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MORPHOLOGICAL AND TECHNOLOGICAL STUDIES ON SOME CANOLA (*Brassica napus, L.*) GENOTYPES

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ABSTRACT

Morphological and technological traits were utilized to identify among canola (*Brassica napus, L.*) genotypes namely Pactol, Serw 6, Serw 10 and Serw 4. Two field experiments were carried out at the Farm of El-Serw Agricultural Research Station during 2006/2007and 2007/2008 seasons. The results revealed that plants of Line Pactol can be identified by leaf length (blade and petiole), leaf petiole length, plant height (171.1 cm), oil content (44.7%) and branches point (60cm) and its lowest Line in cotyledon length and width, number of siliqua/ plant (286,8) number of seed/ siliqua (22) and seed yield/plant (32.1 g). Plants of Line Serw 6 can be identified with higher number of leaf dentation, plant height (175.9 cm), 1000-seed weight (3.40 g), lowest means in number of leaf lobes (4.5), petiole florescence length (39.9 cm), No. of side branches (6.5) and oil content (40.2%). Plants of Line Serw 10 can be identified with its leaf width (10.1 cm), length of flower petals (1.5 cm), branches point (11.5 cm), lowest means in leaf length, no. of leaf dents (19), length of leaf petiole (7.1 cm) and number of leaves/ plant. Plants of cultivar Serw 4 can be identified by higher number of leaf lobes (5.6), number of leaves (10), petiole florescence length (47.9 cm), number of side branches (13), length of beak (1.2 cm), number of siliqua/ plant (888.1), number of seed/ siliqua (30), seed yield/plant (68.6gm), lowest means in leaf length (21.4 cm), width (7.9 cm), branches point (3.4 cm) and 1000-seed weight (2.77 g).

Dice similarity coefficients between genotypes was calculated. Maximum 87% and minimum 62% similarity coefficients were observed between Line Pactol and variety Serw 4, Line Pactol and Line Serw 10, respectively. Base on the cluster analysis, genotypes were grouped into two clusters. Line Serw 10 was in a separate cluster while, Line Pactol, Line Serw 6 and variety Serw 4 were in the second cluster. The results confirmed that some morphological traits and RAPD method could be used for identify among canola genotypes.

Keywords: Canola genotypes, identification, seed yield, oil content and protein content.

INTRODUCTION

The annual edible oil production in Egypt is less than 85000 tons, while the domestic consumption is about 1.1 million tons (FAO. 2008). Canola is one of the promising oil crops which could helps in reducing the gab between the local production and the consumption. It is characterized with high oil content (42%) and a good quality protein in the cake (38%). Canola is the only winter season oil crop and has the ability to be grown in the new reclaimed lands. Little studies have been done in Canola in Egypt, Keshta and Hammad (1999). For varietal identification, Khan *et al.,* (2006 a), reported that number of primary branches/plant and oil contents were less variable traits than plant height, pods/plant, seed/pod, pod length, protein content and seed yield/plant. Phenotypic coefficients of variability were also

greater than respected genotypic ones. Also, Khan *et al.*, (2006 b), found a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield/ plant was positively and significantly correlated with number of primary branches, number of siliqua/ plant, number of seeds/ siliqua, siliqua length and seed yield/plot. On the other hand, liu Yali *et al.*, (2007), concluded that, there were obvious differences among different subspecies on morphological characters such as shape of the leaf, color of flowers and found also that the agronomic traits differences were also significant. Thus, selection for these characters would be effective in improving canola varieties. But the morphological characters of any crop may be affected by environmental factors and soil conditions (Cooke, 1984).

