

Hybrid Performance and Combining Ability Analysis in Rapeseed using Line×Tester Mating Design

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ABSTRACT

Five female moderate maturing lines and four early maturing male testers of rapeseed were used to determine general combining ability (GCA) and specific combining ability (SCA) for phenological traits, yield components and seed yield. Significant mean squares due to lines and testers both indicating of GCA were detected for all the traits except seeds per pod revealed the prevalence of additive genes influencing the traits. Significant variance of parents vs. crosses revealed significant average heterosis for all the traits except days to end of flowering and seeds per pod. High narrow-sense heritability estimates for all phenological traits indicating the prime importance of additive genetic effects for these traits. The crosses including L41×R420 and Zafar×R420 took less days to maturity and had high seed yield which are desirable in rapeseed breeding.

Keywords: Genetic variation, heritability, line × tester, seed yield.

INTRODUCTION

Oilseed Brassicas are the dominant oilseed crop in Iran and their production has witnessed a stable upward movement by the aim of conventional and modern plant breeding approaches (Abtali *et al.*, 2009; Rameeh, 2010). The most promising crop type for high seed yield combined late maturity with early flowering (Amiri Oghan *et al.*, 2016). Genetic information of rapeseed flowering and maturity could aid orienting breeding strategies for short or long growing seasons. Advanced in the phenological traits, yield components and seed yield of brassica requires certain information regarding the nature of combining ability of parents available for use in the hybridization program (Ali *et al.*, 1995; Rameeh, 2014). In addition, information about the nature of gene action involved in expression of quantitative and qualitative traits of economic importance is also required to develop desirable lines. Studies on combining ability have been done earlier (Kumar *et al.*, 2011; Nasimi *et al.*, 2006; Singh *et al.*, 2010). The utilization of genetic variability in any crop species is considered to be critical for making more genetic improvement in seed yield as well as other economically important characteristics

(Inamullah *et al.*, 2006; Mahmood *et al.*, 2003; Rameeh *et al.*, 2012; Rehman *et al.*, 2009; Wang *et al.*, 2010). In rapeseed breeding 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. The variance for GCA includes the additive section of the total variance, while that for SCA comprises the non-additive portion of the total variance, arising largely from dominance and epistatic deviations (Malik *et al.*, 2004; Teklwoold and Becker, 2005; Variath *et al.*, 2009; Rameeh and Andarkhor, 2017). Information and exact study of combining ability can be useful in regard to selection of breeding methods and selection of lines for hybrid combination (Nassimi *et al.*, 2006; Rameeh 2011). Due to the various theoretical and practical advantages of this technique, in recent years the choice of parental forms on the basis of combining ability has been extended. Genetic gain of *Brassica* requires definite information concerning 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 (Akbar et al., 2008; Huang et al., 2010; Singh et al., 2010; Yadav et al., 2005). Variability of results designated clearly that the inheritance patterns of plant traits imparting yield varies with the genetic material and the climatic vagaries that proposed exploring the genetic information about the present material before performing selection. The objectives of the present study were therefore to examine the combining ability abilities patterns of selected rapeseed (*Brassica napus* L.) genotypes in a line × tester analysis, to assess genetic parameters of phenological traits, yield components and seed yield to determine superior candidates for promising hybrid cross combinations.

MATERIALS AND METHODS

The genotypes under study were contained five moderate-maturing of spring rapeseed (*Brassica napus* L.) genotypes including L41, Zafar, L56, L31, L22B as lines and four early-maturing genotypes including Foma2, R42, R41 and R38 as testers which were crossed using line × tester crossing method during 2010-11. Eighteen F₁S 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 2012-13. 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 F₁ 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. Phenological traits and seed yield (adjusted to kg ha⁻¹) 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, pods per plant and seeds per pod. Data for the genotypes were subjected to line×tester analysis (Mather and Jinks, 1982) 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 traits were calculated.

RESULTS AND DISCUSSION

Table1. Mean squares (MS) from ANOVA, narrow-sense heritability and component of variability for plant height, yield components, seed yield and oil content of rapeseed (*Brassica napus* L.) genotypes based on line × tester fashion.

