

Pedigree Selection to Improve the Seed Yield in Two Segregating Populations of Faba Bean (*Vicia faba* L.)

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Received on: 28/6/2018

Accepted for publication on: 2/7/2018

Abstract

The present investigation was conducted at El Mattana Agricultural Research Station, Luxor Governorate, Egypt during three successive seasons i.e., 2013/2014, 2014/2015 and 2015/2016. The objective of this study was to achieve two cycles of pedigree line selection for improving seed yield/plant using two segregating populations of faba bean in the F4 and F5 generations. Remarkable variations among families of the both base populations as well as the selected families in cycle 1 and cycle 2 of pedigree line selection were observed for all studied traits. In Pop. I, families no. F233, F141, F182, F187 and F086 were the best families in most studied traits and out yielded both parents and bulk's mean after two cycles of pedigree selection. In Pop. II, families no. F203, F177, F111, F076 and F036 were the best families and surpassed both bulk sample and better parent. The selected families of Pop. II were higher for seed weight, seed index, biological yield, pods weight and pods number than the selected families of Pop. I. These families could be considered as promising material for seed yield production. Accordingly, the pedigree selection would be reasonably effective for selecting the superior genotypes for seed yield/plant.

Keywords: *Faba bean (Vicia faba L.)*, *pedigree selection*, *heritability*, *genetic advance*, *segregating generation*,

Introduction

Faba bean (*Vicia faba* L.) is a globally important legume crop whose main originated in between the oriental Mediterranean countries and Afghanistan (Cubero, 1974 and O'Sullivan and Angra, 2016). Faba bean is a valuable protein-rich food that provides a large sector of the human populations in developing countries with a cheap protein source thus partly compensating for the large deficiency in animal protein sources (Haciseferogullari *et al.*, 2003 and O'Sullivan and Angra, 2016). Faba bean is one of the essential legume crops grown in Egypt. The total production of faba bean in Egypt in 2016

was about 119104 tons obtained from 34314 ha (FAOSTAT, 2016).

Great efforts from plant breeders in continuously searching for more effective and efficient method to improve yield of the field crops. There are several selection methods that can be used to improve yield and its attributes in faba bean. Pedigree selection is a widely used method of breeding self-pollinated species (and even cross-pollinated species such as corn and other crops produced as hybrids) to enhance crop productivity. It has long been successful method for improving faba bean productivity in Egypt (Ahmed *et al.*, 2008 and Ahmad, 2016).

The success of an autogamous plant-breeding program depends on the choice of populations capable of producing progeny with desired seed yield and its attributes. Selection in the promising segregating populations can isolate lines with superior performance compared to their parents and local cultivars (Oliveira *et al.*, 1996 and Abreu *et al.* 2002).

Many investigations reported that the selection in early segregating populations, within local and exotic populations may give promising results in improving faba bean performance (Ahmed *et al.*, 2008; Bakheit and Metwali, 2011; Ahmad, 2016). Ahmed *et al.* (2008) compared three selection methods, i.e. mass selection, pedigree selection and picking-pod, and found that pedigree selection is a preferable method for improvement yielding ability in faba bean and is recommended for faba bean breeding.

Bakheit and Metwali (2011) reported that the selection for seed weight/plant after two cycles of pedigree selection increased the criterion of selection in population 1 by 9.94, 60.91 and 71.38% compared to the bulk sample, check cultivar and the best parent, respectively. High heritability estimates followed by high genetic advance for number of pods per plant and seed yield per plant, indi-

cating the scope for their improvement through selection (Bora *et al.*, 1998). Ibrahim (2015) stated that heritability estimates in broad sense and expected genetic advance from selection for seed yield/plant were high through selection inside segregating generations of faba bean. Ahmed (2016) found that the values of phenotypic coefficient variation for most studied characters were close to the corresponding genotypic coefficient of variation values indicating little environment effect on the expression of these characters.

The objective of the current investigation was to study the effectiveness of pedigree selection method in isolating high yielding lines in two segregating populations of faba bean.

Materials and Methods

The present study was carried out at El Mattana Agricultural Research Station, Luxor Governorate, Egypt during three successive winter seasons i.e., 2013/2014, 2014/2015 and 2015/2016.

The breeding materials were used in this study, 300 F₃-families from each population traced back to random F₂ plants from two crosses i.e. (Nubariah 2 × Rena Mora) as population I (Pop. I). and (Misr 1 × Rena Mora) as population II (Pop. II). The pedigree of the parents and their sources are given in Table 1.

Table 1. Description of the parental varieties of faba bean (*Vicia faba* L.).

