Multivariate Analysis of Genetic Variation in Winter Rapeseed (Brassica napus L.) Cultivars

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ABSTRACT

Designing breeding programs for winter rapeseed (Brassica napus L.) cultivars with improved seed and oil yields requires information about the genetic variability of traits. In this study, 28 winter rapeseed cultivars were evaluated for genetic variation and relationships between 11 agro-morphological characters during 2010 and 2011. Cultivars and cultivar × year interaction showed significant variation for all studied traits. Genotypic coefficients of variation indicated that yield, number of branches per plant, and plant height had the highest variation. Broad sense heritability estimates ranged from 6% to 87% for seed yield and pod length, respectively. Positive correlation was found between seed yield with number of pods per plant, number of branches per plant, days to flowering, and days to ripening. The result of factor analysis showed three independent factors that explained 71% of the total variability, which were named 'productivity', 'phenology and oil', and 'pod length', respectively. According to the first factor, RGS003, Opera, and Hayola were identified as high seed yielding cultivars. Based on all three factors, Lilian, Licord, and Ella were identified as the best cultivars concerning seed yield and oil content.

Keyword: Diversity, Factor analysis, Genetic variability, Selection.

INTRODUCTION

Oilseed rape (Brassica napus L.) is the second most important oilseed crop in the international oilseed market following soybean (Hasan et al., 2006). 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). Breeders have aimed to produce high yield and high quality cultivars and increase rapeseed production efficiency. Evaluation of genetic diversity wild and cultivated populations can be used for conservation of genetic resources, identification of suitable parents for crosses, broadening of the genetic base, and practical applications in breeding (Kresovich *et al.*, 1992; Diers and Osborn, 1994; Hallden *et al.*, 1994; Cruz *et al.*, 2007).

There are various techniques available for evaluation of crop genetic variability, including morphological, bio-chemical, and molecular markers (Hu et al., 2003; Beigi et al., 2011). However, morphological traits are the first to be used in the classification and evaluation of the germplasm (Smith and Smith, 1989; Smith et al., 1991). Also, basic information such as magnitude and pattern of genetic and phenotypic variability and heritability of yield related traits, and the relationship between these traits would facilitate improvement of varieties and helps to select a suitable breeding procedure. Seed yield and oil content are quantitative traits,

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whose expression is highly affected by plant genotype, environment, and their interaction (Diepenbrock, 2000; Engqvist and Becker, 1993; Gunasekera et al., 2006). 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 (Hristov et al., 2009). The estimation of heritability of traits is needed for an efficient breeding strategy because heritability represents the ratio between genotypic and phenotypic variance and is used to estimate selection gain (Johnson et al., 1955; Seidler-Łożykowska et al., 2010). Correlations whether between traits indicate selection for one trait has an effect on another. In order to exclude environmental effect, genetic correlations should be calculated instead of phenotypic ones (Engqvist and Becker, 1993). Path coefficient analysis has an advantage over simple correlation coefficient because it allows partitioning of the correlation coefficient into its components (direct and indirect effects) (Dewey and Lu, 1959). Factor analysis is a multivariate statistical method used to summarize the variation observed variables through among number of unobserved variables called factors (Johnson and Wichern, 2007).

Genetic variations, broad heritability, and genetic progress parameters have been evaluated in rapeseed by Naazar et al. (2003) and Akbar et al. (2007). Also, some studies were carried out to determine traits related to seed yield which could be used as selection criteria (Olsson, 1960; Thurling, 1974; Engqvist and Becker, 1993; Jeromela et al., 2007 and 2008). Choudhary and Joshi (2001) evaluated genetic variation of some genotypes derivatives of Brassica inter-specific hybrids and found high genetic diversity for days to flowering, plant height, number of branch per plant, and 1000-seed weight. In a study, days to flowering and oil percent had the highest heritability while pods number per plant and defoliation had the least heritability (Khan et al., 2000).

Genetic variation and relationship among 63 oilseed canola accessions was carried out by Hu *et al.* (2007) for nine important agronomical traits using cluster analysis. Results indicated that European accessions could be separated from China's. Thurling (1974) reported a significant correlation between number of pods per plant and seed yield in *B. napus* and *B. Campestris*.

