Journal of Basic and Environmental Sciences, 6 (2019) 273-281

ISSN
Online: 2356-6388
Print: 2536-9202

Research paper Open Acces

Genetic Variability and association of some quantitative characters and protein fingerprinting in some canola genotypes

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Abstract

The aim of this study was to estimate the genetic parameters and genetic advance from the selection of yield and its components, which can provide basic information for the explanation of valuable lines and check variety combinations of canola and protein fingerprinting. Fifteen lines and check variety were planted in 2015/ 2016 and 2016 / 2017, at Bahteem Agricultural, Research Station. The selection was practiced in the first season on the basis of 50% flowering, physiological maturity, seed yield/plant and seed oil content. A total of 150 selected plants were evaluated in a replicated trial in 2016/ 2017 season at Bahteem Res. Station. Genetic variability, heritability, Phenotypic and genotypic coefficient of variation, and genetic advance from selection were estimated. Significant differences were observed among check variety serw-4 selected plants in both seasons for most studied traits. Broad sense heritability estimates in the second season ranged from 1.00 to 81.00%. High heritability coupled with high genetic advance from selection was recorded for seed yield/plot, seed yield/plant, first silique height, and physiological maturity. Hence selection for these traits is expected to be effective. There was a positive and highly significant genotypic correlation coefficient between seed yield/plot and seed oil percentage, indicating the possibility of increasing oil content with high seed yield/plot.

The electrophoresis profile of seed storage protein for fifteen lines and check variety. The Molecular weight 188 polypeptide bands of diver's molecular weight ranging from 12 to 155 KD. Based on molecular weight the banding pattern revealed specific regions (12 to 35 KD) comprised 8 bands.

Keywords: Canola, Brassica Napus, population selection criteria, Genetic advance, Heritability, correlation advance, correlation coefficient, molecular markers.

Received; 24 June 2019, Revised form; 18 July 2019, Accepted; 18 July 2019, Available online 1 Oct. 2019.

1. Introduction

Canola (*Brassica napus, L.*) is an important species and a high-value crop for oil industries content and could be used for producing edible vegetable oil. It is among the important oil crops in the world [1]. There is about 95-99 %., shortage of edible vegetable oils in Egypt. The Egyptian strategy aimed to increase the edible oil production through increasing the areas devoted to oil crops, such as canola as a winter oil crop, in Egypt. And also increasing their seed yield productivities. Development of high seed and oil yielding hybrids or cultivars of canola crop would meet the Egyptian strategy. Studying the genetic components for main agronomic characters is the goal of the breeding strategy for canola crop. Heritability is one of the popular indices, between help phenotypic and breeding value, [7] The local production of edible oil from all oil seed crops and cotton seed is only sufficient to meet about one %of the domestic consumption with remaining being met through heavy imports [19]. These imports are continuously increasing annually at an alarming rate thus Egyptian spends a huge foreign exchange on the import of edible oil to meet the local consumption [7]. Studying of the genetic components for main agronomic characters is the goal of the breeding strategy for canola crop, [9] and has direct effect on selection [15] reported high genetic variability for number of racemes/plants, plant height and seed yield among 11 rapeseed varieties. In addition, high heritability and genetic advance (GA) for these traits were reported [20]. Also reported similar results in a diallel cross among 8 varieties [8] who showed that estimation of some genetic parameter for yield and its components in canola. Basic proteins with low molecular weight (15- 26 KDa) are structural proteins associated with oil bodies and constitute 2-8% of the total canola seed proteins [13] and [1])

The objectives of this study were to estimate the genetic parameters, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (h^2_b), genetic advance (Δ G) from selection for yield components, and protein fingerprinting of canola which can provide the basis for the exploitation of valuable lines combinations in future breeding programs.

2. Materials and methods

Fifteen lines and check variety, the study pertaining to genetic variability, heritability, phenotypic correlation and protein fingerprinting for quality character, were planted in two winter seasons, 2015/2016 and 2016/2017 respectively. The planting was done in a randomized complete block design with three replications. Each experimental plot consisted of five rows 4-m long and 60-cm width the plot area was 12.00m^2). Spacing between plants within the row was kept at 20 cm. Thinning was practiced after 21 days from planting, leaving one

plant/hill. All other agronomic practices were applied according to recommendation. About sixty single plants per replication (total of 180 plants from each in first season) were selected individually in pedigree methods.

