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RESEARCH PAPER

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Multivariate analysis of important morphological traits in some rapeseed (*Brassica napus* L.) Genotypes

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Abstract

In order to determine traits relationship and genetic diversity in some commercial genotype in Canola based on morphological traits, an experiment was conducted with eight Canola varieties in a Randomized Complete Block Design (RCBD) with three replications in experimental field of Sari Agriculture and Natural Resources University of Iran. The correlation coefficients illustrated that there are a positive and highly significant genotypic character association between plant height and Percent of oil per plant (0.511),plant height and Percent of protein (0.840),seeds per siliqua and siliqua length (0.914), 1000-seed weight and Percent of oil (0.762). Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for high yield. Stepwise regression indicated that 85/37% total variation exists in these traits accounted by the traits 1000- seed weight and Percent of glucosinolate. Principal component analysis (PCA) and factor analysis were used for understanding the data structure and traits relationship. Results of principal component analysis of genotypes showed that first three factor represent 87.5 percent of variance. Cluster analysis based on agro morphological traits divided 8 accessions into 3 Clusters. PCA appears to be a useful technique to differentiate between cultivars/breeding lines for selection purposes.

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Introduction

Rapeseed (*Brassica napus* L.) is now the second most important source of vegetable oil in the world. Canola oil is also considered healthy for human nutrition due to its lowest content of saturated fatty acids among vegetable oils and moderate content of polyunsaturated fatty acids (Stamer *et al.*, 1999). Total demand for edible oil in Iran based on 13.5 each person consumption with 70 million population reaches to 945 thousand tons per year, giving a huge drain to the economy (yasari *et al.*, 2007).

Improvement of seed yield in canola (Brassica napus L.) has been the primary objective of canola breeders for many years. Average yield of rapeseed is very low compared to its genetic potential. Different statistical techniques have been used in modeling crops yield, including correlation, regression, path analysis, factor analysis, principal components and cluster analysis (Leilah et al., 2005). Assessment of relationship using correlation coefficient analyses help breeders to distinguish significant relation between traits. Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contributions to yield variables (Semahegn, 2011; Marjanovic, 2009). Correlation between traits for evaluation and planning on breeding programs is useful. In other words, when an evaluation is conducted on a trait, knowing its effects on the other traits is totally important. Also by knowing if correlation exists between important traits, interpretation on previous results would become easier and the basis for effective future plans would be provided. Also correlation between important and non-important traits provides plant breeding experts with a significant assistance in indirect selection of important traits, through nonimportant traits which their measurement is easier (Qulipor et al., 2004). Moreover Correlation coefficient, which is used as a standard of measuring linear relationship between two variables only has one mathematical interpretation, and does not refer to cause and effect relationships (Abozary, 2002). Step-wise regression can reduce effect of nonimportant traits in regression model, in this way traits accounted for considerable variations of dependent variable are determined (Agrama, 1996). Principal component analysis (PCA) and factor analysis were used for understanding the data structure and trait relations.

An study on 30 rapeseed varieties demonstrated that pods per plant have the highest correlation with seed yield (Khan *et al.*, 2006). A researcher reported that there is a positive and significant correlation between Plant height traits, grains per pod and 1000- grain weight with grain yield (Shirany rad, 1994). A positive and significant relation among oil yield and the traits seed yield, plant height and 1000-seed weight was reported.(Bagheri *et al.*, 2008). The objectives of the present study were to estimate the correlation coefficient of variation, relationship among associated traits for improving content oil in spring type of rapeseed cultivars and also classify the genotypes via factor analysis.

Materials and methods

Agricultural practices

This research was conducted in the agronomic year of 2012-2013, in Randomized Complete Block Design (CRBD) with three replications, in the experimental field of Sari Agriculture and Natural Resources University of Iran, (53°, 13' N longitude and 36°, 42' E latitude, 16 m above sea level). The plots consisted of four rows 5 m long and 30 cm apart. The distance between plants on each row was 5 cm resulting in approximately 400 plants per plot, which were sufficient for statistical analysis. Crop management factors like land preparation, crop rotation, fertilizer, and weed control were followed as recommended for local area. All the plant protection measures were adopted to make the crop free from insects. Pods per main raceme and pods per plant were recorded based on 10 randomly plants of each plot (Table 1).

Statistical analysis

The correlation coefficients between the traits were estimated and then factor analysis on the base of major factors analysis was done on the data. Principal component analysis and cluster analysis were performed (Sneath and Sokal, 1973) to classify the genotypes. Content oil measured using soxhlet method (Joshi *et al.*, 1998), content protein measured using Kjeldahl method. This method for the quantitative determination of nitrogen in chemical substances developed by Johan Kjeldahl in 1883, and content glucosinolate performed using spectrophotometer. Also Correlation, Eigen values, percent variance, variance and cumulative percentage share of each of the extracted factors, stepwise regression were calculated. All the analyses were performed using Excel 2013, Minitab software version 16.1. spss 16 and SAS version 9.1.

Traits Genotypes	Plants height (cm)	Pod length (cm)	Number of seeds in pod		Percent of protein		Percent of glucosinolate
Topas ARC185	141.6	4.25	15.25	1.9	35.58	5.6	0.29
Global ARC187	141	4.35	19.03	2.1	38.57	9.29	0.71
SW sailorARC188	144	4.38	20.96	2.5	37.25	6.99	0.06
Brita ARC189	150.6	5.3	21.5	4	35.73	12	0.04
Line ARC192	150	1.92	3.35	2.5	41.06	9.33	0.17
Star lightARC193	152	5.11	21.73	2.5	35.66	7.7	0.08
Omega ARC194	136.3	4.41	19	2.3	34.6	7.5	0.05
Hanna ARC199	122.6	4.91	20.13	2.3	26/3	7.3	0.07

Table 1. Mean of measured traits of the genotypes.

