
THE STUDY OF GROWTH, YIELD AND QUALITY FOR TWELVE OF BRASSICA GENOTYPES USING CORRELATION, PATH AND CLUSTER ANALYSIS.

Asoz. O. Abdulla Bahar J. Mahmood Sirwan T. Salih
Salahaddin University–Erbil, College of Agricultural Engineering Sciences, Field Crops Dept.

Email: bahar.mahmmod@su.edu.krd

ABSTRACT

The comparative study was conducted among twelve (*Brassica napus* L.) genotypes at Grdarash field, College of Agriculture, Salahaddin University-Erbil during the growing season of 2014-2015. The randomized complete block design with three replicates was used. The results of statistical analysis indicated to record the highest value of protein for the seeds and cake (27.75 and 28.74 %) from Rendy genotype respectively. The highest values (60.19 and 20.93 %) of oleic and linoleic acid was recorded from Bacara genotype, while the highest value (5.835) of Linolenic obtained from Pactol genotype. The significant correlation coefficient was obtained between seed yield secondary branches, number of siliques, seed index, biological yield and harvest index with $r=0.79^{**}$, 0.66^{*} , 0.75^{**} , 0.86^{**} and 0.74^{**} respectively. The path coefficient analysis confirming direct and indirect effects seed yield, the maximum positive direct effect on seed yield was obtained by the traits biological yield (0.832) confirm the positive contribution of this traits on seed yield followed by harvest index (0.324) and days of elongation (0.263) while days of flowering, days of physiological maturity, number of secondary branches and number of silique per plant recorded negative direct effect on seed yield with (-0.142, -0.126, -0.022 and -0.078) respectively. Cluster analysis or dendrogram classified the genotypes into three main clusters depending on growth stage, Agronomic characteristics and quality of them.

Keywords: Rape seeds yield, Rape seeds quality, Cluster analysis, Path analysis.

Received: 25/6/2019, Accepted: 30/9/2019

INTRODUCTION

Rapeseed considers as one of the useful crops which regarded as cash and one of the industrial crops which belongs to the Brassica family. in the same time, it is one of the important sources of the vegetable oil throughout the world (Baghdadi et al. 2013) which ranks third (Soybean, Palm then rape seed) for the production of vegetable oils, also reported as the second most important oilseed crop in the international oilseed market as a source of vegetable oil (Hasan et al, 2006), and fifth in the production of proteins. It has the potential to bridge up the gap between the domestic demand and supply due to higher oil and protein content (Malik et al, 2004).

Rapeseed oil is used widely as cooking and salad oil, and in making margarine. It has the lowest saturated fat content of all edible vegetative oils available today (Sharifi, R.S., 2012). A part from its role in direct feeding by humans and animals, it is very healthy oil because it contains omega 3, 6 and 9 essential fatty acids (Sami, 2015), it regards as a conventional edible oil seed crops, impose health concern it contains high level of fatty acids 40-49 % and 61% unsaturated oleic acids 21%, 11% linoleic acid and 7% saturated fatty (Molazim et al, 2013).

Rapeseed globally has an industrial use as a source of bio-fuel in recent years (Kandil, 2012) its oil contains high level of glucosinolates (more than 100 micromole g⁻¹ of dry meal) and low levels of oleic and linoleic acid (El-Nakhlawy and Bakhashwain, 2009).

It regarded as a source of protein for the livestock, it content 35-39% protein after oil extraction the seed meal also content 43.6% protein. (Iqbal et al, 2009). The genotype is an important factor affected rapeseed yield (Armin et al., 2013). Turhan et al (2011) recorded the influence of different genotypes on fatty acid synthesis of rapeseed they found that oleic acid has a maximum value 64.80% in Titan genotype as well as Viking genotype record highest value of linoleic acid.

Punitha et al. (2010) stated that cluster analysis is a powerful tool in quantifying the degree of genetic divergence among parents. Importance of genotypic and phenotypic variability, heritability and character association have proved by many scientists (Ali et al., 2002; Lekh et al., 1998), for further genetic improvement. Positive and significant correlations of seed yield with plant height, branches and silique per plant were recorded by (Sandhu and Gupta, 1996).

In Indian mustard positive correlation of seed yield with pods per plant, 1000 seed weight were also reported by (Khubli and Pant, 1999), whom described the simple correlation analysis could not fully give details link among the characters. Therefore, path coefficient analysis is optional to utilize for more and complete determination of impact of independent variable on dependent one. So direct and indirect effects can clearly be understood by path analysis. Many researchers have widely used this analysis to explain the direct and indirect effects of different traits on yield in different crop species.

