

**ESTIMATES OF GENETIC VARIABILITY AND ASSOCIATION STUDIES  
IN QUANTITATIVE PLANT TRAITS OF *ERUCA* SPP. LANDRACES**

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Bozokalfa Kadri M., D. Esiyokhulya Ilbi, and T. Kaygisiz Ascioğul (2010): *Estimates of genetic variability and association studies in quantitative plant traits of Eruca spp. Landraces*. Genetika, Vol 42, No. 3, 501 -512

Despite the increasing of economical importance of rocket plant limited information is available on genetic variability for the agronomic traits among *Eruca* spp. Hence, heritability and association studies of plant properties are necessities for a successful further rocket breeding programme. The objective of this study was to examine phenotypic and genotypic variability, broad sense heritability, genetic advance, genotypic and phenotypic correlation and mean for agronomic traits of rocket plant.

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The magnitude of phenotypic coefficient of variation values for all the traits were higher than the corresponding values and broad sense heritability estimates exceeded 65% for all traits. Phenotypic coefficients of variability (PCV) ranged from 7.60 to 34.34% and genotypic coefficients of variability (GCV) ranged between 5.58% for petiole thickness and 34.30% for plant weight. The results stated that plant weight, siliqua width, seed per siliqua and seed weight could be useful character for improved *Eruca* spp. breeding programme.

*Key words:* Brassicaceae, genetic advance, germplasm, heritability, variability

#### INTRODUCTION

The genus *Eruca*, a member of the Brassicaceae Family comprises of three species, viz. *E. pinnatifida*, *E. sativa* and *E. vesicaria* (WARWICK *et al.*, 2007). The distribution of these genera occurs in southern Europe, Central Asia and Mediterranean countries. *E. sativa* subsp. *sativa* cultivated in southern Europe, north and north-east Africa, the Middle East, central Asia and north central India (WARWICK *et al.*, 2007). The rocket plant (*Eruca sativa*) is important leafy vegetables and cultivated vegetable most of countries where they are used (either wild or cultivated) in many ways, as condiment in salads, cooked vegetables, medicinal and functional plants (KIM *et al.*, 2006). Besides its popular uses as vegetables, rocket is also considered a medicinal plant. Rocket is today a much appreciated vegetable in Europe, North America and (to a lesser extent) in Asia. It is also becoming popular in some other countries viz Argentina and South Africa due to introductions made by Italian immigrants the same crop is largely underutilized in most countries in the lower Mediterranean countries. Moreover rocket could be grown as an oil crop in Western Canada (WARWICK *et al.*, 2007). The rocket is widely cultivated and used as vegetable in traditional Turkish foods and *Eruca cappadocica* Reut. ex Boiss (syn. *Eruca vesicaria* subsp. *sativa*) is also has been cultivated in Central Anatolia for oil production for a centuries (ERTUG, 2000) and has the potential to become an oil crop in future for Turkey.

The assessment genotypic correlation for determining the relationships among agronomic traits in genetically diverse population at genotypic level also would attend as an effective tool for making progress in crop improvement (BELLO *et al.*, 2006). High phenotypic variation (such as presence of green and purple types, spreading habit with numerous basal branches and erect types with few secondary branches) *Eruca* germplasm gathered in North-West of India has been reported (DUHOON and KOPPAR, 1998). Even though many researches has been carried out on the evaluation, heritability, genetic advance and correlation between agronomic traits in *Brassica* species there is no detailed scientific evaluation in *Eruca* spp. genotypes. While rocket cultivation increase in most countries very limited rocket cultivars are available and variety selection have undergone (MORALES *et al.*, 2006). Various researches indicate genetic parameters to determine the selection criteria for yield and quality improvement on vegetable but limited information is available on the

nature of variability, magnitude of heritability and correlation of *E. sativa* genotypes, in spite of largely underutilized in most countries.

The objective of the present study was to estimate the genetic variation, genetic interrelationships, and heritability's for additional quantitative agronomic and seed traits in accessions of *Eruca* spp. and to evaluate suitable selection criteria for their further breeding.