Results and discussions

Analysis of variance

Significant mean square of genotypes for the traits including plant height, pods per plant, seeds per pod

1000-seed weight, content oil, content protein and content glucosinolate indicating significant genetic variation for these traits (Table 2).

Table 2. Analysis of variance of traits in the genotypes.

protein of oil glucosinolate	1000- weigh	seeds in pod	Pod length (cm)	Plants height (cm)	df	S.O.V
605.98 89.44 2.37	8.5	773.72	23.84	1970.2	7	Tteatments
1.15 3.5 0.006	0.0	0.47	0.08	6.38	2	Replication
51.37 4.4 0.03	0.3	16.39	1.90	114.93	14	Error
5.2 6.63 18.12	6.6	6.13		2.01		CV
1.15 3.5 51.37 4.4	0.0 0.3 6.6	0.47 16.39 6.13	0.08 1.90	6.38 114.93 2.01	14	Replication Error

* and **: Significant at 5% and 1% probability levels, respectively.

Correlation analysis

Correlation studies were also great interest for plant breeders in determining the traits which are correlated with main breeding objectives. The genotypic and phenotypic correlations between the ten characters are also summarized (Table 3) at 1% and 5% significant level.

A positive and highly significant genotypic character association was found between plant height and Percent of oil per plant (0.511),plant height and Percent of protein (0.840),seeds per silique and silique length (0.914), 1000- seed weight and Percent of oil (0.762).

A positive and highly significant genotypic character association between silique per plant and yield per plant was also found by Tuncturk and Ciftci (2007). Highly positive correlation found between plant

	X _{1:} Plants height	X₂:Pod length	X ₃ : Number of seed in pod	X ₄ : 1000- seed weight	X ₅ : Percent of protein	X ₆ : Percent of oil	X ₇ : Percent of glucosinolate
X_1	1	-0.212	-0.222	0.381	**0.840	* 0.511	0.012
X_2		1	**0.914	0.309	-0.277	0.068	-0.197
X_3			1	0.206	200	0.058	-0.010
X_4				1	0.042	**0.762	-0.38
X_5					1	0.305	0.229
X6						1	0.046
X_7							1

Table 3. Correlation among the traits in the genotypes.

Principal Component Analysis

In order to, assess the diversity and grouping genotypes based on the characteristics and parameter was performed Principal Component Analysis. PCA shows that the first three traits correspond to the whole percentage of the variance in the dataset. The first three main PCAs are extracted from the complicated components, the total cumulative variance of these three factors amounted to 87.5% and these components had eigenvalues >1. The PCA grouped the estimated Canola variables into three main components which PCA1 accounted for about 37.236% of the variation; PCA2 for 33.26%; PCA3 17.038%. The first PCA was related to Plants height, Percent of protein and Percent of oil. Where as the second PCA was related to Pod length, Number of seed in pod 1000- seed weight; The third PCA contrasts variables that are related solely to Percent of glucosinolate (Table 4). Cluster analysis based on agro morphological traits divided 8 accessions into 3 Clusters(Fig 1).

On the basis of scattering of the genotypes based on their scores for three factors, the genotypes ARC189 and ARC192 were classified as the same group and all of these had high oil yield. PCA appears to be a useful technique to differentiate between cultivars/breeding lines for selection purposes. Scattering of genotypes based on their scores for related factors can be used as suitable method for grouping and classifying the genotypes for more important yield associated traits. **Table 4**. Factor analysis for 7 studied traits in canola cultivars.

	Component			
	PCA1	PCA2	PCA3	
Plants height	0.931	0.063	0.109	
Pod length	-0.381	0.847	0.296	
Number of seed in pod	-0.384	0.783	0.462	
1000- seed weight	0.499	0.759	-0.337	
Percent of protein	0.823	-0.175	0.363	
Percent of oil	0.715	0.508	-0.022	
Percent of glucosinolate	0.094	-0.361	0.797	
Eigen value	2.607	2.328	1.193	
Cumulative %	37.236	70.496	87.534	

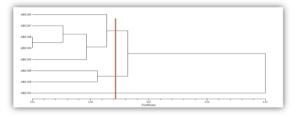


Fig. 1. Grouping and dendrogram based on UPGMA method in the genotypes.

Stepwise regression analysis

In Stepwise regression analysis, Percent of oil was considered as a dependent variable while other traits were considered as independent variables. All the traits were put into regression model and finally two traits of1000- seed weight and Percent of glucosinolate remained in the regression model. This model generally justified 85.37 percent of changes, related to the Percent of oil trait (Table 5).

Other traits which were studied did not have a significant influence on this model, therefore different varieties according to Percent of oil, are because of differences in the mentioned traits above. In a research project in stepwise regression analysis of traits of pod per plant verified 64% of coefficient, the number of grains per pod 67%, 1000- grain weight 72%, oil percentage78% and the number of nodes in stem verified 80% coefficient changes in regression model, which were related to Canola varieties comparison (Baradaran *et al.*, 2006). In regression model conducted by some researchers, in order to determine effective traits on bean yield, traits of 100 grain weight, total number of pods and the number of grains per pod were entered into the model (Rahnamaee *et al.*, 2007).

Table 5. The stepwise regression for oil yield(dependent variable) in the canola genotypes.

Variable added	The stepwise regression			
to model	1	2		
Constant	1.74028	-0.32452		
1000- seed weight	2.67418	3.23276		
glucosinolate		2.74626		
Coefficient R2 (%)	0.6833	0.8537		

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