The goals of this study were to classify these genotypes to different clusters using dendrogram and path analysis.

MATERIALS & METHODS

Comparison study was done at Grdarasha Research Field / College of Agriculture Engineering Sciences / University of Salahaddin - Erbil during the winter growing season (2014-2015) to study the variation between those genotypes in some quality characters and arrange them in different clusters.

The experiment was arranged with Randomized Complete Block Design (RCBD) using three replicates under supplemental irrigation condition. each experimental unit area was (1*2) m², Sowing was done manually with a seed rate of 4 kg ha⁻¹

(Hashim,2016) in 40 cm row spacing on a well-prepared seed bed at 3cm depth. A recommended dose of N, P, K fertilizer was applied before sowing, Twelve genotypes were selected [Pactol (Local), Bonanza, Hybrirock , Rally (France), Rapifera Rendy (Swedin), Heroz (British) and Bard-1, Dunckled , Coscar ,Sultan, Bacara (Hindi)]. Some other agricultural practices such as irrigation, thinning after the emergence stage, weeding, disease control was done., The soil texture was silty clay with organic matter, available P and available K content of (0.9%,0.1,4.3,4.5 $\mu\text{g. g}^{-1}$ and 180 $\mu\text{g. g}^{-1}$) respectively. The amount of rainfall was 269.4 mm during the growing season.

Ten plant were selected randomly to study the agronomic characters, seed samples were taken to determine protein% and oil extraction to identify variation in fatty acids % .The analysis was performed by the General Company for Vegetable Oils/Baghdad to diagnose fatty acids in oil un saturated fatty acids oleic ,linoleic, linolenic acid were determined.

The Duncan's multiple range test at level of significance 5% was used to compare between means. Mature plants were harvested on July 20, of 2017. The seed yield, yield components and growth rate were estimated. Total Nitrogen was determined using Kjeldahl method (A.O.A.C, 1980) then protein percentage was determined as follow: $\text{Protein\%} = \text{N\%} \times 6.25$

Correlation Analysis for determining the degree of association of characters with seed yield and among all the criteria studied the correlation coefficient was conducted. Phenotypic correlations were computed between the characters in the growing season using the formula given by (Singh and Chaudhary, 1985).

Path Coefficient Analysis: The path coefficient analysis was done as mentioned by (Dewey and Lu,1959). Seed yield was kept as resultant variable and other characters as causal using Analysis of Moment Structures (AMOS) Ver. 18 Software.

Cluster analysis was found to be useful tool for classification of genotypes into homogenous groups. In this experiment the cluster analysis was conducted between genotypes and the studied variables using XLSTAT-Premium Program.

RESULTS AND DISCUSSION

The protein content of rapeseed depends on various factors, including genetically and environmental factors, as well as the interaction between them. Table (1) and appendix (1) shows significant differences between the protein % of genotypes, the highest value was recorded for Rendy, while the lowest value was recorded for Bacara with the values of (27.75 and 23.10 %) respectively. Similar results was obtained by (Vujaković et al., 2015) in two-year study, in their experiment protein content ranged from 18.06% to 20.00% in 2007/2008 growing season, in mutant lines of winter rapeseed, presented similar results for this trait .The highest value of protein in seed cake recorded also in Rendy genotypes.The same table and appendix explain the significant differences among the genotypes for quality characters .The table exhibits that Bacara was superior in oleic and linoleic acid content (60.19, 20.93 %) respectively, while the

highest value of linolenic acid was recorded for Pactol and the lowest value of oleic and linoleic acid was obtained for Dunkled genotype, the Rapifera has the lowest value for linolenic acid these results agree with those recorded by (Mohammad ,2018).

Abdulkhaleq et al. (2018) stated that different varieties of rapeseed affect the quality and quantity of rapeseed growth, yield and oil percentage formation production, which was typically characteristic of a species, the genetic variations among the varieties

Table (1): Effect of rapeseeds genotypes on some quality traits (criteria).