The 180 plants were grown in the second season 2016 / 2017 using the same planting method and agronomic practices as applied in first season Fifty single plants were selected in each replication (total of 150 plants from each in the first season) along with check cultivar. The selection was practiced among and within rows in the second season 2016 /2017.

In the two season, individual plant selection (pedigree method) was practiced. At maturity, data were recorded on, 50% flowering date(days), physiological maturity(days), plant height(cm), number of racemes/plant, first silique height (cm), 1000- seed weight(g), seed yield /plant (g), seed yield / fad(kg) and seed oil content (%). All data subjected to analysis of variance based on randomized complete block design at the seasons. Combined analysis of variance was performed, after confirmed of homogenous of both seasons [10]. Data were genetically analyzed to estimate variance as well as genetic parameters i.e., genotypic coefficient of variability (GCV %), and phenotypic coefficient of variability (PCV %), broad-sense heritability (h^2_b) and expected genetic advance (Δ G). From selection. Genetic analysis was computed according to [3]. Expected genetic advance was calculated on the first season (180/300) x 100 = 60 selection intensity 10%, also in the second was (150/300) x 100 = 50 from selection was calculated on 10 % selection intensity. Correlation coefficient analysis was conducted following the procedure developed by [24] and applied by [5]. Seed yield/plant was kept as a resultant variable and correlation of other components and characters as causal variables. The components of variance including error variance ($\delta^2e=MS_2$) genotypic variance $\{\delta^2g=MS_1-MS_2/r\}$ and phenotypic variance $\{\delta^2ph= \delta^2e+ \delta^2g\}$ were estimated, according to the following formula. Heritability ($h^2_b= \delta^2e + \delta^2p_h$ x100 Broad sense heritability) was estimated according to [23]. The coefficients of genotypic and phenotypic variation were calculated according to Burton formula [2]. The genetic advance (GA) from selection was estimated based on formula of [1]. [GA= (K) (h^2) ($\sqrt{\delta^2_P}$)] assuming 10 % (ca.10%) selection intensity. Meanwhile, the phenotypic and genotypic correlation between variable x and y.(r(xy)p) and r(xy)g), were also estimated following [16].

SDS-protein electrophoresis:

For miniscale preparations of all fifteen lines and check variety in canola samples, 0.3 mg of leaf tissue (10 Days old) were grinded with phosphate buffer (pH: 7) and pelted down then only 20ul with (80 ug) protein concentration was added to equal volume of Laemmli Sample Buffer, 5µl of 10%SDS and 5µl of β–mercaptoethanol then boiling the mixture for 5 min and centrifugation to obtain the supernatant which contains the protein fractionations. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was performed according to the method of [[17]. Samples prepared by adding Protein fractionation electrophoresis was performed on 12% acrylamide gel using the apparatus manufactured by BioRad. Gels were analyzed using Total Lab TL100.

Data analysis

The photographs of SDS- PAGE gel was used to study the protein profile of all lines and check cultivar. The bands were designated on the basis of their molecular weight. The presence of protein band was scored as (+) positive and its absence (-) negative as shown in Tables (5) only bright, clearly distinguishable bands were used in genetic analysis

2. Results and discussion

Combined analysis of variance (ANOV) for all traits over the two seasons is presented in Table (1): Data revealed a highly significant difference among genotypes, for all studied characters.

Table 1 combined analysis of variance for nine traits in 16 lines of canola tested across two growing seasons.

s.o.v	d.f	50% flowering (days)	Physiological Maturity (days)	Plant height (cm)	No of racemes/ plant	First silique Height	1000-seed weight	Seed Yield/ plant	Seed yield/ fad	Seed oil content
Rep	2	0.021	1.65	1.08	0.14	4.58	0.20	9.94	3894..04	0.03
Geno	15	35.37**	376.41*	368.14**	2.33**	317.24**0	0.59**	126.47**	5784.41**	1.05**
Error	30	0.81	0.73	6.40	0.16	9.00	0.04	9.96	7558.17	0.05

For all studied characters. Besides, genotypes exhibited highly significant for all studies characters, out of the nine characters studied assuming less effect of changes caused by different years on the genetic performance of the entries. These results are in agreement with [8].

The means of all studied characters for each of the fifteen lines and cheek cultivar (serw-4) are presented in Table (2). The results showed different responses of the nine agronomic characters in the two seasons. In the first season, days to 50 % flowering ranged from 72.00 to 91.67 days and the line 12 was the earliest, while cheek cultivar (serw -4) was the latest in 50% flowering date.

