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Line × tester analysis in rapeseed: Identification of superior parents and combinations for seed yield and its components

ABSTRACT

This research was carried out to investigate the genetic structure of the 20 F1s rapeseed hybrids established from five female moderate maturity lines and four early maturity male testers, to determine parents showing general combining ability (GCA) and detect crosses showing specific combining ability (SCA). Significant variance of parents and crosses for all the traits indicated the existence of significant genetic variation among the parents and their F1 cross combinations. Significant variance of parents *vs.* crosses revealed significant average heterosis for all the traits except first pod height and seeds per pod. High narrow-sense heritability estimates for number of branches and pods length, indicate the importance of additive genetic effects for these traits. Hybrid performance was generally better than parental performance for all the traits except number of branches and also the genetic variation of lines × testers for all the traits were more than lines and testers. Most of the crosses with high mean value of pods per plant were yielded from the parental lines with high mean value of this trait. The crosses including L41×Foma2, Zafar×R42 and L22B×R38 with significant positive SCA effects of seed yield had also high mean values (3400, 3311.3 and 2904.2 kg ha^{-1} , respectively) of this trait.

Keywords: genetic variation, heritability, line × tester**,** seed yield**.**

INTRODUCTION

The oilseed *Brassicas* are the world's third most important source of oils and their production has witnessed a steady upward movement with the aim of conventional and modern plant breeding approaches (16). Seed yield of rapeseed is a quantitative trait, which is largely influenced by the different environmental conditions and hence in most of the cases it has low heritability (3, 4, 12, 21, 24). The exploitation of genetic variability in any crop species is considered to be critical for making further genetic improvement in seed yield as well as other economically important traits (6, 7, 14, 15, 22). Inter and intra *Brassica* species crosses are suitable ways to make genetic variations and develop the new varieties 2, 11). In rapeseed breeding2 program for hybrid and open pollinated varieties, general and specific combining ability effects (GCA and SCA) are important indicators of the potential of inbred lines in hybrid combinations. To incorporate desirable characters to maximize economic yields, the knowledge of combining ability is valuable to get information on selection of parents and nature of gene actions involved. The variance for GCA includes the additive portion of the total variance, whereas that for SCA includes the non-additive portion of the total variance, arising largely from dominance and epistatic deviations (8, 18, 19). Information and exact study of combining ability can be useful in regard to selection of breeding methods and selection of lines for hybrid combination (10, 13). Due to the numerous theoretical and practical advantages of this method, in recent years the choice of parental forms on the basis of combining ability has been extended. Genetic gain of *Brassica* requires certain information regarding the nature of combining ability of parents available for use in the hybridization program. Most of previous studies on combining abilities have shown significant GCA and SCA effects for yield and its component characters. These results indicate that both additive and non-additive gene action are important in the inheritance of these traits (1, 5, 17, 23). Variability of results indicated clearly that the inheritance patterns of plant traits imparting yield varies with the genetic material and the climatic vagaries that suggested exploring the genetic information about the present material before performing selection. Since different genetic materials display different genetic parameters, the objectives of the present study were therefore to examine the combining abilities patterns of selected rapeseed (*Brassica napus* L.) genotypes in a line × tester analysis, to assess genetic parameters of some agronomic traits, to determine superior candidates for promising hybrid cross combinations.

MATERIALS AND METHODS

Five female moderate maturity spring rapeseed (*Brassica napus* L.) genotypes including L41, Zafar, L56, L31, L22B as lines were crossed with four early maturity male spring testers including Foma2, R42, R41 and R38 based on line × tester crossing scheme during 2010-2011. Eighteen F_1s along with their parents were grown in a randomized complete block design with three replications at Baykola Agriculture Research Station, located in Neka, Iran (53°, 13′ E longitude and 36° 43′ N latitude, 15 m above sea level) during winter 2012-2013. Each plot consisted of four rows 5 m long and 40 cm apart. The distance between plants in each row was 5 cm resulting in approximately 300 plants per plot, which was sufficient for F_1 genetic analysis. The soil classified as a deep loam soil (Typic Xerofluents, USDA classification) contained an average of 280 g clay kg^{-1}, 560 g silt kg^{-1}, 160 g sand kg^{-1}, and 22.4 g organic matter kg^{-1} with a pH of 7.3. Soil samples were found to have 45 kg ha^{-1} (mineral N in the upper 30-cm profile. Fertilizers were applied at the rates of 100: 50: 90 kg ha^{-1} of N: P: K, respectively. All the plant protection measures were adopted to make the crop free from insects. Seed yield (adjusted to kg/ha) was recorded based on two middle rows of each plot. The data were recorded from ten randomly competitive selected plants of each entry of each replication for first pod height, number of branches, pods on main raceme, pods per plant, pods length, and seeds per pod. Data for the genotypes were subjected to line × tester analysis (9) to estimate GCA and SCA effects. A *t*-test was used to test whether the GCA and SCA effects were different from 0. Narrow-sense heritability estimates of the traits and Pearson coefficient correlation between the traits were calculated.