#### MATERIALS AND METHODS

A total 26 genotypes of *Eruca* spp. were grown during two growing seasons (2005 and 2006) at the experimental fields of Ege University, Faculty of Agriculture, Department of Horticulture in Bornova, Izmir Province, Turkey. The evaluated accessions/genotype collected different countries of the world were used to estimate genetic variations and assessment plant properties (Table 1).

Seeds were sown on February in a 20 liter volume and 75 x 26 x 21 cm size pots, containing a mixture of peat and perlite (3:1 v/v) as a growing media in both experiment years. These pots consisting 15 plants and were placed in a polyethylene covered glasshouse until the appearance of the first true leaves, and then placed in open field condition. The experimental design was randomized complete block with three replications.

The fifteen agronomic traits: Leaf width (LW) (cm), leaf length (LL) (cm), leaf petiole length (LPL) (cm), leaf petiole width (LPW) (cm), leaf petiole thickness (LPT) (cm), plant height (PH) (cm), plant width (PW) (cm), plant weight (PWE) (g), number of leaves (NL), siliqua length (SL) (cm), siliqua width (SW) (cm), siliqua pedicel length (SPL) (cm), siliqua beak length (SBL) (cm), number of seeds per siliqua (NSS), 1000 seed weight (SWE) (g) were evaluated based on the IPGRI Descriptors for Rocket (*Eruca* spp.) (IPGRI, 1999).

To estimate the extent of magnitude of variation among these traits, all data were subjected to analysis of variance for two separate years. Mean, standard error, range were analyzed according to SINGH and CHAUNHARY (1985). Components of variance  $\sigma^2_g$  = genotypic variance,  $\sigma^2_p$  = phenotypic variance and  $\sigma^2_e$  = error variance were estimated using the following formula (WRICKE and WEBER, 1986);

$$\sigma^2_g = (MSG - MSE / r)$$

$$\sigma^2_p = (MSG / r)$$

$$\sigma^2_e = (MSE / r)$$

where MSG, MSE and  $r$  are the mean squares of genotypes, mean squares of error and number of replication, respectively (BAYE, 2002).

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as the following formula proposed by SINGH and CHAUDHARY (1985) was used:

$$PCV = \left( \sigma_p / \bar{X} \right) \times 100$$

$$GCV = \left( \sigma_g / \bar{X} \right) \times 100$$

where,  $\sigma_p$ ,  $\sigma_g$ , and  $\bar{X}$  are the phenotypic, genotypic standard deviation and grand mean of the traits respectively. Heritability in the broad sense ( $h^2$ ) was estimates on genotypic mean described by ALLARD (1999) as:

$$\text{Heritability } (h^2) = \frac{\sigma^2_g}{\sigma^2_p}$$

Expected genetic advance (GA) and percentage of GA calculated according to SHUKLA *et al.* (2006). Expected genetic advance  $(GA) = i\sigma_p h^2$

$$GA(\%) = \frac{GA}{\bar{X}} \times 100$$

where,  $i$ : standardized selection differential, a constant (2.06),  $\sigma_p$ : phenotypic standard deviation. Genotypic and phenotypic correlation coefficients were calculated as proposed by JOHNSON *et al.* (1955).

## RESULTS AND DISCUSSION

Morphological and physiological plant properties are given table 1. Large variability observed for qualitative and qualitative plant properties (petiole width, plant width, plant weight, seeds per siliqua and seed weight) in examined collections. The least range of variation was showed for leaf width, leaf length, petiole length and thickness, plant height, number of leaves, siliqua length and width, siliqua pedicel and beak length.

To compare the variation among various plant properties, estimation of variance components ( $\sigma^2_g$ ,  $\sigma^2_p$ ,  $\sigma^2_e$ ), phenotypic (PCV) and genotypic coefficient of variability (GCV), broad sense of heritability ( $h^2_B$ ) and genetic advance are given in Table 3. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits were higher than the corresponding (GCV) values indicating that these characters may influenced of environmental effect. Phenotypic coefficients of variability ranged from 7.60 to 34.34% and the highest PCV obtained from plant weight and the lowest from petiole thickness. Broad sense heritability estimates was high for leaf width and length, petiole length and width, plant height, plant width and weight, number of leaves, siliqua length and width while comparing lower values of other traits.