In the second season, the results revealed that line 5, was the earliest in 50% flowering date and had high seed yield/plant. These variations in lines and check variety in two seasons, for flowering date, depends on interaction between genetically and environmental or a minor gene complex. There are some valuable sources for earliness. The present results agreed with those [7].

In the first season, physiological maturity ranged from 104.00 to 142.33 days and line 4 was the earliest one, while serow-4 was the latest in physiological maturity. The results in the second season revealed that line 4 was the earliest, while serw – 4 and line 9 were the latest in physiological maturity.

Also, plant height in the first season ranged from 132.67 to 196.33 cm. The tallest plant height was recorded in line3, while serw- 4 gave the shortest one. While in the

second season, plant height was ranged from 137.13 to 207.67cm. The tallest plant height was recorded in line 14, while serw-4 was the shortest one.

In the first season, mean number of racemes/ plant ranged from 5.44 to 7.39, the highest number of racemes was recorded in line 14, while the lowest number of racemes was recorded in line 15 .While in the second season, number of racemes was ranged from 4.90 to 8.83, the highest number of racemes was recorded in line 7, while the lowest number of racemes was recorded in line10, these results are agreement with [7].

For the first silique height in the first season, it ranged from 87.00 to 136.22cm ,the lowest first silique height was recorded in cheek variety (serw-4) , while the highest of first silique height was recorded in line 7, While in the second season the first silique height ranged from 105.17 to 139.17cm, the lowest in first silique recorded in line 1, while the highest of first silique height was recorded in line 7.

Table 2: Mean values of agronomic traits for 15 lines and cheek variety (serw-4) evaluated in two seasons.

Characters / Genotypes	50% flowering (days)			Physiological maturity (days)			Plant height(cm)		
	First season	Second season	Combined	First season	Second season	Combined	First season	Second season	Combined
Serw - 4	91.67	92.00	91.83	142.33	139.00	140.67	132.67	137.13	134.90
1	78.67	79.00	78.83	109.00	111.00	110.00	161.89	173.33	167.61
2	80.00	82.00	81.00	129.00	131.00	130.00	179.67	195.44	187.56
3	82.00	85.00	83.50	107.00	109.33	108.17	196.33	196.11	196.22
4	82.00	81.00	81.50	104.00	106.00	105.00	171.44	196.81	184.13
5	81.00	76.00	78.50	135.00	136.33	135.67	163.11	166.72	164.92
6	82.00	81.00	81.50	131.33	134.00	132.67	179.56	179.47	179.51
7	80.33	79.00	79.67	133.00	132.33	132.67	182.22	204.17	193.20
8	81.00	82.00	81.50	134.00	134.00	134.00	192.44	202.50	197.47
9	81.00	82.00	81.50	140.33	139.00	139.67	183.00	195.17	189.08
10	79.00	80.00	79.50	138.00	135.00	136.50	176.22	182.50	179.36
11	80.33	82.00	81.17	123.33	132.00	127.67	170.89	173.00	171.94
12	72.00	83.00	77.50	132.33	135.00	133.67	174.11	182.33	178.22
13	73.33	81.67	77.50	134.67	135.00	134.83	173.78	188.67	181.22
14	83.00	81.00	82.00	131.67	136.00	133.83	194.78	207.67	201.22
15	83.00	86.33	84.67	134.67	134.00	134.33	175.00	192.00	183.50
Mean	80.65	82.06	81.35	128.73	129.94	129.33	175.44	185.81	180.63
LSD5%	2.12	1.71	1.50	2.37	1.96	2.17	6.84	7.60	7.22
CV	1.58	1.25	1.11	1.11	0.91	0.66	0.97	2.45	1.40

Table 2 continued.