Cultivar name	Origin	Pedigree
Nubariah 2	Egypt	Hybrid 735 (Radiation 2095/76 × ILB 1550)
Rena Mora	Spain	Introduced from Spain
Misr 1	Egypt	Single cross (Giza 3 × A123/45/76)

Field procedures:

A. Season 2013/2014 (F3 generation)

300 plants from F_3 of each population with the original parents were sown individually in a breeding nursery in non-replicated rows of two-meter-long, 60 cm wide and 20 cm between hills on one side of the ridge with one seed per hill. The recommended cultural practices were adopted throughout the growing season. At flowering time and harvest, a total of 300 plants were taken at random from each population to measure the following traits:

- 1- Days to first flower (FD).
- 2- Days to maturity (MD).
- 3- Plant height (PH); cm.
- 4- Number of branches/plant (BN/P).
- 5- Number of pods/plant (PN/P).
- 6- Number of seeds/plant (SN/P).
- 7- Pods weight/plant (PW/P); g.
- 8- Biological weight/plant (BY/P); g.
- 9- Seed yield/plant (SY/P); g.
- 10- Harvest index (HI); %, and
- 11- Hundred-seed weight (SI); g.

The first cycle of pedigree line selection (early selection) was applied on the F_3 population for seed yield/plant as a selection criterion. The best 50 families (16.5%) were selected based on seed yield/plant and saved to the next generation.

B. Season 2014/2015 (F4 generation; the first cycle of pedigree selection)

The 50 selected F_4 -families from each population with the origi-

nal parents, F_4 -bulked random sample (a mixture of equal number of seeds from each plant to represent the generation mean) were sown at 3th November in separate experiments in a randomized complete block design (RCBD) with three replications. Each plot of them was represented by single row 2 m long, 60 cm apart, 20 cm between hills in each replication. The second cycle of pedigree selection was applied on the 50 selected families for some selection criterion. The best ten families (20%) were selected and saved for the next generation.

C. Season 2015/2016 (F5 generation; the second cycle of pedigree selection)

The 10 selected F_4 -families from each population from each population with the original parents, F_5 -bulked random sample were sown on 5th November. The same procedures and experimental design of the previous season were followed. Each family was a single row 2 m long, 60 cm between rows and 20 cm between hills. Data were recorded as previously mentioned.

1. Statistical analysis:

1.1. Analysis of variance and heritability estimates

For each season, estimates of phenotypic and genotypic variance as well as heritability estimates were calculated from EMS of the variance components of the selected families as presented in Table 2.

Table 2. The analysis of variance as well as mean square expectations.

S.O.V.	d.f.	M.S.	Expected mean square
Rep.	r-1	M3	$\sigma_e^2 + f\sigma_r^2$
Families	f-1	M2	$\sigma_e^2 + r\sigma_f^2$
Error	(r-1)(f-1)	M1	σ_e^2

Where: r and f = number of replications and families, respectively.

σ_e^2 and σ_f^2 = error variance and genetic variance, respectively.

Based on expected mean squares, the estimates of genotypic (σ^2_g) and phenotypic (σ^2_p) variances among family averages as well as all entries including respective parents and bulk sample from each population were calculated as given by Al-Jibouri *et al.* (1958).

- The genotypic variance $\sigma^2_g = (M_2 - M_1) / r$
- The phenotypic variance $\sigma^2_p = \sigma^2_g + \sigma^2_e$
- Heritability in broad-sense; $H^2 = (\sigma^2_g / \sigma^2_p) \times 100$

The phenotypic and genotypic coefficients of variability were estimated using the formula developed by Burton (1952).

- Phenotypic coefficient of variability (PCV %):

$$PCV \% = \frac{\sigma_p}{\bar{X}} \times 100$$

- Genotypic coefficient of variability (GCV %):

$$GCV \% = \frac{\sigma_g}{\bar{X}} \times 100$$

Where: σ_p and σ_g are the phenotypic and genotypic standard deviations of the family means, respectively, and \bar{X} is a family mean for a given trait.

1.2. The expected genetic advance:

The expected genetic advance (GA) expressed as a percentage of the mean value with an assumed 16.5 and

20% intensity of selection pressure for cycle 1 and cycle 2, respectively. The GA was computed by the formula given by Singh and Chaudhary (1985) as: $GA = k \cdot H_b \cdot \sigma_p$

Where: k = 1.50 and 1.37 constants for nearly 16.5 and 20% selection intensity (i.e. the highest-performing are selected), H_b = broad-sense heritability, and σ_p = Phenotypic standard deviation of the population.

1.3. The observed response to selection:

The observed response to selection was measured as the deviation percentage of the mean of the selected families from mid-parent, better parent and bulk sample. Comparing the observed response to selection was calculated using Revised L.S.D.

Where;

L.S.D. = Least significant differences between means of parents, bulk and selected families or only selected families mean as R.L.S.D. $\alpha = t_\alpha \times S_a$

Results and Discussion

1. Description of the two base populations

Data in tables 3 and 4 represent the summary statistics of the two populations in the F3 non-replicated families (generation), respectively.

