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DEVELOPMENT OF NEW BROAD BEAN LINES BY SELECTION

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ABSTRACT: From segregating F_3 populations, promising 17 lines of broad bean were selected in F_7 and evaluated during successive winter seasons of 2004/05 to 2008/09 at El-Gemmiza Agriculture Research Station, Gharbia Governorate. Promising selected lines were evaluated with two commercial cultivars. Estimates of coefficient of variance (C.V.%) values in the new lines for the studied characters revealed high homogeneity within lines and it became similar to the check cultivars. These new lines are enough homogeneous and could be considered as new pure lines .The lines S-10, S-14,S-17, S-19, S-20, and S-22 showed the lowest C.V.% values for most studied traits, indicating that they became more homogeneous. About 40 % of all lines were significantly exceeded the mean of the check cultivars by a value reached to 35.4%. The percentages of this increment were 35.36, 24.87, 24.26 and 15.10 % in the lines S-10,S-8,S-11 and S-1, respectively. Thun, it could be concluded that the lines S-10,S-8,S-11 and S-1 are promising compared with check cultivars and could be recommended as new lines.

The results revealed significant differences among the new lines in all studied traits. Analysis of the phenotypic variances revealed that 76% to 97% were due to genetic factors. Also a high broad-sense heritability which ranged from 57.48% to 94.22%, was found indicating small environmental effects and large additive genetic components of the phenotypic variation for these traits. Accordingly, selection based on phenotypic observations could be effective in the segregating generations for improving these traits. Based on the correlation coefficient, number of seeds per pod, pod number, weight and length, seed pod weight and 100-seed weight appeared to be the principal yield attributes for indirect selection.

Key words: Selection, broad bean, lines, heratibility, association.

INTRODUCTION

Broad bean (*Vicia faba* var. *major*) is an excellent source of low-cost and a basic food for the poorer groups of the population. Cultivated area was limited and great demands have increased as a result of the continuous rise of the population. So, the improvement of broad bean productivity through breeding methods, such as pure line selection, mass selection and introducing high yielding genotypes was considered of national interest. Evaluation trials of broad bean genotypes were conducted by Link *et al.*(1994), Mulat (1998), Bassiouny (2001), Abd-ElKader-Helmy (2001),Farag and Helal (2004), Farag (2007and 2008) and Farag and Morsy (2009). They found significant varietal differences among faba bean genotypes regarding plant growth, yield and yield components.

Good understanding for the genetic of yield and its component traits are the pre-requests for planning suitable breeding methodology. Many investigators used selection or recommended selection in breeding programs to obtain new lines of broad bean. Farag and Helal (2004), Farag and Darwish (2005), Farag *et al.* (2005) and Farag (2007 and 2008) found significant progress for improvement of broad bean yield and its components could be achieved in the segregating generations through selection. The high-yielding stable genotypes and possibility of improving broad bean yield may be occur through obtaining pure lines selection programs (Abd-ElKader-Helmy, 2001, Abd El-Rahim *et al.*, 2003. They selected new broad bean genotypes varied from the local variety. Also, Farag and Darwish (2005) after obtaining large values of heritability suggested the possibility of improving broad bean traits through selection programs.

Heritability estimates are helpful in predicting the expected genetic gain from selection in segregating populations. High heritability in the F_2 populations indicates more importance of genetic factors in controlling a trait and possibility of its improvement by breeding programs (Saeidi, 2008). Estimates of heritability for broad bean traits were reported by Farag and Darwish (2005), which were moderate to high values. Attia *et al.* (2006) reported that heritability values were high in all crosses for all traits and concluded that selection for these traits should be effective and satisfactory for successful breeding program.

A complex character like yield influenced by a number of agronomic traits. To select effectively for high yield, it is necessary to understand the inter-relationships between yield-contributing characters and grain yield. Vandana and Dubey (1993) found that seeds per plant were the most important contributory factor for seed yield in the studied genotypes. Adak *et al.* (1999) reported that the number of seeds per pod should be a priority in selecting promising lines among the accessions evaluated. They found significant positive correlation between number of pods per plant and each of first pod height and plant height, number of seeds per pod and each of seed yield per plant and 100-seed weight, and finally 100-seed weight and seed yield per plant. Farag (2007) and Farag *et al.* (2005) reported that number of seeds per pod, pod weight, length, and 100-green seed weight, appeared to yield attributes for which selection can be effective.

