.39 **	1.91	0.14	0.38	0.06	27.03 **	-17.19 **
BL1 × Ceres	3.33	11.36 **	0.02	-1.89 *	-0.11	-34.00 **	-10.39 **
BL1 × Regent	7.69 **	2.29	-0.11	-0.09	-0.04	30.72 **	-7.33 *
BL1 × Darmor	0.01	12.64 **	-0.07	1.92 *	-0.03	21.14 *	7.83 *
BL1 × Shiralee	-5.44 **	-9.37 **	0.10	2.31 **	0.03	-59.03 **	2.30
Falcon×PF7045/91	2.97	3.79	0.13	1.87	0.04	28.74 **	3.10
Falcon× BL2	5.50 **	15.79 **	-0.05	-0.70	0.22	-1.27	-4.39
Falcon × Ceres	2.30	2.23	0.26	2.25 **	0.21	63.59 **	8.54 *
Falcon × Regent	-0.48	8.38 *	-0.03	-0.26	0.10	49.09 **	35.17 **
Falcon×Darmor	0.48	-0.05	-0.06	-1.20	0.08	-53.01 **	5.15
Falcon × Shiralee	1.77	6.58	0.17	0.87	-0.32 *	-55.28 **	-1.42
PF7045/91×BL2	0.59	-2.34	0.20	0.77	0.18	34.05 **	2.27
PF7045/91× Ceres	2.24	-10.75 **	-0.17	-2.18 **	0.14	-5.03	-36.81 **
PF7045/91×Regent	-4.06 *	2.39	-0.36 *	2.57 **	-0.18	-26.41 **	14.96 **
PF7045/91×Darmor	-1.15	7.85 *	-0.06	3.09 **	-0.02	19.87 *	16.02 **
PF7045/91× Shiralee	4.29 *	5.26	0.24	-1.69	0.09	7.82	-5.79
BL2× Ceres	-5.50 **	-13.05 **	-0.50 **	-0.80	-0.13	-49.83 **	48.88 **
BL2 × Regent	-2.10	1.51	0.35 *	1.08	0.02	-16.77	-9.94 **
BL2 × Darmor	-4.85 **	6.86	-0.03	-0.02	-0.22	-18.34	2.74
BL2 × Shiralee	-1.31	4.72	-0.17	1.50	-0.12	27.89 **	8.41 *
Ceres × Regent	-1.80	-3.04	0.13	3.76 **	-0.31 *	0.64	7.51 *
Ceres ×Darmor	3.57 *	5.56	-0.08	-0.41	0.11	-2.19	-4.12
Ceres ×Shiralee	4.23 *	-3.52	0.17	0.24	0.13	68.14 **	20.63 **
Regent × Darmor	3.24	0.37	-0.32	-0.91	0.09	31.98 **	-38.84 **
Regent × Shiralee	1.65	5.64	0.10	-0.28	0.12	23.35 *	-18.64 **
Darmor× Shiralee	2.54	-4.74	0.45	0.09	0.01	42.27 **	5.19

*, ** Significant at $p<0.05$ and 0.01 probability levels, respectively.

sica species have been reported. The top five combinations with significant positive high parent heterosis on seed yield were Falcon × Regent, Falcon× Ceres, Falcon× PF7045 / 91, BL1×Falcon and Regent× Darmor with seed yields of 5569.8, 5403.5, 5286.83, 5683.33 and 4928.17 kg/hectare, respectively. Since crosses with high *sca* effects for yielded more than those with high heterosis for seed yield, it can be concluded that the *sca* effect is a more realistic criterion than high parental heterosis for seed yield prediction.

Significant *c* mean squares, indicating maternal effects, were observed for yield and yield components except for LOP (Table 1). Therefore, the direction of crosses is important for these traits and in crosses with significant negative reciprocal effects, (Table 5) their reciprocal crosses must be used. Significant maternal effects have been reported for yield components and seed yield in *B. napus* [2] and *B. rapa* [19].

Total Glucosinolate

Significant *a* and *b* mean squares were observed for total glucosinolate, indicating the importance of additive and non- additive genetic effects for this trait (Table 1). A significant ratio of *a* to *b* mean squares, a low degree of dominance and a high narrow-sense heritability estimate were observed for total glucosinolate, indicating a greater importance of additive genetic effects for this

Table 4. Estimates of high parent heterosis for yield components, yield and total glucosinolate, in the diallel crosses of eight parents of *B. napus*.