DNA-based markers are a powerful tool for studies of genetic diversity, therefore it is used for genetic studies and evaluation of genetic diversity. One of suitable DNA-based markers for genetic diversity studies is RAPD (Random Amplified Polymorphic DNA). This marker has a high potential in order to polymorphic evaluation in all races of plants and animals and for identification and study of races is very valuable (Welsh *et al.*, 1991). Recently, identification methods have focused on the application of DNA markers. DNA based markers have a number of advantages over other tests for cultivar discrimination in that DNA is unaffected by environmental factors or the developmental stage of the organism. Further, the RAPD methodology has an advantage over the DNA fingerprinting methods in that is fast, requires no radioactive handling facilities, and the costs are relatively minimal. The success in breeding program of a crop species largely relies on the presence of genetic diversity in the germplasm and knowledge about the characteristics of the genotypes and there genetic relationship. Therefore, the methods that evaluate and identify the genotypes more precisely during the growing season, espcialy at early stage, are preferred by plant readers (Major, 2002).

The objective of this study was to identify some canola genotypes using some morphological, technological and biochemical traits.

MATERIALS AND METHODS

Field and laboratory experiments were carried out at El- Serw Agriculture Research Station Farm, ARC, Domitta governorate and Seed Technology Research Station, ARC, Giza during 2006/2007 and 2007/2008 seasons. Canola seeds were sowen by hand in Randomized Complete Block Design with four replicates. Each experimental plot consists of for rows and 3 m long. The sowing dates were 19 and 25 of November in the first and second seasons, respectively. All agricultural practices were carried out according to the outlined by the Ministry of Agricultural and Land Reclamation recommendations. The morphological characters were determined using the descriptors issued by the International Union for the Protection Of New Varieties of plants (UPOV, 2002). The euricic acid for the studied genotypes was present in line Serw 6 (4.6%), but it absent in line Patcol, Serw 10 and

varity Serw 4 with total percentage (1.3%, 0.6% and 0.2%), respectively, as estimated by the Oil Crops Research Section, Agricultural Research Center (ARC). The studied traits were

1-The morphological characters

a- Leaves: leaf green color, number of lobes (fully developed leaf), dentition of margin, length (blade and petiole), width (widest point), varieties with lobed leaves only (length of petiole).

b- Flowers: time of flowering, color of petals, length of petals, width of petals, production of pollen

c- Plant: height (at full flowering), total length including side branches and branches point

d- Siliqua: number of siliqua/ plant, length (between peduncle and beak), length of beak.

e- Seeds: Cotyledon length and width, number of seeds/siliqua, seed weight /plant, 1000 seed weight.

Data of quantative characters were subjected to statistical analysis of variance using Mstatc computer program, Russell (1994).

2- Chemical components

Percentage of oil (oil percentage was determined using soxhelt apparatus using n- hexane according to AOAC. 1990), and erucic acid content in the oil (erucic acid as estimated by the oil crops section, ARC).

Data Collected data for each season were statistically analyzed by the technique of analysis of variance and the least significant differences (L.S.D.) of treatments (Gomez and Gomez, 1984). Bartlett test was done to the homogeneity of error variances. The test was insignificant for all traits thus the data of both years were combined for these traits except, cotyledon width, branches point, width of petals, siliqua length and 1000-seed weight.

4- Molecular marker

Plant material and DNA extraction

For genomic DNA isolation, seeds of each of the canola genotypes were germinated and grown to the four-leaf stage. The seedlings were used for DNA extraction by DNeasy plant minikit (Quigen Inc., Cat.no.69104, and USA). The DNA concentration of the final samples was measured by ultraviolet (UV) spectrophotometer at 260nm. The integrity of the DNA was checked by electrophoresis in a 1.2% agarose gel in TAE buffer

RAPD- PCR analysis :

A final set of 7 RAPD primers selected based on their polymorphism and repeatability were used to evaluate the rapeseed genotypes with the 5′ → 3′ sequences as shown in Table 1.

