

**VARIABILITY OF YIELD DETERMINING COMPONENTS IN WINTER  
RAPESEED (*Brassica napus* L.) AND THEIR CORRELATION  
WITH SEED YIELD**

Ana MARJANOVIĆ -JEROMELA<sup>1</sup>, Radovan MARINKOVIĆ<sup>1</sup>, Sonja  
IVANOVSKA<sup>2</sup>, Mirjana JANKULOVSKA<sup>2</sup>, Anto MIJIĆ<sup>3</sup>, Nikola HRISTOV<sup>1</sup>

<sup>1</sup>Institute of Field and Vegetable Crops, Novi Sad, Serbia

<sup>2</sup>Faculty of Agricultural Sciences and Food, Skopje, Macedonia

<sup>3</sup>Agricultural Institute Osijek, Osijek, Croatia

Marjanovic-Jeromela A., R. Marinkovic, S. Ivanovska, M. Jankulovska, A. Mijić, and N. Hristov (2011): *Variability of yield determining components in winter rapeseed (*Brassica napus* L.) and their correlation with seed yield.*- Genetika, Vol 43, No. 1, 51 -66.

Designing breeding programs for rapeseed (*Brassica napus* L.) cultivars with improved seed and oil yields require information about the genetic variability of traits effecting seed and oil production. This investigation was undertaken in order to examine phenotypic and genetic variability, broad-sense heritability, genetic gain under selection and interrelationships of some agronomic and seed quality traits of investigated genotypes.

---

*Corresponding author:* Ana Marjanovic Jeromela, Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia fax: +38121 6413 833 e-mail [jeromela@ifvcns.ns.ac.rs](mailto:jeromela@ifvcns.ns.ac.rs)

Genotypes, years and their interaction showed significant variation for all studied characters. Phenotypic variability coefficients were higher than genetic ones. Broad-sense heritability estimates ranged from 12.66% (for ripening period) up to 52.12% (for days to first pods filling). Expected genetic gain was lowest for days to maturity (0.45%) and highest for height to the first lateral branch (12.94%). The analysis of genetic correlations revealed that seed yield per plant is highly and positively associated with pods per plant, oil content, plant height and ripening period, although significant negative correlations were found between seed yield per plant and leaves per plant, days to maturity, protein content, days to first pods filling, days to flowering, height of the first lateral branch and 1000 seed weight.

Genetic path-coefficient analysis indicated that pods per plant and oil content were the most important components of seed yield per plant. Their direct effects on seed yield per plant were  $p=0.472$  and  $p=0.082$ , respectively. Protein content had highly significant negative direct effect on seed yield ( $p=-0.365$ ), followed by 1000 seed weight ( $p=-0.017$ ) and height to the first lateral branch ( $p=-0.081$ ). These observations will support the selection of genotypes with desired traits for further rapeseed seed and oil yield improvement.

*Key words:* *Brassica napus* L., genetic correlations, genetic path coefficient, heritability, rapeseed, yield

## INTRODUCTION

Oilseed rape (*Brassica napus* L.) is after soybean the second most important source of vegetable oil in the world (data from FAOstat: <http://faostat.fao.org/>). The seeds of modern varieties typically contain 40 to 45 % oil, which provides a raw material for many other products ranging from rapeseed methyl ester (biodiesel) to industrial lubricants and hydraulic oils, for detergent and soap production and biodegradable plastics (FRIEDT *et al.*, 2007). In order to fill the developing gap in the supply and demand for high quality oilseed crops for human food, animal feed and biofuels within South-eastern Europe, it is necessary to create genotypes adapted to the specific climate conditions and performing highest seed and oil yield in this region. This will promote and assist the move of agriculture to a more sustainable platform, reduce the dependence on imported oil and thereby increase South-eastern European competitiveness on the market.

---

Abbreviations used: PH (plant height), HFLB (height to the first lateral branch), LB (lateral branches per plant), PP (pods per plant), LP (leaves per plant), SW (1000 seed weight), SYP (seed yield per plant), DFF (days to first flower), DFPF (days to first pod filling), DM (days to maturity), RP (ripening period), FP (flowering period), OC (oil content), PC (protein content)

For conducting any breeding program successfully, some basic information such as magnitude and pattern of genetic and phenotypic variability and heritability of some yield related traits, and the relationship between these traits would facilitate the improvement of the species and help to select a suitable breeding procedure. Success in the breeding process mainly depends on selection of most superior genotypes from a population. However because the selection of elite genotypes is mostly based on phenotypic values, in many cases the effectiveness of the selection is very low, especially when the phenotypic differences are not under strong genetic control (MARJANOVIĆ-JEROMELA *et al.*, 1999).

Seed yield and oil content are quantitative traits. Their expression is determined besides genotype by environmental effect and genotype by environment interaction (DEGENHARDT and KONDRA, 1984; HÜHN and LÉON, 1985; ENGQVIST and BECKER, 1993; GUNASEKERA *et al.*, 2006). Genotypes by environment interaction reduce the association between genetic and phenotypic values. Measuring genotype by environment interaction is very important in order to determine an optimum breeding strategy for releasing cultivars with adequate adaptation to target environments (FOX *et al.*, 1997; HRISTOV *et al.*, 2009; MARJANOVIC-JEROMELA *et al.*, 2009). The ideotype concept provides opportunity to define the desired high-yield phenotype in terms of several relatively simple plant characters (THURLING, 1991). Therefore, the estimation of heritability of desired traits needs to be performed in order to apply an efficient breeding strategy. Heritability represents the ratio between genotypic and phenotypic variance and expresses extent to which individual's phenotypes are determined by their genotypes (BOROJEVIĆ, 1990). Heritability accompanied with genetic gain is more useful than heritability alone in the accurate prediction of the effects of selection (JOHNSON *et al.*, 1955).