This study aimed to developing and release of some new broad bean lines that released through pure line selection program to be replaced of the old cultivars.

MATERIALS AND METHODS

This investigation was conducted out at El-Gemmiza Agriculture Research Station, Gharbia Governorate, Egypt, during the successive winter seasons from 2004/2005 to 2008/2009. Using the progeny of 168 selected plants which were obtained from the F_3 generations to continue the research scheme done by Farag and Helal (2004) and Farag and Darwish(2005). Pure line selection program was done through three cycles of individual plant selection and inbreeding superior homozygous inbred lines according to the following steps:

1. On the winter season of 2004/05, plants from the progeny of each selected plants (168) were sown on October 8^{th}. Observations and selection were made between and within the F_3 populations, in order to ,choose the best plants (short plant height, early flowering), with the best pod characters (long pod, high seed number per pod, high 100 green-seed weight and high total green pod yield). From about 17200 plants, 216 ones were selected, selfed, picked each individual and seed were separately collected to produce the F_4 generation. At

least 5 inflorescences from each selected plant were bagged for selfing. During developing period of pods, the characteristics of green pods were observed. After harvesting dry seeds of the individual selected plants, the best one hundred plants were chosen to be grown in the next season, according to the performance of pods number, number and weight of dry seeds per plant, pod and seed size, as well as the characters of earliness and total fresh green-pod-yield and its components.

2. In the next winter season of 2005/06, the progenies of the selected plants were sown on October in separate rows, with the same cultural practices. Each population contain 105 plants distributed in three replications, Observations and selection were continued. At flowering time, the best 9 plants within each family were bagged to self-polination. Each plant was separately harvested and the following data were recorded as averages per plant: flowering time, number, weight and length of green pods, number and size of green seeds per pod as well as plant height and number of tillers per plant at the end of harvesting. According to the previous data, the best twenty seven superior and homogenous inbred were chosen with considering the markedly variations between such inbred in the most studied characters.

3. The seeds of F_5 population were sown in October, 2006, the selected 27 inbred were preliminary evaluated and compared with 2 commercial check cultivars: Kassasein-1, and Aquadulce. Seeds of each entry were sown in 6 rows, 0.70 cm wide, 4 m length, with 30 cm between hills. During flowering time, 3 plants from each row were selected and selfed. Observations and selection were made between and within the different populations. 10 populations were excluded, because they showed high heterogeneity. The remaining populations were separately collected.

4. On November 2007 and 2008, the best varied 17 lines were selected from further evaluation with the same check commercial cultivars. Evaluation trial was designed as a randomized complete blocks design with three replicates. The plot size was 16.8 m^2, containing six

rows, each 4 m length and 0.70 cm width, with 25 cm within plants. The agricultural practices were applied according to the recommendations of Ministry of Agriculture. Data were recorded on the following characters: Ten plants per plot were randomly labeled in each plot and at the end of growing season, plant height (cm) and number of tillers per plant were recorded and the means were estimated. Days to 50% flowering; number of nodes to 1st pod; 1st pod height (stem length to first pod cm) and pod number per plant were estimated at the proper time. Five green pods were randomly taken from each plant and average of the following characters were recorded : pod weight(g) ;pod length (cm); seed number per pod and seed-index (100 green-seed weight, g). Data for total green pod yield was recorded as averages of ten individual plant taken randomly. Mean values representing the various investigated genotypes were compared by the Duncan multiple range test (Duncan, 1955). All recorded data were subjected to statistical as illustrated by Snedecor and Cochran (1987). Coefficient of variability (C.V.%) was calculated by using the formula of Steel and Torrie (1980). Components of variances, genotypic (G.C.V.) and phenotypic (P.C.V.) coefficient of variation and broad-sense heritability were estimated according to Singh and Chaudhary (1995). Correlation analysis was used to determine the relationship between some pairs of characters by estimating the correlation coefficients (Steel and Torrie, 1980).

