

*Full Length Research Paper*

# Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.)

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Information of the variability and the extent and type of relationship of some quantitative characters in rapeseed is important for an efficient breeding program. In addition, the association between seed yield and quality characters, oil and protein content, is of major interest. 10 winter rapeseed genotypes were evaluated for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for 2 years. The results revealed significant differences for all yield and quality characters indicated the presence of sufficient genetic variability for effective selection. Variability, broad sense heritability, genetic advance were maximum for oil yield, seed yield followed by protein yield. In addition, very strong correlations were estimated among them. Simultaneous selection regarding seed yield would be an effective way to increase oil yield and protein yield. Plant height was associated with seed yield, oil yield, protein yield, number of pods on main stem and pod length. In conclusion, plant height, pod length, oil yield and protein yield were efficient characters as selection criteria.

**Key words:** Genetic correlation, genotypic coefficient of variation, heritability, yield, quality, *Brassica napus* L.

## INTRODUCTION

Knowledge of the relative magnitude of various genetic parameters of seed yield, yield and quality characters are important for an efficient breeding program. A character which have higher range of genetic variability, high heritability and high genetic advance would be an effective tool to improve seed yield. Besides, the genetic background of any pair of characters is unlikely to be under totally separate control. Therefore, for plant breeders it is essential to examine correlations to see the relationships between

pairs of characters in order to decide for the suitable selection criteria for a breeding program.

Efforts are underway to develop better rapeseed genotypes. Genetic variability, broad sense heritability, genetic advance parameters were estimated in some studies (Naazar et al., 2003; Akbar et al., 2007) and phenotypic correlation coefficients between seed yield and yield determining characters have been analyzed in rapeseed (Kumar and Yadava, 1978; Özer and Oral, 1999; Khan et al., 2000; Marinkovic et al. 2003; Jeromela et al., 2007, 2008). The influence of environmental effects can be excluded by calculating genetic correlations which are rarely investigated in winter rapeseed (Malik et al., 2000;

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Akbar et al., 2003) and just only few investigations include genetic correlations between seed yield, yield and quality characters (Engqvist and Becker, 1993; Khan et al., 2006).

The present investigation were planned to find out the extent of genetic variability, broad sense heritability and genetic advance between seed yield, yield and quality characters of 10 winter rapeseed genotypes. And beside phenotypic correlations, genetic correlations were also estimated among yield and quality characters to devise suitable selection criteria for further yield improvements.

## MATERIALS AND METHODS

This research was carried out during 2003 and 2004 in Eskisehir (39°48' N, 30°31' E, 789 m elevation), at research fields of Faculty of Agriculture of Eskisehir Osmangazi University, Turkey. The experimental design was a completely randomized block with 4 replications. Individual plot consists of 5 rows. 10 winter rapeseed (00 types) cultivars, Ceres, Zorro, Falcon, Express, Hansen, Chang, Bienvenue, Darmor, Synergy and Samourai were used as material. The cultivars were sown on September 5, 2003 and September 10, 2004, using a seed rate of 10 kg ha<sup>-1</sup> in 40 cm spaced lines on a well prepared seed bed. The experiment was fertilized respectively before sowing with 150 kg N ha<sup>-1</sup> as ammonium nitrate and 50 kg P<sub>2</sub>O<sub>5</sub> ha<sup>-1</sup> as diammonium phosphate. The crop was irrigated once just after sowing. The thinning was done to maintain 15 cm distance between the plants. Weeds were controlled by hand weeding.

At maturity, yield components such as plant height (H) in cm, number of branches per plant (B), number of pods per plant (PP), number of pods on main stem (PMS); pod length (PL) in cm were measured. Approximately 3 months after harvesting as international seed testing association (ISTA) suggests, 1000 seeds weight (TSW) was calculated by counting 8 replicated 100 seeds from each plot and was weighted in g and the mean was multiplied with 10. Seed yield (Y) in kg ha<sup>-1</sup> were taken by harvesting the central 3 rows of the plot by hand. Crude oil yield (OILY) were calculated from yield and crude oil content (OIL). Crude protein yield (PRY) from yield and crude protein content (PR). For crude oil analysis the samples were extracted with petroleum ether (Soxhlet, Gerhardt 2000 digital system) (Doğan and Basoglu, 1985; Bilsborrow et al., 1993). Seed protein content were determined by kjeldahl method (protein = 6.25 x N) (Diepenbrock and Geisler, 1979; Bilsborrow et al., 1993). Genetic parameters, genotypic and phenotypic correlation coefficients were computed according to the methods suggested by Singh and Chaudhry (1979). Data were processed with microsoft excel 2003 software and statistically analyzed by ANOVA, taking  $p < 0.05$  and  $p < 0.01$  as significant according to LSD test.