Polymerase chain reaction (PCR) conditions :

DNA amplification was carried out in PCR tubes concentaining 25 µL reaction mixture, having 1 µL template DNA, 1 µL RAPD primer, 15 µL of dd H_2O and 7 µL PCR mix. Amplification was carried out in a PTC- 200 thermal cycler (MJ Research, Watertown, USA) programmed as follows: Denaturation, 94 °C for 2 minutes, then for 40 cycles. Each cycle consisted

of 1 minute at 94 °C , 1 minute at 37 °C, 2 minutes and 30 second at 72 °C, followed by a final extension time of 12 minutes at 72 °C and 4 °C (infinitive).

Table 1: Random primer names and their sequences for RAPD-PCR analysis.

Primer name	Sequence
0P- A07	5'GAAACGGGTG3'
0P-A12	5'TCGGCGATAG 3'
0P-D02	5'GGACCCAACC3'
0P-D03	5'GTCGCCGTCA 3'
0P-D05	5' TGAGCGGACA3'
0P-D15	5'CATCCGTGCT 3'
0P-D18	5' GAGAGCCAAC3'

Gel electrophoresis:

Gel electrophoresis was applied according to Sambrook *et al.* (1989). The run was performed for one hour at 80 volt in pharmacia submarine (20 x 20 cm). Bands were detected on UV – transilluminator and photographed by Gel documentation 2000, Bio- Rad. Fragment sizes of RAPD were estimated from the gel by comparison with the 100+1.5 kb ladder marker. The bands were recorded as either present or absent into a database of "0"and "1"'s

RESULTS AND DISCUSSION

Data in Table (2) showed the differences among canola genotypes in morphological traits i.e. leaf lobes, leaf green color, time of flowering, color of petals, production of pollen and tendency to form inflorescences. Leaf lobes and production of pollen was presented in all genotypes. Leaf green color and color of petals were dark and yellow in all genotypes, respectively. Varity Serw 4 was earlier genotype in the time of flowering, while, Lines Pactol and Serw 6 were late. On the other hand, Line Serw 10 was medium in the time of flowering. Tendency to form inflorescences which was medium in all genotypes except the verity Serw 4 was strong. The differences among canola genotypes in flowering dates might be due to the genetical factors and heredity variation among the studied genotypes which differ in flowering dates.

Table (2): Morphological characters of tested canola genotypes in 2006 /2007 and 2007/2008 seasons.

Genotypes	leaf lobes	leaf green color	time of flowering	color of petals	production of pollen	Tendency to from inflorescences
Pactol	present	dark	late	yellow	present	medium
Serw 6	present	dark	late	yellow	present	medium
Serw 10	present	dark	medium	yellow	present	medium
Serw 4	present	dark	early	yellow	present	strong

Data in Table (3) showed that canola genotypes were significantly differed in all studied traits. On the contrast, plant characters (total length including side branches) showed insignificant variation.

Cotyledon length of variety Serw 4 was the tallest followed by Lines Serw 10 and Serw 6, meanwhile, Line Pactol has the shortest one. The highest number of leaf lobes was obtained from Serw 4 followed by Serw 10 and Pactol while, leaves of Line Serw 6 have the lowest number of lobes. Leaves of Line Pactol characterized with its highest of margin, tallest Length of leaf (blade and petiole) and length of petiole. Leaves of Line Serw 6 characterized with the highest number of dents, plant hight, leaves of variety Serw 4 characterized with its shortest means of leaf length (blade and petiole). Leaves of Line Serw 10 have the lowest means of margin dentations, length of petiole, number of leaves and number of dents, on contrast, its leaf width was the highest one. Plants of Line Serw 6 characterized with their highest plant height (175.9 cm) followed by Line Pactol, Line Serw 10 and the lowest length (121.1cm) was recorded from variety Serw 4 plants. With respect to the plants total length (including side branches) plants of Line Serw 10 recorded the highest means (120.3 cm) and it followed by Line Serw 6 (120.2 cm), Line Pactol (111.8 cm) and variety Serw 4 (117.7 cm).