Characters / Genotypes	No. of racemes/plant			First silique height (cm)			1000-seedweight(g)		
	First season	Second season	Combined	First season	Second season	Combined	First season	Second season	Combined
Serow4	5.67	5.22	5.45	87.00	120.83	103.92	2.82	2.92	2.87
1	5.56	6.83	6.20	92.24	105.17	98.71	4.77	4.39	4.58
2	6.10	7.67	6.89	110.67	125.83	118.25	4.20	4.09	4.14
3	6.11	6.67	6.39	116.00	113.89	114.95	4.37	5.12	4.74
4	5.69	6.89	6.29	94.66	116.11	105.39	4.24	4.29	4.27
5	5.72	5.61	5.67	130.44	122.56	126.50	4.38	3.96	4.17
6	6.44	6.33	6.39	115.99	109.50	112.75	4.21	3.52	3.86
7	6.67	8.83	7.75	136.22	139.17	137.70	4.38	4.45	4.42
8	5.78	6.73	6.26	125.44	128.50	126.97	4.23	4.40	4.32
9	5.67	4.97	5.32	116.33	130.00	123.17	4.28	3.74	4.01
10	6.00	4.90	5.45	113.56	119.17	116.36	4.40	4.18	4.29
11	5.89	5.67	5.78	103.89	122.50	113.19	4.53	4.47	4.50
12	5.78	5.70	5.74	106.45	111.01	108.73	4.35	5.20	4.78
13	7.33	8.80	8.07	111.45	114.84	113.14	4.17	4.33	4.25
14	7.39	7.67	7.53	122.78	126.67	124.72	3.86	4.24	4.05
15	5.44	5.00	5.22	116.33	138.44	127.39	3.65	4.31	3.98
Mean	6.08	6.47	6.27	112.47	121.51	116.99	4.18	4.23	4.20
LSD5%	0.98	0.85	0.90	6.32	8.63	7.48	0.48	0.52	0.32
CV	6.67	7.90	7.19	14.26	17.16	15.71	6.85	7.35	4.54

Table 2 continued.

Characters / Genotypes	Seed yield / plant (gm)			Seed yield/fad (kg)			Seed oil content/fad (kg)		
	First season	Second season	Combined	First season	Second season	Combined	First season	Second season	Combined
Serow4	15.00	15.43	15.22	399.74	570.78	485.26	172.81	248.29	210.55
1	31.53	38.46	35.00	390.74	520.07	455.41	167.24	226.59	196.69
2	37.17	52.48	44.82	417.38	315.95	366.67	178.35	222.38	156.75
3	29.07	43.55	36.31	442.26	694.26	568.26	187.34	300.27	243.27
4	30.67	41.11	35.89	491.09	513.45	502.27	214.56	301.59	218.84
5	30.75	58.89	44.82	566.37	568.58	567.48	247.39	221.89	247.76
6	28.33	35.91	32.12	685.44	857.12	771.12	297.48	375.42	336.21
7	30.76	36.35	33.56	740.57	770.18	755.38	323.33	335.41	329.35
8	30.75	45.12	37.94	729.54	850.19	789.87	326.40	379.69	353.07
9	32.98	40.60	36.79	842.31	897.75	870.03	368.26	396.90	382.47
10	33.27	36.73	35.00	556.29	772.38	644.34	241.76	335.83	280.09
11	36.05	42.38	39.21	853.97	520.38	687.18	374.98	225.75	301.33
12	32.24	39.01	35.63	713.48	734.58	724.05	320.00	322.48	321.33
13	27.66	38.12	32.89	628.11	719.78	673.95	281.27	317.28	299.44
14	32.32	38.37	35.34	575.19	559.44	567.32	256.36	246.60	251.49
15	30.48	36.95	33.72	705.60	860.58	783.09	315.05	381.84	348.55
Mean	30.56	39.97	35.27	608.59	599.18	603.89	266.38	262.02	264.20
LSD5%	5.68	9.78	9.23	4.66	2.876	3.77	1.91	1.73	1.92
CV	7.23	14.67	19.95	774.90	906.90	840.90	441.69	743.66	580.22

In the first season weight of 1000- seed ranged from 2.82 to 4.77g. The heaviest 1000- seed recorded by line 1, while the lightest was for cheek variety serw-4. While in the second season it ranged from 2.92 to 5.20 g. The heaviest 1000-seed recorded by line 12 while the lightest was for cheek variety serw-4.

Data revealed that the range for seed yield per plant in the first season was from 15.00 to 38.33 g. The highest value was obtained by line 6, while the lowest seed yield/ plant was obtained from the cheek variety serw-4.

Also, this trait ranged from 15.43 to 58.89 g in the second season the heaviest value was obtained by line 5 while the lowest seed yield/ plant was obtained from the cheek variety serw-4.

Data in Table (2) illustrated seed yield / faden in the first season was ranged from 853.47 to -390.47 kg. The line11 recorded the highest yield, while line 2 recorded the lowest seed yield / faden. While in the trait second seasons ranged from315, 95-to 897.75kg. The line 9 recorded the highest yield, while the line 2 recorded the lowest seed yield /faden.