Canola is an important oil seed crop which is highly cultivated in Iran during the last decades (Bybordi and Tabatabaei, 2009). However little is known about the genetic diversity of cultivated varieties and hybrids in Iran. This study was conducted to investigate the genetic variation of yield, oil, and agro-morphological traits of 28 canola varieties in Iran, to study the relationship among traits, to estimate heritability of traits, and to identify superior cultivars.

MATERIALS AND METHODS

Experimental Site, Cultivation Practices, and Data Collected

The experiment was conducted at the Isfahan University of Technology Research Farm, located at Lavark Najafabad, Iran (40 km south-west of Isfahan, 32° 32′ N and 51° 23' E, 1630 m asl), in 2010-2011. This location has a Typic Haplargid clay loam soil (pH = 7.5). The mean annual precipitation and temperature are 140 mm and 15 °C, respectively. Summers are dry and there is usually no rain from the end of May to mid-October. The plant material of this study was 28 winter rapeseed cultivars, which were obtained from Seed and Plant Improvement Institute, Iran (Table 1). The cultivars were sown in the field according to a randomized complete block design with four replications in September 2010 and 2011. Each plot contained six rows of three meter long, 30 cm apart with 10 cm plant spacing. General crop production operations included broadcasting urea and phosphate fertilizers prior to planting, weed control (hand weeding), and chemical control of

Table 1. Name and origin of the studied winter rapeseed cultivars.

Num.	Cultivar	Origin	Num.	Cultivar	Origin
1	Anatol	France	15	NK Bravour	France
2	Billy	France	16	NK Fair	France
3	Eldo	France	17	Oase	France
4	Ella	France	18	Okapi	France
5	ES Astrid	France	19	Olphi	France
6	ES Betty	France	20	Olpop	France
7	ES Saphir	France	21	Opera	Sweden
8	ESC 6152	Russia	22	RPC 2023	France
9	GK Helena	Hungary	23	SM046	Germany
10	GKH 1103	Hungary	24	Smart	France
11	GKH 305	Hungary	25	Talaye	Germany
12	Lilian	France	26	RGS003	Germany
13	Lioness	France	27	Hayola 041	Canada
14	Modena	Danmark	28	Licord	Hungary

rapeseed aphid (*Rhopalosiphum pseudobrassica*). During the growth stage, agro-morphological traits including days to flowering, days to ripening, plant height, number of branches per plant, number of pods per main stem, pod length, 1000-seed weight, number of seeds per pod, seed yield per plant, and oil content were measured. The measurements were done using 20 randomly selected plants per plot. Percent oil content was determined using a NIR machine (Perten Instrument, Inframtic 8600 model).

Statistical Analysis

Analysis of variance was carried out to differences examine between years, cultivars, and their interaction and also to estimate the variance components, using the general linear model (GLM) of SAS (SAS Institute, 2002). The means comparisons were conducted using least significant Broad-sense difference (LSD) test. heritability (h²) was estimated for all agromorphological traits (Hallauer and Miranda, 1988).

Genotypic coefficient of variation (GCV) was calculated for each trait. Simple correlation coefficients between seed yield and its components were estimated to determine the association between traits.

Pearson's correlation coefficient between agro-morphological traits was estimated by SAS software. To test the significance of correlation coefficients we applied T-test. The genetic correlations between traits were estimated from the variance and covariance components using SAS software.

Stepwise multiple linear regressions were achieved for determination of the best model accounting for the majority of total seed yield variability. Plant traits were used as independent variables and seed yield as the dependent variable. After the first independent variable was added to the model, stepwise regression added those variables that were not auto correlated but could significantly improve the model.

Variables that did not produce an F statistic at p < 0.05 level were dropped. Path coefficient analysis was conducted on the basis of yield (cause) on seed yield (effect) to estimate direct and indirect effects of components of seed yield (Montgomery, 2006). Factor analysis was carried out using SPSS (SPSS Inc, 2001) packages and the 3D-plot was drawn using StatGraphics.

RESULTS

Analysis of variance for the measured traits showed significant effect (p<0.01) among the cultivars. The interaction effect



of genotype \times year was significant for all the measured traits. The year effect was not significant (p<0.05) for all traits, except for the number of branches per plant (Table 2).

