Genetic Analysis for Yield and Yield Components in Rapeseed

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Abstract

Information on estimates of combining ability and heritability of the promising lines of breeding material is important for evolving higher yielding varieties of rapeseed (*Brassica napus* L.). To estimate the combining ability and heritability of F_2 populations of 4 x 4 full diallel crosses and parents, an experiment was carried out at The University of Agriculture, Peshawar, in growing season 2012-2013. Four parental lines and F_2 populations of six direct and six reciprocal crosses were planted in the experiment using randomized complete block design. Data were recorded on yield and yield components. Analysis of variance revealed significant variation among genotypes for all the parameters studied. Yield plant^{-1} ranged from 4.27 to 9.17 g, pods main- raceme^{-1} ranged from 42 to 89 and seeds pod^{-1}ranged from 8 to 18. Among parents highest yield plant^{-1} and seeds pod^{-1}were observed for AUP-402. Cross AUP-402 x AUP-401 produced the highest seed yield plant^{-1} and more pods plant^{-1}. The results of combining ability analysis showed that general combining ability was significant at p ≤ 0.01 for pods main-raceme^{-1}and seeds pod^{-1}. SCA and reciprocal effects were significant at p ≤ 0.01 for pods main-raceme^{-1}, seeds pod^{-1} and seed yield. Genotype AUP-401 was best general combiner for several parameters. Crosses AUP-403 x AUP-404 and AUP-401 x AUP-402 were best specific combiners for seed yield plant^{-1}. Heritability (bs) estimates were high (>70%) for seeds pod^{-1}. Moderate heritability values were observed for seed weight and seed yield plant^{-1}. The variance components of specific combining ability (SCA) were greater than respective general combining ability (GCA) components of all the characters signifying the presence of non-additive genetic effects in transfer of these traits and for that reason selection in the later generations should be practiced for improvement of these traits.

Key words: Combining ability, rapeseed, heritability

Introduction

Rapeseed (*Brassica napus* L.)*,* is chiefly grown for seeds which contain 35-45 % oil and oil extracted from its seed is mainly used for edible purpose. Plant oils are one of the high value agricultural commodities, and thus rapeseed as a source of plant oil is an important oilseed crop.

Yield is a complex polygenic trait and is thus subject to more changes by the environmental conditions. The magnitude of genetic variations is responsible for improvement in complex polygenic traits. Knowledge of genetic variation of yield and yield components are essential for improvement of varieties. Creation, manipulation and evaluation of genetic differences in any crop species including rapeseed are important for genetic improvement in yield and related traits (Mahmood et al., 2003).

The breeding programs mostly depend upon selection of plants on the basis of phenotype. When the phenotype of a trait is not due to genetic makeup, the selection process is not very effective thus; selection is affected greatly by the heritability of a trait for which selection is done (Marjanovic et al., 2011). Selection of phenotypically superior genotypes for hybridization programs may produce poor recombinants in the segregating generations. Determination of combining ability; the capability of a genotype to produce superior progeny upon hybridization with other genotypes, is important for selection of parents for hybridization programs. Diallel mating design may be used by breeders to select suitable parents for hybridization. Heritability of yield and yield components,

magnitude of genetic and phenotypic variability and combining ability of genotypes are important for success of breeding programs, as such information assists improvement of the populations.

Materials and Methods

This experiment was conducted to evaluate combining ability and heritability of important traits in F_2 diallel populations and their parental lines at Agriculture Research Farm of The University of Agriculture, Peshawar, Pakistan in growing season of 2012-13.

The genetic material comprised of a set of four *B. napus* L. genotypes introduced from China; the genotypes along with their original codes are given below:

Genotypes	Original Code
AUP-401	Topas-7038/DH/7/401-3
AUP-402	Topas-7038/DH/7/402-9
AUP-403	Topas-7038/DH/7/403-10
AUP-404	Topas-7038/DH/7/404-10

The genotypes were crossed in full diallel fashion. F_2 generations of 12 possible crosses (six direct crosses and six reciprocal crosses) and the four parents were evaluated in the study under irrigated condition.

