

Selection of suitable genotypes based on physiological and morphological traits in rapeseed (*Brassica napus* L.)**Abstract**

Aims: Rapeseed (*Brassica napus* L.) as one of the most important oilseeds in the world, has a special role in cultivation and plant breeding research. Especially, the properties of rapeseed oil compounds, which have high oleic acid, antioxidant and positive effects on cholesterol, blood sugar control, blood pressure and cancer, make it one of the healthiest and most important edible oils in the world and an alternative to use Other vegetable oils have been introduced in recent years.

Study design: In order to conduct the experiment, a randomized complete block design was used in three replications.

Place and Duration of Study: This study was conducted in Varamin region in 2019-2020.

Methodology: Each experimental plot had 4 rows of cultivation at a distance of 50 cm. The seeds were planted at a distance of 10 cm from each other and all steps such as watering and weeding were done regularly and manually.

Results: The results of analysis of variance at the level of 0.01 indicated that the evaluated genotypes have significant differences in terms of all traits except the number of grains in the pod. In the means comparison of the traits of grain yield and oil percentage, which were selected as the most important traits, the Licord genotype was selected as the most favorable genotype. Based on the correlation analysis between the traits, the trait of grain yield had a positive and significant correlation with the traits of thousand grain weight, number of pods in the main stem, pod weight, days to flowering and oil percentage. Based on analysis of the main components, the first five components accounted for more than 74% of the variance of the total data. The drawn polygon diagram also identified Licord, Hyola-401, SLM046, Modena and Option 500 genotypes as desirable genotypes.

Conclusion: Non-invasive independent predictors for screening esophageal varices may decrease medical as well as financial burden, hence improving the management of cirrhotic patients. These predictors, however, need further work to validate reliability.

Keywords: rapeseed, correlation, PCA, oil percentage, graphical analysis

1. Introduction

The special characteristics of rapeseed and its adaptability to the climate conditions of most places have caused the cultivation of this plant to be intensively developed, therefore, it is important to choose the right cultivar for the success of the crop production. In this regard, performance comparison tests are used as one of the methods of selecting high yield varieties [1]. Evaluation of genotypes using a set of traits increases the probability of finding ideal genotypes [2]. The main goal of rapeseed research is to investigate the creation of diverse germplasm and achieve higher yields. Quantitative traits are affected by a large number of small alleles, which make it difficult to determine the number of chromosomal locations of alleles and the relative contribution of each allele to the expression and phenotypic distribution of a quantitative trait [3]. Seed yield is a complex trait determined by several traits that have positive or negative effects on the trait. It is important to examine the contribution of each trait in order to pay more attention to those that have the greatest impact on seed yield. Therefore, the information related to the relationship between traits and grain yield is of great importance for defining the selection criteria for rapeseed breeding in terms of yield. In general, correlation coefficients show the relationships between independent characteristics and the degree of linear relationship between these characteristics [4]. The use of appropriate statistical methods is a useful tool for the initial characterization and classification of genotypes, as it allows plant breeders to identify and select valuable genetic resources for direct

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use 25 farmers or for implementation in a breeding program to improve various plant traits [5]. Multivariate analysis is used to evaluate a large number of accessions for different traits in a germplasm pool. This analysis assigns 27 genotypes to qualitatively homogeneous groups based on response similarities and also helps classify genotypes [6]. The present study was conducted to investigate 7 canola cultivars using multivariate and graphical analyses. The purpose of this study is to investigate the relationship between grain yield and other traits and suggest the most suitable genotype(s) in terms of different morphological and physiological traits.

2. Materials and Methods

In order to investigate different rapeseed genotypes in terms of morphological and physiological traits and relationships between grain yield trait and other traits, an experiment was conducted in the form of a randomized complete block design (RCBD) in three replications. Each experimental plot had 4 rows of cultivation at a distance of 50 cm. The seeds were planted at a distance of 10 cm from each other and all steps such as watering and weeding were done regularly and manually. Sampling was done to remove marginal effects from the middle two rows. Table 1 shows the code and name of genotypes and traits studied in the experiment and Table 2 shows the properties of cultivated soil. Excel, SAS.V9 and Genstat.V12.1 software were used for analyses.