RESULTS AND DISCUSSION

Line × tester analysis of variance

Lines × tester analyses were performed on all the traits for which crossed genotypes gave significant differences. Results of these analyses are summarized in Table 1. Significant differences were found among the treatments, parents and their crosses for first pod height, number of primary branches, pods on main raceme, pods per plant, pods length, seeds per pod and seed yield indicating sufficient genetic variations for the genotypes and their cross combinations for these traits (Table 1). For all of the traits except pods length, genetic variations among the lines were greater than the testers, therefore although lines had significant genetic diversity for all the traits, the testers had not significant genetic difference for pods on main raceme and seeds per pod. Parents vs crosses mean squares which indicate average heterosis were significant for all the traits except first pod height and seeds per pod. High narrow-sense heritability estimates were found for the number of branches, pods length and seeds per pod, indicating the prime importance of additive genetic effects for these traits. In earlier studies (3, 12, 22) high narrow-sense heritability estimates for some of yield components in rapeseed were reported.

Means performances and general combining abilities of the parents

The mean values of the parents including lines and testers for all the traits were presented in Table 2. Among the testers, first pod height varied from 97.8 to 108.6 cm in R38 and R42, respectively and also among the lines, this trait ranged from 88.38 to 115.59 cm in L31 and L41, respectively. The GCA and SCA genetic effects are shown in Table 2. Two parental genotypes, R38 and L31, were characterized by significantly high negative GCA effects for first pod height and therefore will have reduction effects for this trait in their cross combinations. Number of branches had less variation than the other traits in parental lines. Foma2 and Zafar with 5.20 and 5.22 branches per plant, respectively had high mean values of this trait. Significant positive correlation of GCA effects was detected between the number of branches and pods per plant, therefore the GCA effect of this trait can be used as indirect selection criterion for improving of pods per plant (Table 4). Pods on main raceme ranged from 46.7 to 49.6 in testers and also they varied from 41.98 to 54.82 in female lines. The GCA effect of this trait had significant positive correlation with GCA effect of seed yield, therefore it can be used as suitable indicator of good combiners genotypes for seed yield. Pod per plant was more correlated to seed yield and the genotypes including Foma2, L41 and Zafar with high mean values of this trait were favoured. High narrow-sense heritability (0.80)

Table 1. Anaysis of variance (ANOVA), narrow-sense heritability and component of variability for yield components and seed yield of rapeseed (*Brassica napus* L.) genotypes based on line × tester method

Source of variance	df	MS						
		First pod height	Number of branches	Pods on main raceme	Pods per plant	Pods length	Seeds per pod	Seed yield
Replication	2	774.8**	2.95**	383.4**	11.1	0.97	198.0**	1203007.4**
Treatment	28	778.0**	1.63**	348.6**	1889.8**	1.29**	30.2**	391951.8**
Parents	8	642.9**	1.90**	682.6**	990.7**	1.64**	33.0**	621857.3**
Parents vs crosses	1	25.3	2.13*	47.8**	4893.1**	1.34**	2.1	412194.1*
Crosses	19	874.5**	1.49**	223.8**	2110.3**	1.14**	30.5**	294084.1**
Lines	4	1341.5**	2.22**	396.3**	2484.1**	1.27**	48.2**	295939.5**
Testers	3	297.7*	2.62**	23.5	1515.9**	2.40**	18.0	151393.5
Line x tester	12	863.0**	0.97**	216.4	2134.3**	0.79**	27.8*	329138.2**
Error	56	84.2	0.44	28.2	142.4	0.31	8.5	65305.6
Heritability		0.15	0.82	0.31	0.19	0.80	0.50	0.05
Variations due to lines		32.30	31.37	37.28	24.78	23.45	33.27	21.19
Variations due to testers		5.38	27.76	1.66	11.34	33.24	9.32	8.13
Variations due to lines × testers		62.33	41.12	61.07	63.88	43.77	57.57	70.69

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

estimated for pod length, indicating the prime importance of additive genetic effects for this trait. Foma2 and L56 with significant positive GCA effects for pod length are good candidate for improving this trait.