Crosses	No. of pods on main axis	No. of pods per Plant	Length of pod	No. of Seeds per Pod	1000-Seed Weight	Yield	Total glucosi-nolate
BL1 ×Falcon	7.11	24.38**	0.21	3.45	-0.34	101.55**	6.48
BL1×PF7045/91	10.51**	12.18	-0.59	3.08	0.04	92.10**	1.18
BL1 1 × BL2	3.96	16.88 *	0.11	1.90	-0.25	58.49**	-7.63
BL1 × Ceres	10.61**	4.78	-0.07	-1.00	-0.31	-3.93	-52.82**
BL1 × Regent	10.58**	17.58 *	-0.39	1.63	-0.55	88.45**	-49.58**
BL1 × Darmor	3.73	35.40**	-0.23	4.68**	-0.27	52.53 *	-24.17**
BL1 × Shiralee	0.55	-2.83	-0.27	4.44 *	-0.26	-9.86	-15.39
Falcon×PF7045/91	10.92**	7.10	0.28	3.50	0.13	104.45**	-16.02 *
Falcon× BL2	5.28	39.49**	-0.04	0.38	0.29	19.91	-0.05
Falcon × Ceres	10.79**	-7.13	0.22	2.70	-0.12	121.66**	52.49**
Falcon × Regent	3.60	33.90**	0.07	1.05	0.07	131.64**	43.44**
Falcon×Darmor	5.40	28.94**	-0.18	1.10	-0.13	6.11	14.26
Falcon × Shiralee	8.96 *	10.35	0.32	2.60	-0.32	-16.13	10.07
PF7045/91×BL2	1.03	-7.33	-0.21	0.53	0.21	66.58**	9.60
PF7045/91× Ceres	10.08**	-11.15	-0.63	-3.06	0.03	48.16 *	-81.49**
PF7045/91×Regent	0.67	-2.28	-0.66	-2.52	-0.36	51.26 *	-29.54**
PF7045/91×Darmor	4.42	10.65	-0.60	4.07 *	-0.02	74.20**	-18.23 *
PF7045/91×Shiralee	12.14**	9.35	-0.02	-1.23	0.14	58.32**	-25.72**
BL2× Ceres	-5.85	-30.70**	-0.64	0.78	-0.53	-51.16 *	27.68**
BL2 × Regent	-2.30	17.23 *	0.01	0.53	-0.18	6.37	-30.97**
BL2 × Darmor	-6.16	27.55**	-0.23	1.32	-0.50	-18.35	-8.04
BL2 × Shiralee	-0.99	0.20	-0.59	1.37	-0.19	48.91 *	11.94
Ceres × Regent	2.15	-20.38**	-0.26	2.58	-0.91**	66.29**	-9.77
Ceres ×Darmor	8.36*	-4.30	-0.35	0.30	-0.44	40.12	-20.56 *
Ceres ×Shiralee	11.29**	-12.10	-0.30	-0.53	-0.26	84.78**	6.56
Regent × Darmor	6.24	21.38**	-0.78 *	-0.24	-0.39	101.25**	-55.53**
Regent × Shiralee	6.28	1.44	-0.21	0.88	-0.14	64.47**	-32.53**
Darmor× Shiralee	8.00 *	-1.48	-0.09	1.18	-0.25	64.99**	1.55

*, ** Significant at p<0.05 and 0.01 probability levels, respectively.

trait. In previous studies, the importance of additive genetic effects for glucosinolates in *B. napus* [11,16] and also in *Brassica juncea* was emphasized [14]. The parents BL1, PF7045/91 and BL2 with significant negative *gca* effects and low gluciosinolate content (< 30μM gr-1dry meal) were considered as good combiners for this trait (Table 2).

The *b*1, *b*2 and *b3* mean squares were significant for total glucosinolate, indicating significant average heterosis, directional dominance and significant *sca* effects, respectively (Table 1). Significant negative *sca* effects of total glucosinolate were exhibited for the crosses which had one parent with a significant negative *gca* effect (Table 3). The crosses BL1× PF7045/91, BL1 × BL2, BL1 × Regent, PF7045/ 91 × Shiralee and Regent×Darmor with low or significant negative *sca* effects had a low total glucosinolate content (9.61,13.29, 27.08, 29.59 and 21.56 μM gr-1dry meal, respectively), so they can be considered as good combinations for improving total glucosinolate.