40 **Table 1. Code and name of genotypes and traits evaluated in the experiment**

Genotype code	Genotypes	Trait Code	Trait	Trait Code	Trait
G1	Sunday	YLD	Grain yield	DF	days to flowering
G2	Modena	NPM	Number of pods on the main stem	DM	days to maturity
G3	Option500	WTG	the weight of 1000 grain	NB	Number of branches
G4	Licord	PLH	Plant height	HI	Harvest Index
G5	Okapi	WP	Weight of pod	OP	oil percentages
G6	Hyola-401	LP	Length of pod		
G7	SLM046	NGP	Number of grains in a pod		

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Table 2. Characteristics of the soil used in the experiment

OC %	PH	Ec Ds/m	B ppm	Fe ppm	Sand %	Silt %	Clay %	P ppm	K ppm	N %
2.8	6.9	7.5	4.3	19.8	26	54	20	374	2850	0.28

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3. Results and Discussion

3.1 Analysis of variance and mean comparison

The results of analysis of variance showed that the effect of the block in the grain yield traits, the number of pods on the main stem, pod weight, days to maturity and the number of branches had a significant difference at the probability level of 0.01 and 0.05, and also the evaluated genotypes in terms of all traits, showed a significant difference except for the number of seeds in the pod trait. The highest coefficient of variation (CV%) was related to the trait number of branches (26.5) and the lowest was related to the trait oil percentage (3.15) (Table 3). Considering that the traits of seed yield and oil percentage are among the most widely used and important traits in rapeseed cultivation, the mean comparison analysis was done on these traits. Based on the average comparison of the grain yield trait (Figure 1-a), G6 and G4 genotypes were identified as favorable genotypes and G2 and G7 genotypes were identified as unfavorable genotypes. Also, in the comparison of averages on the trait of oil percentage (Figure 1-b), G4, G2 and G3 genotypes were identified as genotypes with high performance in this trait and G5 genotype was identified as an unfavorable genotype. Comparing these two

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graph 60 related to the traits, G4 genotype can be selected as the optimal genotype in terms of grain yield traits and 61 percentage (Figure 1).

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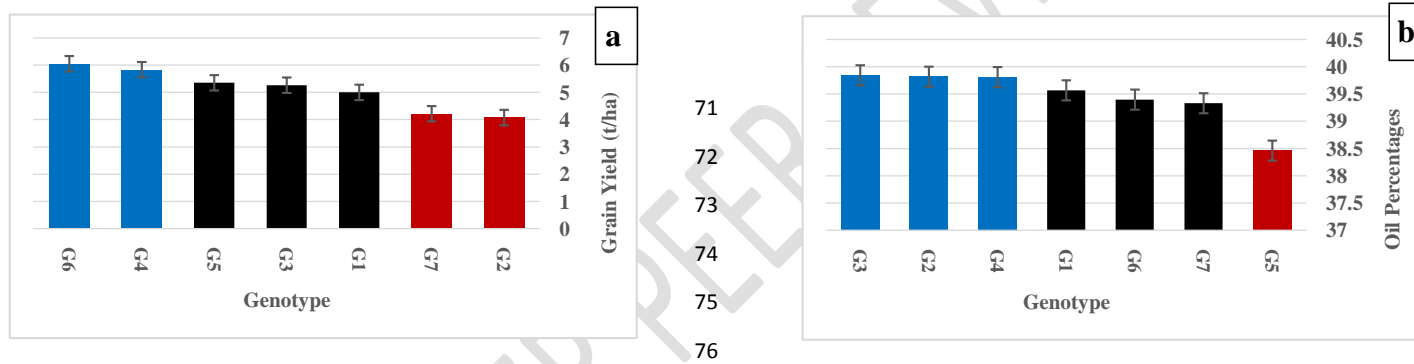
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Table 3. Variance analysis of traits evaluated in the experiment

S.O.V	df	YLD	NPM	WTG	PLH	WP	LP	NGP	DF	DM	NB	HI	OP
Block	2	26.8*	16010.8*	0.8 ^{ns}	175.7 ^{ns}	0.001*	5.2 ^{ns}	8.2 ^{ns}	198.5 ^{ns}	462.6*	69.7*	0.005 ^{ns}	0.06 ^{ns}
Genotype	6	1.68*	1133.6**	0.47*	41.4*	0.0006**	0.83*	11.8 ^{ns}	48.6*	93.7**	10.12*	0.002*	0.7*
Error	12	13.7	3493.6	0.6	145	0.0007	2.5	7.18	105.8	120.6	10.02	0.002	1.5
CV%	-	20.9	20.4	25.9	18.6	17.09	17.09	11.14	6.5	10.9	26.5	25.1	3.15

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**Figure 1. Means comparison of grain yield and oil percentage traits on evaluated 7 rapeseed genotypes, a: Means comparison on grain yield trait, b: Means comparison on oil percentage trait**

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3.2 Correlation and Principal Components Analysis