All the 16 genotypes (12 crosses and four parents) of rapeseed were sown on October 18, 2012 in well prepared seedbeds after pre-sowing irrigation using a randomized complete block design with three replications. Each experimental unit had three rows, 5 meters long with 60 cm distance between rows. Sowing was done at thicker rate with a hand drill. At seedling stage, 30 cm plant to plant distance was maintained by thinning. Recommended doses of nitrogen and phosphorous at the rate of 80 kg ha^{-1} and 50 kg ha^{-1} respectively for rapeseed crop were applied to the experiment. Uniform standard cultural practices for entire experiment were followed to raise the crop. Ten guarded plants from the central row were randomly selected in each experimental unit and tagged for recording data. Data were recorded on pods main-raceme^{-1}, seeds pod^{-1}, seed weight, and seed yield plant^{-1}, of the tagged plants. Selected plants were harvested, pods form the plants were separated and threshed; the seeds were cleaned and weighed with an electronic balance to record yield plant^{-1}.

Statistical Analysis

Data for each trait were subjected to method of analysis by Griffing (1956) as explained by Singh and Chaudhry (1985). Combining ability analysis was done to partition genotypic variance into variances for general combining ability (GCA), specific combining ability (SCA) and reciprocal effects (RE). Griffing (1956) Method 1, Model 1 (Fixed effect) was used for combining ability analysis. GCA (gi) effects of the parents and SCA (sij) as well as RE (rij) for the crosses were calculated.

From the expected MS (mean squares) for Model 1 of ANOVA for combining ability analysis, the genetic components due to GCA, SCA and RE were calculated as follows:

$$\frac{1}{n-1}\Sigma gca_i^2 = \frac{(MSgca - MSError)}{2n}$$

$$\frac{2}{n(n-1)}\Sigma\Sigma s_{ij}^2 = \frac{(MSsca - MSError)}{2n}$$

$$\frac{2}{n(n-1)}\Sigma\Sigma r_{ij}^2 = \frac{(MSreciprocal\ effects - MSError)}{2}$$

The ratio of genetic component due to GCA and SCA was calculated; the ratio is important and denotes the relative significance of additive and non-additive gene effects.

Heritability (h^2) expressed as percent was calculated for each trait using following formula (Singh, 1993).

$$h^2 = \left[\left(\frac{Vg}{Vp}\right)x100\right]$$

Where Vg is genotypic variance and Vp is phenotypic variance: Vg and Vp were calculated from MS genotypes and MS error of preliminary ANOVA for RCB design using the following formulae based on expected mean sum of squares (Singh, 1993):

Vg (genetic variance) = $\frac{(MSgenotypes - MSError)}{number\ of\ replications}$

Ve (environmental variance) = Error MS

Vp (phenotypic variance) = Vg + Ve

For further exploration about the potential of the crosses for producing promising lines in later generations of the crosses; some of the basic statistics relevant to varietal improvement were calculated from data on 30 plants of each cross; the basic statistics are criteria for variability of plants in F_2 generations of the crosses. As variation is the basis for improvement, variances were calculated for each cross. Minimum, maximum, median, skewness, and third quartile were also calculated for each cross. Skewness was calculated using the following formula (Muhammad, 2000).

$$Skewness = \frac{3(mean - median)}{Standard\ deviation}$$

If mean is higher than median the distribution is positively skewed in which case the tail extend to the right side or higher value side indicating less number of plants on higher side of mean but having comparatively greater values: If mean is lower than median, the distribution is negatively skewed in which case there are comparatively more plants with values greater than mean. If the third quartile of the cross is more than better parent mean, more than 25 % of the plants have higher values than the better parent and these plants have potential to produce better lines in F_4 to F_6 generations. Percent of the plants having higher values than better parent were also calculated and it also indicates the potential of the cross for producing better lines in later generation.

Result and Discussion

The preliminary analysis of variance showed significant differences among genotypes for pods raceme[-1], seeds pod[-1], seed yield plant[-1] and seed weight (Table 1). Similar results in rapeseed were also reported by Turi et al. (2011), Amiri-oghana et al. (2009), Akbar et al. (2008), and Nassimi et al. (2006). Co-efficient of variation (CV) of a trait shows variation due unknown sources as a percent of mean and it is one of the indications for precision of experiment. Low CV values indicate less within experiment environmental fluctuations and hence less experimental error. The CV values of different traits ranged from 4.918 to 20.30% (Table 1). Highest co-efficient of variation was observed for seed yield plant[-1] (20.30) showing high influence of environment on yield; this was followed by seeds pod[-1] (14.47). High CV value for seed yield was also observed by Aytac et al. (2008), Marjanovic et al. (2011) and Sadat et al. (2010).