RESULTS AND DISCUSSION

Degree of Homogeneity

Estimated coefficients of variance C.V.% for all studied genotypes are presented in Table 1. Concerning plant height, all genotypes, except line S-22, could be considered homogeneous, since they gave the lowest variation within their plants. The genotypes S-5, S-19, S-14, S-7 and S-2 showed C.V. % values less than 9.00%. On the other hand the lowest homogeneity were observed in the lines S-22,S-15, and S-11, where they gave the highest C.V.% values18.25,13.54 and 13.46%, respectively. Regarding to days to 50% flowering, data in Table 1 showed that the highest homogeneity was observed within plants of the genotypes S-22,S-10

Table 1. Estimates of coefficient of variation (C.V.%) for some characters of the new breeding lines and the check cultivars

Genotype	Plant height	Days to flowering	1st pod height	Number of nodes to 1st pod	Pod length	Seed number /pod	Pod weight	Seed pod weight
Lines								
S-1	10.06	11.54	11.15	14.67	9.85	16.35	16.01	14.79
S-2	8.78	18.02	9.56	11.12	7.11	16.48	12.26	13.76
S-3	10.74	14.08	10.26	10.79	9.40	11.55	12.00	12.19
S-5	4.82	9.53	11.44	13.24	9.12	13.24	12.03	12.83
S-7	8.70	11.59	10.60	10.18	10.86	11.02	16.40	12.57
S-8	11.17	17.73	10.22	9.94	11.14	11.35	20.93	10.05
S-10	11.28	9.53	9.91	8.88	9.34	12.58	14.32	15.11
S-11	13.46	11.38	7.84	11.74	6.28	14.45	11.53	16.39
S-12	12.40	12.98	9.80	11.02	7.10	18.72	17.13	17.22
S-14	8.51	16.70	5.98	9.90	3.74	15.45	12.69	12.55
S-15	13.54	13.48	10.75	13.17	8.37	13.49	13.89	18.50
S-17	12.43	13.76	10.31	10.00	5.54	13.90	6.79	9.92
S-18	10.41	12.67	9.95	10.32	8.89	14.44	22.96	7.87
S-19	7.98	12.58	8.56	9.19	8.81	17.33	14.41	14.07
S-20	11.21	13.15	7.86	10.43	9.50	14.80	11.14	10.73
S-21	9.72	10.16	10.09	11.79	9.57	12.93	13.98	11.51
S-22	18.25	7.09	11.38	12.60	9.29	10.63	20.63	11.37
Check cultivars								
Kassasein-1	5.59	8.19	14.43	15.41	6.23	12.20	16.25	13.18
Aquadulce	14.38	7.90	12.06	15.02	6.40	9.56	12.43	10.72

and S-5, since they gave the lowest C.V.% values (7.09, 9.53 and 9.53%, respectively). While, plants of the genotypes S-2, S-8 and S-14 showed the highest heterogeneity, where they gave the highest C.V. % values (18.02, 17.73 and 16.70%, respectively). The new inbred line S-22 gave C.V. % value lower than the check cultivars.

As for stem length and number of nodes to 1st pod, obtained data in Table 1 showed C.V.% close to those recorded by all check cultivars, indicating that these new genotypes became high homogeneous in these traits. The highest homogeneity were found within plants of the genotypes S-14, S-11, and S-20 for 1st pod height and S-10,S-19, S-14 and S-8 for number of nodes to 1st pod, where they gave the lowest C.V.% values (less than 8.0 and 10.0%, respectively). These lines showed the lowest variation within their plants since they showed C.V.% values close to the check cultivars and became high homogeneous in 1st pod height and number of nodes to 1st pod as shown in Table 1.

In relation to pod length, the coefficient of variance values in the inbred genotypes reflected the highest homogeneity within plants of the genotypes S-15 S-17 and S-11, (Table 1). They gave the lowest C.V.% values (3.74, 5.54 and 6.28%, respectively), indicating that they were more phenotypically uniform than other lines. When these lines evaluated with the check cultivars they showed C.V.% values less than the check cultivars (Table 1).