The phenotypic values of different traits in the same individual are often found to be correlated (LYNCH and WALSH, 1998). In many cases the correlations are highly dependent on the environment and on the studied material. In order to exclude the environmental effect, genetic correlations should be calculated instead of phenotypic ones (ENGQVIST and BECKER, 1993). Correlation studies are of interest to plant breeders because traits that are correlated with main breeding objectives may be useful for indirect selection. When the selection is simultaneous for various traits, the correlation between them may restrict the response to selection.

Path coefficient analysis has an advantage over simple correlation coefficient because it allows partitioning of the correlation coefficient into its components. These components are: i) the path coefficient (or standardized partial regression coefficient) that measures the direct effect of a predictor variable upon its response variable; and ii) the indirect effect(s) of a predictor variable on the response variable through the predictor variables (DEWEY and LU, 1959).

Numerous studies were carried out in rapeseed to determine traits which influence seed yield to a great extent and could serve as selection criteria rather than yield *per se*. Many of these studies reported correlations between different yield related traits (OLSSON, 1960; THURLING, 1974; THURLING and VIJENDRA DAS, 1979;

ENGQVIST and BECKER, 1993; MARINKOVIĆ and MARJANOVIĆ-JEROMELA, 1996; ALI *et al.*, 2002; ALI *et al.*, 2003, OGRODOWCZYK and WAWRZYNIAK, 2004).

Rapeseed breeding strategies are oriented in developing varieties with high and stable seed and oil yield, as well as low content of glucosinolate and erucic acid. Before planning of any breeding programme for genetic improvement, the assessment of genetic variation available in germplasm lines is a necessary step (MARJANOVIĆ-JEROMELA *et al.*, 2003).

Keeping in view the importance of rapeseed as an oil crop, the following study was carried out in order to estimate genetic and phenotypic variability, broad sense heritability and interrelationships between seed yield, oil content and some related characters. Such information will serve as useful tool for establishing suitable breeding program for rapeseed improvement.

#### MATERIALS AND METHODS

*Material.* Thirty *Brassica napus* L. cultivars were sown over three years at the Institute of Field and Vegetable Crops, Novi Sad. Thirteen cultivars originated from Serbia, ten from Germany, two from Hungary, four from France and one cultivar from Sweden (Table 1).

Table 1. Cultivars included in the study

<i>Cultivar</i>	<i>Origin</i>	<i>Cultivar</i>	<i>Origin</i>
Sremica		Falcon	
Banacanka		K-571	
UM-1		K-1550	
UM-2		Alaska	
UM-5		Aligator	Germany
UM-6		H-450	
UM-8	Serbia	Valesca	
UM-9		Orkan	
UM-10		Pronto	
UM-11		Artus	
UM-12		Samurai	
UM-13		Jet Neuf	France
UM-14		B-009	
Oktavija		Duna	
Jana	Hungary	Casino	Sweden

*Field experiment.* The field trial was arranged in a randomized complete block design with three replications at Rimski Šančevi site (near Novi Sad, Serbia) during three growing seasons (from 1997 to 2000). The seed was sown by hand in 4 rows, 4 meters long, 0.25 m apart. Thinning at HB 3 stage (HARPER and BERKENKAMP, 1975)

provided 5 cm distance between plants within a row. The trial was conducted on a chernozem type of soil, according to pedodinamic classification (VASIN *et al.*, 2002), with 2.8% humus content, moderate content of phosphorus and potassium and pH 6.92. Optimal agricultural practices were carried out in all investigated seasons. Data for mean monthly temperatures and total monthly precipitations for the years of investigation and 10-years average for the experimental site are given in Figure 1.

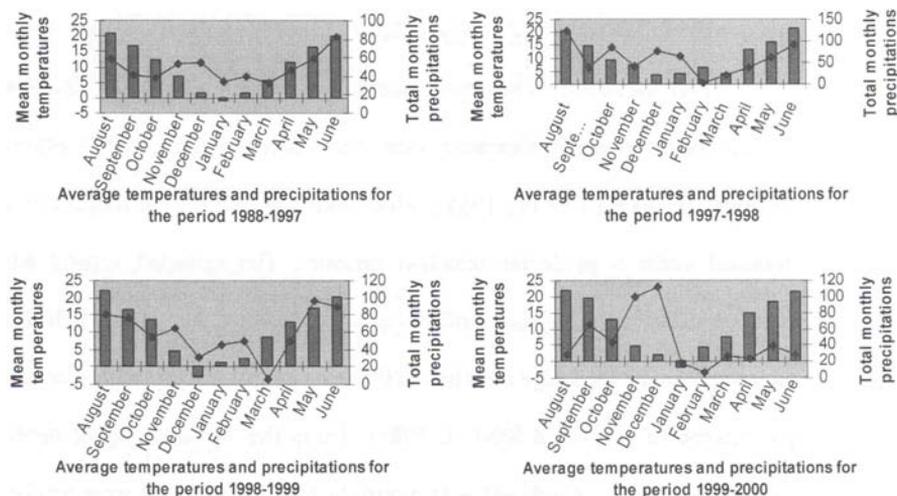


Fig. 1. Mean monthly temperatures and total monthly precipitations for the studied years and 10-years average