Table 1. Mean squares from the ANOVA table for various traits of 4x4 diallel crosses of B. napus

Parameter	Replications (df=2)		Genotypes (df=15)	Error (df=30)	CV (%)
Pods raceme[-1]	166.300	ns	438.200 **	56.890	11.23
Seeds pod[-1]	12.200	*	29.820 **	3.047	14.47
Seed yield plant[-1] (g)	0.317	ns	5.970 **	1.859	4.92
Seed weight (g)	0.003	ns	0.004 *	0.002	20.30

ns = not significant, * = significant at 0.05, ** = significant at 0.01

Mean performance of parents and crosses
Seed yield plant[-1] (g)

Brassica is generally planted as oilseed crop and seed is the most important economic part. Highest seed yield plant[-1] was observed for AUP-402 x AUP-401 (9.17g) which is significantly high than most of the crosses except AUP-401 x AUP-403, AUP-403 x AUP-404 and AUP-404 x AUP-403 (Table 2). Three crosses, AUP-402 x AUP-401 (9.17g), AUP-404 x AUP-403 (8.38g), and AUP-401 x AUP-403 (7.81 g) produced more yield than their better parents. Cross AUP-404 x AUP-403 produced significantly more yield than parental mean yield. Cross AUP-401 x AUP-403 and cross AUP-402 x AUP-403 produced more yield plant[-1] than their reciprocal crosses. Although seed yield of both AUP-403 and AUP-404 is less than mean yield of crosses and other parents but their direct as well as reciprocal cross produced more yield than average of parents and crosses. Highly significant differences for seed yield plant[-1] were also observed by Amiri-Oghana et al. (2009) Azizinia (2012), Sadat et al. (2010), Marjanovic et al. (2011), Aytac et al (2008) and Zare and Sharafzadeh (2012).

Pods main-raceme[-1]

Number of pods per raceme is one of the major yield contributing traits in brassica species.

Maximum number of pods main raceme[-1] was produced by AUP-402 x AUP-401 (89.1 pods raceme[-1]) and the number of pods per main raceme of the cross was significantly more than both parents (Table 3). The next highest number of pods was produced cross AUP-401 x AUP-404 (82.5 pods raceme[-1]). Minimum pods were produced by AUP-404 x AUP-402 (42.2 pods raceme[-1]) although both the parents had more pods than mean values of all the crosses and the other two parents. Generally, the cross with maximum raceme length produced maximum number of pods and the cross with short raceme produced lowest number of plants; F_2 plants of cross AUP-402 x AUP-401 had on the average 93.1 cm long main racemes which produced on the average 89 pods. The results of Aytac et al. (2008), Sadat et al. (2010), Dar et al. (2013), Azizinia (2012) and Gupta et al. (2011) are similar to the results of the present study.

Seeds pod[-1]

Seeds pod[-1] is a component of seed yield of brassica; product of seeds pod[-1] and pods plant[-1] is equal to seed plant[-1] which is an important yield component. Among parents AUP-402 produced maximum seeds pod[-1] whereas among crosses the cross AUP-404 x AUP-402 produced maximum seeds pod[-1] (Table 4). Among the direct crosses only AUP-403 x AUP-404 produced significantly

higher number of seeds pod[-1] than parents whereas among reciprocal crosses AUP-404 x AUP-401, AUP-404 x AUP-402 and AUP-404 x AUP-403 produced significantly more seeds pod[-1] than parents. Similar results were reported by Aytac et al. (2008), Dar et al. (2013) and Qurban et al. (2010) however, Sadat et al. (2010) and Zare and Sharafzadeh (2012) reported not significant variability for seeds pod[-1].