The crosses BL1×PF7045/91, BL1×BL2, BL1×Regent and PF7045/91×Shiralee with significant positive and negative high parent heterosis for seed yield and total glucosinolate, respectively can be considered as good combinations for improving seed yield and total glucosinolate, simutaneously (Table 4).

The *c* mean square was significant for total glucosinolate, indicating the presence of maternal effects and the direction of cross should therefore be considered. In a previ-

Table 5. Estimates of reciprocal effects for yield components, yield and total glucosinolate in the crosses of eight parents of *B. napus.*

Crosses	No. of pods on main axis	No. of pods per Plant	Length of pod	No. of Seeds per Pod	1000-Seed Weight	Yield	Total glucosinolate
BL1 ×Falcon	-2.97	-10.98**	0.12	-0.10	-0.28	-55.93**	-1.22
BL1×PF7045/91	-6.59**	-6.68	-0.22	-0.63	0.24	-20.98	3.03
BL1 1 × BL2	0.31	6.38	-0.07	0.45	-0.17	20.16	-5.62
BL1 × Ceres	0.55	-3.28	0.07	-0.75	0.04	-18.76	-5.03
BL1 × Regent	1.08	-0.33	-0.06	0.48	-0.20	-15.61	-15.27**
BL1 × Darmor	2.58	-5.40	-0.14	0.23	0.18	-1.10	-5.67
BL1 × Shiralee	0.60	4.33	0.17	0.04	-0.19	22.63*	3.26
Falcon×PF7045/91	3.33	15.25	-0.05	-0.40	-0.04	-45.90**	-22.08**
Falcon× BL2	-7.82**	-20.49**	0.23	0.43	0.17	-91.42**	2.06
Falcon × Ceres	1.88	-6.13	-0.13	0.40	-0.05	37.96**	-10.42*
Falcon × Regent	-1.75	-0.30	0.18	-1.20	0.02	-28.93**	-25.56**
Falcon×Darmor	-4.30*	-1.06	0.05	1.10	-0.08	-33.17**	0.54
Falcon ×Shiralee	6.24**	12.75**	-0.30	0.80	0.45**	70.30**	-25.53**
PF7045/91×BL2	1.13	18.68**	-0.15	1.68	-0.09	34.88**	-20.07**
PF7045/91× Ceres	-2.03	5.25	-0.42	-2.61**	-0.20	-47.34**	0.87
PF7045/91×Regent	12.35**	13.63**	0.13	6.73**	-0.13	61.82**	-23.32**
PF7045/91×Darmor	0.63	-9.80**	-0.09	-2.63**	0.17	-22.31*	41.76**
PF7045/91×Shiralee	2.56	24.60**	0.27	2.48**	0.12	72.79**	-2.84
BL2× Ceres	-1.55	-16.80**	-0.07	-1.38	0.23	49.07**	19.39**
BL2 × Regent	-0.05	8.43*	-0.08	-2.18*	0.04	-24.92*	-22.94**
BL2 × Darmor	-0.93	6.85	0.25	1.69	0.44**	-32.48**	18.32**
BL2 × Shiralee	2.86	5.70	-0.08	0.64	0.14	58.54**	-17.90**
Ceres × Regent	-2.10	-1.13	-0.27	-4.08**	0.06	-5.84	23.37**
Ceres ×Darmor	-6.21**	-20.55**	-0.06	1.50	-0.07	-95.21**	-20.03**
Ceres ×Shiralee	4.09*	-11.40	0.01	2.78**	-0.06	-3.06	-3.94
Regent × Darmor	-2.36	-17.78**	-0.02	-1.84	0.18	-50.16**	-5.47
Regent × Shiralee	-2.43	-8.54*	-0.24	-1.63	0.21	61.91**	27.71**
Darmor× Shiralee	2.45	16.53**	-0.18	1.78	0.00	61.99**	5.89

*, ** Significant at p<0.05 and 0.01 probability levels, respectively.

ous study, [14] the importance of maternal effects for glucosinolates was emphasized. In order to obtain combinations with low glucosinolate, the reciprocal crosses of combinations with significant positive reciprocal effects (Table 5), should be used. The correlation between seed yield and total glucosinolate (–0.13) was not significant, so the improvement of total glucosinolate without any considerable change in seed yield is possible.