As regards to seed number per pod, data in Table 1 show that the genotypes S-3,S-7,S-8 and S-22 could be considered the highest homogeneous lines. The obtained C.V.% values were less than 12.0% and close or lower than those of the check cultivar Kassasien-1. On the other hand, the lowest homogeneity were observed in the lines S-12 and S-19, where they gave the highest C.V.% values (18.72 and 17.33%, respectively). In respect to pod weight and seed-pod weight, data showed that the new bred lines S-17 recorded the lowest C.V.% values (6.79 and 9.92%, respectively). Also, three and six ones recorded C.V. % values less than 12% for these traits (Table 1). Comparing with the check cultivars, it is seen that they became high homogenous in this trait and reflected C.V.% values lower than those given by the check cultivars. Generally, the degree of homogeneity (C.V.) varied from genotypes to another in the same characters and from trait to others in the same genotypes. Estimates of C.V. % values in the new lines for the studied characters revealed high homogeneity within plants and similar to the check cultivars.

Mean Performance of the Studied Genotypes

Data in Tables 2 and 3 showed significant differences among all genotypes studied for all traits. Regarding plant height, it ranged from 106.8 in the cv. Aquadulce to 141.1 cm in the line S-21, (Table 2).The overall mean for lines and check cultivars were 122.34 cm. All lines gave plants longer than the general mean except, S-7,S-8, S -10,S-11,S-12 S-14,S-18,and S-22. Comparison of the studied lines with the check cultivars, all lines gave plants taller than the tallest check cultivars, except the line S-12.

Concerning number of tillers per plant, all lines showed number of tillers per plant ranged from 7.00 in line S-17 to 9.50 in line S-15 (Table 2). Comparison of the studied lines with the check cultivars, the mean of lines, check cultivars and overall mean were 8.15, 8.72 and 8.21, respectively. Regarding days to flowering and first pod height showed significant differences between all lines (Table 2). The earlier ones were S-14 (43.0 days) and S-22 (43.7 days) in flowering times and S-5 (23.1 cm) for first pod height, while the latest lines were S-15and S-8 in flowering and S-21 for first pod height. Comparing with the overall means (49.56 days to flowering and 30.17 cm for 1st pod height, the lines S-2, S-8, S-15, S-17 and S-20, flowered after long period, while S-8, S-11, S-14, S-19, S-20 S-21 and S-22 showed long height to 1st pod. For number of nodes to 1st pod, it ranged from 5.3 to 6.8 nodes for lines and from 5.0 to 5.8 nodes in the check cultivars. All lines poded after large number of nodes than the overall mean (6.12 nodes), except the lines S-1, S-2, S-3, S-5, S-7 and S-22.

For pod length and seeds number per pod, data in Table 2 showed significant differences among all lines for these traits .The line S-5 and cv. Kassasien-1 gave the shortest pod and the line S-19 gave less seed number per pod. Conversely, the lines S-8 produced high value for pod length and S-10 for seed number per pod.

Comparing the lines with the overall means showed that the line S-1, S-8, S11, S-12, S-15, S-12 and S-17 surpassed for pod length and lines S-3, S-8, S-10, S-11, S-12 and S-15 for seed number per pod. Comparison of the studied lines with the check cultivars for these traits, data in Table 2 show that all lines gave pods shorter than the mean of the check cultivars, except lines S-8,S-11,S-12S-14,S-15 and S-17 for pod length; and S-3,S10,S-11,S-12 and S-15 for seeds number per pod .Data in Table 3 show that the studied broad bean genotypes greatly differed in number of pods per plant. The line S-1 and CV. Kassasien-1 produced the highest number of pods per plant (24.0 and 25.7, respectively). On the other hand, the line S-20 gave the lowest number of pods per plant, (14.7 pods). Comparison of the studied lines with the check cultivars showed that, all lines were less than the control in their number of pods per plant.

Regarding pod weight and seed-pod weight, significant differences among the lines studied in these traits were observed (Table 3 and Fig 1).The line S-7 produced the lowest pod weight value and the lines S-22 and S-19 gave the lowest seed-pod weight. While, the lines S-15 and S-10 produced the highest values for these traits, respectively. The overall mean values of these traits were 21.871 and 12.073 g, respectively. All the bred lines produced pods heavier than the control cultivars. 65% of the lines produced seed-pod heavier than the control. Comparing all lines with overall means for these traits (21.871 and 12.073 g), showed that seven and eleven lines exceeded these values, respectively.