	Protei% in seed	Protei% in cake	Protein yield	oleic	linoleic	linolenic
Rapifera	26.12 ^{ab}	24.46 ^{cd}	016 ^e	51.43 ^{ab}	18.02 ^{bcd}	1.78 ^b
Bard-1	25.88 ^{ab}	24.05 ^{cd}	2.26 ^a	57.14 ^a	19.62 ^{ab}	2.51 ^b
Dunkled	25.46 ^{ab}	24.39 ^{cd}	2.20 ^{ab}	31.75 ^c	11.31 ^e	1.92 ^b
Bacara	23.10 ^b	22.84 ^{de}	0.69 ^{de}	60.19 ^a	20.93 ^a	2.65 ^b
Rally	25.28 ^{ab}	25.16 ^c	0.70 ^{de}	52.98 ^{ab}	18.49 ^{bcd}	2.32 ^b
Sultan	24.92 ^{ab}	25.38 ^{bc}	1.74 ^{abc}	46.04 ^b	16.22 ^d	2.25 ^b
Heroz	24.74 ^{ab}	24.56 ^{cd}	1.63 ^{bc}	50.14 ^{ab}	17.43 ^{bcd}	3.07 ^b
Bonanza	24.99 ^{ab}	26.87 ^{ab}	1.20 ^{cd}	52.36 ^{ab}	17.33 ^{bcd}	2.74 ^b
Hybriroc	25.13 ^{ab}	21.04 ^f	1.62 ^{bc}	53.30 ^{ab}	18.84 ^{abc}	2.71 ^b
Coscar	25.03 ^{ab}	21.37 ^{ef}	1.81 ^{ab}	49.77 ^{ab}	18.63 ^{bc}	2.47 ^b
Pactol	26.13 ^{ab}	24.84 ^c	1.82 ^{ab}	57.57 ^a	16.50 ^{cd}	5.83 ^a
Rendy	27.75 ^a	27.84 ^a	0.98 ^d	46.05 ^b	17.21 ^{cd}	3.14 ^b

Appendix (1) Mean squares of variance analysis for the studied characters

S.O.V	df	Protei% in seed	Protei% in cake	Protein yield	Oleic	Linoleic	linolenic
Blocks	3	28.32	0.68	0.15	68.56	21.37	18.17
Genotypes	11	3.58*	11.64**	1.31**	163.00**	16.80**	3.24**
Exp.Error	22	2.40	0.91	0.09	31.88	1.49	0.39

Table (2) explains the results of correlation between the studied characters of plant, the significant correlation coefficient was recorded between seed yield and each of secondary branches, number of silique per plant, seed index, biological yield harvest index and oil yield with the correlation coefficient values (r) equal to 0.79*, 0.66*, 0.75**, 0.86**, 0.74** and 0.98** respectively.

There are many studies on the correlation of *Brassica* species, in most of them includes silique per plant and number of seeds per silique on the main stem had a significant positive correlation with seed yield (Arshad et al, 2017) and (Basalma, 2008).

Table (3) shows the path coefficient analysis confirming direct and indirect effects seed yield, the maximum positive direct effect on seed yield was obtained by the traits

biological yield (0.832) confirm the positive contribution of this traits on seed yield followed by harvest index (0.324) and days of elongation (0.263) while days of flowering, days of physiological maturity, number of secondary branches and number of silique per plant recorded negative direct effect on seed yield with (-0.142, -0.126, -0.022 and -0.078) respectively. Similar results were obtained (Rameeh, 2011) and (Tahira et al, 2011).

Cluster analysis is a valuable tool in classifying the material into different groups according to variation present among them. Knowledge about the variation of different genotypes is one of the principles in breeding programs. (Arshad et al. 2017).

Multivariate methods are used to reveal differences, similarities or relationships between individuals, considering several different genotypes and types of measurement at the same time (e.g. height, weight,). From Figure (1) it can be seen that the genotypes are discern to three main clusters, the 1st included (. Bonanza, Rapifera , Rendy, bacara, Rally) ,the 2nd cluster is (Dunkled genotype)alone while the 3rd cluster included (Sultan, Heroz, Bard-1 ,Hybriroc ,Coscar and Pactol) fig (2) each genotypes was similar to each other in one cluster .It explain that is much more similar to the variables have more practical importance than others.

Bacara, Rally is more closers than Rally and Rendy in the first cluster at the same time Pactol and Coscar is the same like Heroz and Sultan.

Table (2): Correlation analysis among the studied characters of rapeseeds genotypes.