CONCLUSION

On the basis of the ratios of *a* to *b* mean squares, degree of dominances and narrow-sense heritability estimates, it was concluded that additive genetic effects were more important for total glucosinolate and 1000-seed weight, while non-additive genetic effects were more important for other yield components and seed yield. Therefore, the efficiency of selection for total glucosinolate and 1000-seed weight will be high, but other traits should be improved on the basis of hybridization methods. Among yield components, NPM and NPP had a significant positive correlation with seed yield, therefore, they can be considered as good criteria for improving seed yield. On the other hand, the narrow-sense heritability of NPM and NPP were low and it was high for 1000-seed weight, and so defining an index for selection based on these traits will be effective in a breeding program. The correlation be-

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tween seed yield and total glucosinolate was not significant, so reduction of total glucosinolate without any considerable change in seed yield is possible. In general, the parents BL1, BL2 and PF7045/91 and the crosses BL1 × Falcon, BL1 × PF7045/91 and BL1 ×BL2 were respectively good combiners and combinatons with regard to improving all the traits, simultaneously.

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برآورد پارامترها ي ژنتيكي براي عملكرد، اجزاء عملكرد وميزان گلوكوزينولات در كلزا

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چكيده

هشت ژنوتيپ كلزا شامل شش رقم و دو لاين اصلاح شده جهت برآورد پارامترهاي ژنتيكي تعداد غلاف در ساقه اصلي، تعداد غلاف در بوته، طول غلاف، تعداد دانه در غلاف، وزن هزار دانه، عملكرد دانه و ميزان گلوكوزينولات كل مورد استفاده قرار گرفتند. تجزيه واريانس بر اساس روش هيمن مبين قابليت تركيبپذيري عمومي(a) و خصوصي (b) معنيدار براي خصوصيات مورد مطالعه به استثناء وزن هزار دانه بود، كه نشان دهنده اهميت اثرات افزايشي و غير افزايشي در كنترل ژنتيكي آنها است. براي وزن هزار دانه فقط قابليت تركيبپذيري عمومي معنيدار گرديد. برآورد نسبت ميانگين مربعات قابليت تركيبپذيري عمومي به قابليت تركيبپذيري خصوصي معنيدار و قابليت توارث خصوصي بالا براي وزن هزار دانه و گلوكوزينولات كل مبين اهميت بيشتر اثرات افزايشي در كنترل ژنتيكي خصوصيات مزبور بود ودر نتيجه كارايي انتخاب براي آنها بالا خواهد بود. برآورد ميانگين مربعات معني دار انحراف ميانگين والدين از هيبريدها (b1) براي تمامي خصوصيات به استثناء طول غلاف و وزن هزار دانه نمايانگر غالبيت جهتدار ودرنتيجه هتروزيس متوسط معني دار براي كليه خصوصيات مورد مطالعه به استثناء دو صفت مزبور ميباشد. برآورد ميانگين مربعات معنيدار اثرات مادري (c) براي تمامي خصوصيات به استثناء طول غلاف نشان دهنده اهميت اثرات مادري براي كليه خصوصيات مورد مطالعه به استثناء صفت مزبور ميباشد. در بين اجزاء عملكرد، تعداد غلاف در ساقه اصلي و تعداد غلاف در بوته داراي همبستگي مثبت معنيداري با عملكرد دانه بودند، لذا بعنوان صفات مناسب جهت بهبود عملكرد قابل استفاده ميباشند. عدم وجود همبستگي معنيدار بين گلوكوزينولات كل و عملكرد دانه امكان كاهش اين خصوصيت نامطلوب مرتبط با كيفيت را بدون تغيير قابل ملاحظه در عملكرد دانه ميسر ميسازد. در اين بررسي والدهاي PF7045/91 و BL1 داراي تركيبپذيري عمومي مناسب و

تلاقي‌هاي PF7045/91 x Shiralee و PF7045/91 x Bl1 داراي تركيب‌پذيري خصوصي مناسب براي عملكرد دانه و ميزان گلوكوزينولات كل بودند.

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