Data in Table (3) showed that flowers of Line Serw 10 characterized with the highest petals length (1.5 cm) followed by Line Pactol, Line Serw 6, and variety Serw 4 was (1.4 cm). Florescence of variety Serw 4 have the highest petiole length (47.9 cm) and it followed by Line Serw 10 (44.1 cm) and Line Pactol (41.1 cm), meanwhile, florescence of Line Serw 6 have the lowest florescence petiole length (39.9 cm).

The results in Table (3) indicated that, the four canola genotypes significantly differed in length of siliqua peak and number of siliqua/ plant. The highest length of siliqua peak (1.2 cm) was obtained by variety Serw 4 followed by Line Serw 10 (1.1 cm), Line Serw 6 (0.9 cm) and finally Line Pactol (0.9 cm). Number of siliqua/ plant in variety Serw 4 reached to (888.1), meanwhile, in Line Serw 6 was (479.5) followed by (359.1) for Line Serw 10 and finally (286.8) for Line Pactol.

With respect to the number of seed/ siliqua, significant differences among genotypes were noticed as presented in Table (3). The highest number of seed/ siliqua (30) was produced from variety Serw 4 followed by (27) for Line Serw 10, and (22) for siliqua of Lines Pactol and Serw 6. The genotypes significantly varied with respect to the seed oil as illustrated in Table (3). The highest mean of seed oil content (44.7) was obtained from Line Pactol followed by variety Serw 4 (42.9), Line Serw 10 (41.5) and (40.2) for Line Serw 6 seed.

The results in Table (3), indicated that, genotypes significantly differed in seed yield/ plant. The highest average of plant seed yield (68.6 gm) was obtained by variety Serw 4. Vice versa, the lowest means of plant seed yield (32.1 gm) were produced from Line Pactol. On the other side, averages of plant seed yield for Line Serw 6 and Line Serw 10 were (45.3 and 41.2 gm), respectively. The significant differences in these traits among the studied genotypes revealed that these characters are valuable for identification among canola genotypes and could be useful in breeding programs. The results agreed with those obtained by Khan et al., (2006 a), Abdalla, Safia T. *et al.*, (2004) and Lui yali *et al.,* (2007) they concluded that, there were

obvious differences among different subspecies morphological characters such as shape of the leaf, color of flowers and found also that the number of primary branches/ plant and oil contents were less variable traits than plant height, pods/ plant, seed/ pod, pod length, grain yield/ plant, and seed yield/ plant.

Table (3): Differences in some characters of Pactol, Serw 6, Serw10 and Serw 4 canola genotypes (combined data over 2006/2007 and 2007/2008 seasons).

Characters	Pactol	Serw 6	Serw 10	Serw 4	LSD 0.0 5%
1-Cotyledon length (cm)	0.4	0.4	0.5	0.6	0.1
2-Leaf : no. of lobes	5.3	4.5	5.4	5.6	0.8
3-Leaf: dentation of margin	8.5	7.3	4.1	7.0	1.0
4-Leaf: length of blade and petiole (cm)	27.3	25.7	23.1	21.4	4.3
5-Leaf: length of petiole (cm)	13.7	12.9	7.1	7.9	2.6
6-No. of leaves	9.0	8.0	7.0	10.0	1.5
7-Leaf: no. of dents	18	19	15	17	2.6
8-Leaf: width (cm)	9.7	9.1	10.1	7.9	1.6
9-Plant height (cm)	171.1	175.9	131.6	121.1	13.7
10-Plant: total length (including side branches)	111.8	120.2	120.3	117.7	NS
11-Flower: length of petals (cm)	1.4	1.4	1.5	1.4	0.1
12-Petiole florescence length (cm)	41.1	39.9	44.1	47.9	5.8
13-No. of side branches	7.5	6.5	8.0	13.0	1.6
14-Siliqua: length of beak (cm)	0.9	0.9	1.1	1.2	0.2
15-No. of Siliqua/plant	286.8	479.5	359.1	888.1	50.6
16-No of seed /Siliqua	22	22	27	30	3.1
17-Oil content	44.71	40.2	41.5	42.9	1.0
18-Seed yield/plant (gm)	32.1	45.3	41.2	68.6	3.1