To compare the variation among various traits, descriptive statistics (mean values and range), genetic coefficient of variation (GCV), and broad sense heritability (h²) are given in Table 3. The highest genotypic coefficient of variation (GCV) was observed for plant height (11.46%) and number of branches per plant (11.43%) in 2010, while the highest GCV was observed for seed yield (30.49%) and number of branches per plant (16.52%) in 2011. There were slight differences between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for some morphological traits indicating the negligible effect of environment. Broad sense heritability (h²) estimates ranged from 6% to 87% for measured traits. The highest values of h² were observed for pod length (87%) followed by plant height (47%) and number of seeds per pod (36%), while the lowest values were found for the seed yield (6%), number of pods per plant (12%), and pods per main stem (11%).

Means comparison for the measured traits over years are shown in Table 4. Cultivars had considerable variation in flowering and ripening time. Values for days to flowering ranged from 179 to 190 in 2010 and from 180 to 210 in 2011. Among the studied cultivars, Anatol, ES Astrid, Opera, ES Saphir and Lilian in 2010 and Okapi, Lilian, Ella and SLM046 in 2011 were identified as floweringcultivars. Cultivars late RGS003, Olphi, Oase and ES Betty in 2010 and Olphi, Oase, ES Betty, and GKH 1103 in 2011 had the lowest values for days to flowering. The cultivars NK Fair, Oase, and Smart in 2010 and RGS003, Hayola, SLM046 and Oase in 2011 had the highest seed yield. The lowest seed yield belonged to cultivars GK Helena and RPC 2023 in both years. The highest number of pods per plant was observed for cultivar Lioness, SLM046, Oase and Hayola in 2010. In 2011 cultivars Hayola, RGS003, NK Fair and

Lioness had the highest number of pods per plant. These results showed that cultivars with higher number of pod per plant had higher seed production.

Cultivars ES Betty, Anatol, ESC 6152, and GK Helena in 2010 and Hayola, RGS003, Opera, and Modena in 2011 had the highest value for number of branches per plant. Number of seeds per pod ranged from 15.3 to 22.3 in 2010 and from 4.8 to 28.8 in 2011 (Table 2). The highest number of seeds per pod was observed for cultivars Olpop, Billy, Talaye, and Modena in both years. Also, cultivars ES Betty, RPC 2023, NK Bravour and GK Helena in 2010 and Okapi, Modena, Lilian, and ES Betty in 2011 had the highest value of oil content. The highest value for 1000-seed weight belonged to cultivars NK Bravour, ES Betty, ES Astrid and Ella in 2010 and cultivars SLM046, Okapi, Ella, and Eldo in 2011.

Pearson's and genotypic correlation coefficients of studied variables presented in Table 5. In most instances, there was a close agreement between genotypic and phenotypic correlations. Strong significant and positive correlations were found between seed yield with days to flowering, days to repining, number of branches per plant and number of pods per whereas significantly correlations were observed with pods per main stem, plant height and number of seeds per pod. Number of pods per plant had positive correlation with days to flowering and number of branches per plant. There were negative and low genetic correlations between pod length and 1000-seed weight. There was no significant correlation between oil content and seed yield. However, oil content had positive and significant correlation with days to ripening.

Result of stepwise regression (Table 6) showed that the number of pods per plant, number of seeds per pod, 1000-seed weight and plant height explained more than 87% of the total variation of seed yield. The number of pods per plant was the most important component of seed yield (Partial R²=72%).

Table 2. Mean squares for agro-morphological traits of 28 Brassica napus cultivars during 2010-2011.

OIL^{κ}	5.33 ^{n.s}	8.84	0.29	.0.79**	6.29	5.56
	60.94 ^{n.s}					
SP'	13.28 ^{n.s}	32.12	19.95^{**}	12.83^{**}	5.92	15.21
$^{\prime\prime}$ ASM $^{\prime\prime}$	0.06 ^{n.s}	0.24	0.51^{**}	0.40^{**}	0.04	6.04
PL^g	$0.01^{\rm n.s}$	0.04	0.53^{**}	0.11^{**}	0.04	6.04
PMS^{J}	128.66 ^{n.s}	23.03	73.69^{**}	65.47^{**}	10.52	9.61
PP^{ℓ}	712.46 ^{n.s}	1653.64	1534.58**	1096.15^{**}	177.82	11.65
\mathbf{B}^{d}	13.28^*	1.28	5.77**	4.71	0.65	12.13
\mathbf{H}_c	556.51 ^{n.s}	219.91	506.55**	268.40**	49.06	6.7
$DR^{ b}$	33.96 ^{n.s}	86.79	57.84**	39.47**	3.70	0.76
DF^{a}	ı	59.63	123.42^{**}	95.28^{**}	5.93	1.29
ф	1	9	27	27	78	
Sources	Year	Block(Year)	Cultivar	Cultivar×Year	Error	CV%

^a days to flowering, ^b days to ripening, ^c plant height, ^d number of branches per plant, ^e number of pods per plant, ^f number of pods in main stem, ^g pod length, ^h 1000-seed weight, ⁱ number of seeds per pod, ^j seed yield and, ^k oil content. ns=non-significant, * and **significant at P < 0.05 and P < 0.01, respectively.