On the subject of shell-out percentage and seed index, significant differences among the lines studied in these traits were observed (Table 3).The lines S-7 and S-11 produced the highest shell-out percentage and seed index, respectively. The overall mean values of these traits were 54.732 and 251.807g, respectively . Comparing of the studied genotypes with check cultivars showed that, the lines S-1, S-2 and S-7 gave higher shell-out percentage than the check cultivars. While, the lines S1,S-10,S-11,S15 and S-18 gave heavier 100-green seed weight than the higher check cultivar (Aquadulce).

Highly significant differences among the evaluated breed lines were observed in total green-pod yield (Table 3 and Fig 2). The total green-pod yield per plant ranged

Table 2. Mean performances of the evaluated broad bean lines and check cultivars for some plant characters

Genotypes	Plant height (cm)	Tillers number /plant	Flowering time (day)	Number of nodes to 1st pod	1st pod height	Pod length (cm)	Seeds number /pod
Lines							
S-1	127.4 d	7.50 i	48.0 de	5.8 h	29.6 efg	16.60 cd	4.44 ef
S-2	131.3 c	7.83 gh	56.0 b	5.4 i	25.5 i	14.59 g	4.25 gh
S-3	126.0 d	8.00 fg	48.0 ef	5.9 gh	26.1 i	13.55 h	4.64 cd
S-5	138.6 b	8.17 ef	44.7 hi	5.3 i	23.1 j	13.57 h	4.32 fg
S-7	114.2 g	7.83 gh	47.0 fg	5.8 h	30.5 de	14.30 g	4.17 hi
S-8	118.5 ef	8.67 c	62.0 a	6.5 cd	35.1 b	18.40 a	4.52 de
S-10	120.8 e	7.67 hi	48.3 ef	6.5 cd	28.9 fgh	15.05 f	4.97 a
S-11	109.5 hi	9.17 b	45.0 hi	6.4 d	32.8 c	16.71 cd	4.73 bc
S-12	107.1 ij	8.50 cd	47.0 fg	6.5 cd	28.3 gh	17.18 b	4.78 b
S-14	118.6 ef	8.00 fg	43.0 j	6.7 ab	32.7 c	16.63 cd	4.33 fg
S-15	130.6 c	9.50 a	62.3 a	6.5 cd	30.8 de	17.19 b	4.77 bc
S-17	131.3 c	7.00 j	50.0 d	6.1 ef	28.2 h	17.02 bc	4.15 hi
S-18	117.5 f	8.33 de	44.7 hi	6.2 e	31.1 d	14.37 g	4.16 hi
S-19	138.6 b	7.17 j	48.0 ef	6.8 a	32.9 c	15.65 e	4.08 i
S-20	127.3 d	8.17 ef	55.0 bc	6.6 bc	32.4 c	16.49 d	4.32 fg
S-21	141.1 a	8.67 c	49.0 de	6.7 ab	36.7 a	13.84 h	4.44 ef
S-22	111.0 h	8.17 ef	43.7 ij	6.0 fg	34.7 b	14.46 g	4.42 ef
Mean	124.08	8.15	49.51	6.21	30.54	15.62	4.44
Check cultivars							
Kassasin-1	108.3 ij	7.67 hi	46.0 gh	5.0 j	24.0 j	14.67 fg	4.06 i
Aquadulce	106.8 j	9.17 b	54.0 c	5.8 h	30.0 def	17.22 b	5.00 a
Mean	107.55	8.72	50.00	5.41	27.00	15.95	4.53
MEAN	122.34	8.21	49.56	6.12	30.17	15.66	4.45

* Mean within a column followed by different letters are significantly different at 0.05 level.

Table 3. Mean performances of the evaluated broad bean lines and check cultivars for some pod characters