Source of variance	df	Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per plant	Number of seeds per pod	Seed yield
Replication	2	38.7**	34.2	7.9	13.1*	15.2	11.1	198.0**	1203007.4**
Treatment	28	1023.4**	121.6**	750.6**	539.5**	844.1**	1889.8**	30.2**	391951.8**
Parents	8	14336.3**	96.0**	1121.1**	786.2**	715.3**	990.7**	33.0**	621857.3**
Parents vs crosses	1	13348.5**	31.9	1098.3**	420.3**	238.6	4893.1**	2.1	412194.1*
Crosses	19	711.3**	137.1**	576.3**	441.9**	930.2**	2110.3**	30.5**	294084.1**
Lines	4	1332.7**	241.5**	1050.1**	596.0**	1372.7**	2484.1**	48.2**	295939.5**
Testers	3	1717.5**	131.3**	974.7**	1221.1**	418.2*	1515.9**	18.0	151393.5
Line x tester	12	252.7**	104.4**	318.7**	195.7**	910.7**	2134.3**	27.8*	329138.2**
Error	56	6.6	18.6	12.5	2.7	109.1	142.4	8.5	65305.6
Heritability		0.97	0.79	0.92	0.95	0.22	0.19	0.50	0.05
Variations due to lines		39.44	37.08	38.36	28.39	31.07	24.78	33.27	21.19
Variations due to testers		38.13	15.12	26.70	43.63	7.10	11.34	9.32	8.13
Variations due to lines × testers		22.44	48.09	34.93	27.97	61.83	63.88	57.57	70.69

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

Analysis of Variance

Results of the analyses are summarized in Table 1. Significant differences were found among the

treatments, parents and their crosses for days to flowering, days to end of flowering, duration of flowering, days to maturity, plant height, pods

per plant, seeds per pod and seed yield indicating sufficient genetic variations for the genotypes and their cross combinations for these traits. For all of the traits except days to maturity, genetic variations among the lines were greater than the testers. Parents vs crosses mean squares which indicate average heterosis were significant for all the traits except days to end of flowering, plant height and seeds per pod. High narrow-sense heritability estimates were found for phenological traits, and also its average mean value was detected for seeds per pod, indicating the prime importance of additive genetic effects for phenological traits. In earlier studies (Diepenbrock, 2000; Wang et al., 2007; Rameeh, 2010) high narrow-sense heritability estimates for some of yield components in rapeseed were reported.

Means Performances and General Combining Abilities of the Parents

The means value of the parents including lines and testers for all the traits were shown in Table 2. Among the testers, days to flowering varied from 87 to 109.2 in R308 and Foma2, respectively and also among the lines, this trait ranged from 85.58 to 112 in Zafar and L22B, respectively. The GCA and SCA genetic effects are shown in Table 3. Most of parental genotypes had significant negative GCA effects for days to flowering and therefore will have reduction effects for this trait in their cross combinations. In earlier studies (Hung, et al., 2010; Sabaghnia, et al., 2010; Rameeh 2011) were reported significant negative GCA effects for days to flowering. The data regarding, days to end flowering and duration of flowering manifested meaningful differences among lines and testers. Days to end of flowering ranged 161.2 to 167.3 in R308 and Foma2, respectively and among the lines, it was varried from 156.75 to 167.67 in L31 and L22B, respectively (Table 2). The parental genotypes including Foma2 and

L41 with significant positive GCA effects for days to end of flowering had increasing effect for this trait (Table 3). In rapeseed, maximum duration of flowering is desirable which is shown by R420 and Zafar i.e. 74.9 and 78.92 days, respectively. Days to maturity ranged from 191.3 to 212.5 days in R420 and Foma2, respectively and it also was varried from 190.58 to 210.42 days in Zafar and L22B, respectively. In rapseed due to minnum value of days to maturity is desirable, therefore the genotypes including R420 and Zafar will be preferred. The genotypes viz R420, R308 and Zafar with significant negative GCA effects for days to maturity will have reduction effects in their cross combinations for this trait (Table 3).