Table 3. Mean values, genotypic coefficients of variation (GCV) and broad-sense heritability (h^2) of traits evaluated on 28 cultivars of winter rapeseed during 2010 and 2011.

Parameter	Range (N	fin-Max)	Mean	ın	CC	V(%)	h^2 (%)
	2010	2011	2010	2011	2010	2011	2010-2011
Days to flowering	179-190	180-210.2	184.36	194.44	1.39	3.22	22.81
Days to ripening	232-256	244-262.6	248.78	251.62	1.70	1.12	31.77
Plant height (cm)	89-145	59.1-135	110.48	95.23	11.46	60.9	47.02
Number of branches per plant	4.7-7.3	4.6-15.5	5.80	7.96	11.43	16.52	18.05
Number of pods per plant	85-125	90-303.93	105.04	273.13	8.63	8.47	11.76
Pods per main stem	30.8-44.8	14.8-43.9	37.15	28.53	8.88	13.70	11.16
Pod length (cm)	4.8-6.7	4.8-6.7	5.52	5.48	7.46	3.16	87.50
1000-seed weight (g)	2.6-4.3	2.6-4.8	3.51	3.65	8.05	10.78	14.28
Number of seeds per pod	15.3-22.3	4.8-28.8	17.39	13.86	5.92	16.31	35.64
Seed yield (g/plant)	5.6-7.42	5.6-17.2	6.33	12.17	4.46	30.49	5.95
Oil content (%)	41.1-48.1	35.2-59.2	45.12	44.89	3.89	80.9	31.41

JAST

Table 4. Means comparison of agro-morphological traits for 28 cultivars of winter rapeseed evaluated in 2010 and 2011.