Concerning Seed oil content, it ranged from 167.24 to 368.76% in the first season the highest seed oil content /faden was observed for line 9, and the lowest was by lin1, while it the second seasons ranged from222.38 to396.90. % the highest oil content/faden was observed for line 8, and the lowest one by line2. Line 9 was high seed oil content / faden and high seed yield / faden. These results are in agree with [7].

The results in Table (3) indicated that for all studied traits in two seasons, the phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all characters in two seasons, but in many cases, the two values differed only slightly.

The results in Table (3) indicated that for all studied traits in two seasons the genotype, phenotype and environmental variances were significant for all characters except No. of racemes, 1000-sed weight and of seed oil content/faden%, indicating the presence of sufficient genetic variability for effective selection helping to identify the superior genotypes as shown in Table (3). Although significant results have experienced the variation between the genotypes was not broad for No. of racemes (0.24-1.56), 1000-seed weight, 0.17-0.27 and seed oil content (0.59 and 1.8). The genotypes significantly differed for the last two characters in two seasons. However, selected efficiency is related to magnitude of heritability and genetic advance [14]. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all characters in two seasons, but in many cases, the two values differed only slight. The highest values were shown in the second seasons, plant height and seed yield/plant except first season Physiological maturity, first silique height, and seed yield/fedan. These results are in agreement with those of [7].

Therefore, it is essential to assess the relative effect of genotypes and environmental to have an estimate of the extent to which improvement is possible in the traits under consideration. The results are in agreement with those of [6] and [7]. The results showed highly significant variation for two seasons indicating the presence of sufficient genetic variability for selection helping to identify the superior hybrid.

As for phenotypic coefficient of variability values for seed yield /faden was (159.38), first silique height in

second seasons was (121.51), seed yield/ plant (87.07g) number of racemes (9.39), and plant height was (58.26). High genotypic and phenotypic coefficient of variability was recorded for seed yield/ plot physiological maturity, first silique height, seed yield/ plant, and plant height. The present data means that selection based on phenotype performance may be useful for yield improvement. These results are similar to those reported by [15, 4], and to those by [7].

Results of broad-sense heritability estimates were high in the first season and ranged from 0.67 to 1.00 while in the second seasons it ranged from 0.86 to 1.00 for all characters. The estimates were high due to high genotypic influence. The highest value was obtained for physiological maturity, plant height, 50% flowering date and first silique height in two seasons. Heritability estimates indicated that these traits are less influenced by environmental conditions. Heritability accompanied with high genetic advance is rather useful than heritability alone for predicting the selection effect.

These results are in agreement with those reported by [14]. The excepted genetic advance expressed as a percentage of the mean varied from (0.44 and 0.67 in 1000- seed weight in two seasons and oil content 1.29 and 0.51 respectively as shown in Table3. The high expected genetic advance was observed for seed yield per faden, and plant height, in two seasons. These results are in agreement with those of [15].

Meanwhile, second seasons ranged from (1.00 to 81.00). All studied characters showed high heritability coupled with high genetic advance for seed yield per faden, seed yield per plant, first silique height and physiological maturity indicated the percentage additive gene effects and that these traits could be improved by selection. Therefore, genetic advance as a percentage of mean was also computed in these studies. High heritability and moderate genetic advances were shown in some characters, planted. 50% flowering date and plant height indicating moderate magnitude of additive gene effects. High heritability for the previous characters in second seasons showed that two characters with moderate genetic advance could be consisted indication that improvement can be done by selection.

The selection is advocated for those characters because data indicated the presence of additive gene effects, hence their improvement can be done through selection. Also high heritability coupled with moderate genetic advance was shown in first silique height, meanwhile high heritability of seed oil content per faden (0.81) coupled with low genetic advance (1.17) indicated that influence of dominant and epistatic effect on this trait also indicates that non additive gene effects are more important and selection on phenotypic value may not be much effective to improve this trait. These results confirm the findings of [22,21].

Table 3: Genotypic, Phenotypic and environmental variances, Genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), broad-sense heritability (h^2_b) and genetic advance (GA) from selection for the studied traits in canola.