Table 2. Average Seed yield plant[-1] of *B. napus*, GCA of parents, SCA, RE and descriptive statistics of crosses

Parents and crosses	Mean	GCA, SCA, RE	Descriptive statistics‡						
			Var	Min	Max	Mdn	SK	Q-3	P>BP
									Parents
AUP-401	7.63	0.26 *	13.13	--	--	--	--	--	--
AUP-402	7.76	0.09 ns	12.88	--	--	--	--	--	--
AUP-403	5.52	-0.22 *	7.55	--	--	--	--	--	--
AUP-404	5.79	-0.14 ns	9.99	--	--	--	--	--	--
									Direct crosses
AUP-401xAUP-402	6.16	0.68 **	20.98	1.18	17.06	4.71	0.95	8.19	26
AUP-401xAUP-403	7.81	-0.32 *	27.92	1.76	23.76	4.65	1.80	8.54	29
AUP-401xAUP-404	6.01	-0.83 **	37.32	1.25	28.81	3.82	1.08	7.37	22
AUP-402xAUP-403	6.71	-1.01 **	11.59	0.69	14.60	6.45	0.24	8.33	27
AUP-402xAUP-404	6.53	-0.61 **	20.37	1.63	17.29	5.49	0.69	7.57	23
AUP-403xAUP-404	8.15	2.00 **	28.66	2.15	24.99	7.31	0.47	9.82	55
									Reciprocal crosses
AUP-402xAUP-401	9.17	-1.51 *	35.90	1.81	21.28	7.74	0.72	7.80	37
AUP-403xAUP-401	4.88	1.47 *	12.09	0.46	13.99	4.47	0.36	6.38	17
AUP-404xAUP-401	5.83	0.09 ns	26.78	0.68	20.05	3.87	1.14	7.70	21
AUP-403xAUP-402	4.27	1.22 ns	15.09	0.69	19.25	3.49	0.60	4.76	10
AUP-404xAUP-402	5.41	0.56 ns	24.03	1.19	25.56	3.98	0.88	5.99	10
AUP-404xAUP-403	8.38	-0.12 ns	47.06	0.86	32.25	6.10	1.00	11.44	48

‡ Min (Minimum), Max (Maximum), Mdn (Median), Sk (Skewness), Q-3 (Third quartile), P>BP (Percent plants having greater value than better parent), * = significant at the 5 % level of probability, ** = significant at the 1 % level of probability, and ns = not significant.

Thousand Seed weight (g)

Seed weight is one of the major yield components; heavier seeds result in higher economic yield. Thousand seed weight ranged from 7.75 g to 8.63 g in parents and from 7.72 g to 8.93 g in crosses (Table 5). Parents AUP-403 and AUP-404 produced heavier seeds than other two parents. Cross AUP-403 x AUP-402 produced heavier seeds among crosses followed by cross AUP-402 x AUP-401. Rameeh (2011), Gupta et al. (2011), Sadat et al. (2010) and Qurban et al. (2010) also observed significant differences among genotypes for seed weight.

Combining ability

Combining ability studies are important in determining the type of gene action involved in controlling the inheritance of a trait and parents with good general combing ability can be used in hybridization program for varietal improvement. Best performance of a particular cross showing desirable specific combining ability can be used as hybrids and can be a source of better lines in segregating generations in self-pollinated species.

Seed yield plant[-1] (g)

Seed yield is the most important character in rapeseed. Mean squares for SCA and reciprocal effects were significant while variance for GCA was not significant for the seed yield (Table not reported). These results agree with Sincik et al. (2011) and Saeed et al. (2013) who reported not significant GCA mean squares and significant SCA and RCA mean squares. However, significant mean squares for GCA and SCA were observed by Amiri-Oghana et al. (2009), Aghao et al. (2010), Rameeh (2010), Arifullah et al. (2012) and Azizinia (2012).

The result of general combining ability estimates showed that genotype AUP-401 showed significant positive general combining ability effects, which are important for developing new genotypes with high yielding characteristics and two genotypes showed negative GCA (Table 2). Six crosses exhibited significant SCA effects. Two crosses showed positive SCA effects while rest of the crosses exhibited negative SCA. Maximum SCA was observed for AUP-403 x AUP-404 (2.00), both the parents of this cross exhibit negative GCA effects. Next highest SCA was recorded for AUP-401 x AUP-402 (0.68) with one parent having

significant positive GCA. The highest SCA of cross AUP-403 x AUP-404 was due to higher SCA for seeds pod^{-1} while that of the cross AUP-401 x AUP-402 was due to higher SCA for pods main-raceme^{-1}. Reciprocal effects ranged from -1.51 for AUP-402 x AUP-401 to 1.47 for AUP-403 x AUP-401. Maximum reciprocal effects was observed for the cross AUP-403 x AUP-401; which shows that direct cross is better than reciprocal cross and it indicates that the use of AUP-401 as female and AUP-403 as male is better than AUP-401 as male and AUP-403 as female. The lowest significant reciprocal effect (-1.6) indicates that reciprocal cross AUP-402 x AUP-401 is better than its direct cross AUP-401 x AUP-402 in term of average yield plant^{-1}.