Daily observations were taken to obtain number of days from emergency to the different growth stages. Growth stages were determined on a plot basis, according to HARPER and BERKENKAMP (1975), as following:

1. Days to first flower: recorded when 50% of the plants had first flower open (HB4.1);
2. Days to first pod filling: recorded when 50% of the lower pods started filling (HB4.4)
3. Days to maturity: recorded when 50% of the plants had brown seeds in lower pods of the main raceme (HB5.4).
4. Ripening period: number of days from HB4.4 to HB5.4
5. Flowering period: number of days from first flower (HB4.1) to last flower (HB4.4);

The plots were hand-harvested at HB5.4 stage. Randomly selected 10 plants from the middle 2 rows of each plot were used to measure plant height (cm), height to the first lateral branch (cm), lateral branches per plant, pods per plant and leaves per plant.

Seed oil content was determined by magnetic resonance analyzer (Newport 4000 NMR analyzer) and the protein content by a classical micro method according to Kjeldahl. 1000 seed weight and seed yield per plant were determined in laboratory, after each plant was harvested.

*Statistical analyses.* Variance components were estimated from the mean squares in the analysis of variance (SINGH *et al.*, 1993; HILL *et al.*, 1998). Broad sense heritability ( $h^2$ ) was estimated according to SINGH *et al.* (1993) as:

$$h^2 = \sigma_g^2 / \sigma_p^2 \cdot 100 (\%)$$

where  $\sigma_g^2$  and  $\sigma_p^2$  are the genetic and phenotypic variances, respectively.

Expected genetic advance (GA) and GA as percent of the mean assuming selection of the superior 10% of the genotypes were estimated in accordance to JOHNSON *et al.* (1955) and FALCONER (1989) as

$$\begin{aligned} GA &= k(\sigma_p)h^2 \\ GA(\text{as \% of the mean}) &= (GA / \bar{x}) \times 100 \end{aligned}$$

where  $k$  is a standardized selection differential (with 10% selection intensity it is 1.755),  $\sigma_p$  is the phenotypic standard deviation,  $h^2$  is the broad sense heritability, and  $\bar{x}$  refers to the mean of the character.

Genetic correlation coefficients were calculated from the analysis of covariance as described by SINGH and CHAUNDHARY (1979).

Path analysis partition the total correlation coefficients into direct and indirect effects of various characters and helps to understand the relationship among variables based on a priori model. Direct and indirect path coefficients were calculated as described by SINGH and CHAUNDHARY (1979), WILLIAMS *et al.* (1990) and LYNCH and WALSH (1998) as:

$$r_{yi} = P_{yi} + \sum_{i'=1}^k r_{ii'} P_{yi'} \quad \text{For } i \neq i' \quad \text{and } i' \neq 1$$

where  $r_{yi}$  is the simple correlation coefficient between the  $i$ -th causal variable ( $X_i$ ) and effect variable ( $y$ ),  $r_{ii'}$  is the simple correlation coefficient between the  $i$ -th and  $i'$ -th causal variables,  $P_{yi}$  is the path coefficient (direct effect) of the  $i$ -th causal variable ( $X_i$ ),  $r_{ii'} P_{yi'}$  is the indirect effect of the  $i$ -th causal variable via the  $i'$ -th causal variable. To determine  $P_{yi}$  values, square matrices of the correlation coefficient between independent traits in all possible pairs were inverted and then multiplied by the correlation coefficients between the independent and dependent traits.

## RESULTS

Genotypes differed significantly ( $p < 0.01$ ) for all investigated traits (Table 2), confirming the possibility of improving these traits through selection. Moreover,

genotypes responded differently to changes in the environmental conditions within three years, as genotype x year interaction and year mean squares were highly significant ( $p < 0.01$ ) for all the characters. This indicates that experiments should be performed in different environmental conditions for evaluating the divergence between genotypes.

Table 2. Analysis of variance for seed yield per plant and yield related characters

	Replication	Year (Y)	Genotype (G)	Interaction G x Y	Error (residual)
PH	731.11**	99260.94**	256.53**	91.95**	32.37
HFLB	348.32**	49869.58**	388.15**	76.01**	21.89
LB	0.23	80.74**	3.72**	1.67**	0.58
PP	502.75	75782.05**	2611.22**	1403.82**	197.62
LP	15.06**	497.29**	6.61**	2.01**	1.05
PC	1.87	127.11**	12.84**	2.28**	0.84
OC	2.13	1278.05**	19.43**	2.87**	1.41
SW	0.01	6.08**	0.54**	0.12**	0.02
SYP	0.09	1994.22**	16.18**	9.14**	1.86
DFP	0.47	424.46**	93.16**	36.10**	0.78
DLPF	0.45	2455.72**	56.95**	12.54**	0.53
DM	5.56**	6430.34**	28.57**	12.28**	0.54
RP	3.60*	13434.86**	12.11**	7.92**	0.86
FP	0.63	2673.23**	13.90**	6.53**	0.51

\*, \*\* - significant at 0.05 and 0.01 level, respectively

PH (plant height), HFLB (height to the first lateral branch), LB (lateral branches per plant), PP (pods per plant), LP (leaves per plant), SW (1000 seed weight), SYP (seed yield per plant), DFP (days to first flower), DFPF (days to first pod filling), DM (days to maturity), RP (ripening period), FP (flowering period), OC (oil content), PC (protein content)

To compare the variation among various traits, descriptive statistics (mean values and range), estimates of variance components ( $\sigma_p^2$ ,  $\sigma_g^2$ ,  $\sigma_{gy}^2$ ), phenotypic (PCV) and genetic coefficient of variability (GCV), broad sense heritability ( $h^2$ ), genetic advance and genetic advance (GA) as a percentage of mean are given in Table 3. For all traits, genetic variances were lower as compared to phenotypic ones, demonstrating the environmental influence in their expression.