Table 1. Names and origins of *Eruca* spp. genotypes and qualitative value of morphological/physiological characters

Genotype	Country of origin	Donor	Seedling <sup>¶</sup> pubescence	Stem hairiness	Leaf blade shape	Leaf apex shape	Leaf hairiness	Stem color	Plant growth habit	Branching density	Petal color
PI 120927	Turkey	USDA-ARS*	5	7	3	4	5	4	2	5	1
PI 164936	Turkey	USDA-ARS	5	7	3	3	5	4	3	5	4
PI 170361	Turkey	USDA-ARS	7	5	4	3	3	2	3	3	1
PI 170362	Turkey	USDA-ARS	7	7	3	4	5	4	1	5	4
PI 173902	Turkey	USDA-ARS	7	5	3	3	5	2	1	3	4
PI 175720	Turkey	USDA-ARS	3	5	4	3	3	2	1	3	4
PI 178901	Turkey	USDA-ARS	7	5	4	3	3	2	1	3	4
PI 179279	Turkey	USDA-ARS	7	5	4	3	3	2	1	3	4
PI 183233	Egypt	USDA-ARS	3	5	3	4	5	4	1	5	1
PI 217829	Pakistan	USDA-ARS	7	5	3	4	3	2	1	3	1
PI 251490	Iran	USDA-ARS	3	3	4	3	3	4	2	5	4
PI 255664	Afghanistan	USDA-ARS	7	5	3	4	3	2	1	3	3
PI 261629	Spain	USDA-ARS	3	7	4	3	5	4	2	5	1
PI 311742	Poland	USDA-ARS	3	7	3	4	3	4	1	5	4
PI 344365	Turkey	USDA-ARS	5	7	3	4	5	4	2	5	4
PI 390143	Pakistan	USDA-ARS	7	7	3	3	3	2	1	5	4
PI 407630	Turkey	USDA-ARS	5	5	4	3	3	2	1	5	4
PI 426198	Afghanistan	USDA-ARS	5	5	4	3	3	2	1	3	4
PI 432339	Cyprus	USDA-ARS	5	5	3	4	5	4	2	5	4
PI 597835	Pakistan	USDA-ARS	7	7	4	3	3	4	2	5	1
PI 603033	England	USDA-ARS	7	7	3	4	3	2	1	3	1
PI 633202	Algeria	USDA-ARS	5	7	3	4	3	4	2	5	4
PI 633210	China	USDA-ARS	7	7	3	4	3	2	1	3	1
<i>E. sativa</i>	Local cultivar- Italy	FRC	5	7	3	4	5	2	2	5	4
<i>E. cappadoica</i>	Konya-Turkey	LF	3	3	4	3	3	2	1	3	4
<i>E. sativa</i> Mill.	Local cultivar- Turkey	LC	3	7	3	4	3	4	2	5	1

\*ARS-GRIN: United States Department of Agriculture Agricultural Research Service North Central Regional Plant Introduction Station, Ames, USA, FRC: Received from foreign researchers Jules Janick collected in Italy, LF: Local farmer supported, LC: Local cultivar sales in market. <sup>¶</sup> Plant qualitative traits were evaluated and scored basis on *Eruca* spp. descriptor using with visual rating, seedling pubescence 3: very sparse, 5: intermediate, 7: dense, stem hairiness 3: sparse, 5: intermediate, 7: high, leaf blade shape 3: obovate, 4: spatulate, leaf apex shape 3: rounded, 4: broadly rounded, leaf hairiness 3: sparse, 5: intermediate, stem color 2: green, 3: dark green, plant growth habit 1: elongate branching stems supporting leaves, 2: elongate, non-branching stem terminating in floral apex, 3: elongate branching stems terminating in pre-floral apices, branching density 3: low, 5: intermediate, petal color 1: white, 2: cream, 3: cream yellowish, 4: yellow.