Cross AUP-403 x AUP-404 had maximum SCA though both parents of the cross had negative GCAs, RE of this cross was not significant showing both direct and reciprocal crosses have better SCAs. The variance of the yield of 30 F$_2$ generation plants of cross AUP-404 x AUP-403 is highest showing promise for developing high yielding lines in later generations of this cross; the plant with the highest maximum yield (32.25 g plant^{-1}) among crosses, the highest quartile-3 and the second highest percentage of plants showing more yield than better parent (only exceeded by its direct cross) also show that this cross have great promise for generating better yielding lines in later generations. Cross AUP-401 x AUP-404 with the next highest variance and the next highest maximum yield producing F$_2$ plant and cross AUP-402 x AUP-401 with the highest mean performance, greater variance (variation is basis for Improvement), greater percentage of plants producing more yield than better parent may have greater promise for selection of high yielding lines in F$_4$ to F$_6$ generations.

Table 3. Average pods raceme^{-1} of *B. napus,* GCA of parents, SCA, RE and descriptive statistics of crosses

Parents and crosses	Mean	GCA, SCA, RE	Descriptive statistics‡						
			Var	Min	Max	Mdn	SK	Q-3	P>BP
									Parents
AUP-401	69.0	4.67 **	490.7	--	--	--	--	--	--
AUP-402	71.4	0.69 ns	370.9	--	--	--	--	--	--
AUP-403	72.7	-0.70 ns	162.6	--	--	--	--	--	--
AUP-404	71.8	-4.66 **	491.7	--	--	--	--	--	--
									Direct crosses
AUP-401 x AUP-402	69.5	6.79 **	513.5	17	110	63.5	0.79	85.8	43
AUP-401 x AUP-403	67.0	0.10 ns	611.6	28	109	65.5	0.18	90.0	43
AUP-401 x AUP-404	82.5	0.56 ns	570.0	33	121	84.5	-0.25	100.8	73
AUP-402x AUP-403	74.2	-1.06 ns	548.2	35	139	73.0	0.15	80.8	53
AUP-402xAUP-404	66.9	-8.63 **	458.8	32	114	66.5	0.06	80.3	37
AUP-403xAUP-404	63.2	-5.94 **	385.1	28	118	62.5	0.11	73.0	30
									Reciprocal crosses
AUP-402xAUP-401	89.1	-9.83 *	505.3	48	141	90.0	-0.12	88.0	73
AUP-403xAUP-401	75.5	-4.25 ns	389.4	18	111	74.5	0.15	90.3	60
AUP-404xAUP-401	52.9	14.78 *	226.3	27	89	52.0	0.19	61.5	10
AUP-403xAUP-402	58.0	8.12 *	421.1	30	103	50.0	1.16	75.5	27
AUP-404xAUP-402	42.2	12.35 *	215.2	3	66	44.0	-0.37	51.5	0
AUP-404xAUP-403	48.5	7.38 *	163.5	29	84	46.0	0.58	58.0	3

‡ Min (Minimum), Max (Maximum), Mdn (Median), Sk (Skewness), Q-3 (Third quartile), P>BP (Percent plants having greater value than better parent), * = significant at the 5 % level of probability, ** = significant at the 1 % level of probability, and ns = not significant.

The estimates of GCA and SCA variances showed higher magnitude of SCA variance than GCA variance signifying the pre-dominance of non-additive gene action for seed yield (Table 6). Selection in later generations after hybridization procedure would be effective for improving seed yield plant^{-1}. Non-additive gene action for the inheritance of seed yield plant^{-1} was previously reported by Farshadfar et al. (2013), Nasrin et al. (2011), Akbar et al. (2008) and Sincik et al. (2011). In earlier studies additive gene effects were observed for this trait by Saeed et al. (2013), Noshin et al. (2007) and Turi et al. (2011).

Pods main-raceme^{-1}

Highly significant mean squares due to general, specific and reciprocal combining abilities were observed for pods raceme^{-1}. These results of significant combining ability agree with the findings of Nassimi et al. (2006) and Noshin et al. (2007). Sincik et al. (2011) reported significant GCA and

SCA mean squares and not significant RCA mean squares for this trait.