Data in Table (4), showed variation in cotyledon width, branches point, width of flower petals, siliqua length and 1000-seed weight. Significant differences among canola genotypes in cotyledon width was existed in the two seasons. The highest value of cotyledon (1.07 and 1.03 cm) was obtained from variety Serw 4 in 2006/2007 and 2007/2008 seasons respectively, followed by Line Serw 10 (0.82 and 0.78), Line Serw 6 (0.77 and 0.73) and (0.77 and 0.69) from Line Pactol.

Table (4): Differences in cotyledon width, branches point, width of petals, siliqua length and 1000-seed weight among canola varieties in 2006/2007 and 2007/2008 seasons.

Genotype	Cotyledon width (cm)		Branches point (cm)		Width of flower petals (cm)		Siliqua length (cm)		1000-seed weight (gm)	
	2006/ 07	2007/ 08	2006/ 07	2007/ 08	2006/ 07	2007/ 08	2006/ 07	2007/ 08	2006/ 07	2007/ 08
Pactol	0.77	0.69	60.0	58.7	0.75	0.74	8.8	8.7	3.41	3.29
Serw 6	0.77	0.73	56.3	55.1	0.75	0.74	8.1	8.0	3.40	3.39
Serw 10	0.82	0.78	11.5	11.2	0.72	0.71	9.2	9.1	3.40	3.88
Serw 4	1.07	1.03	3.5	3.4	0.72	0.71	9.1	9.0	2.77	2.89
LSD 0.05%	0.12	0.16	23.4	16.0	ns	ns	ns	ns	0.27	0.35

Branches point significantly differed among genotypes, while, they reached the highest length (60.0 and 58.7cm) for Line Pactol followed by Line Serw 6 (56.3 and 55.1cm) and (11.5 and 11.2cm) for Line Serw 10 and they reached its lowest mean (3.5 and 3.4 cm) in variety Serw 4. The significant differences in this trait which is a good character for identification among canola genotypes and is useful in breeding programs. It could be arrange the studied canola genotypes according to the branches point as follows Lines Pactol, Serw 6, Serw 10 and variety Serw 4. Insignificant differences among canola genotypes were noticed in the two seasons for both width flower petals and siliqua length as presented in Table (4).

The canola genotypes significantly differed in 1000-seed weight. The heaviest weight (3.88 g) was obtained by genotype Line Serw 10 in the second season followed by Lines Pactol, Serw 6, and the lowest means of 1000-seed weight (2.77 and 2.89 g) were recorded by variety Serw 4 in the two seasons, respectively. These findings might be attributed to the differences in their genetical constitution and it could be easily recognized them with its 1000-seed weight. However they could be arranged as follows; Line Serw 10, Line Serw 6, Line Pactol and variety Serw 4. The results agreed with those obtained by Khan *et al.,* (2006 b) he found a wide range of genetic variation existed among all the characters under study except 1000-grain weight.

Molecular marker

The 7 RAPD primers produced 72 bands in the 4 canola genotypes under study, 44 bands of them were polymorphic (Table 5). Number of bands ranged from 7 (Primer OP-D02) to 14 (Primer OP-A12). Size of amplified DNA fragments was in the range of 72 to 2447 bp.

Table 5: Levels of polymorphism and unique cultivar-specific band sbased on APD analysis .