Traits	Seasons	$\delta^2 g$	$\delta^2 ph$	$\delta^2 e$	GCV	PCV	h^2	GA	GA%	SI%
50% Flowering	First	17.72	19.34	1.62	7.32	7.99	0.97	38.71	48.01	9.07
	Second	12.30	13.36	1.06	5.00	5.43	0.97	26.79	32.65	7.54
Physiological maturity	First	138.79	140.82	2.03	35.94	36.46	1.00	289.11	224.59	24.48
	Second	115.24	116.63	1.39	29.56	29.92	1.00	239.65	184.43	22.28
Plant height	First	228.69	231.59	2.9	34.45	44.00	1.00	475.76	271.18	31.40
	Second	304.00	324.78	20.78	54.54	58.26	0.98	655.09	352.55	37.18
No. of racemes	First	0.24	0.58	0.34	1.31	3.20	0.67	0.81	13.34	1.58
	Second	1.56	1.82	0.26	8.05	9.39	0.95	3.56	55.07	2.79
First silique height	First	178.19	184.90	6.71	52.81	54.80	0.99	28.05	376.72	28.05
	Second	86.15	112.92	26.77	30.98	121.51	0.91	211.08	137.71	21.92
1000- seed weight	First	0.17	0.25	0.08	1.33	1.99	0.86	0.44	10.58	1.03
	Second	0.27	0.36	0.09	2.10	2.86	0.89	0.67	15.78	1.24
Seed yield / plant	First	21.81	26.70	4.90	23.79	29.12	0.93	51.25	167.68	10.66
	Second	70.01	104.39	34.38	58.39	87.07	0.86	185.07	463.05	21.08
Seed yield / faden	First	231.45	239.35	7.9	399.25	412.88	0.99	488.23	252.65	100.93
	Second	609.65	909.46	299.81	106.84	159.38	0.86	161.20	847.46	196.74
Seed Oil content/ faden	FirstS	0.59	0.65	0.06	0.45	0.49	0.97	1.29	2.95	1.66
	Second	0.18	0.31	0.13	0.14	0.23	0.81	0.51	1.17	1.15

Phenotypic and genotypic correlation coefficients between different traits in two seasons are presented in Table (4). However, the discussion will focus on second seasons only. The results revealed that 50% flowering date had highly significant and positive correlation with seed yield per plant (-0.770), regarding 1000-seed weight had significant and negative (-0.592) Meanwhile plant height showed positive and significant correlation with number of racemes /plant and 1000-seed weight. First silique height in second seasons had positive and highly significant with

1000 – seed weight. Meanwhile 1000 – seed weight in second seasons had positive and significant correlation with seed yield per plant. Regarding seed yield per faden in second season it had positive and high significant correlation with of seed oil content faden.

Table (4): Phenotypic (P) and genotypic (G) correlation coefficient of canola traits in the first and second seasons.

Traits	Season		Physiological maturity	Plant height	Number of racemes	First silique height	1000-seed weight	Seed yield /plant	Seed yield/plot	Seed yield/fad
50 % flowering	First	G	-0.090	-0.363	-0.272	-0.181	-0.762**	-0.603	-0.292	-0.367
		P	0.094	-0.350	-0.195	-0.180	-0.592*	-0.516*	-0.291	-0.339
	Second	G	0.117	-0.391	-0.311	0.087	-0.297	0.770**	-0.488	0.070
		P	-0.104	-0.357	-0.305	0.071	-0.237	-0.585*	-0.390	0.003
Physiological maturity	First	G		-0.170	0.187	0.353	-0.502*	-0.191	0.0.410	-0.48
		P		-0.171	0.101	-0.345	-0.385	-0.230	0.396	0.417
	Second	G		-0.183	-0.219	0.469	-0.449	-0.147	0.433	0.428
		P		-0.172	-0.206	0.412	-0.362	-0.135	0.348	0.334
Plant height	First	G			0.491	0.645**	0.516*	0.640**	0.337	0.160
		P			0.296	0.629**	0.395	0.564	0.333	0.163
	Second	G			0.514*	0.375	0.556*	0.462	0.427	0.270
		P			0.453	0.355	0.499*	0.352	0.372	0.226
Number of racemes	First	G				0.437	0.021	0.060	0.045	0.343
		P				0.311	-0.019	-0.014	0.061	0.129
	Second	G				0.024	0.319	0.138	-0.067	-0139
		P				0.025	0.146	0.145	-0.037	-0.100
First silique height	First	G					0.296	0.362	0.955	0.265
		P					0.230	0.315	0.450	0.251
	Second	G					0.806**	0.123	0.303	0.309
		P					0.326	-0.026	0.232	0.231
1000-seed weight	First	G						0.362	0.455	0.265
		P						0.649**	0.179	-0.133
	Second	G						0.499*	0.098	-0.006
		P						0.288	0.034	0.015
Seed yield /plant	First	G							0.355	0.066
		P							0.299	0.059
	Second	G							0.171	-0.100
		P							0.115	-0.157
Seed yield / faden	First	G								0.6.11*
		P								0.587*
	Second	G								0.848**
		P								0.447
seed oil content		G								
		P								
		G								
		P								