Table 3. Mean values, range of variance components, broad sense heritability, and genetic advance in rapeseed cultivars

	Mean	Minimum	Maximum	Estimates of variability				PCV%	GCV%	h <sup>2</sup>	GA	GA%
				$\sigma_p^2$	$\sigma_g^2$	$\sigma_{gy}^2$	$\sigma_{e^2}$					
PH	123.50	69.5	172	70.52	18.29	19.86	32.37	6.80	3.46	25.93	3.83	3.10
HFLB	54.61	15.3	89.5	74.61	34.68	18.04	21.89	15.82	10.78	46.48	7.07	12.94
LB	6.45	3.6	10.8	1.17	0.23	0.37	0.58	16.77	7.40	19.47	0.37	5.75
PP	128.01	62.7	261.4	733.84	134.16	402.06	197.62	21.16	9.05	18.28	8.72	6.81
LP	10.29	5.4	16.5	1.88	0.51	0.32	1.05	13.32	6.95	27.20	0.66	6.38
PC	19.48	16.01	25.36	2.49	1.17	0.48	0.84	8.10	5.56	47.04	1.31	6.71
OC	44.87	36.23	52.41	3.74	1.84	0.49	1.41	4.31	3.02	49.21	1.67	3.73
SW	3.76	2.97	4.68	0.10	0.05	0.03	0.02	8.49	5.73	45.55	0.26	6.81
SYP	8.97	1.58	19.81	5.07	0.78	2.43	1.86	25.09	9.86	15.43	0.61	6.82
DFF	215.50	196	222	18.89	6.34	11.77	0.78	2.02	1.17	33.57	2.57	1.19
DLPF	226.10	212	238	9.47	4.93	4.01	0.53	1.36	0.98	52.12	2.82	1.25
DM	280.81	269	292	6.26	1.81	3.91	0.54	0.89	0.48	28.91	1.27	0.45
RP	54.70	36	68	3.68	0.47	2.35	0.86	3.51	1.25	12.66	0.43	0.78
FP	21.40	12	31	3.34	0.82	2.00	0.51	8.54	4.23	24.53	0.79	3.69

$\delta_g^2$  (genetic variance),  $\delta_p^2$  (phenotypic variance),  $\delta_{gy}^2$  (variance of genotype x year interaction),  $\delta_{e^2}$  (error variance), GCV (genetic coefficient of variability), PCV (phenotypic coefficient of variability), h<sup>2</sup> (broad sense heritability), GA (genetic advance), GA % (genetic advance as percent of mean), PH (plant height), HFLB (height to the first lateral branch), LB (lateral branches per plant), PP (pods per plant), LP (leaves per plant), SW (1000 seed weight), SYP (seed yield per plant), DFF (days to first flower), DFPF (days to first pod filling), DM (days to maturity), RP (ripening period), FP (flowering period), OC (oil content), PC (protein content)

Genetic and phenotypic variances were high for pods per plant (134.16 and 733.84, respectively), followed by height of the first lateral branch (34.68 and 74.61) and plant height (18.29 and 70.52). Lowest variances were observed for 1000 seed weight (0.05 and 0.1) and lateral branches per plant (0.23 and 1.17).

Genetic coefficient of variation (GCV) ranged from 10.78 for height of the first lateral branch to 0.48 for days to maturity. Phenotypic coefficients of variation (PCV) had similar trend. Seed yield per plant (25.09), pods per plant (21.16) and lateral branches per plant (16.77) had highest, and days to maturity (0.89) the lowest PCV.

Broad sense heritability ( $h^2$ ) estimates range from 12.66% for ripening period to 52.12% for days to first pods filling. Genetic gain as a percent of mean varied between 0.45% and 0.48% for days to maturity and ripening duration, respectively, to 6.81% for pods per plant and 1000 seed weight, 6.82% for yield per plant and 12.94% for height of the first lateral branch. Days to maturity and ripening period combined low heritability and low GA. Moderate heritability and relatively low GA were observed at days to first pod filling and oil content. Low heritability and relatively high GA were observed for seed yield per plant, pods per plant and 1000 seed weight. Height to the first lateral branch showed moderate heritability and relatively high GA values. The GA values suggest that population means for some of the characters included in this study may be improved substantially by selecting the superior 10% of the materials compared.

Genetic correlations between the characters are shown in Table 4. The strongest positive genetic correlations were observed between phenological traits such as days to flowering, days to first pods filling and days to maturity. These traits also showed significant positive correlations with plant height, height to the first lateral branch, leaves per plant and protein content and strong negative associations with 1000 seed weight, oil content and seed yield per plant. Seed yield per plant had significant positive correlations with pods per plant ( $r=0.445$ ), oil content ( $r=0.306$ ) and plant height ( $r=0.171$ ). Except with phenological traits, seed yield per plant also showed significant negative correlations with leaves per plant ( $r=-0.572$ ), protein content ( $r=-0.368$ ), height to the first lateral branch ( $r=-0.252$ ) and 1000 seed weight ( $r=-0.135$ ). Oil content had significant positive associations with seed yield ( $r=0.306$ ) and plant height ( $r=0.151$ ), and positive, but nonsignificant correlations with branches per plant and pods per plant. All other traits were negatively correlated with oil content. The positive association between oil content and seed yield per plant indicate the possibility of simultaneous improvement of these most important traits in rapeseed.