The results of the correlation analysis between the assessed traits indicated that the grain yield trait with the traits of thousand-grain weight, number of pods in the main stem, pod weight, days to flowering and oil percentage had a positive and significant correlation and with the traits of days to maturity and number of branches had a negative and significant correlation. The trait of number of pods in the main stem had a positive and significant correlation with the number of grain in the pod trait and a negative and significant correlation with the days to maturity trait. In the examination of the thousand grain weight trait, a positive and significant correlation was observed with the pod weight trait and a negative and significant correlation was observed with the days to flowering trait. Also, the trait of plant height showed a positive and significant correlation with traits of pod weight and days to maturity. Pod weight and pod length traits showed positive and significant correlation with days to maturity trait and day to flowering and day to maturity traits, respectively. The trait of number of grain in the pod also had a significant positive correlation with the trait of harvest index and the trait of days to maturity with the trait of the number of branches (Table 4). Jeromela et al. (2007) studied 30 rapeseed varieties and demonstrated that the number of pod/plant has maximum correlation with seed yield [7]. Khan et al. (2006) also reported, the positive significance between seed yield and plant height, number of branch/plant, number of pod/plant, number of seed/pod and pod length [8]. Based on principal component analysis (PCA) performed on the traits evaluated in the experiment, the five components accounted for more than 74% of the variance of the total variance. The first component covered 24%, the second component 20%, the third component 11%, the fourth component 9% and the fifth component 8% of the total variance of the data. 1000 grain weight, plant height, pod weight, pod length, number of grain per pod, days to maturity, number of branches and oil percentage had a positive effect on the first component. The most positive effect was related to the traits of days to maturity (0.41) and the number of branches (0.39). Also, all the traits, except the traits of weight of 1000 grains, plant height and the number of branches, had a positive effect on the second component, and among these traits, the harvest index (0.47) and the number of seeds in pods (0.43) traits were the most had a positive effect. In the examination of the traits affecting the third component, the traits number of pods per main stem, weight of 1000 grains, plant height, weight of pods, number of grain per pod and harvest index have a positive effect, and the traits weight of 1000 grain (0.45) and number grain in pods (0.45) had the most positive effect on this component. Grain yield traits, 1000 grain weight, pod weight, pod length, days to flowering and number of lateral branches also had a positive effect on the fourth component, among which, 1000 grain weight (0.54) and grain yield (0.39) traits had the most positive impact. In the investigation of the effects of traits on the fifth component, all traits except the traits of weight of 1000 grain, number of grain in a pod and percentage of oil have a positive effect, and the traits of plant height (0.41) and days to flowering (0.38) are the most had a positive effect on this component (Table 5). Different researchers also used the analysis of analysis into main components in order to select the best components [9].

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Table 4. Correlation analysis between the evaluated traits in the experiment of 7 canola genotypes

	YLD	NPM	WTG	PLH	WP	LP	NGP	DF	DM	NB	HI
NPM	0.3*										
WTG	0.3*	-0.3									
PLH	-0.2	-0.14	0.13								
WP	0.19*	-0.11	0.18*	0.16*							
LP	0.1	-0.3	-0.02	-0.06	0.33						
NGP	0.009	0.16*	0.14	0.13	0.33	0.21					
DF	0.51**	0.33	-0.46*	-0.22	-0.08	0.08*	0.04				
DM	-0.4*	-0.3*	-0.2	0.27*	0.37*	0.3*	0.18	-0.19			
NB	-0.41*	-0.36	0.22	0.1	0.22	0.35	-0.06	-0.26	0.3*		
HI	0.2	0.15	-0.18	-0.06	0.33	0.1	0.5**	0.24	0.2	-0.17	
OP	0.07*	-0.11	-0.13	-0.1	0.2	0.2	0.35	-0.17	0.3	-0.02	0.18

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Table 5. The eigenvalues and Principal Component Analysis (PCA) based on the traits evaluated in the experiment

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
YLD	-0.36	0.28	-0.12	0.39	0.06	0.43	0.03	-0.05	0.00	0.36	-0.10	0.54
NPM	-0.39	0.11	0.23	-0.19	0.01	-0.13	0.67	0.29	-0.27	-0.15	0.29	0.12
WTG	0.25	-0.22	0.45	0.54	-0.06	-0.11	-0.12	0.09	0.14	-0.25	0.41	0.34
PLH	0.22	-0.06	0.33	-0.33	0.41	0.58	-0.14	0.34	-0.01	0.20	0.20	-0.08
WP	0.24	0.36	0.15	0.31	0.23	0.30	0.41	-0.36	0.09	-0.31	-0.13	-0.36
LP	0.25	0.31	-0.40	0.30	0.09	-0.05	-0.17	0.40	-0.59	-0.10	0.16	-0.12
NGP	0.10	0.43	0.45	-0.01	-0.13	-0.23	-0.11	0.41	0.09	0.03	-0.58	0.08
DF	-0.36	0.25	-0.24	0.01	0.38	-0.12	-0.21	0.27	0.57	-0.34	0.18	-0.08
DM	0.41	0.23	-0.20	-0.44	0.08	-0.01	0.04	-0.19	0.01	-0.34	0.01	0.62
NB	0.39	-0.08	-0.23	0.12	0.27	-0.33	0.44	0.18	0.31	0.51	0.02	0.05
HI	-0.04	0.47	0.27	-0.11	0.14	-0.34	-0.24	-0.42	-0.11	0.37	0.41	-0.08
OP	0.16	0.31	-0.13	-0.09	-0.71	0.25	0.09	0.15	0.33	0.10	0.35	-0.14
Eigenvalue	2.93	2.41	1.41	1.15	1.05	0.8	0.65	0.62	0.34	0.32	0.13	0.08
Proportion	0.24	0.2	0.11	0.09	0.08	0.07	0.054	0.051	0.028	0.027	0.011	0.007
Cumulative	0.24	0.44	0.56	0.66	0.74	0.81	0.87	0.92	0.95	0.98	0.99	1