## RESULTS

### Genetic variation

Genotypic differences were highly significant ( $p < 0.01$ )

for all yield and quality characters studied among 10 cultivars for 2 years (Tables 1 and 2). Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance (GA) as mean percentage were calculated for various traits (Table 1 and 2). There were slight differences between PCV and GCV for almost all characters. Highest GCV, PCV, genotypic variance and phenotypic variance were shown for oil yield, seed yield and protein yield followed by number of pods per plant both year. Lowest values were obtained from oil and protein content.

Broad sense heritability estimates ranged from 37.0 to 99.2% for all characters. Highest values were obtained from 1000 seeds weight, seed yield, oil yield, number of pods per plant, plant height and protein yield, and moderate value was found for the number of branches per plant.

In order to estimate the selection effects, heritability accompanied with genetic advance is rather useful than heritability alone (Johnson and Hanson, 2003). Heritability and genetic advance were maximum for oil yield, seed yield followed by protein yield, number of pods per plant and 1000 seeds weight for both years.

### Correlation between characters

55 genetic and phenotypic correlation coefficients among 10 characters for both years are presented in Tables 3 and 4. In most instances, there was a close agreement between genetic correlations and phenotypic correlations. 64% of genetic correlations and 18% of phenotypic correlations were statistically significant at 5% level. Both years, strong significant positive genetic and phenotypic correlations found between seed yield, oil yield and protein yield. Seed yield was significantly and positively correlated with plant height, number of branches per plant and pods on main stem in one of the years whereas it has negative and low genetic and phenotypic correlations with TSW and protein content both years.

Plant height has positive genetic and phenotypic correlations with pods per main stem, pod length, oil yield and protein yield. Likely, branches per plant have positive genetic and phenotypic correlation with oil content, oil yield and protein yield for both experimental years. Number of pods per plant has positive genetic and phenotypic correlation with oil yield, protein yield, pod length, plant height and branches per plant for second year. But the values for the first year were negative. Pod length was

**Table 1.** Genetic parameters of yield and yield components of winter rapeseed genotypes (2003).

Parameter	Range	Mean square	Mean	SE(±)	CD	CV (%)	$\sigma^2g$	$\sigma^2p$	$h^2$ (%)	GCV	PCV	GA
Plant height (cm)	124.2-141.6	18.77**	134.6	1.74	3.56 <sup>1</sup> 4.81 <sup>2</sup>	0.33	26.77	32.80	81.6	0.10	0.11	0.18
Branches per plant	5.6-6.9	23.49**	6.3	0.14	0.29 0.39	0.12	0.22	0.26	84.8	0.19	0.20	0.19
Number of pods per plant	94.9-129.9	20.36**	115.1	3.40	6.97 9.42	0.71	111.76	134.85	82.8	0.23	0.25	0.43
Pods per main stem	28.9-37.7	1.90	35.0	2.49	5.12 6.91	0.94	2.79	15.24	18.3	0.12	0.28	0.11
Pod length (cm)	6.78-7.98	3.36**	7.29	0.29	0.59 0.80	0.24	0.098	0.26	37.0	0.11	0.18	0.13
1000-seed weight	3.83-5.05	498.67**	4.36	0.02	0.05 0.06	0.02	0.13	0.13	99.2	0.21	0.21	0.43
Seed yield (kg ha <sup>-1</sup> )	277-389.5	21.39**	318.1	10.16	20.86 28.16	1.27	1053.22	1259.84	83.6	0.26	0.28	0.48
Oil content (%)	38.32-42.78	3.84**	40.72	0.82	1.69 2.28	0.29	0.96	2.32	41.5	0.06	0.09	0.08
Oil yield (kg ha <sup>-1</sup> )	107.4-159.9	14.98**	129.7	5.62	11.52 15.56	1.10	220.39	283.48	77.7	0.29	0.32	0.52
Protein content (%)	20.83-22.70	3.31**	21.91	0.43	0.88 1.18	0.20	0.21	0.57	36.6	0.05	0.09	0.07
Protein yield (kg ha <sup>-1</sup> )	62.2-81.2	8.75**	69.6	2.70	5.54 7.48	0.72	28.22	42.79	65.9	0.19	0.24	0.32

SE = Standard error; CD = critical difference <sup>1</sup>5% and <sup>2</sup>1%; CV = coefficient of variation;  $\sigma^2g$  = genotypic variances;  $\sigma^2p$  = phenotypic variances;  $h^2$  = broad-sense heritability; GA = genetic advance; PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation; \*\*significant at 1 % level.