Table 4. Seeds pod^{-1} of *B. napus,* GCA of parents, SCA, RE and descriptive statistics of crosses

Parents and crosses	Mean	GCA, SCA, RE	Descriptive statistics‡						
			Var	Min	Max	Mdn	SK	Q-3	P>BP
									Parents
AUP-401	10.8	-0.84 **	13.01	--	--	--	--	--	--
AUP-402	11.8	-0.24 ns	16.93	--	--	--	--	--	--
AUP-403	10.8	-0.11 ns	15.56	--	--	--	--	--	--
AUP-404	9.1	1.19 **	8.40	--	--	--	--	--	--
									Direct crosses
AUP-401xAUP-402	12.1	0.50 *	30.19	4.0	26.7	11.00	0.61	14.0	46
AUP-401xAUP-403	12.3	-1.13 **	32.05	2.0	24.7	12.00	0.13	16.0	55
AUP-401xAUP-404	9.6	0.17 ns	21.56	3.7	22.3	8.33	0.82	10.6	25
AUP-402xAUP-403	11.4	-1.88 **	19.92	4.0	26.0	11.17	0.16	12.6	47
AUP-402xAUP-404	10.8	1.15 **	24.88	4.0	29.0	9.33	0.86	12.5	30
AUP-403xAUP-404	16.9	4.02 **	47.90	4.7	29.3	17.33	-0.18	22.3	79
									Reciprocal crosses
AUP-402xAUP-401	10.9	0.63 ns	6.14	6.7	16.3	10.33	0.63	13.9	29
AUP-403xAUP-401	7.7	2.27 *	7.35	3.0	12.0	7.83	-0.14	9.5	17
AUP-404xAUP-401	15.6	-2.98 *	49.51	1.7	30.0	15.17	0.17	20.0	71
AUP-403xAUP-402	8.3	1.57 ns	8.80	2.0	14.3	8.00	0.27	10.3	10
AUP-404xAUP-402	17.5	-3.39 *	44.81	6.0	32.3	17.67	-0.05	22.3	72
AUP-404xAUP-403	17.4	-0.22 ns	37.63	6.7	16.3	10.33	0.63	13.9	29

‡ Min (Minimum), Max (Maximum), Mdn (Median), Sk (Skewness), Q-3 (Third quartile), P>BP (Percent plants having greater value than better parent), * = significant at the 5 % level of probability, ** = significant at the 1 % level of probability, and ns = not significant.

Positive combining ability values are desirable for yield contributing traits like pods main-raceme^{-1} to increase yield. AUP-401 was identified as a good general combiner for pod main raceme^{-1} with maximum GCA value of 4.67 (Table 3); the GCA estimate for AUP-404 was negative. Four crosses showed positive and three crosses showed negative SCA ability values and the rest being non-significant. The cross AUP-401 x AUP-402 was the best specific combiner. Highest positive reciprocal effect shows that direct cross AUP-401 x AUP-404 had better performance than reciprocal cross. The highest negative reciprocal effect for AUP-402 x AUP401 shows that use of AUP-402 as female parent with AUP-401 as male parent is better than their use in reverse order and that may be the reason for the highest positive greater SCA of the cross involving AUP-401 and AUP-402. The best cross based on pods main-raceme^{-1} involved parents with positive general combining abilities with the highest GCA parent used as male. Based on maximum values of pods plant^{-1} of the F$_2$ plants of the crosses, quartile-3 values, percent plants showing more pods than better parent, variance of the F$_2$ plants and mean performance; crosses AUP-402 x AUP-401, AUP-402 x AUP-403, and AUP-401 x AUP-404 show promise for increasing pods plant^{-1} to increase seed yield.

Estimates of components of variance due to GCA and SCA showed that SCA effects were higher than GCA effects suggesting the predominance of non-additive gene action over additive gene action for pods raceme^{-1} (Table 6). The efficiency of improvement through selection for this trait will be high in late segregating generations. Non-additive gene actions for pods main raceme^{-1} were also reported by Dar et al. (2013), Rameeh et al. (2003), Gupta et al. (2011) and Sincik et al. (2011). However, Azizinia (2012), Rameeh (2010), Noshin et al. (2007) and Nassimi et al. (2006) reported the presence of additive effects.