Genotypes	Pods number /plant	Pod weight (gm)	Seed pod weight (gm)	Shell-out (%)	Seed index	Total green-pod yield /plant(gm)
Lines						
S-1	24.0 c	20.52 g	12.39 de	60.4 b	266.3 cd	492.5 c
S-2	19.7 f	19.40 i	12.36 de	63.5 a	251.2 ef	382.9 j
S-3	21.3 e	20.43 gh	11.83 G	57.9 bc	251.3 ef	431.2 f
S-5	19.7 f	20.00 h	11.23 H	56.1 cde	258.6 de	386.2 j
S-7	16.0 k	19.00 i	12.28 de	64.6 a	227.3 g	301.3 l
S-8	23.7 c	22.82 d	12.87 C	56.4 cd	241.9 f	534.3 b
S-10	23.0 d	25.50 b	13.62 A	53.4 ef	276.1 bc	579.2 a
S-11	21.0 e	25.50 b	12.47 D	49.0 g	294.5 a	531.7 b
S-12	19.3 g	24.30 c	12.78 C	46.0 h	247.0 ef	468.2 d
S-14	18.0 i	23.20 d	12.15 ef	52.4 f	246.5 ef	411.2 gh
S-15	16.3 k	27.60 a	13.22 B	47.9 gh	271.4 bc	452.1 e
S-17	18.0 i	23.00 d	13.37 ab	58.1 bc	242.9 f	412.0 gh
S-18	16.7 j	24.30 c	12.07 efg	49.7 g	280.5 b	400.8 hi
S-19	18.3 i	20.50 g	10.63 I	45.8 h	252.9 ef	375.6 j
S-20	14.7 l	22.10 e	12.16 def	55.0 def	209.8 h	317.4 k
S-21	18.7 h	21.30 f	11.88 fg	56.0 cde	258.5 de	390.5 ij
S-22	19.3 g	22.20 e	10.53 I	48.8 g	240.7 f	423.5 fg
Mean	19.27	22.452	12.225	54.167	253.964	428.859
Check cultivars						
Kassasin-1	25.7 a	15.81 k	9.42 j	59.6 b	208.5 h	409.0 gh
Aquadulce	24.7 b	18.04 j	12.14 ef	59.3 b	258.4 de	446.8 e
Mean	25.17	16.928	10.781	59.454	233.470	427.917
MEAN	19.89	21.871	12.073	54.732	251.807	428.67

* Mean within a column followed by different letters are significantly different at 0.05 level.

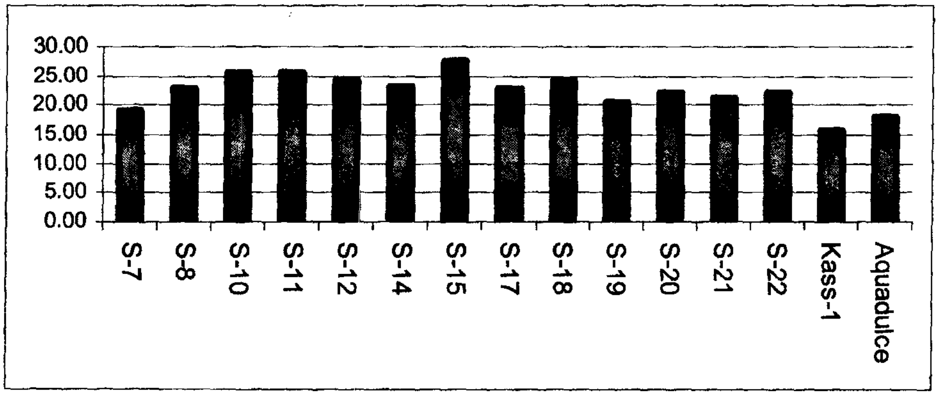

Fig. 1. Green-pod weight for some broad bean genotypes (gm)