Primer	Total bands	Poly morphic Bands	Mono morphic Bands	Poly morphism %	Unique bands	
					Genotypes	MS
OP-A07	9	2	7	22.2	Pactol	1118bp
OP-A12	14	12	2	85.7	Serw 4	1618bp
OP-D02	7	6	1	85.7	-	-
OP-D03	9	5	4	55.6	Pactol	1127, 975bp
OP-D05	11	8	3	72.7	Serw 10	207bp
OP-D15	9	6	3	66.7	Serw 6	1777, 1497,1261, 917,439bp
OP-D18	13	5	8	38.5	Pactol Serw 10	884,365bp116
Total	72	44	28	61.1		

Level of genetic polymorphism observed among the genotypes were in the range of 22.2% to 85.7%. The highest level of polymorphism was observed in primers OP-A12 and OP-D02 which were (85.7 and 85.7%), while the lowest level of polymorphism was 22.2% in primer OP-A07 (Table 5). Primers with higher polymorphic bands are more efficient in studying genetic diversity and discrimination of the genotypes (Pradhan *et al.*, 2004, Roman *et al.*, 2004 and Vladislav CUm Zaludova, 2007).

All genotypes can identified by Unique bands. Line Serw 6 can be identified by lage set of bands at 1777, 1497, 1261, 917 and 439bp of primer OP-D15, while Line Pactol has many specific bands in primers OP-A07 at 1118bp, OP-D03 at 1127, 975bp and OP-D18 at 884, 365bp. There is only one specific band for variety Serw 4 at 1618bp of primer OP-A12, while Line Serw 10 has two bands at 207 and 116bp of primer OP-D05 and OP-D18 respectively. These results are in agreement with those Abdalla, Safia, *et al.*, (2004), they found that DNA analysis was considered essential to distinguish among genotypes while, protein banding patterns were effective in providing resolution for soybean genotypes.

The genetic similarity matrix was calculated among 4 studied genotypes based on RAPD analysis ranged between 87 % and 62%. Maximum (87%) and minimum (62%) genetic similarity coefficients were observed in Line Pactol and variety Serw 4 and Line Pactol and Line Serw 10, respectively as shown in Table 6 .

Based on genetic similarity coefficient, clustering analysis was also carried out for all genotypes based on RAPD analysis (Figure 1) in which the dendrogram separated the genotypes into two clusters, where Line Serw 10 in a separate cluster while, Line Bactol, Line Serw 6 and variety Serw 4 were in the second cluster. These result are in agreement with Moghaddam *et al.*, (2009) who found that RAPD marker can be used as a suitable tool for genetic assessment of rapeseed germplasm. Also, random amplified polymorphic DNA (RAPD) techniques were employed to estimate the genetic diversity within 13 varieties of Chinese, 26 varieties of Japanese and 11 varieties of Korean, European and Canadian B. napus. MAC, *et al.*, (2000).

Table 6: Similarity matrix among the four canola genotypes based on RAPD analysis.

	1	2	3
2	.831		
3	.874	.829	
4	.625	.750	.652

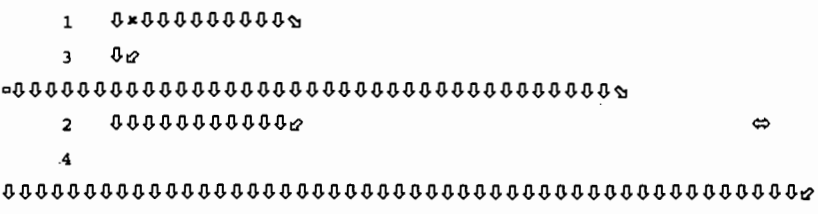

Figure 1: Dendrogram of the genetic distances between the four canola genotypes based on RAPDs analysis.