Means performances and specific combining abilities of the crosses

The genetic variation of lines × testers for all the traits were more than lines and testers (Table 1). Hybrid performance was generally better than parental performance for all the traits except the number of branches (Table 5). Mean values of first pod height ranged from 70.67 to 117.1 cm in Zafar × R38 and L22B× R41, respectively. Most of the crosses with high mean values of first pod height had at least one parent with high mean value of this trait. Due to high mean value of first pod height makes susceptible to lodging, therefore the cross combinations with low mean value of this trait including Zafar × R38, Zafar × R41 and L31×R41

Table 2. Means of parents for yield components, seed yield

Parents		First pod height (cm)	Number of branches	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod	Seed yield (kg ha^{-1})
Testers	1-Foma2	104.3	5.2	49.6	154.4	7.0	25.0	2799.9
	2-R42	108.6	4.5	47.3	131.5	6.6	25.0	2791.7
	3-R41	103.0	4.3	48.2	146.9	6.7	24.1	2755.2
	4-R38	97.8	4.4	46.7	137.9	6.0	22.7	2585.1
Lines	5-L41	115.59	4.96	54.82	159.41	6.62	26.66	2977.92
	6-Zafar	110.32	5.22	52.32	154.28	6.32	22.63	2762.00
	7-L56	98.47	4.43	41.98	128.26	6.98	24.02	2611.38
	8-L31	88.38	4.28	42.46	143.10	6.20	21.89	2581.25
	9-L22B	104.33	4.28	48.08	128.34	6.79	25.68	2732.21
LSD (α=0.05)		14.98	1.08	8.67	19.49	0.91	4.76	417.31
LSD (α=0.01)		19.93	1.44	11.53	25.92	1.21	6.33	555.02

Table 3. Estimates of GCA effects for yield components and seed yield and oil of rapeseed (*Brassica napus* L.) genotypes based on line × tester fashion

Parents		First pod height (cm)	Number of branches	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod	Seed yield (kg ha^{-1})
Testers	1-Foma2	0.9	0.63**	1.65	11.73**	0.42**	0.81	66.93
	2-R42	5.16*	–0.12	–0.66	–11.16**	0.03	0.81	58.71
	3-R41	–0.39	–0.3	0.24	4.23	0.09	–0.12	22.23
	4-R38	–5.67*	–0.18	–1.23	–4.77	–0.54**	–1.50*	–147.84*
Lines	5-L41	12.18**	0.33	6.90**	16.74**	0.03	2.49**	244.98**
	6-Zafar	6.9	0.60**	4.38**	11.61**	–0.27	–1.53	29.04
	7-L56	–4.95	–0.21	–5.94**	–14.43**	0.39*	–0.15	–121.59
	8-L31	–15.03**	–0.36	–5.46**	0.42	–0.39*	–2.28**	–151.71*
	9-L22B	0.9	–0.36	0.15	–14.34**	0.21	1.5	–0.75
S.E. GCA (tester)		2.37	0.17	1.37	3.08	0.14	0.75	65.98
S.E. GCA (line)		2.65	0.19	1.53	3.44	0.16	0.84	73.77

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

Table 4. Pearson coefficients of correlation estimates among the means, GCA effects of parent and SCA effects of the crosses for yield components and seed yield

Means (n=20)

Traits	First pod height	Number of branches	Pods on main raceme	Pods per plant	Pods length	Seeds per pod	Seed yield
First pod height	1						
Number of branches	0.05	1					
Pods on main raceme	0.01	0.52*	1				
Pods per plant	0.08	0.45*	0.57**	1			
Pods length	0.31	0.06	0.31	-0.16	1		
Seeds per pod	0.15	0.24	0.34	0.13	0.51*	1	
Seed yield	0.16	0.23	0.46*	0.70**	-0.02	0.23	1