**Table 2.** Genetic parameters of yield and yield components of winter rapeseed genotypes (2004).

Parameter	Range	Mean square	Mean	SE(±)	CD	CV (%)	$\sigma^2g$	$\sigma^2p$	$h^2$ (%)	GCV	PCV	GA
Plant height (cm)	120.4 - 135.3	17.36**	130.8	1.57	3.221 4.352	0.31	20.13	25.05	80.3	0.09	0.10	0.16
Branches per plant	5.2 - 6.9	8.64**	6.0	0.22	0.46 0.62 4.88	0.20	0.19	0.29	65.6	0.22	0.18	0.30
Number of pods per plant	82.1 - 105.6	23.58**	96.2	2.38	6.60	0.54	63.95	75.28	84.9	0.21	0.23	0.39
Pods per main stem	21.9 - 33.4	12.46**	28.7	1.56	3.21 4.33	0.65	13.99	18.87	74.1	0.33	0.38	0.58
Pod length (cm)	6.67 - 7.62	2.44*	7.07	0.30	0.63 0.84	0.26	0.07	0.25	26.5	0.18	0.09	0.10
1000-seed weight	3.67 - 4.40	17.19**	3.85	0.09	0.18 0.24	0.10	0.06	0.07	80.1	0.16	0.18	0.30
Seed yield (kg ha <sup>-1</sup> )	202.3 - 312.3	55.40**	263.2	7.79	15.99 21.60	1.07	1652.27	1773.76	93.1	0.39	0.40	0.77
Oil content (%)	37.03 - 41.92	11.04**	39.57	0.62	1.27 1.71	0.22	1.91	2.67	71.5	0.09	0.10	0.15
Oil yield (kg ha <sup>-1</sup> )	82.5 - 130.9	56.96**	104.4	3.44	7.06 9.53	0.75	330.88	354.54	93.3	0.44	0.45	0.87
Protein content (%)	18.27 - 20.17	8.45**	19.11	0.33	0.68 0.92	0.17	0.41	0.64	65.1	0.08	0.10	0.14
Protein yield (kg ha <sup>-1</sup> )	40.8 - 62.4	48.62**	50.4	1.72	3.54 4.78	0.54	70.73	76.67	92.2	0.42	0.43	0.837

SE = Standard error; CD = critical difference <sup>1</sup>5% and <sup>2</sup>1%; CV = coefficient of variation;  $\sigma^2g$  = genotypic variances;  $\sigma^2p$  = phenotypic variances;  $h^2$  = broad-sense heritability; GA = genetic advance; PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation; \*\*significant at 1 % level.

**Table 3.** Genetic and phenotypic correlation coefficients of winter rapeseed genotypes among eleven traits in 2003 (below diagonal) and 2004 (above diagonal).