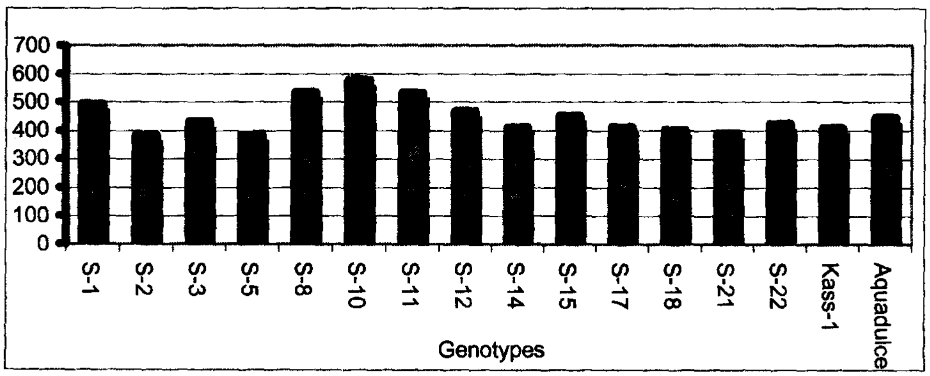

Fig. 2. Total green-pod yield (g/plant) for some broad bean genotypes

from 301.3 in the line S-7 to 579.2 g in the line S-10 , with a mean of 428.76 g per plant. 41 % of these lines significantly out-yielded the mean of the check cultivars by value reached 35.4%. The percentages of these increments were 35.36, 24.87, 24.26 and 15.10 % in the lines S-10, S-8, S-11 and S-1, respectively. Then, it could be concluded that the lines S-10, S-8, S-11 and S-1 are promising compared with all check cultivars and could be recommended as new lines. These results are in agreement with Khare and Singh (1991), Salih *et al.* (1993), Adak *et al.* (1999) and Farag and Helal (2004), Farag *et al.* (2005) and Farag and Morsy (2009),who found significant differences for these traits among studied broad bean genotypes. Among 200 tested genotypes, Mulat (1998) found that 18 genotypes produced 25 – 47 % higher yield than the check cultivars.

Components of Variance

Estimates of genotypic and phenotypic coefficient of variation and broad sense heritability for the studied traits were listed in Table 4. The estimated genotypic/ phenotypic coefficient of variation percent (σ^2GCV/σ^2PCV %) for the studied traits ranged from 75.82 for seed index to 97.07% for green pod weight. These results indicated that about 76 to 97 %of the phenotypic variances were due to genetic ones. Therefore, these traits might be more genotypically predominant and it would be possible to achieve further improvement in them. These results are in agreement with those reported by Farag and Darwish, (2005), and Attia *et al.* (2006). Estimated broad sense heritability ranged from 57.48% for seed-index to 94.22 %for pod weight. The estimated values of genotypic coefficient of variation as well as broad sense heritability indicated less environmental effects and high additive genetic components of the phenotypic variation. Accordingly, selection based on phenotypic observations could be effective in the segregating generations for improving these traits. These findings were in agreement with those obtained by Bakheit (1992) and Farag (2009).

Correlation Coefficients

A significant correlation coefficient value was found between some traits (Table 5). Total green-pod yield showed correlation values with high weight of seed index, large pod weight, and long pod (Farag *et al.*, 2005;

Table 4. Magnitudes of genetic parameters and heritability values for all traits

Parameters	Plant length	Tillers number/ plant	Flowering time	Number of nodes to1st pod	1st pod height	Pod length	Seed number/ pod	Green pod weight	Seed index	Total green pod /plat
MEAN	122.34	8.27	49.56	6.12	30.17	15.66	4.45	21.87	251.81	428.8
σ^2 ph	134.4	0.60	35.54	0.3	16.53	2.44	0.11	8.69	663.01	5269.3
σ^2 G	121.22	0.46	31.41	0.26	12.71	2.09	0.07	8.19	381.12	4824.1
σ^2E	13.18	0.14	4.13	0.04	3.82	0.35	0.04	0.50	281.9	445.2
σ^2PCV	9.48	9.37	12.03	8.9	13.48	9.97	7.44	13.48	10.23	16.93
σ^2GCV	9.00	8.20	11.31	8.26	11.82	9.24	6.11	13.08	7.75	16.2
σ^2GCV/ σ^2 PCV%	94.97	87.53	94.01	92.78	87.68	92.59	82.17	97.07	75.82	95.68
B S H%	90.19	76.62	88.38	86.09	76.88	85.74	67.52	94.22	57.48	91.55

Table 5. Correlation coefficients between some characters of studied genotypes

Characters	Pod number	Green pod weight	Pod length	Seed number/ Pod	Seed - index	Seed pod weight
Total green pod yield	0.626**	0.471*	0.422*	0.682**	0.574**	0.414*
Pod number		-0.384*	0.122	0.343	0.083	-0.181
Green pod weight			0.381*	0.422*	0.569**	0.657**
Pod length				0.341	0.043	0.483*
Seed number/ Pod					0.482*	0.510**
Seed index						0.428*

*Significant at 5% level.