The genetic correlations were analyzed further by the path coefficient technique. Only traits that revealed higher heritability than seed yield per plant combined with relatively high genetic gain (height to the first lateral branch, pods per plant, protein content, oil content and 1000 seed weight) were included in path analysis. The direct effects of traits on seed yield per plant corresponded well with the genetic correlation coefficients. Protein content had highly significant negative direct effect on seed yield ( $p=-0.365$ ), followed by 1000 seed weight ( $p=-0.017$ ) and height to the first lateral branch ( $p=-0.081$ ). The other studied traits expressed negative indirect effect on seed yield through height of the first lateral branch and 1000 seed weight. The direct effect of pods per plant was positive and highly significant ( $p=0.472$ ). Oil content expressed positive, but non significant direct effect on seed yield ( $p=0.082$ ). The lower value of the direct effect than the simple correlation coefficient of this trait on seed yield is mainly due to the positive indirect effect of protein content.

Table 4. Genetic correlations between seed yield per plant and yield related characters

	PH	HFLB	LB	PP	LP	PC	OC	SW	SYP	DFP	DLPF	DM	RP
HFLB	0.507**												
LB	0.105	-0.069											
PP	0.122*	-0.143**	0.027										
LP	0.325**	0.787**	0.128*	-0.199**									
PC	-0.151**	0.240**	0.197**	0.124*	0.323**								
OC	0.151**	-0.189**	0.042	0.063	-0.237**	-0.487**							
SW	0.163**	0.066	-0.059	-0.100	0.000	0.164**	-0.061						
SYP	0.171**	-0.252**	0.038	0.445**	-0.572**	-0.368**	0.306**	-0.135**					
DFP	0.283**	0.462**	0.031	0.001	0.477**	0.184**	-0.120*	-0.084	-0.304**				
DLPF	0.343**	0.614**	-0.127*	-0.091	0.562**	0.113	-0.221**	-0.137*	-0.346**	0.929**			
DM	0.224**	0.436**	-0.014	-0.022	0.554**	0.232**	-0.317**	-0.154**	-0.391**	0.910**	0.910**		
RP	-0.400**	-0.662**	0.254**	0.163**	-0.369**	0.112	-0.006	0.061	0.150**	-0.617**	-0.771**	-0.437**	
FP	0.211**	0.324**	-0.360**	-0.134*	0.052	-0.347**	-0.108	0.018	0.008	-0.311**	-0.003	-0.250**	-0.378**

\*, \*\* - significant at 0.05 and 0.01 level, respectively

Table 5. Pathways of association between seed yield per plant and some yield determining characters

	Direct effect	Indirect effect via					r
		HFLB	PP	PC	OC	SW	
HFLB	-0.081		-0.068	-0.087	-0.016	-0.001	-0.252**
PP	0.472**	0.012		-0.045	0.005	0.002	0.445**
PC	-0.365**	-0.019	0.059		-0.040	-0.003	-0.368**
OC	0.082	0.015	0.030	0.178		0.001	0.306**
SW	-0.017	-0.005	-0.047	-0.060	-0.005		-0.135**

\*\* - significant at 0.01 level,

HFLB (height to the first lateral branch), PP (podsperplant), SW (1000 seed weight), OC (oil content), PC (protein content)

## DISCUSSION

Optimizing yield is one of the most important goals for most rapeseed breeders (OZER *et al.*, 1999). Before starting any breeding program, the divergence among available germplasm needs to be examined.

Significant ( $p < 0.01$ ) mean squares for genotypic differences are indicating sufficient variability among examined genotypes and possibility to improve these traits through selection. Phenotypic variability was higher as compared with genetic variability, which is in relation with the findings of ALI *et al.* (2003) and MARINKOVIĆ and MARJANOVIĆ-JEROMELA (1996). Genetic and phenotypic coefficients of variation had similar trend for all traits.

For most of the traits heritability estimates were low as a result of higher phenotypic variances, indicating great environmental influence in their expression. However, estimates of heritability may differ widely in the same crop and same trait (HILL *et al.*, 1998; RASMUSON, 2002), because heritability always refers to a defined population and specific experimental setup (NYQUIST, 1991; HOLLAND *et al.*, 2002). The lowest heritability was estimated for ripening period and seed yield per plant, and the highest for days to lowest pods filling and oil content. Oil content in rapeseed has been found to be highly heritable in the results of WANG and QIU (1990), BECKER *et al.* (1999), MARJANOVIĆ-JEROMELA *et al.* (2007) and WU *et al.* (2006). Such findings are different from those of ALI *et al.* (2003), who reported highest heritability for days to maturity, followed by flowering duration and seed weight.

High heritability does not necessarily mean high genetic gain. The utility of heritability estimates is, therefore, increased when they are used to estimate genetic advance (JOHNSON *et al.*, 1955), which indicates the degree of gain in a character obtained under a particular selection pressure. The expected genetic advance is a function of selection intensity, phenotypic variance and heritability. Thus, the genetic advance has an added edge over heritability as a guiding factor to breeders in a selection programme (SINGH and SINGH, 1981). Traits that revealed higher heritability than seed yield per plant combined with relatively high genetic gain were height to the first lateral branch, pods per plant, protein content, oil content and 1000 seed weight. Phenological traits exhibited the lowest genetic gain.