	Yield	Plant height	Primary branch	Secondary branch	No. Silique	Seed	Seed index	Biological yield	HI	Oil %	Oil yield	Protein seed	Cake protein	Protein yield	Oleic	Linoleic
Plant height	.46															
Primary br.	-.23	.23														
Secondary	.79**	.59*	.07													
No. Silique	.66*	.16	-.18	.52												
Seed	.17	-.43	-.09	-.09	.41											
Seed index	.75**	.25	-.14	.35	.58*	.25										
Bio. yield	.86**	.46	-.06	.85**	.62*	.15	.61*	.								
HI	.74**	.38	.11	.77**	.58*	-.08	.68*	.79**								
Oil%	.51	.24	-.29	.39	.35	-.04	.35	.31	.38							
Oil yield	.98**	.46	-.24	.79**	.65*	.13	.74**	.83**	.74**	.63*						
Protein seed	.04	.27	-.05	-.17	-.13	-.12	-.02	-.32	-.31	.34	.09					
Cake	-.37	-.20	-.22	-.61*	-.19	.27	-.18	-.49	-.66*	.27	-.29	.51				
Protein	-.32	.09	.12	-.21	-.15	-.58*	-.22	-.19	-.16	-.21	-.31	.23	-			
Oleic	-.31	-.08	.21	.05	-	-.48	-.45	-.14	-.02	.03	-.26	-.27	-	-		
Linoleic	-.41	-.23	.27	-.06	-	-.46	-.58*	-.29	-.13	-.22	-.39	-.29	-	.01	.89**	
Linolenic	.46	.08	-.25	.14	-.21	.01	.04	.06	.08	.43	.19	.22	.14	.39	.29	0.08

*, ** significant at the probability level 1 and 5% respectively

Table (3): Shows pathway analysis of data.*

Traits	Days to elongation(EL)	Days to flowering(FL)	Days to physiological maturity Aturity(DPH)H	No. secondary branch (NSB)	No. silique plant ⁻¹ (NSPP)	Seed index(SI)	Biological yield (BY)	Harvest index (HI)	Correlation with SEED Yield (YI)
DEL	<u>0.263*</u>	-	-	0.014	0.0489	-	-0.691	-0.215	-0.860
DFL	0.252	<u>0.142</u>	-	0.013	0.047	-	-0.611	-0.214	-0.793
DPH	0.225	-	<u>0.126</u>	0.013	0.065	-	-0.622	-0.177	-0.770
NSB	-0.166	0.083	0.077	<u>0.022</u>	-	0.020	0.601	0.235	0.789
NSP	-0.165	0.087	0.105	-	<u>0.078</u>	0.033	0.501	0.189	0.661
SI	-0.166	0.084	0.068	-	-	<u>0.057</u>	0.539	0.220	0.749
BY	-0.218	0.104	0.094	-	-	0.037	<u>0.832*</u>	0.176	0.963
HI	-0.174	0.094	0.069	-	-	0.039	0.452	<u>0.324*</u>	0.742

*Bolted number= Direct effect and Non-Bolted number= indirect effect

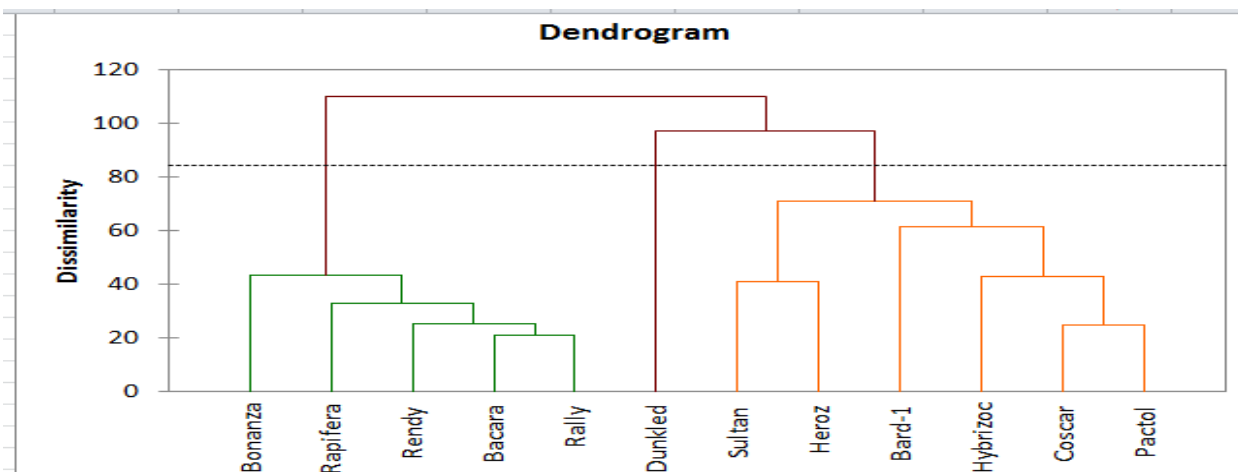


Fig (1) Dendrogram obtained from a cluster analysis of the genotypes.

Table (4) shows the proximity matrix which refers to similarity and dissimilarity, the highest value (187.65) refers to higher dis-similarity. Relationship between the two genotype Dunkled and Papifera , the same dis-similarity between Dunkled and Rendy (173.41) it means there is highest differences between them while the value of 24.89 refers to the similar relation between Pactol and Coscal.