Seeds pod^{-1}

Highly significant mean squares for general, specific and reciprocal combining abilities were found for seeds pod^{-1}. Akbar et al. (2008), Saeed et al. (2013), Arifullah et al. (2012) also observed similar results. Farshadfar et al. (2013) and Azizinia et al. (2012) reported not significant GCA and SCA mean squares for seeds pod^{-1}.

GCA effects ranged from -0.84 to 1.19, SCA effects ranged from -1.9 to 4.0 and the reciprocal effects ranged from -3.4 to 1.6 (Table 4). Only one parent (AUP-404) showed positive GCA value

(1.19) for seed pod[-1]. Cross AUP-403 x AUP-404 showed maximum SCA value followed by AUP-402 x AUP-404, both involving the best general combiner as male parent. The reciprocal effects of AUP-404 x AUP-402 and AUP-404 x AUP-401 were negative which reveal that these reciprocal crosses had better performance than direct crosses. The three significant reciprocal effects show special genetic types of interactions among the four parents in diallel crosses.

Table 5. Thousand seed weight of *B. napus,* GCA of parents, SCA, RE and descriptive statistics of crosses

Parents and crosses	Mean	GCA, SCA, RE	Descriptive statistics‡						
			Var	Min	Max	Mdn	SK	Q-3	P>BP
									Parents
AUP-401	7.75	-0.07	1.74	--	--	--	--	--	--
AUP-402	7.89	-0.05	1.48	--	--	--	--	--	--
AUP-403	8.63	0.03	0.49	--	--	--	--	--	--
AUP-404	8.60	0.09	0.94	--	--	--	--	--	--
									Direct crosses
AUP-401 x AUP-402	8.20	0.30	4.74	3.8	10.0	9.25	-1.45	9.60	60
AUP-401 x AUP-403	8.29	-0.14	3.01	5.2	10.0	8.90	-1.05	9.60	70
AUP-401 x AUP-404	8.47	0.22	1.54	6.7	10.0	8.25	0.52	9.75	70
AUP-402xAUP-403	7.72	0.08	2.54	5.0	9.6	7.45	0.50	8.90	40
AUP-402xAUP-404	8.24	-0.12	1.81	5.0	9.8	8.30	-0.14	8.73	60
AUP-403xAUP-404	8.49	-0.25	1.85	5.7	9.9	8.60	-0.25	9.73	80
									Reciprocal crosses
AUP-402xAUP-401	8.69	-0.25	3.29	5.0	10.0	9.20	-0.85	9.85	80
AUP-403xAUP-401	7.89	0.20	11.16	4.2	9.9	8.05	-0.15	9.80	50
AUP-404xAUP-401	8.54	-0.04	1.74	7.2	9.9	9.10	-1.27	9.90	75
AUP-403xAUP-402	8.93	-0.61*	1.32	7.0	10.0	9.50	-1.48	9.85	70
AUP-404xAUP-402	8.12	0.06	2.35	4.5	9.5	8.35	-0.46	9.23	50
AUP-404xAUP-403	7.78	0.36	7.40	1.0	9.2	8.85	-1.18	9.08	80

‡ Min (Minimum), Max (Maximum), Mdn (Median), Sk (Skewness), Q-3 (Third quartile), P>BP (Percent plants having greater value than better parent), * = significant at the 5 % level of probability, ** = significant at the 1 % level of probability, and ns = not significant.

Table 6. Estimates of components of variance due to GCA, SCA and RCA of various traits of *B. napus* and ratios of the component of variance of GCA and SCA

Parameters	Components of variance				Total	GCA/SCA
	GCA	SCA	RE	Error		
Pods raceme[-1]	14.020	72.390	90.990	20.090	197.500	0.19
Seeds pod[-1]	0.600	11.460	4.230	1.020	17.300	0.05
1000 seed weight	-0.003	0.071	0.067	0.066	0.202	-0.04
Seed yield plant[-1](g)	-0.040	1.920	0.770	0.540	3.180	-0.02

Table 7. Genetic variance (Vg), environmental variance (Ve), phenotypic variance (Vp) and heritability (h^2) estimates of various traits of parents and F_2 population of *B. napus*

Parameters	Vg	Ve	Vp	h^2 (%)
Pods raceme[-1]	127.100	19.000	146.100	87.0
Seeds pod[-1]	8.925	1.016	9.941	89.8
1000 seed weight	0.078	0.066	0.144	54.4
Seed yield plant[-1](g)	1.370	0.620	1.990	68.9

Overall assessment based on SCA, RE, Variance, Maximum, skewness, Q3 show that direct cross AUP-403 x AUP-404 and reciprocal crosses AUP-404 x AUP-402, and AUP-404 x AUP-401 are more promising than the other crosses to produce lines with more seeds per plant for improving genetic potential of yield per plant.