Genetic advance as percent of the mean was highest for plant weight (70.56%), seeds per siliqua (55.15%) seed weight (51.77%), and siliqua width (51.57%) and the remaining traits showed a moderate to very low amounts of genetic advance. In generally the higher heritability estimates for these traits indicate that environmental factors did not greatly affect phenotypic variation of such characters. Correlation between traits is of interest to determine whether selection for one trait will have an effect on another. Simple correlation coefficient from the combined data across the two years is shown in table 4. Leaf length showed strong positive correlation with leaf width, leaf petiole length, leaf petiole width, leaf petiole thickness, plant height and width, plant weight, siliqua length and width. One of the

two important seed component, number of seed per siliqua exhibited positive association with siliqua width, siliqua pedicel length, seed weight. The other seed component, seed weight revealed positive correlation with leaf petiole width, leaf petiole thickness, plant width, siliqua pedicel length, number of seed per siliqua and negative correlation with plant weight. Phenotypic and genotypic correlation coefficients among various traits are presented in table 5. Among the agronomic traits leaf properties showed high genotypic and phenotypic positive correlation with leaf length, leaf petiole length, leaf petiole width, leaf petiole thickness, plant height, whereas negative correlation with plant width. Seed weight was showed positive correlation with leaf length, leaf petiole width, leaf petiole thickness, plant weight, siliqua pedicel length, number of seeds per siliqua.

Table 2. Mean values, standard error of 26 accessions for 15 agronomic traits in *Eruca* spp.

Genotype	LW <sup>‡</sup> (cm)	LL (cm)	LPL (cm)	LPW (cm)	LPT (cm)	PH (cm)	PW (cm)	PWE (g)	NL	SL (cm)	SW (cm)	SPL (cm)	SBL (cm)	NSS	SWE (g)
PI 120927	6.28	24.24	4.40	0.37	0.34	10.88	38.78	29.45	13.50	2.31	0.24	0.60	0.55	17.51	0.59
PI 164936	6.99	20.37	3.97	0.34	0.33	14.56	27.75	21.18	9.40	1.53	0.36	0.58	0.73	11.64	0.91
PI 170361	7.84	20.36	4.52	0.36	0.30	13.45	24.75	15.30	8.33	2.02	0.50	0.55	0.97	22.51	1.89
PI 170362	8.26	22.08	5.36	0.39	0.35	10.05	26.50	30.12	12.77	1.72	0.37	0.44	0.79	15.93	1.60
PI 173902	8.14	22.10	5.36	0.42	0.34	10.63	22.57	26.50	8.76	1.98	0.48	0.61	0.88	20.16	1.28
PI 175720	6.76	19.16	5.18	0.37	0.31	10.43	16.02	19.16	7.69	1.88	0.52	0.62	0.93	20.47	1.87
PI 178901	8.35	20.74	5.16	0.43	0.33	13.32	15.19	29.26	8.83	2.26	0.37	0.60	0.84	22.49	1.37
PI 179279	8.44	21.73	4.72	0.47	0.37	13.69	19.46	36.74	8.57	1.83	0.41	0.46	0.77	13.35	1.76
PI 183233	8.44	21.34	5.90	0.39	0.34	18.19	25.59	29.39	8.36	1.90	0.47	0.51	0.87	17.19	1.39
PI 217829	8.51	16.30	6.06	0.46	0.35	11.76	21.26	27.61	8.10	2.39	0.47	0.57	0.94	19.24	1.73
PI 251490	7.73	17.33	5.97	0.43	0.34	13.24	25.00	35.73	8.66	1.72	0.50	0.54	0.85	14.56	2.44
PI 255664	7.62	16.02	6.56	0.41	0.33	12.93	20.46	27.99	7.47	1.78	0.48	0.60	0.88	16.76	1.39
PI 261629	6.92	16.71	5.53	0.40	0.34	7.29	31.42	28.53	10.95	1.79	0.31	0.59	0.78	18.26	1.38
PI 311742	6.80	16.50	5.73	0.45	0.33	8.00	26.44	22.32	8.45	1.70	0.46	0.66	0.91	9.52	0.82
PI 344365	6.42	16.74	5.61	0.43	0.34	8.49	26.83	24.88	7.93	1.90	0.38	0.55	0.95	17.77	0.73
PI 390143	6.93	17.29	5.57	0.48	0.33	10.85	25.83	51.20	8.47	2.17	0.55	0.65	1.08	14.19	1.52
PI 407630	5.18	16.40	5.48	0.37	0.32	12.80	24.23	16.06	7.28	2.26	0.58	0.63	0.87	17.54	1.80
PI 426198	6.53	16.32	5.49	0.40	0.35	9.61	23.98	28.63	8.76	1.85	0.56	0.57	0.96	21.55	1.87
PI 432339	6.79	16.26	5.61	0.39	0.33	10.12	31.27	23.68	10.07	1.71	0.25	0.56	0.69	7.11	0.74
PI 597835	4.25	14.48	2.97	0.31	0.25	3.86	29.31	6.81	8.38	1.29	0.15	0.53	0.48	8.69	0.30
PI 603033	5.87	19.10	5.19	0.36	0.33	8.27	22.97	28.18	8.47	1.53	0.37	0.52	0.84	18.96	1.01
PI 633202	7.13	21.83	5.30	0.40	0.37	9.34	32.87	27.48	9.82	1.62	0.37	0.63	0.79	15.95	1.08
PI 633210	7.95	18.76	5.60	0.37	0.37	0.66	25.02	25.60	7.72	2.26	0.38	0.64	0.86	9.14	0.36
<i>E. sativa</i>	6.78	20.55	3.80	0.40	0.32	10.00	29.00	20.39	8.60	1.95	0.44	0.56	0.63	22.11	0.90
<i>E. cappadocica</i>	5.77	18.85	5.45	0.38	0.35	7.01	21.48	13.45	8.26	1.94	0.42	0.62	0.83	19.16	2.08
<i>E. sativa</i> Mill.	6.70	17.56	3.15	0.37	0.34	8.06	24.32	15.59	8.94	1.97	0.30	0.48	0.54	13.31	1.11
Mean	7.05	18.81	5.14	0.40	0.33	10.60	25.32	25.43	8.94	1.89	0.41	0.57	0.82	16.33	1.30
Standart error	1.07	2.52	0.87	0.04	0.02	2.94	5.09	8.68	1.47	0.27	0.10	0.06	0.14	4.42	0.55