Table (4): Proximity matrix (Euclidean distance)

Genotypes	Rapifera	Bard-1	Dunkled	Bacara	Rally	Sultan	Heroz	Bonanza	Hybrizoc	Coscar
Bard-1	162.85									
Dunkled	187.65	85.01								
Bacara	36.08	145.70	176.02							
Rally	25.89	148.09	174.81	20.73						
Sultan	121.11	90.47	74.01	108.57	107.54					
Heroz	83.85	99.91	110.07	68.52	68.46	41.04				
Bonanza	56.17	119.12	162.29	43.53	41.86	104.93	68.93			
Hybriroc	95.96	77.78	109.62	87.21	83.50	68.75	55.16	62.32		
Coscar	109.94	57.02	99.69	91.98	94.72	60.878	50.07	70.71	43.67	
Pactol	117.89	49.11	105.76	101.27	103.29	75.475	67.29	73.39	42.50	24.89
Rendy	36.38	140.26	173.41	26.23	24.04	110.77	72.14	31.71	79.13	88.20

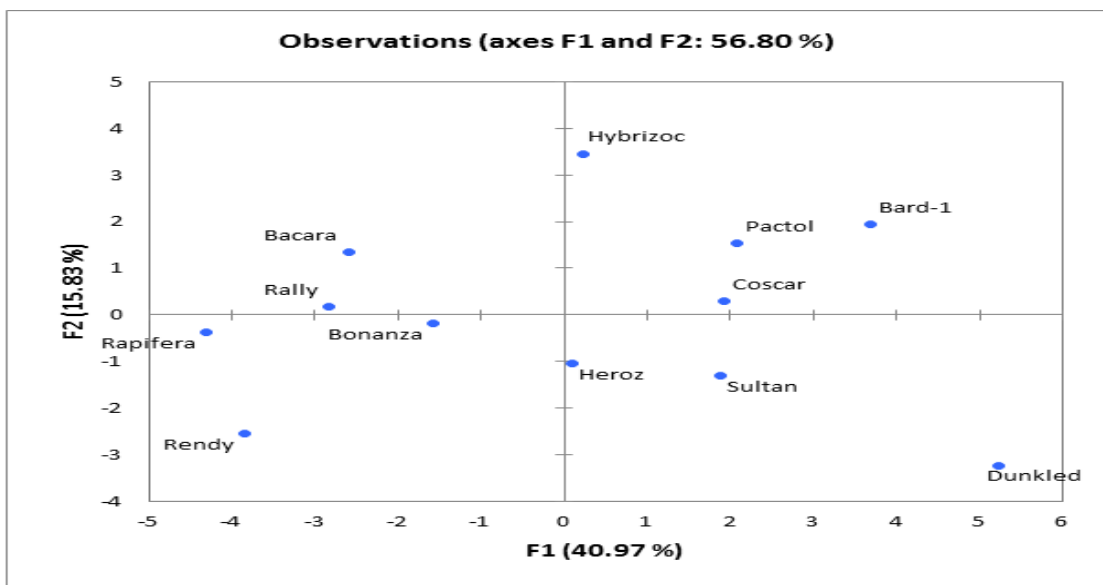


Fig (2): Cluster analysis of the genotype's characteristics

Fig (2) Shows the observations on the studied genotypes it's clear that there are three clusters the first at the right side the closest distance mean more similarity in the same cluster there are different manner between the genotypes Coscar, Pactol ,Bardi-1 and hybriroc was in the positive side while Heroz and Sultan was negative .this explanation is the same for the second cluster. The Dunkled genotype is different among the genotypes this figure is with agreement with fig (1).