	Y	H	B	PP	PMS	PL	TSW	OIL	PR	OILY	PRY
Y		0.63 <sup>a</sup> 0.55 <sup>b</sup>	0.56 0.40	0.42 0.36	0.70* 0.61	-0.15 -0.04	0.17 0.09	0.44 0.37	0.23 0.19	0.98** 0.97**	0.98** 0.97**
H	0.29 <sup>a</sup> 0.31 <sup>b</sup>		-0.07 -0.05	1.00** 1.00**	0.69* 0.58	0.36 0.23	-0.32 -0.24	-0.14 -0.03	-0.34 -0.26	0.54 0.49	0.53 0.46
B	0.78* 0.67*	0.37 0.27		1.00** 1.00**	0.25 0.09	0.008 -0.008	0.76* 0.62	0.73* 0.52	0.47 0.22	0.63* 0.47	0.60 0.41
PP	-0.64* -0.53	-0.36 -0.31	-0.59 -0.56		0.60 0.48	0.49 0.23	0.27 0.22	0.24 0.23	0.28 0.16	0.41 0.36	0.43 0.37
PMS	0.008 0.026	0.88** 0.49	-0.14 -0.05	-0.25 -0.17		0.19 0.23	-0.31 -0.25	0.19 0.13	0.02 -0.05	0.66* 0.57	0.66* 0.56
PL	0.90** 0.46	0.19 0.026	0.81** 0.35	-0.73* -0.33	0.58 0.09		-0.43 -0.16	-0.29 -0.08	-0.50 -0.26	-0.20 -0.06	-0.24 -0.10
TSW	-0.48 -0.44	0.44 0.40	-0.49 -0.46	0.16 0.16	1.00** 0.46	-0.24 -0.15		0.62 0.46	0.59 0.38	0.27 0.19	0.26 0.17
OIL	0.47 0.35	0.12 0.14	0.18 0.046	-0.58 -0.56	-0.33 0.01	0.10 -0.10	-0.04 -0.02		0.99** -0.25	0.59 0.58	0.60 0.32
PR	-1.00** -0.58	-0.15 -0.09	-0.73* -0.4	0.66* 0.25	0.43 -0.07	-0.61 -0.32	0.59 0.35	-0.87** 0.59		0.39 0.30	0.40 0.40
OILY	0.98** 0.96**	0.29 0.31	0.74* 0.59	-0.69* -0.52	-0.06 0.02	0.82** 0.36	-0.43 -0.38	0.59 0.56	-1.00** -0.58		1.00** 0.99**
PRY	1.00** 0.95**	0.32 0.31	0.83** 0.64*	-0.66* -0.53	0.09 -0.004	1.00** 0.42	0.48 -0.39	0.36 0.48	-1.00** -0.32	0.97** 0.91**	

\*\*\*Significant at 5 and 1% level, respectively.

<sup>a</sup> Genetic correlation coefficient, <sup>b</sup> Phenotypic correlation coefficient.

positively and significantly genetic correlated with oil yield, protein yield and seed yield in the first year where-as the results for the second year were low. In addition there were negative and low genetic and phenotypic correlations between pod length and TSW both years. More-over, the correlation between TSW and oil and protein content were generally positive but low. Positive correlation between seed yield and oil content has been found in our study. Protein content has negative genetic and phenotypic correlation with oil content and oil yield in the first year.

## DISCUSSION

Highly significant ( $p < 0.01$ ) genotypic differences for all

characters have indicated the presence of sufficient genetic variability for effective selection (Tables 1 and 2). For all components slightly higher PCV than GCV and similarly higher phenotypic variances compared to genotypic variances indicating the influence of environment. High GCV, PCV were stated for seed yield and number of pods per plant (Akbar et al., 2003; Naazar et al., 2003; Akbar et al., 2007) and high genotypic and phenotypic variance were found for seed yield (Aytaç et al. 2008).

Although genotypes differed significantly, selection efficiency is related to magnitude of heritability and genetic advance (Johnson and Hanson, 2003). Akbar et al. (2003) found high and similar values of broad sense heritability for number of pods per plant and plant height moderate value for branches per plant. But their value for

1000 seeds weight was extremely low. However Richard and Thurling (1978) found low heritability in pod number of plant because this trait is mainly governed by environmental conditions. High values for heritability and genetic advance were stated for seed yield (Akbar et al., 2003 and 2007). A trait having high heritability and high genetic advance is considered under control of additive genes which highlights the usefulness of plant selection based on phenotypic performance.

### Correlation between characters

High value of GCV, PCV, broad sense heritability and genetic advance were stated for oil yield and protein yield. Oil yield were calculated from yield and crude oil content (OIL) and protein yield (PRY) from yield and crude protein content (PR) in this study. Highly significant positive correlations were found among seed yield, oil yield and protein yield both years. In addition, the correlations between oil content and oil yield and between protein content and protein yield were rather low. As a result, the most effective way to increase oil and protein yield is to increase the seed yield. Engqvist and Becker (1993) and Jeromela et al. (2007) also obtained highly significant correlations between seed yield, oil yield and protein yield. These results lead to the conclusion that simultaneous selection regarding seed yield would be an effective way to increase oil yield and protein yield.