	Days to	s to	Day	vs to	Num.	m.	Num. pods	spod	1000-seed	seed	Num. seeds	seeds	Seed yield	yield	Oil content (%)	nt (%)
Cultivar	flowering	ering	ripe	ripening	branches	ches	per plant	lant	weight	ght	per pod	poc	(per plant)	lant)		
	2010	2011	2010	2011	2010 20	2011	2010	2011	2010	2011	2010	2011	2010	2011	2010	2011
Anatol	187.6	188.0	251.6	250.0	6.9	7.2	104.0	104.4	3.5	3.6	16.9	16.2	6.3	6.2	45.5	45.1
Billy	186.3	186.0	250.6	251.0	5.1	5.1	100.0	96	3.4	3.4	19.2	19.5	6.4	6.3	46.2	46.1
Eldo	186.3	185.0	252.0	251.0	5.9	5.5	107.6	95	3.6	4.2	16.2	16.1	6.3	6.3	46.3	46.1
Ella	184.0	206.0	248.0	254.2	5.4	7.6	9.66	117	3.8	4.2	17.4	8.7	6.4	6.4	46.1	43.8
ES Astrid	187.6	188.0	254.6	255.0	5.0	5.1	9.66	100	3.8	3.8	17.2	17.2	6.3	6.3	45.3	45.3
ES Betty	181.0	180.0	248.3	253.0	7.0	7.3	9.96	95	3.9	3.9	16.8	16.9	6.2	6.1	47.7	47.4
ES Saphir	187.0	187.0	249.6	249.0	5.3	5.5	104.0	115	3.6	3.3	17.2	16.9	6.3	6.3	45.9	46.1
ESC 6152	184.0	185.0	250.6	250.0	8.9	6.9	106.6	108	3.2	3.1	18.3	17.9	6.3	6.3	44.5	44.4
GK Helena	189.0	189.0	254.0	253.0	6.7	9.9	92.6	95	3.2	3.2	18.2	17.9	5.9	5.9	47.2	47.2
GKH 1103	182.0	180.0	246.0	246.0	5.5	5.3	102.6	66	3.5	3.7	17.1	16.8	6.3	6.3	44.9	45.1
GKH 305	184.3	183.0	252.3	252.0	6.3	6.3	103.0	66	3.6	3.8	17.1	16.8	6.4	6.3	46.0	46.1
Lilian	187.0	206.3	245.0	253.0	5.4	6.7	120.0	115	3.1	3.1	16.5	14.3	6.3	6.5	46.1	49.2
Lioness	182.0	182.0	245.0	245.0	5.3	5.3	123.0	123	3.1	3.1	16.0	16.0	6.3	6.3	44.1	44.1
Modena	185.3	204.8	249.0	257.3	9.9	8.5	102.6	104	3.2	3.2	18.6	18.6	6.3	7.0	46.6	49.6
NK Bravour	183.0	183.0	253.3	252.0	0.9	5.8	97.3	101	4.0	3.8	16.4	16.2	6.3	6.3	47.3	47.1
NK Fair	182.3	182.0	248.3	247.0	5.0	4.9	117.0	124	3.2	2.8	18.8	18.1	7.1	8.9	42.1	42.1
Oase	180.6	180.0	243.3	244.0	5.6	5.7	119.0	115	3.7	3.7	16.7	16.8	7.1	7.0	45.0	44.1
Okapi	185.0	207.8	253.3	257.1	5.4	6.7	99.3	110	3.7	4.4	17.1	9.3	6.1	6.1	44.0	56.2
Olphi	180.6	180.0	250.0	248.0	5.3	5.3	93.6	06	3.9	3.9	16.4	16.1	6.1	5.9	46.6	46.1
Olpop	182.3	182.0	249.6	248.0	5.9	6.1	105.0	104	3.0	5.6	20.2	22.3	6.3	6.2	43.1	43.1
Opera	187.6	190.2	255.6	248.8	6.2	11.2	92.0	119	3.7	3.0	17.5	8.58	0.9	8.9	42.9	44.7
RPC 2023	188.0	189.0	248.3	250.0	9.6	5.7	106.3	108	3.3	3.1	15.8	16.1	9.9	9.6	47.4	47.1
SLM046	183.3	205.3	247.6	254.0	9.9	8.4	121.6	113	2.8	4.8	17.0	16.0	0.9	7.4	46.3	38.7
Smart	186.0	185.0	246.0	244.0	5.3	5.3	113.6	119	3.3	3.3	17.5	16.5	9.9	9.9	43.3	43.1
Talaye	185.0	185.0	246.3	245.0	5.0	5.4	87.0	06	3.7	3.5	18.9	19.3	6.1	0.9	42.1	42.1
RGS003	179.6	189.8	234.0	249.0	9.9	10.6	113.0	123	3.5	2.8	15.7	8.2	6.3	10.0	42.1	36.0
Hayola	182.0	185.4	247.0	247.8	4.8	11.4	117.6	131	2.9	3.9	18.3	12.6	6.3	8.0	42.1	45.4
Licord	183.0	202.9	246.0	254.8	5.0	8.4	93.3	112	3.8	3.8	17.3	11.5	0.9	6.4	45.6	39.1
Mean	184.3	189.1	248.7	250.3	5.8	6.85	105.0	114.6	3.4	3.5	17.3	15.6	6.3	6.5	45.1	45.1
LSD 5 %	1.31	6.15	2.48	3.80	0.43	2.03	10.39	39.44	0.42	0.03	1.01	8.13	0.17	0.58	99.0	6.52

Table 5. Phenotypic (above diagonal) and genotyping (below diagonal) correlation coefficients of winter rapeseed cultivars for agro-morphological traits.