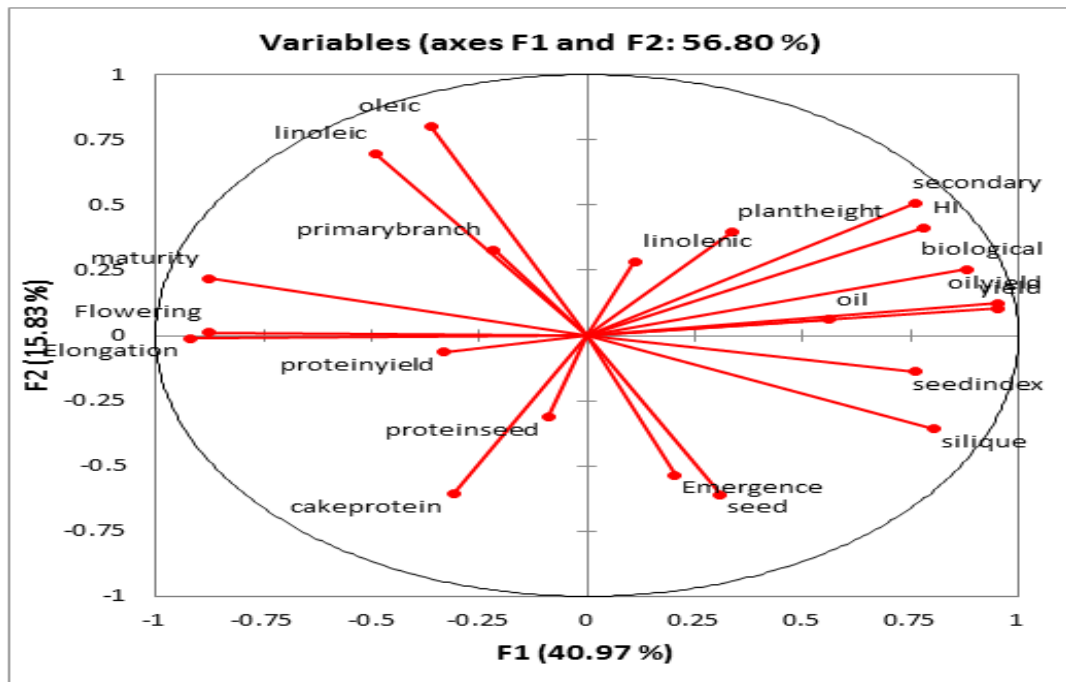


Fig (3): Cluster analysis between variables in the comparison study.

There is very highly correlation between seed yield and secondary branches, number of silique per plant, seed index, biological yield harvest index and oil yield as mentioned in table (2). In real-life situations, clustering variables can be a useful way to discover which traits or groups of traits tend to vary together in a population.

In figure (3) the genotypes and variables are merged and gives different explanation. The variables close to the central there will not be significant differences between them for example in Dunkled genotype the no. of silique is closest variables. Protein seed and cake is closer to Rendy genotype. any of the variable are close mean there are positive reaction between them and the other side has negative reaction with the first one.

The results indicated to significant difference between genotypes depending of correlation, pathway and cluster analysis. Depending on cluster analysis the twelve studied genotypes were classified into three different classes. Cluster analysis showed presence of considerable genetic variation among rapeseed hybrids studied. Correlation and path analysis revealed that the trait pods per plant had the maximum potential of selection for seed yield improvement because it exhibited highly significant positive correlation and maximum positive direct effects with seed yield.

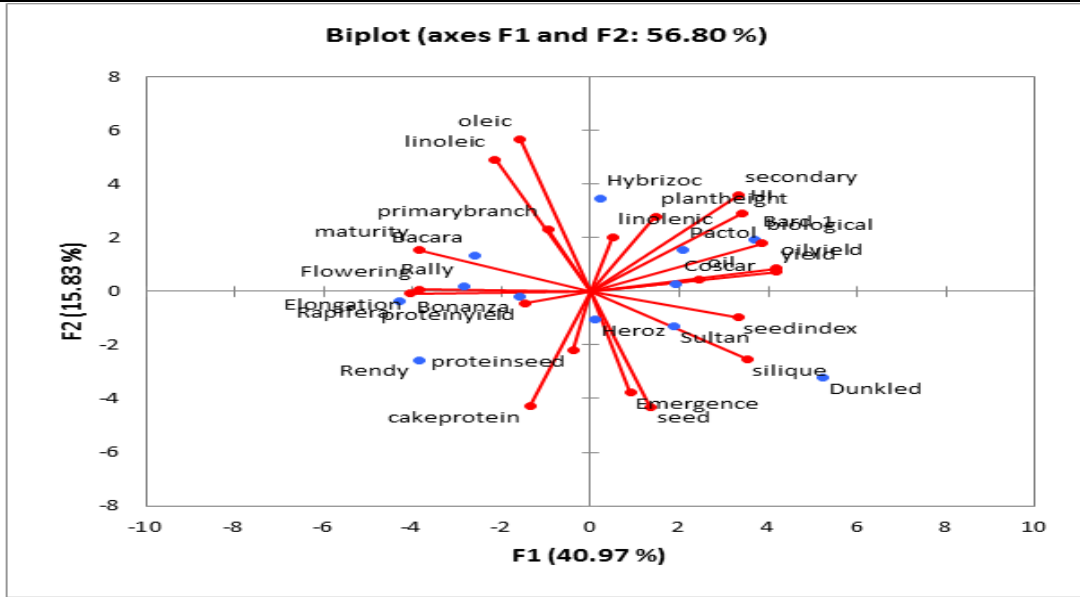


Fig (4): Cluster analysis between genotypes and variables in the comparison research