GCA (n=9)

Traits	First pod height	Number of branches	Pods on main raceme	Pods per plant	Pods length	Seeds per pod	Seed yield
First pod height	1						
Number of branches	0.55	1					
Pods on main raceme	0.87**	0.70*	1				
Pods per plant	0.38	0.75*	0.71*	1			
Pods length	0.25	0.15	0.20	-0.12	1		
Seeds per pod	0.65*	0.18	0.52	0.07	0.67*	1	
Seed yield	0.88**	0.60	0.86**	0.58	0.36	0.79*	1

SCA (n=20)

Traits	First pod height	Number of branches	Pods on main raceme	Pods per plant	Pods length	Seeds per pod	Seed yield
First pod height	1						
Number of branches	0.62**	1					
Pods on main raceme	0.59**	0.40	1				
Pods per plant	0.26	0.21	-0.48*	1			
Pods length	0.34	-0.19	0.19	-0.26	1		
Seeds per pod	0.54*	0.31	0.22	0.15	0.36	1	
Seed yield	0.01	-0.01	0.26	0.76**	-0.32	-0.09	1

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

are preferred. Out of 20 crosses, 7 crosses had significant SCA effects for first pod height (Table 6). High narrow-sense heritability estimates and therefore more important role of additive genetic effects for this trait, most of the crosses had not significant SCA effects of this trait. The crosses including Zafar × Foma2 and L56 × Foma2 had high mean value of this trait. Pods on main raceme differed from 33.8 to 64.8 in L31×R42 and Zafar × R41, respectively. Significant positive correlation of SCA effects was determined between pods on main raceme and seed yield, therefore the SCA effect of this trait can be used as indirect selection criterion for improving seed yield. Zafar × R41 and L41 × Foma2 had high mean performances of this trait. Pods per plant was significant positively correlated with seed yield, therefore the crosses such as Zafar × R41, L41 × Foma2, Zafar × R42, L56 × Foma2 and L31 × Foma2 with high mean value of this trait were good combinations for this trait. Most of the crosses with high mean value of pods per plant were yielded from the parental lines with high mean value of this trait. Pods length was more affected from additive effects and therefore most of the crosses had not significant SCA effects of this trait. The crosses including L41 × Foma2, L56 × Foma2, L56 × R41, L56 × R38, L22B × Foma2 and L22B ×R42 with high mean values of this trait were favoured combinations. The crosses including Zafar × Foma2 and L56 × Foma2 with significant positive SCA effects of seeds per pod were good combinations. Out of 20 crosses, 7 crosses had significant SCA effects for seed yield. The crosses including L41 × Foma2, Zafar × R42 and L22B ×R38 with significant positive SCA effects of seed yield had also high mean value of this trait. Most previous studies on combining abilities have shown significant GCA and SCA effects on yield and its component characters. These results indicated that both additive and non-additive gene actions were important in the inheritance of these traits (1, 5, 17, 23).

CONCLUSIONS

In general pods on main raceme and pods per plant were significantly correlated with seed yield, indicating that these traits can be used as good selection criteria for improving seed yield. Parents *vs* crosses as indicator of average heterosis was significant for all the traits except first pod height and seeds per pod. Hybrid performance was generally better than parental performance for all the traits except the number of branches and also the genetic variation of lines × testers for all the traits were more than lines and testers. Among the yield components, the number of branches and pods length were more heritable than the others. For the traits with low narrow-sense heritability suggested that emphasis should be given to specific crosses followed by selection in progenies rather than pursuing GCA by mass selection.