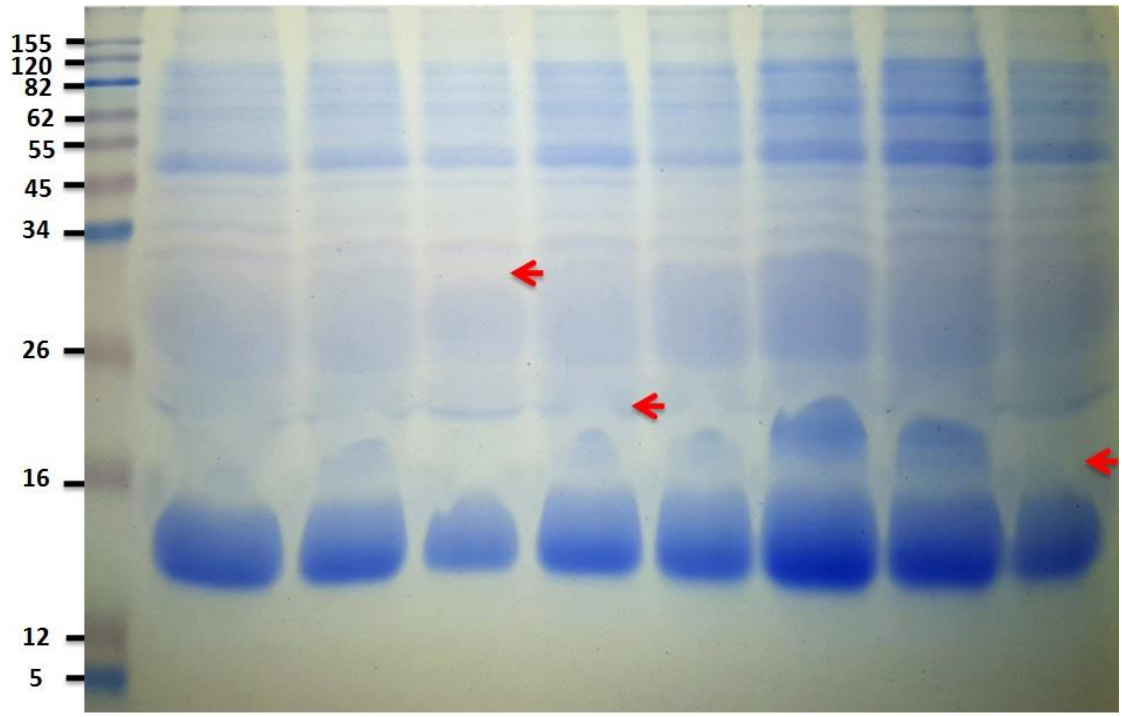

Fig (1): SDS-PAGE profile of seed storage protein of eight canola lines from No. 1check variety 2- 8 lines Protein concentration 25ug/sample. Stained with comassie blue on 12% acrylmide gel.