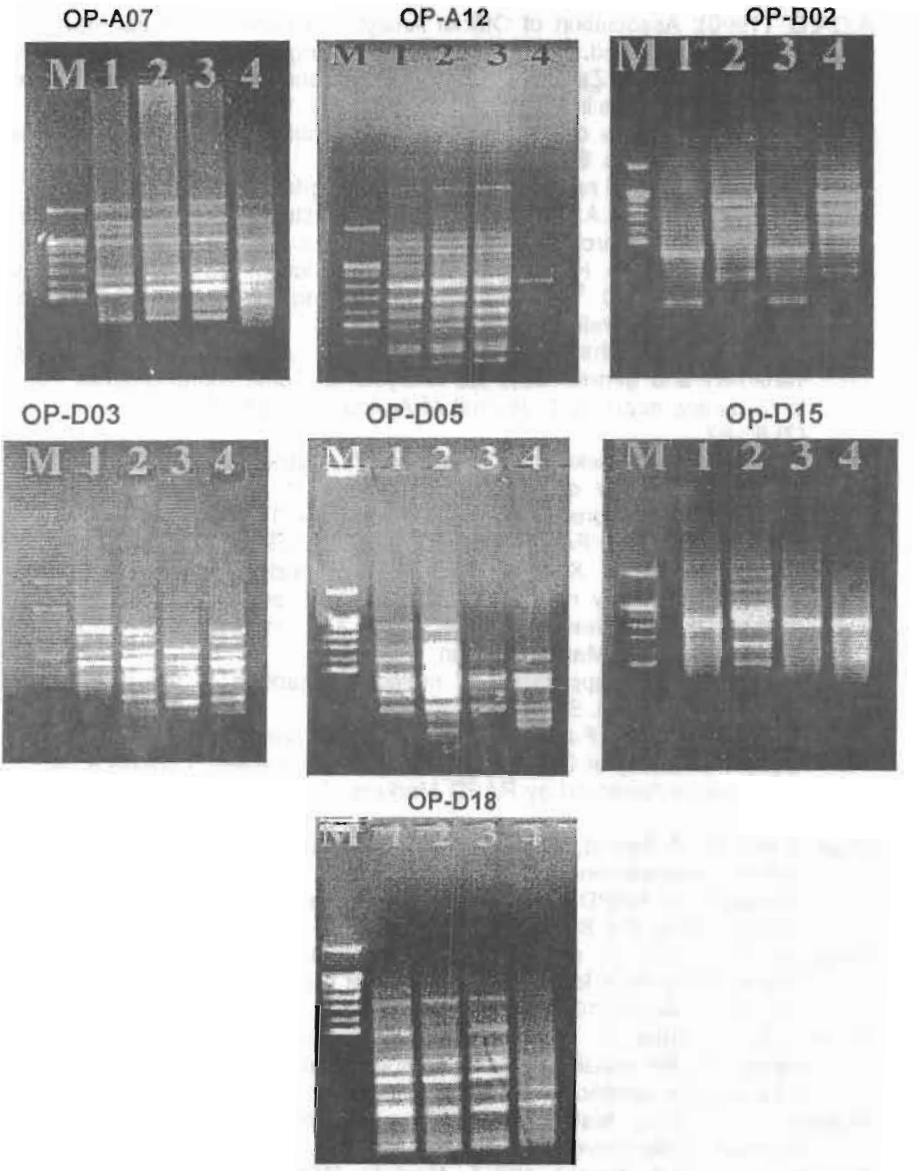

Figure 2: RAPD banding patterns amplified with seven primers

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دراسات مورفولوجية وتكنولوجية على بعض التراكيب الوراثية من الكانولا

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تهدف هذه الدراسة إلى استخدام بعض الصفات المورفولوجية والتكنولوجية والبيوكيميائية لتمييز بعض التراكيب الوراثية لنبات الكانولا وهي: ثلاث سلالات (باكتول، سرو ٦، سرو١٠) وصنف (سرو ٤). لذلك أجريت تجربتان حقليتان بمحطة البحوث الزراعية بالسرو – محافظة دمياط – مركز البحوث الزراعية ، خلال موسمي ٢٠٠٦/٢٠٠٧م، ٢٠٠٧/٢٠٠٨م .١

ويمكن تلخيص أهم نتائج هذه الدراسة فيمايلي:-

بالإضافة إلى محتوى البذور من حامض الإيروسيك فإن الصفات المورفولوجيه مثل نقطه التفريع، ميعاد التذهير، عدد الأفرع الجانبية، وزن الألف بذره ومحصول البذور للنبات الواحد يمكن أن تستخدم للتمييز بين الطرز تحت الدراسة.