Table 5. Means of the crosses for yield components and seed yield

Crosses	First pod height (cm)	Number of branches	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod	Seed yield (kg ha^{-1})
1-L41 x foma2	104.33	5.0	61.6	171.5	7.0	24.9	3400.0
2-L41 x R42	83.67	5.4	57.4	161.9	6.1	23.8	3000.0
3-L41 x R41	98.00	4.6	47.2	153.5	6.7	28.2	2908.3
4-L41 x R38	76.00	4.8	53.1	150.7	6.6	29.7	2603.3
5- Zafar x Foma2	114.00	6.1	54.4	146.0	6.4	22.2	2512.5
6- Zafar x R42	83.67	4.9	44.8	172.7	6.3	23.1	3311.3
7- Zafar x R41	74.00	5.1	64.8	176.5	6.8	24.2	2975.0
8- Zafar x R38	70.67	4.8	45.3	121.9	5.8	21.1	2249.2
9-L56 xFoma2	98.33	5.7	51.4	171.4	7.7	29.8	2847.5
10-L56 x R42	83.67	4.1	45.7	104.9	7.2	25.1	2695.8
11-L56 x R41	85.67	3.9	35.6	96.1	7.4	22.1	2196.7
12-L56 x R38	89.33	4.0	35.3	140.6	5.6	19.1	2705.5
13-L31 x Foma2	112.33	4.4	44.0	171.6	6.9	22.4	2511.7
14-L31 x R42	83.33	3.6	33.8	111.6	6.1	24.7	2537.5
15-L31 x R41	81.33	4.8	46.7	165.6	5.5	22.7	2812.5
16-L31 x R38	83.00	4.3	45.4	123.6	6.3	17.8	2463.3
17- L22B x foma2	117.00	5.1	36.5	111.6	7.1	25.6	2727.7
18-L22B x R42	98.00	4.5	54.7	106.4	7.2	28.3	2413.7
19- L22B xR41	117.00	3.1	46.7	142.7	6.9	23.2	2883.3
20- L22B xR38	116.00	4.3	54.4	152.6	6.0	25.7	2904.2
LSD (α=0.05)	14.98	1.08	8.67	19.49	0.91	4.76	417.31
LSD (α=0.01)	19.93	1.44	11.53	25.92	1.21	6.33	555.02

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Table 6. Estimates of SCA effects for yield components and seed yield of rapeseed (*Brassica napus* L.) genotypes based on line × tester fashion

Crosses	First pod height (cm)	Number of branches	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod	Seed yield (kg ha^{-1})
1-L41 x foma2	–13.77*	–0.6	5.1	0.39	–0.06	–2.58	355.17*
2-L41 x R42	10.92*	0.6	3.24	13.71	–0.51	–3.66*	–36.63
3-L41 x R41	1.83	0.01	–7.86*	–10.11	0.03	1.65	–91.8
4-L41 x R38	0.99	0.03	–0.48	–3.96	0.51	4.59**	–226.74
5- Zafar x Foma2	–2.58	0.24	0.45	–20.04**	–0.36	–1.2	–316.41*
6- Zafar x R42	–8.73	–0.21	–6.87*	29.55**	–0.03	–0.39	490.62**
7- Zafar x R41	17.73**	0.24	12.21**	18.03*	0.39	1.65	190.77
8- Zafar x R38	–6.42	–0.27	–5.79	–27.57**	–0.03	–0.06	–364.98*
9-L56 xFoma2	29.07**	0.66	7.74*	31.41**	0.24	4.95**	169.2
10-L56 x R42	–1.95	–0.21	4.38	–12.15	0.24	0.3	25.74
11-L56 x R41	0.39	–0.21	–6.66*	–36.36**	0.36	–1.83	–436.92**
12-L56 x R38	–27.51**	–0.24	–5.46	17.13*	–0.84*	–3.42*	241.98
13-L31 x Foma2	–4.02	–0.54	–0.12	16.74*	0.3	–0.33	–136.5
14-L31 x R42	–3.03	–0.54	–8.01**	–20.37**	–0.09	1.98	–102.48
15-L31 x R41	–1.86	0.87*	3.99	18.33**	–0.81*	0.96	209.04
16-L31 x R38	8.91	0.21	4.14	–14.67*	0.6	–2.61	29.94
17- L22B x foma2	–8.73	0.24	–13.17	–28.47**	–0.15	–0.84	–71.31
18-L22B x R42	2.79	0.36	7.26*	–10.74	0.39	1.77	–377.13*
19- L22B xR41	–18.06**	–0.87*	–1.65	10.14	0.03	–2.4	129.03
20- L22B xR38	24.00**	0.24	7.59*	29.07**	–0.27	1.5	319.95*
S.E. (SCA)	5.30	0.38	3.07	6.89	0.32	1.68	147.54

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

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