3.3 Graphical analysis

Graphical analysis method was used to investigate and interpret the relationship between grain yield and yield components in rapeseed genotypes. Polygon view was drawn to determine the best genotype for the evaluated traits. This figure is drawn by connecting the genotypes that had the greatest distance from the origin so that other genotypes are placed inside this polyhedron. From the origin, a line is perpendicular to each side of the polygon until the figure is divided into several parts. In this form, figures that are in a section with one or more special traits show good performance in relation to that trait. Based on the polygon diagram drawn in order to evaluate and select the appropriate genotype based on the traits, the first component was 35.13% and the second component was 28.07%, and in total more than 63% of the data variance was justified. Based on this, G4, G7, G2, and G3 genotypes were selected as the most favorable genotypes in terms of all traits, and in each trait, G6 and G7 genotypes were selected in terms of pod length, number of grain in pod, and harvest index for the desired genotypes, G2 and G1 genotypes were identified as desirable genotypes in terms of oil percentage and thousand grain weight and G4 genotype in terms of grain yield and number of pods in the main stem (Figure 2). Different researchers used the polygon diagram, which is one of the diagrams used in graphic analysis, to investigate traits [10,11,12]

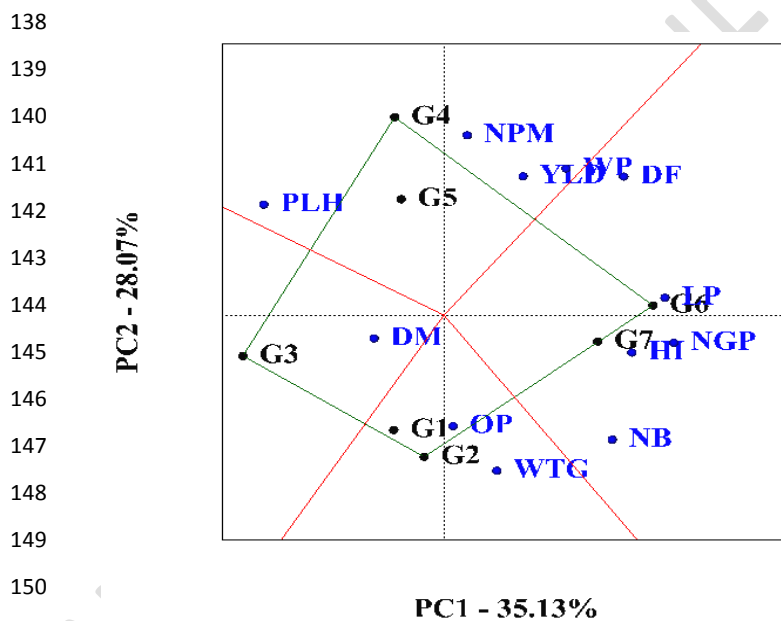


Figure 2. The polygon diagram of the evaluation of the different genotypes evaluated in terms of the traits investigated in the experiment

4. Conclusion

Rapeseed (*Brassica napus* L.) as one of the most important oilseeds in the world, has a special role in cultivation and plant breeding research. The results of analysis of variance at the level of 0.01 indicated that the evaluated genotypes have significant differences in terms of all traits except the number of grains in the pod. G4 genotype can be selected as the optimal genotype in terms of grain yield traits and oil percentage

Hạt đậu nành (*Brassica napus* L.) là một trong những hạt có dầu quan trọng nhất trên thế giới, có vai trò đặc biệt trong trồng trọt và nghiên cứu nhân giống cây trồng. Kết quả phân tích phương sai ở mức 0, 01

chỉ riêng các kiểu gen được đánh giá có sự khác biệt đáng kể về tất cả các đặc điểm ngoại trừ số lượng hạt và tỷ lệ vỏ. Kiểu gen G4 có thể được chọn làm kiểu gen tối ưu về đặc điểm năng suất hạt và tỷ lệ phần trăm dầu

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