وتمييز نباتات السلالة باكتول عن باقى التراكيب الو راثية المدروسة بزيادة درجه تسنين حافه الورقه وطول الورقه وطول عنق الورقه وطول النبات وزياده نسبه الزيت وإرتفاع نقطه التفريع (٦٠ سم) وتميزت نباتاته أيضا بنقص الطول الكلى للنبات (المحتوى على أفرع جانبيه) ونقص عدد القرون/ نبات وعدد البذور بالقرن ومجصول البذور للنبات الواحد. أيضا يمكن تمييز نباتات السلالة سرو ٦ بزياده عدد الأسنان بالورقة وارتفاع طول النبات (١٧٥,٩ سم) وزيادة وزن الألف بذره (٣,٤٠ جم) و قله عدد الفصوص بالورقه وقصر طول عنق الزهرة وعدد البذور بالقرن (٢٢). وتمييز نباتات السلالة سرو ١٠ بالزياده فى عرض الأوراق/ نبات (١٠,١ سم) وطول بتلات الزهره وإنخفاض درجه تسنن حافه الورقه و عنق الورقه (٧,١ سم) وعدد الأوراق/ نبات (٧,٠) وعرض بتلات النوره. كما يمكن تمييز نباتات الصنف سرو ٤ عن نباتات باقى الأصناف المدروسه بالزياده فى طول الأوراق الفلقيه وعرضها وعدد الفصوص بالورقه وعدد الأوراق/ نبات وطول عنق النوره وعدد الأفرع الجانبيه وطول بوز القرن وعدد القرون للنبات (٨٨٨,١) وعدد البذور بالقرن (٣٠) ومحصول البذور/ نبات (٦٨,٥٦ جم) وتميزت نباتاته أيضا بإنخفاض طول الورقه وعرضها وطول النبات (١٢١,١ سم) و نقطه التفريع (٣,٤ سم) ووزن الـ١٠٠٠ بذره (٢,٧٧ جم).

تم استخدام تكنيك RAPD-PCR لتمييز الاختلافات بين التراكيب الوراثية تحت الدراسة وذلك باستخدام سبعة بادئات عشوائية أظهرت ٦١% نسبة اختلاف وأظهر التحليل أن أعلي درجة تشابه كانت ٨٧% بين السلاله باكتول والصنف سرو ٤ بينما أقل درجة تشابه كانت بين السلاله باكتول والسلاله سرو ١٠. قسمت الشجرة التطورية هذه التراكيب الوراثية الي مجموعتين حيث ظهرت السلالة سرو ١٠ في مجموعة مستقلة بينما باقي التراكيب الوراثية (السلالة باكتول، السلالة سرو ٦ والصنف سرو ٤) كانت تنتمي الي المجموعة الثانية.

وتشير نتائج التفريد الكهربي لبروتين التراكيب الوراثية المدروسة باستخدام SDA- PAGE إلى وجود اختلافات بين الطرز المدروسة، حيث كان هناك عدد من روابط البروتين المميز للتراكيب الوراثية المدروسة، حيث أعطى الطراز الوراثي باكتول أعلى عدد من روابط البروتين الكلية بينما أعطى الطراز الوراثي سرو ٦، سرو ٤ أقل عدد من روابط البروتين الكلية.

تعتبر النتائج المتحصل عليها من هذه الدراسة ذات أهمية كبيرة في حفظ حقوق مربو النباتات عند تسجيل التراكسب الوراثية كأصناف تجارية جديدة الا أنة علي مربي النبات الانتخاب من قاعدة وراثية عريضة حتي يمكن الحصول علي صفات مورفولوجية مميزة للسلالات الجديدة عن الأصناف المنزرعة المسجلة وذلك عند تسجيلها كأصناف جديدة مما يسهل التحقق من نقاوة الصنف الجديد أثناء مراحل اكثارة المختلفة.

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