The genetic background of any pair of characters, whether yield, height, or maturity characters is unlikely to be under totally separate control, mainly due to linkage or pleiotropy (ENGQVIST and BECKER, 1993). For plant breeders it is therefore necessary to examine the relationship between pairs of characters in order to decide upon the most appropriate selection criteria for a breeding program. In oil crops, the association between seed yield and the quality characters, oil and protein content, is of major interest (ENGQVIST and BECKER, 1993). In cases where the magnitudes of the genetic and phenotypic correlations were nearly the same, the environmental covariance was very small, which means that the influence of the environment on these correlations was minimal (FALCONER, 1989). Seed yield per plant revealed highest genetic correlations with pods per plant and oil content. Significant correlations between seed yield and number of pods per plant, 1000 seed

weight and seed weight per pod were reported by OLSSON (1960), THURLING and VIJENDRA DAS (1979), TAYLOR and SMITH (1992), OZER *et al.* (1999) and IVANOVSKA *et al.* (2007). ALI *et al.* (2003) found highly significant and positive correlations of seed yield per plant with harvest index and seed weight. ENGQVIST and BECKER (1993) considered 1000 seed weight as most interesting trait to use as an indirect selection criteria for yield, but the correlation between those two traits wasn't significant across years and crosses. Enhancing the oil content while simultaneously improving grain yield and agronomical traits is the major challenge of rapeseed breeders (HAUSKA *et al.*, 2007). Positive genetic correlation between those two traits indicates the possibility for simultaneous improvement of seed and oil yield (MIJIC *et al.*, 2009).

Path coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy (SHIPLEY, 1997; SCHEINER *et al.*, 2000). This approach is based on *a priori* assumptions which traits are to be included in the analysis. Such assumptions are somewhat subjective, but path coefficients may allow a better understanding of the interrelationships between traits than correlation tables with all possible combinations between all traits measured (BAYE and BECKER, 2005). The greatest positive direct effect on seed yield per plant showed pods per plant, followed by oil content. These two traits can be used as selection criteria for seed yield in the early generations. In breeding programs including investigated cultivars, special attention needs to be given to oil content. Its direct effect on seed yield per plant confirms the possibility of their simultaneous improvement. Protein content, height to the first lateral branch and 1000 seed weight exhibited negative direct effect on seed yield per plant. THURLING (1974), OZER *et al.* (1999), ALI *et al.* (2003) and BASALMA (2008) reported highest direct effect of pods per plant and 1000 seed weight on yield per plant. DIEPENBROCK (2000) concludes that number of pods per plant is decisive for seed yield.

In conclusion, the divergence of the studied material represents solid basis for starting effective breeding program for increasing seed yield. Seed yield per plant had significant positive genetic correlations with pods per plant, oil content, plant height and ripening period. The other traits exhibited positive nonsignificant or negative associations with seed yield.

The direct effect of pods per plant on seed yield per plant was positive and highly significant. Oil content expressed positive, but non significant direct effect on seed yield. These two traits need to be considered as selection criteria in future breeding programs for improving seed yield. Such approach will deliver quantifiable increases in the environmental sustainability of rapeseed production within the region. According to the present study, the positive association between oil content and seed yield per plant indicate the possibility of improving these most important traits in rapeseed simultaneously.

## ACKNOWLEDGMENTS

This research results from project TR31025 of Ministry of science and technological development of the Republic of Serbia.

Received, June 3<sup>rd</sup>, 2010

Accepted, February 22<sup>nd</sup> 2011

## REFERENCES

- ALI, N., F. JAVIDFAR and A.A. ATTARY (2002): Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus* L.). Pak. J. Bot. 34 (2): 145-150.
- ALI, N., F. JAVIDFAR, J.Y. ELMIRA and M.Y. MIRZA (2003): Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). Pak. J. Bot. 35 (2): 167-174.
- BASALMA, D. (2008): The Correlation and Path Analysis of Yield and Yield Components of Different Winter Rapeseed (*Brassica napus* ssp. *oleifera* L.) Cultivars. Research Journal of Agriculture and Biological Sciences, 4 (2): 120-125.
- BAYE ,T. and C.H. BECKER (2005): Genetic variability and interrelationship of traits in the industrial oil crop *Vernonia galamensis*. Euphytica, 142: 119–129.
- BECKER, H.C., H. LOPTIEN and G. ROBBELEN (1999): Breeding: an overview. In: Gomez-Campo, C. (Ed.) Biology of *Brassica* coenospecies. Elsevier, Amsterdam, pp 413-460.
- BOROJEVIĆ, S. (1990): Principles and methods of plant breeding. Developments in Crop Science 17. Elsevier Science Publishing Company Inc. New York.
- DEGENHART, D. F. and Z. P. KONDRA (1984): Relationships between seed yield and growth characters, yield components and seed quality of summer-type oilseed rape (*Brassica napus* L.). Euphytica, 33: 885-889.
- DEWEY, D.R. and K.H. LU (1959): A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron. J., 51: 515-518.
- DIEPENBROCK, W. (2000): Yield analysis of winter oilseed rape (*Brassica napus* L.): a review. Field Crops Res., 67: 35-49.
- ENGQVIST, M. G. and H.C. BECKER (1993): Correlation studies for agronomic characters in segregating families of spring oilseed rape (*Brassica napus*). Hereditas, 118: 211-216.
- FALCONER, D.S. (1989): Introduction to Quantitative Genetics. 3rd edn., Longman, London.
- FOX, P.N., J. CROSSA and I. RAMAGOSA (1997): Multienvironment testing and genotype x environment interaction. In: Kempton, R.A. and Fox, P.N. (Eds.), Statistical methods for plant variety evaluation. Chapman & Hall, pp.117-138.
- FRIEDT, W., R. SNOWDON, F. ORDON, and J. AHLEMEYER (2007): Plant Breeding: assessment of Genetic Diversity in Crop Plants and its Exploitation in Breeding. Progress in Botany, 168: 152-177.
- GUNASEKERA C. P., L. D MARTIN, K. H. M. SIDDIQUE and G. H. WALTON (2006): Genotype by environment interactions of Indian mustard (*Brassica juncea* L.) and canola (*B. napus* L.) in Mediterranean-type environments. I. Crop growth and seed yield. European Journal of Agronomy, 25: 1-12.
- HARPER, F.R. and B. BERKENKAMP (1975): Revised growth-stage key for *Brassica campestris* and *B. napus*. Can. J. Plant Sci., 55: 657-658.