<sup>‡</sup> Leaf width (LW), Leaf length (LL), Leaf petiole length (LPL), Leaf petiole width (LPW), Leaf petiole thickness (LPT), Plant height (PH), Plant width (PW), Plant weight (PWE), Number of leaves (NL), Siliqua length (SL), Siliqua width (SW), Siliqua pedicel length (SPL), Siliqua beak length (SBL), Number of seeds per siliqua (NSS), 1000 seed weight (SWE).

Table 3. Estimation of variance components ( $\sigma^2g$ ,  $\sigma^2p$ ,  $\sigma^2e$ ), phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability ( $h^2$ ) and genetic advance (GA) (%) for various agronomic traits in *Eruca* spp.

Traits	$\sigma^2p$	$\sigma^2g$	$\sigma^2e$	PCV			
				(%)	GCV (%)	$h^2$	GA (%)
Leaf width	1.017	0.985	0.032	14.34	14.12	96.89	28.63
Leaf length	6.059	5.886	0.172	13.14	12.95	97.15	26.30
Petiole length	0.950	0.797	0.153	19.04	17.43	83.86	32.89
Petiole width	0.003	0.002	0.001	13.24	11.84	79.91	21.80
Petiole thickness	0.001	0.000	0.000	7.60	5.58	53.94	8.44
Plant height	5.393	5.067	0.327	21.89	21.22	93.94	42.36
Plant width	25.807	25.371	0.436	20.18	20.00	98.31	40.86
Plant weight	76.933	76.729	0.204	34.34	34.30	99.73	70.56
Number of leaves	46.667	41.667	5.000	15.43	14.58	89.29	28.39
Siliqua length	0.069	0.063	0.006	13.96	13.39	92.02	26.47
Siliqua width	0.011	0.010	0.000	25.72	25.37	97.35	51.57
Siliqua pedicel length	0.003	0.002	0.001	9.82	8.50	74.85	15.15
Siliqua beak length	0.019	0.013	0.007	17.39	14.08	65.56	23.49
Seed per siliqua	19.545	19.305	0.240	27.11	26.94	98.77	55.15
Seed weight	0.158	0.130	0.028	30.61	27.74	82.11	51.77