SCA effects were higher than GCA effects suggesting the predominance of non-additive gene action over additive gene action for seeds pod[-1] (Table 6). Selection for increasing seeds pod[-1] will be more efficient in late segregating generations. Non-additive genetic effect was also observed by Rameeh (2011), Dar et al. (2013), Sincik et al.

(2011) for this trait. However, Arifullah et al. (2012) reported presence of additive effects for this trait.

Thousand Seed weight (g)

Combining ability analysis of seed weight revealed not significant mean squares for general and specific combining abilities while significant mean squares for reciprocal effects. Akbar et al. (2008) and Sincik et al. (2011) reported similar results of not significant GCA and SCA mean squares and significant RCA mean squares. Whereas Turi et al. (2011) reported significant mean squares of GCA, SCA and RCA for seed weight.

Though F value for GCA was not significant, AUP-404 had the highest GCA for seed weight (Table 5). Three crosses showed positive SCA and three crosses exhibited negative SCA for seed weight. Maximum SCA of 0.30 was observed for AUP-401 x AUP-402 followed by SCA of AUP-401 x AUP-404. In case of reciprocal effects, one cross (AUP-403 x AUP-402) showed significant negative reciprocal effect which showed that the reciprocal cross produced heavier seeds than its direct cross.

The ratio of GCA variance to SCA variance was less than one indicating the presence of non-additive type of gene action (Table 6). Selection process in later generations after hybridization procedures will result in better improvement for this trait. Azizinia (2012), Dar et al. (2013), and Sincik et al. (2011) reported prevalence of non-additive control for this trait. In studies by Nasrin et al. (2011), Saeed et al. (2013), Rameeh et al. (2003) and Gupta et al. (2011) additive gene effects were observed for seed weight.

Heritability

Heritability ranged from 54.4% to 89.8% for the studied traits (Table 7). Highest heritability was observed for seeds pod[-1] (89.8%) followed by pods raceme[-1] (87.0%). Similar results were also reported by Aytac et al. (2008) and Sadat et al. (2010). However, Zare and Sharafzadeh (2012) reported low heritability for seeds pod[-1]. High h^2 value for seeds pod[-1] was also reported by Aytac et al. (2008). The difference in the results of present and previous studies may be due to the differences in the genotypes used and in environments under which the experiments were conducted. High heritability for pods main raceme[-1] was reported Aytac et al. (2008), Sadat et al (2010) and Zare and Sharazadeh (2012). Moderate heritability was observed for 1000-seed weight (54.4%) and seed yield plant[-1] (68.9%). High heritability has been reported for seed weight and seed yield plant[-1] by Zare and Sharafzadeh (2012) and Sadat et al. (2010). For most of the traits in this study heritability estimates were moderate or high as a result of high genetic variance, signifying less environmental influence. For such traits selection is effective and gain from selection is more.

Conclusion

From the present study it is concluded that *B. napus* genotype AUP-401 was good combiner for seed yield[-1] and pod raceme[-1] and parent AUP-404 was good combiner for seed pod[-1]. Cross AUP-403 x AUP-404 had the highest SCA for seed yield[-1] followed by AUP-401 x AUP-402: The highest SCA of the former cross was due to higher SCA for seeds pod[-1] while that of the later cross was due to higher SCA for pods main-raceme[-1]. Reciprocal effects were significant for some traits in some crosses indicating that there were differences between direct and indirect crosses and maternal effects or cytoplasmic effects are involved. From the conclusions of the present study it is recommended that parental genotype AUP-401 should be used in further breeding programs for evolving genotypes with high yield. Cross AUP-402 x AUP-401 could be exploited for developing high yielding varieties with more pods main-raceme[-1]. Cross AUP-403 x AUP-404 could be exploited for developing varieties with higher yield and more seeds pod[-1]. The double cross (AUP-402 x AUP-401) x (AUP-403 x AUP-404) may be more promising for developing high yielding varieties with more pods raceme[-1] and more seeds pod[-1].

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