- HAUSKA, D., C. OERTEL, L. ALPMANN, D. STELLING and H. BUSCH (2007): Breeding progress towards high oil content in oilseed rape (*Brassica napus* L.) – essential innovations to meet current and future market needs. 12<sup>th</sup> International Rapeseed Congress, Wuhan, China, 1: 159-162.
- HILL, J., H.C. BECKER and P.M.A. TIGERSTEDT (1998): Quantitative and Ecological Aspects of Plant Breeding. Chapman and Hall, London.
- HOLLAND, J.B., W.E. NYQUIST and C.T. CERVANTES-MARTINEZ (2002): Estimation and interpreting heritability for plant breeding: An update. *Plant. Breed. Rev.*, 22: 9–112.
- HRISTOV, N., N. MLADENOV, V. DJURIC, A. KONDIC-SPIKA, A. MARJANOVIĆ-JEROMELA and D. SIMIC (2009): Genotype by environment interactions in wheat quality breeding programs in southeast Europe. *Euphytica*, 174, (3): 315-324.
- HÜHN, M. and J. LÉON (1985): Genotype x environment interactions and phenotypic stability of *Brassica napus*. *Z. Pflanzenzüchtung*, 95: 135- 146.
- IVANOVSKA, S., C. STOJKOVSKI, Z. DIMOV, A. MARJANOVIĆ-JEROMELA, M. JANKULOVSKA, and L.J. JANKULOSKI (2007): Interrelationship Between Yield and Yield Related Traits of Spring Canola (*Brassica napus* L.) Genotypes. *Genetika*, 39, (3): 325-332.
- JOHNSON, H.W., H.F.ROBINSON, and R.E. COMSTOCK (1955): Estimates of genetic and environmental variability in soybeans. *Agron. J.*, 47: 314–318.
- LYNCH, M. and B. WALSH (1998): Genetics and analysis of quantitative traits, Sinauer Associates Inc. Sunderland, MA, USA.
- MARINKOVIĆ, R. and A. MARJANOVIĆ-JEROMELA (1996): Genotypic and phenotypic correlations of some characters of oilrape (*Brassica napus* L.) Proc. of the Eucarpia - Symposium on breeding of oil and protein crops, 5-8 August 1996, Zaporozhye, Ukraina., pp. 127-130.
- MARJANOVIĆ-JEROMELA, A., R. MARINKOVIĆ, M. KRALJEVIĆ-BALALIĆ, D. VASIĆ and J. CRNOBARAC (2003): Genetic divergence of winter oilseed rape (*Brassica napus* L.) genotypes. Proceedings of the 2nd Symposium for Breeding, Vrnjačka Banja, 49 (in Serbian, with English abstract)
- MARJANOVIĆ-JEROMELA, A., R. MARINKOVIĆ, V. RADIĆ, S. IVANOVSKA and M. JANKULOVSKA (2007). Variability and Heritability of Yield Components in Rapeseed (*Brassica napus* L.). *Cruciferae Newsletter*, 27: 46-48.
- MARJANOVIĆ-JEROMELA A., A. KONDIC-SPIKA, D. SAFTIC-PANKOVIC, R. MARINKOVIC and N. HRISTOV (2009): Phenotypic and molecular evaluation of genetic diversity of rapeseed (*Brassica napus* L.) genotypes. *African Journal of Biotechnology*, 8 (19): 4835-4844.
- MIJIC, A., I. LIOVIC, Z. ZDUNIC, S. MARIC, A. MARJANOVIĆ JEROMELA, M. JANKULOVSKA (2009): Quantitative analysis of oil yield and its components in sunflower (*Helianthus annuus* L.). *Romanian Agricultural Research*, 26: 41-46.
- NYQUIST, W.E. (1991): Estimation of heritability and prediction of selection response in plant populations. *Crit. Rev. Plant. Sci.*, 10: 235–322.
- OGRODOWCZYK, M. and M. WAWRZYNIAK (2004): Adoption of the path- coefficient analysis for assesment of relationship and interrelationship of yield and yield parameters of winter oilseed rape. *Rosliny Oleiste*, 25 (2): 479- 492.
- OLSSON, G. (1960): Some relations between number of seeds per pod, seed size and oil content and the effect of selection for these characters in *Brassica* and *Sinapis*. *Hereditas*, 46: 29-70.
- RASMUSON, M. (2002): The genotype-phenotype link. *Hereditas*, 136: 1–6.
- SCHEINER, S.M., R.J. MITCHELL and H.S. CALLAHAN (2000): Using path analysis to measure natural selection. *J.Evol.Biol.*, 13: 423–433.