Table 4. Simple correlation coefficients among the 15 traits of *Eruca* spp. accessions

	LL	LPL	LPW	LPT	PH	PW	PWE	NL	SL	SW	SPL	SBL	NSS	SWE
LW	0.423**													
LPL	0.393**	-0.149												
LPW	0.410**	-0.022	0.365**											
LPT	0.346**	0.234*	0.349**	0.551**										
PH	0.607**	0.366**	0.265*	0.244*	0.225*									
PW	0.330**	0.070	-0.272	-0.171	0.064	-0.217								
PWE	0.524**	0.233*	0.492**	0.451**	0.352**	0.354**	-0.035							
NL	0.123	0.481**	-0.152	0.000	0.188	-0.037	0.595**	0.218						
SL	0.312**	0.215	0.148	0.317**	0.188	0.322**	-0.154	0.174	-0.029					
SW	0.307**	-0.028	0.482**	0.365**	0.200	0.483**	-0.469	0.298**	-0.395**	0.386**				
SPL	-0.069	-0.095	0.214	0.218	0.013	0.052	0.068	0.008	-0.098	0.326**	0.339**			
SBL	0.366**	-0.085	0.628**	0.504**	0.243*	0.339**	0.392**	0.392**	-0.250*	0.358**	0.765**	0.384**		
NSS	0.191	0.306**	0.133	0.098	0.000	0.237*	0.047	0.048	-0.015	0.387**	0.462**	-0.018	0.331**	
SWE	0.309**	0.018	0.375**	0.310**	0.216	0.407**	-0.484**	0.221	-0.082	0.204	0.656**	-0.079	0.504**	0.507**

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

Table 5. Genotypic and phenotypic correlation coefficients among 15 traits of *Eruca* spp. Accessions

Traits		LL	LPL	LPW	LPT	PH	PW	PWE	NL	SL	SW	SPL	SBL	NSS	SWE
LW	G <sup>†</sup>	0.423**													
	P	0.424**													
LPL	G	0.393**	-0.149**												
	P	0.405**	-0.159												
LPW	G	0.410**	-0.022	0.365**											
	P	0.476**	0.005	0.419**											
LPT	G	0.346**	0.234*	0.349**	0.551**										
	P	0.303**	0.275*	0.274*	0.505**										
PH	G	0.607**	0.366*	0.265*	0.244*	0.225*									
	P	0.622**	0.380**	0.302**	0.243*	0.125									
PW	G	-0.330**	0.070	-0.272*	-0.171	0.064	-0.218								
	P	0.310**	0.061	-0.238*	-0.204	0.049	-0.245*								
PWE	G	0.524**	0.233*	0.492**	0.451**	0.352**	0.354**	-0.035							
	P	0.506**	0.154	0.470**	0.577**	0.304**	0.358**	-0.025							
NL	G	0.123	0.481**	-0.152	0.000	0.188	-0.037	0.595**	0.218						
	P	0.089	0.489**	-0.204	-0.146	0.046	-0.038	0.561**	0.172						
SL	G	0.388**	0.215	0.148	0.317**	0.188	0.322**	-0.154	0.174	-0.029					
	P	0.299**	0.186	0.228*	0.291**	0.199	0.291**	-0.166	0.218	0.003					
SW	G	0.381**	-0.023	0.482**	0.365**	0.200	0.483**	-0.469**	0.298**	-0.395**	0.386**				
	P	0.292**	-0.031	0.515**	0.379**	0.160	0.455**	-0.481**	0.310*	-0.419**	0.352**				
SPL	G	-0.086**	-0.095	0.214	0.217	0.013	0.052	0.068	0.008	-0.098	0.326**	0.339**			
	P	0.156	-0.077	0.254*	0.000	0.034	-0.122	0.014	0.006	-0.121	0.202	0.309**			
SBL	G	0.001	-0.085	0.628**	0.504**	0.243**	0.339**	-0.408**	0.392**	-0.250*	0.358**	0.765**	0.384**		
	P	0.370**	-0.051	0.704**	0.390**	0.080	0.315**	-0.433**	0.435**	-0.346**	0.287**	0.785**	0.353*		
NSS	G	0.238**	0.306**	0.133	0.098	0.000	0.237*	-0.318**	0.047	-0.015	0.387**	0.462**	-0.018	0.331**	
	P	0.215	0.317**	0.127	0.128	0.027	0.245*	-0.357**	0.033	-0.047	0.353**	0.447**	0.052	0.360**	
SWE	G	0.384**	0.018	0.375**	0.310**	0.216	0.407**	-0.484**	0.223	-0.082	0.204	0.656**	-0.079	0.504**	0.507**
	P	0.313**	0.039	0.394**	0.296**	0.072	0.407**	-0.512**	0.238*	-0.145	0.172	0.665**	0.002	0.500**	0.499**