The data regarding, plant height showed significant differences for line, tester and their cross combinations. Among testers the mean value of plant height ranged from 152.2 to 163.5cm in R308 and R401, respectively. Among lines, this trait also ranged from 148.58 to 173.42 cm in

L31 and L41, respectively. Sabaghnia et al. (2010) also reported highly significant differences among rapeseed genotypes for plant height. Plant with shorter stem are desirable in rapeseed, L31 and L56 showed low values of plant height in the genotypes studied. The parents including L31 and R308 with significant negative GCA effects for plant height had reduction effects in their hybrid combinations for this trait (Table 3). 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) 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.

Table2. Means of parents for plant height, yield components, seed yield and oil content.

Parents		Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per plant	Number of seeds per pod	Seed yield
Testers	1-Foma2	109.2	167.3	58.1	212.5	163.3	154.4	25.0	2799.9
	2-R420	86.5	161.3	74.9	191.3	163.5	131.5	25.0	2791.7
	3-R401	91.2	164.8	73.6	202.6	160.5	146.9	24.1	2755.2
	4-R308	87.0	161.2	74.2	197.3	152.2	137.9	22.7	2585.1
Lines	5-L41	90.50	167.33	76.83	201.83	173.42	159.41	26.66	2977.92
	6-Zafar	85.58	164.50	78.92	190.58	168.08	154.28	22.63	2762.00
	7-L56	89.25	162.08	72.83	200.25	151.11	128.26	24.02	2611.38
	8-L31	90.00	156.75	66.75	201.50	148.58	143.10	21.89	2581.25
	9-L22B	112.00	167.67	55.67	210.42	158.31	128.34	25.68	2732.21
LSD ($\alpha=0.05$)		4.20	7.04	5.77	2.68	17.06	19.49	4.76	417.31
LSD ($\alpha=0.01$)		5.58	9.37	7.68	3.57	22.69	25.92	6.33	555.02

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

Parents		Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per plant	Number of seeds per pod	Seed yield
Testers	1-Foma2	15.72**	3.66**	-12.06**	11.61**	3.39	11.73**	0.81	66.93
	2-R420	-6.99**	-2.34*	4.68**	-9.66**	3.63	-11.16**	0.81	58.71
	3-R401	-2.28**	1.14	3.39**	1.68**	0.63	4.23	-0.12	22.23
	4-R308	-6.48**	-2.46*	3.99**	-3.66**	-7.65**	-4.77	-1.50*	-147.84*
Lines	5-L41	-2.97**	3.66**	6.63**	0.93	13.53**	16.74**	2.49**	244.98**
	6-Zafar	-7.89**	0.84	8.73**	-10.32**	8.19**	11.61**	-1.53	29.04
	7-L56	-4.23**	-1.59	2.64*	-0.66	-8.79**	-14.43**	-0.15	-121.59
	8-L31	-3.48**	-6.93**	-3.45**	0.57	-11.31**	0.42	-2.28**	-151.71*
	9-L22B	18.54**	3.99	-14.52**	9.51**	-1.59	-14.34**	1.5	-0.75
S.E. GCA (tester)		0.66	1.11	0.91	0.42	2.70	3.08	0.75	65.98
S.E. GCA (line)		0.74	1.24	1.02	0.47	3.02	3.44	0.84	73.77

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

Means Performances and Specific Combining Abilities of the Crosses

Line×tester mean square was significant for days to flowering, days to end of flowering, duration of flowering, days to maturity, plant height, pods per plant, seeds per pod and seed yield indicating sufficient genetic variations for hybrid combinations of these traits (Table 1). Parents vs crosses which is indicating of superiority of crosses than parents was also significant for days to flowering, duration of flowering, days to maturity, pods per plant and seed yield.

Means value of days to flowering ranged from 70.7 in Zafar×R308 to 117 in L22B×Foma2 and L22B×R401 (Table 4). In rapeseed, low value of days to flowering is preferred, therefore the crosses including Zafar×R308, L41×R308 and L41×R308 with 70.7, 74 and 76 days of this trait, respectively will be favoured. Most of the crosses with significant negative SCA effects for days to flowering had at least one parent with significant negative GCA effects of this trait. The crosses including L41×R308, L41×R308 and L22B×Foma2 with highly significant negative SCA effects for days to flowering were good combinations for improving this trait (Table 5).