	DF a	DR^{b}	H^{c}	\mathbf{B}^{d}	PP ^e	PMS^f	PL^g	TSW h	SP i	\mathbf{Y}^{j}	OIL^k
	DI		**		**					- 44	
DF	1	0.71**	-0.53**	0.32	0.53**	-0.56**	0.13	0.29	-0.48*	0.70^{**}	0.15
DR	0.92	1	-0.20	0.19	0.21	-0.41*	-0.03	0.39^{*}	-0.24	0.40^{*}	0.37^{*}
Н	-0.24	-0.20	1	-0.53**	-0.69**	0.57^{**}	0.10	-0.08	0.68^{**}	-0.60**	0.05
В	-0.14	0.01	-0.72	1	0.89^{**}	-0.77**	-0.01	0.05	-0.60**	0.77^{**}	-0.20
PP	0.26	0.32	-0.91	0.86	1	-0.83**	0.03	0.10	-0.74**	0.85^{**}	-0.19
PMS	-0.27	-0.33	0.63	-0.81	-0.88	1	-0.05	-0.23	0.71^{**}	-0.69**	-0.02
PL	0.12	-0.03	0.32	-0.10	-0.07	0.10	1	-0.21	0.24	0.09	-0.21
TSW	0.42	0.40	0.04	-0.05	0.04	-0.07	-0.01	1	-0.24	0.28	0.15
SP	-0.16	-0.19	0.62	-0.35	-0.59	0.66	0.11	-0.17	1	-0.47*	0.05
Y	0.72	0.65	-0.66	0.63	0.78	-0.70	0.05	0.41	-0.19	1	-0.05
Oil	0.27	0.37	0.13	-0.40	-0.32	0.01	-0.36	0.03	0.23	-0.11	1

 $[^]a$ days to flowering, b days to ripening, c plant height, d number of branches per plant, e number of pods per plant, f number of pods in main stem, g pod length, h 1000-seed weight, i number of seeds per pod, j seed yield and, k oil content. ns=non-significant, * and ** significant at P < 0.05 and P < 0.01, respectively.

Table 6. Results of stepwise regression analysis for seed yield of 28 winter rapeseed cultivars.

Variable entered	Parameter Estimate	Partial R ²	Model R ²	F Value
Number of pod per plant	0.03	0.72	0.72	68.14**
Number of seeds per pod	0.73	0.05	0.78	6.49**
1000-seed weight	2.69	0.07	0.85	12.24**
Plant height	-0.05	0.01	0.87	$2.84^{\text{n.s}}$
Intercept	-12.82			

ns, * and **: non-significant, significant at p < 0.05 and p < 0.01, respectively.

Number of seeds per pod and 1000-seed weight justified 12% of seed yield variation. The correlation coefficients were partitioned into direct and indirect effects by path analysis (Table 7). Results showed that number of pods per plant (1.18), number of seeds per pod (0.47), and 1000-seed weight (0.27) had positive direct effect on seed yield.

Results of the factor analysis (Table 8) showed that three main factors accounted for 71% of the total variability. The first factor which explained 38% of total variation emphasized on the number of pods per plant, seed yield, and number of branches per plant and was named as the 'productivity factor'. The second factor, which explained 22% of total variation, included days to flowering, days to ripening, and oil content and was named the 'oil and phenological factor'. The third factor included only the pod length and explained 11% of variability. A 3-D graph

of factor scores based on the first three factors, generated from data studied, is presented in Figure 1. The graph identified superior genotypes based on three factors (productivity, oil and phonological traits and pod length). Cultivars Licord, Ella, and Lilian (labeled in Figure 1) had the highest value of all three factors. Cultivars RGS003, Opera, and Hayola 041 had the highest values of factor 1 (productivity) and cultivars Okapi and Modena had the highest values of factor 2 (oil and phenological).

DISCUSSION

Agricultural production is influenced by environmental conditions that generally lead to wide variations in yield between years (Akbarpour *et al.*, 2014). Highly significant (p<0.01) genotypic differences for all characters in both years indicates the



Table 7. Direct and indirect effects of seed yield components of winter rapeseed of the studied cultivars.

		I	ndirect effect via		
Traits	Direct effect	Number of pods	Number of	1000- seed	r
		per plant	seeds per pod	weight	
Number of pod per	1.18	-	-0.35	0.03	0.86
plant					
Number of seeds per	0.47	-0.87	-	-0.07	-0.47
pod					
1000-seed weight	0.27	0.12	-0.11	-	0.28

Residual= 0.35

Table 8. Factor loadings and Eigen-values in factors analysis of 11 agro-morphological traits in the winter rapeseed cultivars.