<sup>†</sup>G: genotypic correlation coefficient; P: phenotypic correlation coefficient. \*, \*\* Significant at 5% and 1% probability level, respectively

The knowledge of genetic variation and association between agronomic traits is regarded to support considerable help to maintain genetic improved to breeding programme. This will assist plant breeders in choosing which agronomic traits should be used in their breeding programme. In the programme, high range of variability, heritability, genetic advance and positive correlation coefficient among traits could be an excellent tool for improving or selection genotype (AKBAR *et al.*, 2003). Performance of the evaluated genotypically different individuals under similar environmental conditions across two year trial on 15 wide ranges of variation observed in evaluated agronomic traits and results allows a comprehensively understanding the some accessions observed good potential over others. This great variation might be responsible of the different genetic characteristics and physiological development of plant and this type of variation can be reported in several species. Numerous examples are available underline the presence of a great genetic variation for both qualitative and quantitative traits in rocket germplasm. DUHOON and KOPPAR (1998) stated that very range of phenotypic variation among native rocket population in India. CHANDEL and BHANDARI (1989) reported that



rocket exhibited rich genetic variation in plant type, branching pattern, pigmentation, fruit habit, pod size, shape and grain size and color. YADAVA *et al.* (1998) evaluated *E. sativa* accession and great variations were assessed in oil content and fatty acid composition. Variability was also pointed out by BOZOKALFA *et al.* (2009) in mineral concentration among wild (*Diplotaxis tenuifolia* L.) and cultivated rocket plant. Furthermore EGEEA-GILABERT *et al.* (2009) evaluated wild and cultivated *E. vesicaria* population and high variation reported for most of the agronomic and morphological traits. In the present study phenotypic coefficients of variation was higher than that of the genotypic coefficients of variation for all agronomic traits. The variation among genotypes for all examined traits showed promise for their improvements in agronomic traits through selection. Moreover AKBAR *et al.* (2003) reported high phenotypic variability for plant height in summer mustard.

Variability plays an important key role in plant breeding program and observed the limit of selection for different plant properties. STAINFIELD (1971) classify heritability in three groups, traits having heritability values higher than 0.50 describe high, between 0.50 to 0.20 referred medium and lower than 0.20 define low heritability. Regarding heritability accompanied by the genetic advance together for plant weight, silique width, seeds per silique, seed weight showed high heritability and high genetic advance. Leaf width, leaf length, petiole length, plant height and width, number of leaves, silique length showed high heritability with moderate genetic advance. *Eruca* genotype observed moderate heritability and genetic advance for petiole width, silique pedicel length and silique beak length. Furthermore petiole thickness showed low heritability and low genetic advance. The other investigated agronomic traits showed moderate to low values of heritability and genetic advance. In the breeding programme the high amount of heritability alone is not enough to make sufficient improved through selection and genetic advance should be accompanied (SHULKA *et al.*, 2006). The traits having high heritability with high genetic advance are considered under control of additive genes, whereas high heritability low genetic advance under control non-additive (dominant and/or epistatic) genes which limits the scope for improvement through selection (AKBAR *et al.*, 2003). *Eruca sativa* has been extensively cultivated in Asia for several purposes and the species could be grown as an oil crop in some countries such as Canada (WARWICK *et al.*, 2007). In the present study plant weight, seeds per silique, seed weight, and silique width showed very high heritability and genetic advance. These characters can be improved efficiently by individual selection or breeding strategies in the examined population. AKBAR *et al.* (2003) reported high genetic advance in seed yield, plant height, seed weight, and indicate number of silique and seed yield could be useful in improving seed yield.