High narrow-sense heritability estimates for all phenological traits indicating the prime importance of additive genetic effects for these traits (Table 1). High means value of days to end of flowering will be favoured, therefore the crosses including Zafar×Foma2, L22B×R420 and L41×R401 with 171.3, 174.3 and 176.7 days to end of flowering were suitable combinations for improving this trait. (Table 4). Duration of flowering was varied from 48.3 to

93.7 days in L31×Foma2 and Zafar×R401, respectively (Table 4). Due to high mean value of duration of flowering is desirable, the crosses including L41×R308, Zafar×R308 and Zafar×R401 were considered good combinations for improving this trait. Low mean value of days to maturity is favoured in rapeseed breeding. The genotypes including Zafar×R308, Zafar×R401 and L41×R420 with 179.7, 183.7 and 187.7 days to maturity were detected as prior combinations for improving rapeseed. Plant height ranged from 120.5 to 192.5 cm in L56×R308 and Zafar×R401, respectively. Low mean value of plant height make tolerance to lodging, therefore the crosses including L56×R308, L22B×R401, L31×R401, L22B×Foma2 and L31×R420 with low means value of plant height will be preferred (Table 4).

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 favored 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×R420 and L22B×R38 with significant positive SCA

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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 (Yadav et al., 2005; Akbar et al., 2008; Huang et al., 2010; Singh et al., 2010).

Table4. Means of the crosses for plant height, yield components, seed yield and oil content.

Crosses	Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per plant	Number of seeds per pod	Seed yield
1-L41 x Foma2	104.3	169.7	65.3	206.3	169.5	171.5	24.9	3400.0
2-L41 x R420	83.7	157.0	73.3	187.7	188.1	161.9	23.8	3000.0
3-L41 x R401	98.0	176.7	78.7	207.3	173.7	153.5	28.2	2908.3
4-L41 x R308	76.0	166.0	90.0	206.0	162.4	150.7	29.7	2603.3
5- Zafar x Foma2	114.0	171.3	57.3	210.7	165.6	146.0	22.2	2512.5
6- Zafar x R420	83.7	157.7	74.0	188.3	163.9	172.7	23.1	3311.3
7- Zafar x R401	74.0	167.7	93.7	183.7	192.5	176.5	24.2	2975.0
8- Zafar x R308	70.7	161.3	90.7	179.7	150.3	121.9	21.1	2249.2
9-L56 xFoma2	98.3	168.7	70.3	214.3	184.4	171.4	29.8	2847.5
10-L56 x R420	83.7	157.3	73.7	189.3	151.8	104.9	25.1	2695.8
11-L56 x R401	85.7	164.0	78.3	193.7	147.7	96.1	22.1	2196.7
12-L56 x R308	89.3	158.3	69.0	203.7	120.5	140.6	19.1	2705.5
13-L31 x Foma2	112.3	161.3	49.0	214.7	149.8	171.6	22.4	2511.7
14-L31 x R420	83.3	160.3	77.0	189.0	147.6	111.6	24.7	2537.5
15-L31 x R401	81.3	149.3	68.0	214.0	144.5	165.6	22.7	2812.5
16-L31 x R308	83.0	156.0	73.0	188.3	152.4	123.6	17.8	2463.3
17- L22B x Foma2	117.0	165.7	48.7	216.7	147.2	111.6	25.6	2727.7
18-L22B x R420	98.0	174.3	76.3	202.0	166.2	106.4	28.3	2413.7
19- L22B xR401	117.0	166.3	49.3	214.3	144.3	142.7	23.2	2883.3
20- L22B xR308	116.0	164.3	48.3	208.7	175.6	152.6	25.7	2904.2
LSD ($\alpha=0.05$)	4.20	7.04	5.77	2.68	17.06	19.49	4.76	417.31
LSD ($\alpha=0.01$)	5.58	9.37	7.68	3.57	22.69	25.92	6.33	555.02

Table5. Estimates of SCA effects for plant height, yield components, seed yield and oil content of rapeseed (*Brassica napus L.*) genotypes based on line × tester fashion.