Traits	Factor 1	Factor 2	Factor 3
Days to flowering	0.423	0.743	0.248
Days to ripening	0.071	0.876	0.074
Plant height (cm)	-0.764	-0.256	0.057
Number of pods per plant	0.743	-0.295	-0.013
Number of seeds per pod	-0.798	-0.311	0.240
1000-seed weight	0.002	0.280	-0.334
Seed yield (per plant)	0.807	-0.289	0.011
Pod length (cm)	-0.094	-0.007	0.947
Pods per main stem	-0.706	-0.501	-0.125
Branches per plant	0.839	0.125	0.078
Oil content (%)	-0.373	0.573	-0.319
Eigen-value	4.19	2.37	1.23
Explaining proportion	38.13	21.58	11.23
Cumulative (%)	38.13	59.71	70.95

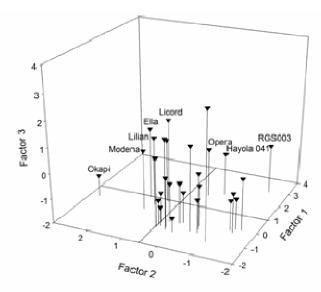


Figure 1. Three-dimensional graph of 28 winter rapeseed cultivars based on the three factors generated from factor analysis. The analysis was performed on 11 agro-morphological attributes. The first, second and third factors were considered as 'productivity', 'phenological factor' and 'pod length' respectively. The cultivars labeled in the figure had the highest score values for all of the three factors.

presence of sufficient genetic variability in the studied germplasm, which is useful for effective selection. In general, high GCV and PCV for a trait indicate the possibility of improvement through selective breeding. However, low difference between these two coefficients will outcome more gain in breeding programs. These results are in agreement with Akbar et al. (2007) and Singh (2004) who state that the highest genotypic coefficient of variation (GCV) was observed for seed yield, number of pod per plant, number of branches per plant and 1000-seed weight. Heritability estimates provide an indication of the potential genetic variation available in a population. High broad sense heritability was observed for pod length, plant height, and number of seeds per pod, in agreement with other researches (Singh, 2004; Kumar and Misra, 2007). Low heritability estimates were obtained for seed yield, pods per main stem, and number of pods per plant indicating that these traits were strongly influenced by environment. High heritability for seed yield-related traits such as pod length, number of seeds per pod, number of pods per plant, number of branches per plant, and 1000-seed weight indicating that selection for these traits may be effective for indirect improvement of seed yield. Blum (2011) reported that indirect selection via yield components and other traits could be more efficient than direct selection if yield components and other traits have a higher heritability.

Evaluation of relationships between pairs of traits is necessary for deciding upon the most appropriate selection criteria in breeding programs. Therefore, determining the relationship between yield and its components could lead to effective criteria for indirect selection. Correlation coefficient is an important statistical parameter to determine the relationship among variables (Johnson and Wichern, 2007; Kozak *et al.*, 2010). Results of correlation coefficients indicated that seed yield had positive correlation with number of pods per plant, number of branches per plant, days to

flowering, and days to ripening. These results are in conformity with the findings of Ohlsson (1972) who stated that there was a big correlation between number of pods per plant and grain yield. Many researchers found positive correlations between pods per plant and seed yield in rapeseed (Özer and Oral, 1999; Khan et al., 2006; Jeromela et Most of the phenotypic al., 2007). correlations in this study were confirmed by genotypic correlations. Little differences between values of genetic and phenotypic correlations signify little environmental effects.

Although correlation coefficients estimate the type and magnitude of association of yield with other traits, they do not give clear information about the interrelationship between the causal and resultant variables. In this study, stepwise regression indicated that number of pods per plant, number of seeds per pod, and 1000-seed weight explained more than 87% of the total variation of seed yield. Results of path analysis showed that number of pods per plant had the highest direct effect on seed yield, followed by the number of seeds per pod and 1000-seed weight, which confirmed that these traits can be used as selection criteria to improve seed yield in the early generations. These strong direct effects may indicate that these traits were controlled by additive type of gene action (Aslam et al., 1992). Thurling (1974), Ozer and Oral (1999), Diepenbrock (2000), and Basalma (2008) reported that number of pods per plant and 1000-seed weight possessed strong direct effect on seed yield of rapeseed accessions. The number of pods per plant had indirectly negative effect on number of seeds per pod. This negative effect resulted in negative correlation of number of seeds per pod with seed yield. Number of pods per plant had negative indirect effect on seed yield through number of seeds per pod. Result of path analysis indicated that indirect selection would be better for increasing seed yield in rapeseed.