دراسة مقارنة بين اثنا عشر تركيب وراثي من محصول السلجم لصفات النمو الحاصل و النوعية مستخدما
تحليل الانحدار، المسار و العنقودي

ناسوز عمر عبد الله بهار جلال محمود سيروان طه صالح
جامعة صلاح الدين - اربيل \كلية علوم الهندسة الزراعية \ قسم المحاصيل الحقلية

Email: bahar.mahmmod@su.edu.krd

الخلاصة

اجريت دراسة مقارنة بين اثنا عشر تركيب وراثي من محصول السلجم (*Brassica napus* L) في حقل كرده ره شه التابعة لكلية الزراعة /جامعة صلاح الدين- اربيل خلال موسم النمو 2014-2015. استخدم فيها تصميم القطاعات العشوائية (RCBD) و بثلاث مكررات. بينت نتائج التحليل الاحصائي وجود فروقات معنوية في الصفات النوعية للسلجم حيث سجلت اعلى قيمة لها في البذور و الكيك اي البذور بعد استخلاص الزيت بحوالى (27.75 و 27.84) في التركيب الوراثي (Rendy) على التوالي. وعلى قيمة (60.19, 20.93) كانت للحوامض الامينية (oleic, linoleic) و المدونة ضمن التركيب الوراثي (Bacara) بينما كانت اعلى قيمة ل (linolenic) ضمن التركيب الوراثي (Pactol) بقيمة (0.835). بينت الدراسة ان هناك ارتباط معنوي بين حاصل البذور مع التفرعات الثانوية، عدد القرينات، دليل البذار، الحاصل البيولوجي و دليل الحصاد فكانت قيم الارتباط = (0.74, 0.86, 0.75, 0.66, 0.79) على التوالي. قدرت معاملات الارتباط الوارثي بين حاصل البذور والصفات المدروسة الأخرى لتجزئته باستخدام تحليل معامل المسار إلى تأثيرات مباشرة وغير مباشرة لتحديد الصفات الأكثر تأثيرا في حاصل البذور. حيث كان التأثير الموجب المباشر على حاصل البذور كانت ضمن الحاصل البيولوجي (0.832) يعقبه دليل الحصاد (0.324)، اما الفترة من البذار الى الاستطالة (0.263) بينما الفترة من البذار الى الازهار، بينما الى النضج الفسيولوجي، عدد الافرع الثانوية و عدد القرينات لكل نبات سجلت تأثيرا سالبا مباشرا على حاصل البذور القيم هي (-0.142, -0.126, -0.022 and -0.078) على التوالي. تم تقسيم التراكيب الوراثية الى قلادة مجاميع رئيسية اعتمادا على الصفات المدروسة والتي تتضمن صفات النمو و الحاصل و النوعية. الكلمات المفتاحية: التراكيب الوراثية للسلجم، النوعية، تحليل المسار و تحليل المجاميع العنقودية.