Correlation between agronomic traits are useful tools to determine whether selection for one trait will effect on another and highly heritable traits can be correlated to a more complex trait in selection process (NAIR *et al.*, 2004). Correlation coefficient reported in many researchers for several species including Brassicaceae family. KHAN *et al.* (2006) in *Brassica napus* L. reported that seed per silique was highly significant and positive correlation with silique length at

genotypic level, these findings supported present result. CHOWDHURY *et al.* (1987) indicate that siliqua length had positive and significant correlation with seed yield which is related number of seed per siliqua. Seed per siliqua showed positive correlation with seed weight and non significant relationship find on seed weight with siliqua length at genotypic and phenotypic level in examined collections. Number of seeds per siliqua was positive and highly correlated with seed weight both at phenotypic and genotypic level. Present outcomes are similar to that obtained by KHAN *et al.* (2006) who reported that genotypic correlation coefficients were higher than their phenotypic correlation coefficients for all traits such as plant height, and seeds per siliqua, siliqua length, seed yield in *Brassica napus* L. except seed weight. Correlation among the investigated agronomic traits demonstrated that it is possible to simultaneously improve seed and leaf yield of *Eruca* spp.

FALCONER (1989) argue that heritability is a property of a character only for the population and estimation of variability depends on magnitude of all the variance components, and in any one of these will affect heritability. Estimation of genetic parameters such as heritability, genetic variation and genetic correlation are fundamental role in to predict gains (DA SILVA *et al.*, 2008). Variability alone is not sufficient in determining the heritable portion of variation and heritability has important place in plant breeding and can be adequate to assess the degree to which a character may be transmitted from parents to offspring (SHUKLA *et al.*, 2006). Moreover heritability it is not enough to make sufficient improvement thought selection generally in advance generations unless accompanied by substantial amount of genetic advance (JOHNSON *et al.*, 1955). In the present study broad sense heritability exceeded 65% for all characters moderate to high genetic advance for some traits indicate that improvement or selection could be made basis on this characters. Particularly plant weight, siliqua width, seed per siliqua and seed weight could be useful character in improved *Eruca* spp. breeding programme.

*Eruca* spp. not only vegetable it's also oil crop and well adapted to diverse environmental condition. *Eruca* has generated increased interest among researcher and farmers, and also variety selection have undergone. The present research revealed that there is genetic variability for the various agronomic traits among *Eruca* spp. genotypes and showed effectiveness of different agronomic traits on *Eruca* genotypes for further breeding.

Received January 26<sup>th</sup>, 2010

Accepted December 6<sup>th</sup>, 2010

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### UTVRĐIVANJE GENETIČKE VARIJABILNOSTI I ISPITIVANJE KVANTATIVNIH OSOBINA SLAČICE (*Eruca spp.*)

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#### I z v o d

Uprkos porastu ekonomskog značaja postoje ograničene informacije o genetičkoj varijabilnosti agronomski značajnih osobina slačice, *Eruca spp.* Zbog toga su ispitivanja naslednog karaktera različitih osobina značajna za uspešne programe oplemenjivanja slačice. Predmet ovih ispitivanja je varijabilnost fenotipa i genotipa, način nasleđivanja, genetička dobit kao i fenotipske i genotipske korelacije agronomskih osobina. Magnituda koeficijenta variranja fenotipa za sve ispitivane osobine je veća od odgovarajuće vrednosti opšte naslednosti i prelazi 65 % za sve ispitivane osobine. Koeficijent fenotipske varijabilnosti (Phenotypic Coefficient of variability – PCV) varira od 7,60 do 34,34 % a genotipski (GCV) varira od 5,58 % za debljinu latica cveta do 34,34 za visinu biljke. Dobijeni rezultati ukazuju da težina biljke, širina osnove omotača semena, broj semenki po cvetu kao i težina semena mogu da budu korisne osobine za unapređenje programa oplemenjivanja slačice, *Eruca spp.*

Primljeno 26. I. 2010.

Odobreno 06. XII. 2010.