Crosses	Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per plant	Number of seeds per pod	Seed yield
1-L41 x Foma2	-1.89	-1.32	0.57	-7.11**	-7.35	0.39	-2.58	355.17*
2-L41 x R420	0.18	-8.01**	-8.16**	-4.53**	11.04	13.71	-3.66*	-36.63
3-L41 x R401	9.78**	8.19**	-1.56	3.81**	-0.36	-10.11	1.65	-91.8
4-L41 x R308	-8.04**	1.14	9.18**	7.83**	-3.33	-3.96	4.59**	-226.74
5- Zafar x Foma2	12.69**	3.18	-9.51**	8.46**	-5.88	-20.04**	-1.2	-316.41*
6- Zafar x R420	5.07**	-4.5	-9.57**	7.41**	-7.77	29.55**	-0.39	490.62**
7- Zafar x R401	-9.33**	2.04	11.34**	-8.61**	23.79**	18.03*	1.65	190.77
8- Zafar x R308	-8.46**	-0.69	7.74**	-7.26**	-10.14	-27.57**	-0.06	-364.98*
9-L56 xFoma2	-6.66**	2.91	9.57**	2.46*	29.94**	31.41**	4.95**	169.2
10-L56 x R420	1.41	-2.43	-3.84	-1.26	-2.88	-12.15	0.3	25.74
11-L56 x R401	-1.32	0.78	2.1	-8.28**	-4.08	-36.36**	-1.83	-436.92**
12-L56 x R308	6.54**	-1.29	-7.83**	7.08**	-22.95**	17.13*	-3.42*	241.98
13-L31 x Foma2	6.6**	0.93	-5.67**	1.56	-2.16	16.74*	-0.33	-136.5
14-L31 x R420	0.33	5.91*	5.58**	-2.85**	-4.65	-20.37**	1.98	-102.48
15-L31 x R401	-6.39**	-8.55**	-2.16	10.83**	-4.71	18.33**	0.96	209.04
16-L31 x R308	-0.54	1.71	2.25	-9.51**	11.49	-14.67*	-2.61	29.94
17- L22B x Foma2	-10.74**	-5.67*	5.07*	-5.37**	-14.55**	-28.47**	-0.84	-71.31
18-L22B x R420	-6.99**	9.00**	15.99**	1.23	4.26	-10.74	1.77	-377.13*
19- L22B xR401	7.26**	-2.46	-9.72**	2.22*	-14.64*	10.14	-2.4	129.03
20- L22B xR308	10.47**	-0.87	-11.34**	1.89	24.9**	29.07**	1.5	319.95*
S.E. SCA	1.48	2.49	2.04	0.95	6.03	6.89	1.68	147.54

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

CONCLUSION

In general high narrow-sense heritability estimates for all phenological traits indicating the prime importance of additive genetic effects for these traits. The lines and crosses had highly significant genetic difference for phenological traits, plant height, pods per plant, seeds per pod and seed yield. Parents vs crosses as indicator of average heterosis was significant for all the traits except days to end of flowering and seeds per pod. Among the yield components, seeds per pod was 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. The crosses including L41×Foma2, Zafar×R420 and L22B×R38 with significant positive SCA effects of seed yield had also high mean value of this trait considered as good combinations for improving seed yield.

RECOMMENDATIONS

On the basis of conclusions given above the following recommendations can be made: High narrow-sense heritability estimates for all phenological traits indicating the prime importance of additive genetic effects for these traits and therefore these traits can be improved by selection breeding program. L41 × R420 and Zafar × R420 took less days to maturity and had high seed yield which are desirable in rapeseed breeding. Most of crosses with significant negative SCA effects for plant height had at least on parent with highly significant negative GCA effect for this trait, therefore in future breeding program, GCA effect of parents can be used as good selection criterion for improving plant height.

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