** Significant at 1% level.

Farag, 2007) high number of pods (Bakheit and Mahady, 1988). Pod weight was associated with long pod, high number of seeds per pod, high weight of seed index, and seed pod weight (Farag, 2007). Seed index was associated with large pod weight and seed number per pod. High seed number per pod was associated with seed index and seed pod weight. Similar results were reported by many investigators who studied the relationship between yield and its components, among them were Ashmawy *et al.* (1998), Abdel Aziz *et al.* (2005), Farag *et al.* (2005) and Farag (2007). Based on the correlation coefficient, number of seeds per pod, pod number and weight, pod length, seed pod weight and 100-seed weight appeared to be the principal yield attributes for indirect selection.

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إستنباط سلالات جديدة من الفول الرومي بالانتخاب

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خلال المواسم ألشتوية المتتالية من ٢٠٠٤/٢٠٠٥ إلى ٢٠٠٨/٢٠٠٩، أجريت هذه الدراسة في المزرعة البحثية بمحطة البحوث الزراعية بالجميزة – محافظة الغربية، باستخدام طريقه الانتخاب مع تسجيل النسب لعشيرة من الفول الرومي، بداية من الجيل الثالث وحتى الجيل السابع. كما تم الانتخاب بين وداخل السلالات على أساس عدد من الصفات مثل عدد الأفرع، وعدد القرون/نبات، وعدد البذور بالقرن، والتبكير في الإزهار، وطول ووزن القرن، ومحصول القرون الخضراء، كما تم تقديرُ التباين وحساب درجه التجانس عن طريق تقدير معامل الاختلاف داخل ١٧ سلالة تم انتخابها وتقييمها في الجيل السادس، ولقد أظهرت النتائج المتحصل عليها أن هذه السلالات أصبحت على درجه عالية من التجانس مقارنة بالأصناف الكنترول: قصاصين–١ واكوادولسى، وفي الموسم الشتوي ٢٠٠٨/ ٢٠٠٩ تم تقييم السلالات (F_7) المتحصل عليها من الموسم السابق مقارنه بالأصناف ألاختباريه سالفة الذكر، و أظهرت نتائج الدراسة مايلى:

١- وجود اختلافات معنوية بين السلالات وبعضها من حيث الصفات التي درست.

٢- السلالات س-١٠، س-١٤، س-١٧، س-١٩، س-٢٠، س-٢٢ أعطت قيماً منخفضة لمعامل الاختلاف (C.V%) لمعظم الصفات التي درست مما يشير إلي إنها أصبحت أكثر تجانسا وتماثلا مثل الأصناف التجارية. لقد أعطت ٤٠% من كل السلالات تحت الدراسة تفوقا في محصولها الكلي علي ألأصناف المقارنة. حيث وصلت نسبة الزيادة إلى ٣٥,٣٦ % في السلالة س-١٠، ٢٤,٨٧% في السلالة س-٨ ،٢٤,٢٦% في السلالة س-١١، ١٥,١٠% في السلالة س-١. إن التفوق ودرجة التماثل العالية لتلك التراكيب الو راثية الجديدة يجعلها سلالات مبشرة ومتفوقة في محصولها الكلي من القرون الخضراء مقارنة بالأصناف التجارية.

٣- أظهرت النتائج أيضاً قيماً عالية لمعامل الاختلاف الراجع للتباين الوراثى من معامل الاختلاف الراجع إلى التباين الكلى (الظاهري) حيث تراوحت من ٧٦ إلى ٩٧%. أيضا الكفاءة الوراثة على النطاق الواسع حيث تراوحت من ٥٧,٤٨ إلى ٩٤,٢٢%، مما يدل على صغر تأثير البيئة على هذه الصفات وان الجزء الأكبر من المكون الوراثى الكلى (الظاهري) راجع إلى المكونات الو راثية لعوامل الإضافة وأنة يمكن تحسين تلك الصفات بالانتخاب على أساس شكلها الظاهري.

٤- بناءا علي قيم الارتباط تتضح أن عدد القرون وعدد البذور بالقرن، متوسط وزن وطول القرن، وزن ١٠٠ بذرة هي المكونات الرئيسية للمحصول والتي يمكن أن يكون الانتخاب لها فعالاُ.