In this study, factor analysis revealed three factors which explained 71% of the



total variability, in agreement with the results of previous studies on canola and other crop plants (Mohamed, 1999; Leilah and Al-Khateb, 2005; Ashkani et al., 2007; Naderi and Emam, 2010). The first factor was considered as 'productivity' which emphasized on seed yield, number of pods per plant, and number of branches per plant. The second and third factors considered as the 'oil and phenological' and 'pod length' factors, respectively. The sign of the loading indicates the direction of the relationship between the factor and the variable. Thus, two variables with high magnitude of loading in the same factor would be expected to exhibit a high correlation (Seiler and Stafford, 1985). Thus, the traits may be influenced by the gene or genes and advantageous for suitable rapeseed genotypes screening. Selection of cultivars based on the first factor will increase seed yield while selection of cultivars based on the first two factors could introduce late flowering cultivars with high yield and oil content. This can be easier and more reliable selection based only on the seed yield. In other words, each factor can be utilized as a selection index. Wide distribution of accessions on 3-D graph (Figure 1) indicates high variation among cultivars. For example, cultivars Licord, Lilian, and Ella (labeled in Figure 1) had the highest value of all three factors and could be used as superior cultivars. Results indicated that factor analysis could be a rapid way to identify appropriate cultivars for different purposes. For example, suitable cultivars can be cultivated under specific conditions or be selected for crossing with other parents in order to conduct subsequent researches. Rameah (2012) states that scattering of genotypes based on factor analysis can be used as suitable method for grouping and classifying the genotypes.

In conclusion, results of this study show that large genetic variation exists in the rapeseed cultivars that are currently cultivated in Iran. Assessment of the relationship among the traits using different multivariate methods indicated that number of pods per plant, number of branches per plant, number of seeds per pod and 1000-seed weight can be used for constructing selection index to indirectly improve seed yield in rapeseed. Differentiating accessions using the factor analysis could be a rapid way to identify superior rapeseed cultivars for different purposes. In this study, cultivars Licord, Lilian, and Ella had the highest values of the three factors. The variation found in this study can be used to construct future breeding projects and to plan mapping populations for genome studies.

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تحلیل چند متغیره تنوع ژنتیکی در ارقام کلزا

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چکیده

طراحی برنامههای اصلاحی بهبود عملکرد دانه و روغن در ارقام پاییزه کلزا گلیزه از نظر (مانیزه کلزای پاییزه از نظر (مانیزه کلزای پاییزه از نظر اینزه اطلاعات درباره تنوع ژنتیکی صفات میباشد. در این مطالعه ۲۰۱۸ و موروبط بین صفات با استفاده از ۱۱ صفت مورفولوژیک و زراعی طی سالهای ۲۰۱۰ و تنوع ژنتیکی و روابط بین صفات با استفاده از ۱۱ صفت مورفولوژیک و زراعی طی سالهای ۲۰۱۱ مورد ارزیابی قرار گرفتند. اثر رقم و اثر متقابل رقم × سال تفاوت معنی داری را برای صفات مورد مطالعه نشان دادند. صفات عملکرد، تعداد شاخه فرعی و ارتفاع بو ته بیشترین ضریب تنوع ژنتیکی را به خود اختصاص دادند. وراثت پذیری عمومی از ۶ تا ۸۷ درصد برای عملکرد دانه و طول غلاف متغییر بود. بین صفت عملکرد دانه با صفات تعداد غلاف در بو ته، تعداد شاخه فرعی، روز تا گلدهی و روز تا رسیدگی همبستگی مثبت مشاهده شد. بر اساس نتایج همبستگی، رگرسیون مرحلهای و تجزیه علیت، صفات تعداد غلاف در بو ته، تعداد شاخه فرعی، تعداد دانه در غلاف و وزن هزار دانه به عنوان شاخص مناسب انتخاب در بهبود عملکرد شناسیی شدند. نتایج تجزیه به عامل نشان داد که سه عامل اول ۷۱ درصد از تغییرات کل را توجیه نمود که به ترتیب عامل تولید، فنولوژی وغن و طول غلاف نام گذاری شدند. بر اساس تجزیه به عامل ها ارقام RGS003 ، POpera به عنوان ارقام به عنوان ارقام پر تولید و ارقام الفام در وغن و عملکرد معرفی شدند. تجزیه خوشهای ارقام را در ۴ گروه دسته بندی نمود که با نتایج تجزیه به عامل ها تطابق بالا