تاريخ تسليم البحث: 2019/6/25، تاريخ القبول: 2019/9/30

REFERENCES

- A. O. A. C. (1980). Association official of analytical chemists. Official Methods of Analysis 14th Ed Washington, D.C., U.S.A.
- Abdulkhaleq, D. A; J. H. Shara; M. A. Rozhgar; and, I. T. Sherwan (2018). Response of some Rapeseed (*Brassica napus* L.) varieties of Zn fertilizer Under Dryfarming Conditions. *Journal of Zankoi Sulamani, JZS Special Issue (Part-A) (Pure and Applied Sciences.)*.
- Ali, N; F. Javidfar; and A. A. Attary (2002). Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus* L.). *Pak. J. Bot.*34:145-150.
- Armin, A and A. Golparvar (2013). Effect of planting dates on seed and oil yield of canola (*Brassica napus* L) cultivars, *International Journal of Modern Agriculture* 2(2), 81-84.
- Arshad, T. M: A. K. Muhammad and A. K. Mubashar (2017). Cluster Analysis Association and Path Coefficient Analysis for Seed Yield Improvement in Rapeseed. *Pakistan Journal of Agricultural Research*.
- Baghadi, H: S. Taspinar: M. Yousefi and A. Hosseinpour (2013). Influence of different sowing dates on grain yield of canola (*Brassica napus* L) cultivars in Qazvin area. *International Journal of Agriculture: Research Review* 2 (5) 1092-1096.
- Basalma, D. (2008). "The Correlation and Path Analysis of yield and yield components of different winter rapeseed (*B. napus* ssp. *oleifera* L.) Cultivars". *Res. J. Agri. Biol. Sci.*, 4: 120-125.
- Dewey, D. R and K.H. Lu (1959) "A correlation and path-coefficient analysis of components of crested wheat grass grain production". *A. J.*, 51:515-518.
- Different Sowing Dates and Seeding Rates. Salahaddin University, Erbil, MSc thesis.
- El-Nakhlawy, F. S and A. A. akhashwain (2009) Performance of Canola (*Brassica napus* L) seed yield, yield components and seed quality under the effect of four genotypes and nitrogen fertilizer rates. *JKAU: Met, Env. and Arid Land Agric.Sci*, Vol.20,NO.2,PP:33-47.
- Hashim, J. J. (2016). Response of Rapeseed (*Brassica napus* L.) Genotypes to
- Iqbal, M: N. Akhtar: S. Zafar and I. Ali (2009). Genotypic responses for yield and seed oil quality of two Brassica species under semi-arid environmental conditions. *South African Journal of Botany* 74 (2008) 567–571.
- Kandil, A. A; A. E. Sharief, W. A. E. Abido and M. M. O. Ibrahim (2012). "Response of some canola cultivars (*Brassica napus* L.) To salinity stress and its effect on germination and seedling properties". *J. Crop Sci.*, 3: 95-103.
- Khubli, S. K. and D. P. Pant (1999). Correlation and path coefficient analysis of yield and its components in Indian mustard. *Crop Res. Hisar.* 17:371-375.
- Lekh, R; S. Hari; V. P. Singh; L. Raj and H. Singh (1998). Variability studies in rapeseed and mustard. *Ann. Agric. Res.* 19(1):87-88.

- Malik, M. A; I. Aziz; H. Z. Khan and M. A. Wahid (2004). Growth, seed yield and oil content response of canola (*Brassica napus*) to varying levels of sulphur. *International Journal of agriculture and biology* 6, 6(1153-1155).
- Mohammad, B. I. (2018). Evaluation of some quality and quantity characteristics of canola varieties in response to foliar application of manganese. *Polytechnic Journal* 8, 3 (132-147).
- Molazim, D: J, Azimi and T, Dideban (2013). Measuring the yield and its component, in the canola in different planting date and plant density of the West Guilan. *Int.J.Agri.Crop Sci.* 6:869-872.
- Punitha, B. P; Vindhiyavarman and N. Manivannan (2010). Genetic divergence study in sunflower (*Helianthus annuus* L.). *Electron. J. Plant Breed*, 1(4):426-430.
- Rameeh, V. (2011). "Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components". *J. of Oilseed Brassica*, 2(2):56-60.
- Sami, S. (2015). Effect of plant nutrition on canola (*Brassica napus* L.) growth. *Trakya University Journal of Natural Science*, 16 (2):87-90.
- Sandhu, S. K. and V. P. Gupta (1996). Genetic divergence and correlation studies In Brassica Species. *Crop Improv.* 23: 253-256.
- Sharifi, R. S. (2012). "Study of yield, yield attribute and dry matter accumulation of canola (*Brassica napus* L.) cultivars in relation to sulfur fertilizer". *Int. J. of Agric. and C. Sci.*, 4(7): 409-415 (2012).
- Singh, R. K. and B. D. Chaudhar (1985). "Biometrical Methods in Quantitative Genetic. Analysis". Revised Edition, Kalyani Publishers, Ludhiana, New Delhi, India.
- Snowdon, R. J. (2006). Analysis of genetic diversity in the *Brassica napus* L. gene pool using SSR markers. *Genet. Resour. Crop Evol.* 53: 793-802.
- Tahira, T. M; M. S. Mahmood; U. Tahir; M. Saleem and M. S. Hussain (2011). "The estimation of heritability, association and selection criteria for yield components in mustard (*Brassica juncea*)". *Pak. J. Agri. Sci.*, 48(4): 251-254.
- Turhan, H; M. K. Gul; C. O. Egesel and F. Kahrman (2011). Effect of sowing time on grain yield, oil content, and fatty acids in rapeseed (*Brassica napus* subsp, *Oleifera*) *Turk. Journal. Agri. Forestry*, 35:225-234.
- Vujaković, M. A; D. J. Marjanović-Jeromela and R. Marinković. (2015). Dependence of rapeseed quality and yield on density, variety and year of production. *Field Veg. Crop Res.* 52: 61-66.