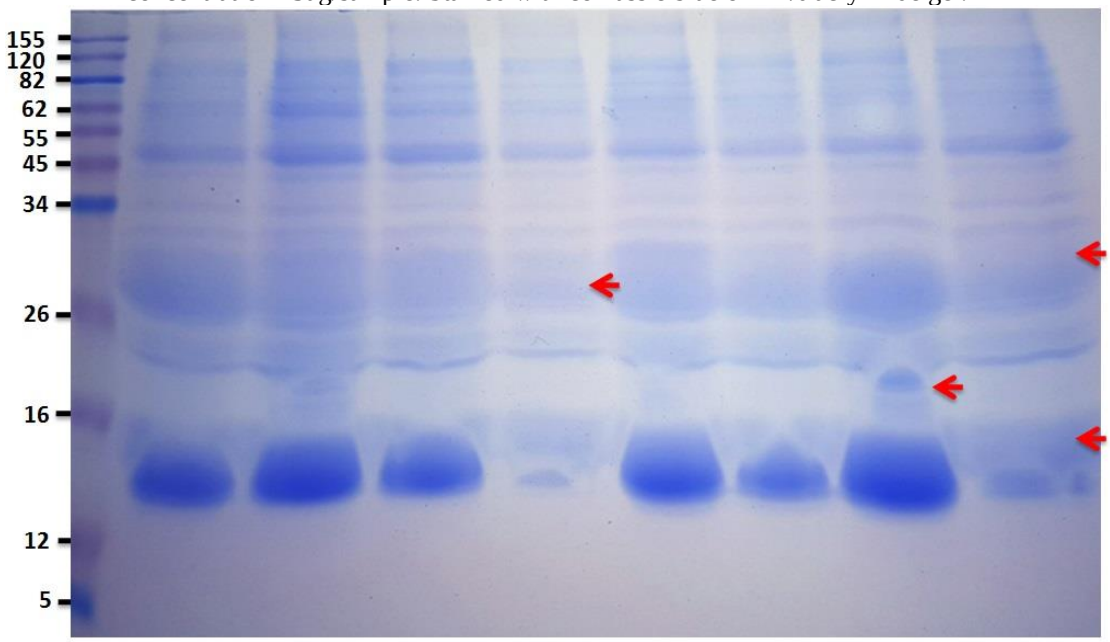

Fig (2): SDS-PAGE profile of seed storage protein of canola lines from 9 -16 lines Protein concentration 25ug/sample. Stained with comassie blue on 12% acrylmide gel.

The electrophoresis profile of seed storage protein for fifteen lines and check variety of serw-4 divided into two groups, Group 1 (1 to 8), No.1 check variety (serw-4) 2,3,4,5,6,7 and 8 lines Group 2 (9,10,11,12,13,14,15 and 16) lines in second season were studied and reveal qualitative and quantitative intra and interspecific variations in terms of band number, staining intensity and molecular weight (Figs. 1,2). 243 protein polypeptide bands of diverse molecular weights ranging from 12 to 155kD were detected via SDS electrophoresis pattern, only six polypeptide bands were polymorphic. Our SDS-PAGE lines band number ranged from 100 - 220 bands. Among the quantitative variation between the three groups of canola lines we notice each line.

Group1 revealed 3 to 4 polymorphic bands even there are two specific polypeptides band (100, 32 and 14kD) excised in all canola lines groups as distinguish band for all different lines and check variety. Bands (100.6kD), (62.5kD), (45.6kD) and (14.8kD) were common in all the genotypes whereas band (30.0kD) was missing in lines Table (4, 5) these bands can be considered as species-specific (Fig. 1 and 2), table (5 and 6). Band with molecular weight 30kD showed stain intensity variation between lines of group No. 2. It was high intensity in

genotype 12 and 17. Fig. 2. Based on molecular weights the banding pattern revealed specific regions (12-35kD) comprised 8 bands, which could be used as signature for SDS-PAGE profile pattern for seed storage protein of canola.

Table (5): Molecular weights and polymorphic bands presence or absence in group1 genotypes of canola (*Brassica* L.)

Band MW	Genotypes							
	1	2	3	4	5	6	7	8
155	+	+	+	+	+	+	+	+
100	+	+	+	+	+	+	+	+
80	+	+	+	+	+	+	+	+
62	+	+	+	+	+	+	+	+
48	+	+	+	+	+	+	+	+
40	+	+	+	+	+	+	+	+
34	+	+	+	+	+	+	+	+
30	+	+	+	-	+	-	+	-
28	+	+	+	+	+	+	+	+
25	+	+	+	+	+	+	+	+
20	-	+	-	-	+	-	+	-
16	+	+	+	+	+	+	+	+
12	+	+	+	-	+	+	+	-
Total	12	13	12	10	13	11	13	10

Table (6): Molecular weights and polymorphic bands presence (+) or absence (-) in group 2 genotypes of canola (*Brassica* L.).

Band MW	Genotypes							
	9	10	11	12	13	14	15	16
155	+	+	+	+	+	+	+	+
100	+	+	+	+	+	+	+	+
80	+	+	+	+	+	+	+	+
62	+	+	+	+	+	+	+	+
48	+	+	+	+	+	+	+	+
40	+	+	+	+	+	+	+	+
34	+	+	+	+	+	+	+	+
30	+	+	-	+	+	+	+	+
28	+	+	+	+	+	+	+	+
25	+	+	+	+	+	+	+	+
20	-	-	+	-	-	+	-	+
16	-	+	-	+	+	+	+	-
12	+	+	+	-	+	+	+	+
Total	11	12	11	11	12	13	12	12

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