- SHIPLEY, B. (1997): Exploratory path analysis with applications in ecology and evolution. *The American Naturalist*, *149* (6): 1113-1138.
- SINGH M., S. CECCARELLI and J.HAMBLIN (1993): Estimation of heritability from varietal trials data. *Theor. Appl. Genet.*, *86*: 437-441.
- SINGH, R. K., and B. D. CHAUDHARY (1979): Biometrical methods in quantitative genetic analysis. Kalyani Publishers, NewDelhi.
- SINGH, S.P. and H.N. SINGH (1981): Gene system involved and their implication in breeding lablab bean (*Dolichos lablab*). *Z. Pflanzenzüchtung*, *87*, 240–247.
- THURLING, N. (1974): Morphophysiological determinants of yield in rapeseed (*Brassica campestris* and *Brassica napus* ). II. Yield Components. *Aust. J. Agric. Res.*, *25*: 711-721.
- THURLING, N. (1991): Application of the ideotype concept in breeding for higher yield in the oilseed brassicas. *Field Crops Res.*, *26*: 201-219.
- THURLING, N. and L.D. DAS VIENDRA (1979): The relationship between pre-anthesis development and seed yield of spring rape (*Brassica napus* L.). *Aust. J. Agric. Res.*, *31*: 25-36.
- VASIN J., P. SEKULIĆ and M. BELIĆ (2002): Characteristics of the chernozem soil at Rimski Šančevi experiments field of Institute of Field and Vegetable crops. Sesiunea anuala omagiala de comunicari si referate stiintifice “ 80 de ani de la nasterea prof. dr. Iulian Dracea”, 9-10 May 2002., Temisoara, Romania, pp. 153-160.
- WANG F. and J. QIU (1990): Studies on the inheritance of seed protein content and its correlation with other characters in *Brassica napus* L. *Scientia Agricultura Sinica*, *23* (6): 42-47
- WILLIAMS, W.A., M.B. JONES and W. DEMMENT (1990): A concise table for path analysis statistics. *Agron. J.*, *82*: 1022-1024.
- WU, J.G., C.H. SHI, and H.Z. ZHANG. (2006): Partitioning genetic effects due to embryo, cytoplasm and maternal parent for oil content in oilseed rape (*Brassica napus* L.). *Genet. Mol. Biol.*, *29*: 533-538.

## VARIJABILNOST KOMPONENTI PRINOSA OZIME ULJANE REPICE (*Brassica napus* L.) I NJIHOVA KORELACIJA SA PRINOSOM SEMENA

Ana MARJANOVIĆ-JEROMELA<sup>1\*</sup>, Radovan MARINKOVIĆ<sup>1</sup>, Sonja IVANOVSKA<sup>2</sup>, Mirjana JANKULOVSKA<sup>2</sup>, Anto MIJIĆ<sup>3</sup>, Nikola HRISTOV<sup>1</sup>

<sup>1</sup> Institut za ratarstvo I povrtarstvo, Novi Sad, Srbija

<sup>2</sup> Fakultet za zemljodelske nauke i hranu, Skoplje, Makedonija

<sup>3</sup> Poljoprivredni institute Osijek, Osijek, Hrvatska

### I z v o d

Za organizovanje dobrog oplemenjivačkog programa na uljanoj repicu (*Brassica napus* L.) neophodno je poznavanje genetičke varijabilnosti svojstava koja utiču na prinos semena i ulja. Istraživanja su sprovedena da bi se ispitala fenotipska i genotipska varijabilnost, heritabilnost u širem smislu, genetička dobit od selekcija i međuzavisnost agronomskih važnih osobina i svojstava kvaliteta semena kod ispitivanih genotipova. Genotipovi, godine i njihova interakcija signifikantno su varirale za sva ispitivana svojstva. Fenotipski koeficijent varijacije bio je veći od genotipskog. Heritabilnost u širem smislu kretala se od 12.66% (za vreme sazrevanja) do 52.12% (broj dana do formiranja prve mahune). Očekivana genetička dobit bila je najniža za broj dana do sazrevanja (0.45%) i najviša za visinu do prve bočne grane (12.94%). Analiza genetičkih korelacija ukazala je na visoku i pozitivnu vezu prinosa semena po biljci sa brojem ljuski po biljci, sadržajem ulja, visinom biljke i vremenom sazrevanja, a negativna korelacija je utvrđena između prinosa semena po biljci i broja listova po biljci, dana do zrenja, sadržaja proteina, broja dana do formiranja prve mahune, broja dana do cvetanja, visine prve bočne grane i težine 1000 semena

Analiza koeficijenta putanje ukazala je da su broj ljuski po biljci i sadržaj ulja najvažnije komponente prinosa semena po biljci. Njihovi direktni efekti na prinos po biljci su bili  $p=0.472$  i  $p=0.082$ . Sadržaj proteina imao je visokoznačajan negativan direktan efekat na prinos semena ( $p=-0.365$ ), potom masa 1000 semena ( $p=-0.017$ ) i visina do prve bočne grane ( $p=-0.081$ ). Ova istraživanja predstavljaju osnov za dalje oplemenjivanje uljane repice poboljšanog prinosa semena i ulja.

Primljeno 03. VI.2010.

Odobreno 22.II.2011.