Winter rapeseed breeding programs are dealing with plant height as a quantitative character that determines final plant density. Besides genetic effects, environmental effects also play an important role in expression of this trait. The results stated positive genetic and phenotypic correlations for plant height with seed yield, oil yield, protein yield, number of pods per plant, number of pods on main stem and pod length. The values of broad sense heritability for plant height were also high in both years. Positive genetic and phenotypic correlations for plant height with seed yield were stated (Musnicki, 1974; Kumar and Yadava, 1978; Schuster and Sra, 1979; Schuster, 1979; Akbar et al., 2003; Naazar et al., 2003). Jeromela et al. (2008) reached similar results regarding correlations between plant height with pods per plant and with number of branches per plant. As a result, an increase of plant height leads to the increase of the recent yield components that is, seed yield, oil yield, protein yield, number of pods per plant, number of pods on main stem and pod length. So this trait should be paid attention

in rapeseed breeding programs.

The results of this study stated positive genetic and phenotypic correlations between number of pods per plant and seed yield and between number of pods per plant and oil yield, protein yield, pod length, plant height and branches per plant for the second year. But the correlations among these traits were negatively correlated in the first year. The differences between values of genetic and phenotypic correlations and within the years of this trait are signifying the environmental effects (Schuster and Taghizadeh, 1980; Ehdaie and Waines, 1989). Although our results stated high value of broad sense heritability and genetic advance for number of pods per plant both years, Richard and Thurling (1978) found low heritability for this trait because it is mainly governed by environmental conditions as it mentioned above. Therefore, selection for large pod number per plant reveals no selection response. Many researchers found positive correlations between pods per plant and seed yield (Özer and Oral, 1999; Khan, 2000; Malik et al., 2000; Naazar et al., 2003; Khan et al., 2006; Jeromela et al. 2007) whereas Marinkovic et al. (2003) reported negative correlations.

TSW is an important component of seed yield and depends on environmental conditions (Schuster and Taghizadeh, 1980; Diepenbrock, 2000). It is easier to determine than yield itself and generally has a high heritability. Heritability values found for this trait for both years were high but the correlation between TSW and seed yield was negative and low in the second year. In general there is a weak correlation between seed weight and yield (Engqvist and Becker, 1993; Malik et al., 2000). Although genetic variation in seed weight exists, the selection for high seed weight would have a negative effect on other yield components (Diepenbrock, 2000). However some findings stated strong positive correlations between TSW and oil and protein content (Röbbelen, 1978; Bengtsson, 1985; Jeromela et al., 2007). As a result, selection for large seeds can not be expected to be effective in increasing oil and protein content. So, it is better to improve seed yield and oil and protein content at the same time (Engqvist and Becker, 1993).

Pod length was positively and significantly genetic correlated with oil yield, protein yield and seed yield in the first year. Although our results revealed low values for the second year and low heritability estimates in both years, many researchers stated that the effect of pod length on yield depends to a great extent on the genetic background of the material (Chay and Thurling, 1989; Leon and Becker, 1995). The genetic and phenotypic correla-

tions between pod length and TSW were negative in both years whereas pod length was significantly correlated with seed yield. This means that longer pods obtain more seeds and seed yield depends mainly on number of seeds per pod instead of TSW. Chay and Thurling (1989) also revealed that long pods have more seeds and resulting in a greater seed yield per plant.

Seed oil content, besides seed yield, is one of the highly demanding criteria in developing rapeseed cultivars (Engqvist and Becker, 1993). Positive correlation between seed yield and oil content has been found in this study and stated by Engqvist and Becker (1993), Khan et al. (2006) and Jeromela et al. (2008). Thus, it is essential to improve yield and oil content at the same time. Jeromela et al. (2008) also determined positive correlations between number of branches per plant and seed oil content. Protein content has negative genetic and phenotypic correlations with oil content which is in accordance with Khan (2007) and Özer and Oral (1999). The values for the second year were positive. This is due to different environmental conditions.

A trait which had high range of genetic variability, heritability and genetic advance, degree of positive and significant correlation coefficient would be very effective tool to improve seed yield. Such traits in this study were plant height, pod length, oil yield and protein yield.

## Conclusion

Very strong correlations were estimated between oil yield, protein yield and seed yield consistent in both years. Simultaneous selections regarding seed yield would be an effective way to increase oil yield and protein yield. An increase of plant height leads to the increase of seed yield, oil yield, protein yield, number of pods on main stem and pod length. Pod length was positively and significantly genetic correlated with oil yield, protein yield and seed yield. Finally, effective tools which largely influence the response to selection, in order to improve seed yield were plant height, pod length, oil yield and protein yield.

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