A. Coefficients of variation and means

By looking to the variances of the two population, it can be observed that families of the Pops. I and II

show a remarkable variation in all studied traits. Judging by the range and coefficients of variation for each trait, it is quite obvious that Pop. I showed more genetic coefficient variation than Pop. II in most of studied traits (Tables 3 and 4). Number of days to maturity (MD) exhibited a minimum coefficient of variation in the two populations, since it was 5.40 and 4.36% in Pop I and Pop II, respectively. While seed yield/plant (SY/P) showed the maximum coefficient of variation in both populations and was 71.56 and 63.90 % for the Pop. I and Pop. II, respectively. High differences among the F3 families in all studied traits in both populations, indicating the presence of sufficient genetic variation for pedigree selection. The coefficients of variation in the F3 generation of the two populations was very high for all traits compared to their respective parents. This might be due to the homogeneity of the parents. These results are matching with those obtained by Bakheit and Metwali (2011) who reported highly significant differences among F3 families in two populations for all studied traits. They also detected satisfactory genotypic coefficients of variation for selection of no. of

Pods/main stem and seed yield/plant. Ahmed *et al.* (2008) stated that F4 progenies had the highest means for all traits in all crosses except for days to maturity, plant height and 100-seed weight compared to F2 progenies. As an average, the Pop. II was superior in SY/P (65.43 g), SI (79.93 g), BY/P (184.39 g), SN (80.35), PW/P (88.70 g), PN/P(27.98) and BN/P (7.55) than the same traits in the Pop. I. While, the Pop. I was earlier in flowering (42 days) and maturity (134.92 days). Also, it had shorter plants (88.98 cm) and higher in harvest index (36.16 %) than in Pop. II. The superiority of the Pop. II in seed yield/plant may due to the superiority in yield components such as pods number, seed number and seed index. With comparison of parents of the two populations, it can be noticed that the range of both populations fall outside the range of the two parents that formed the population. This result reflects the presence of transgressive segregation among the F3 families of the two populations. Suso *et al.* (1993), who found significant difference in days to flowering among Spanish faba bean cultivars. Similar results were obtained by Ahmed *et al.* (2008).

Table 3. Descriptive statistics of the base population I and its parents as well as heritability in broad sense in the F3 generation

Variable	FD	MD	PH	BN	PN	PW	SN	BY	HI	SI	SY
Base population I											
Mean	42.00	134.92	88.98	6.83	27.72	82.55	73.77	161.98	36.16	76.19	59.35
SE	0.28	0.42	0.83	0.15	0.88	3.03	2.51	4.73	0.91	1.44	2.45
Variance	23.91	53.06	204.40	6.82	233.53	2747.32	1891.86	6724.14	248.44	624.88	1803.82
Minimum	32.00	125.00	45.00	2.00	1.00	6.30	3.00	27.40	0.97	7.87	1.20
Maximum	60.00	156.00	120.00	15.00	97.00	283.90	230.00	393.95	59.89	111.67	220.00
C.V. %	11.64	5.40	16.07	38.25	55.12	63.49	58.96	50.62	43.58	32.81	71.56
Nubariah (P1)											
Mean	47.80	137.00	85.40	7.40	46.80	88.98	105.20	237.98	27.79	62.53	65.76
SE	0.37	0.45	1.63	0.24	0.80	4.55	3.44	6.95	1.79	1.82	2.86
Variance	0.70	1.00	13.30	0.30	3.20	103.48	59.20	241.43	16.02	16.59	40.93
Minimum	47.00	136.00	80.00	7.00	45.00	82.45	99.00	221.90	24.32	55.71	60.72
Maximum	49.00	138.00	90.00	8.00	49.00	106.90	117.00	258.65	34.57	65.75	76.72
C.V. %	1.75	0.73	4.27	7.40	3.82	11.43	7.31	6.53	14.40	6.51	9.73
RenaMora (P2)											
Mean	36.40	126.40	65.00	7.00	15.40	94.39	55.20	142.41	52.58	135.54	74.62
SE	0.51	0.51	2.74	0.45	1.47	1.28	1.77	5.48	1.63	4.40	1.97
Variance	1.30	1.30	37.50	1.00	10.80	8.17	15.70	150.24	13.24	96.85	19.37
Minimum	35.00	125.00	55.00	6.00	10.00	91.60	51.00	127.00	48.73	126.43	69.00
Maximum	38.00	128.00	70.00	8.00	18.00	98.56	61.00	159.11	56.88	151.33	78.80
C.V. %	3.13	0.90	9.42	14.29	21.34	3.03	7.18	8.61	6.92	7.26	5.90
σ^2_E	1.00	1.15	25.40	0.65	7.00	55.82	37.45	195.84	14.63	56.72	30.15
σ^2_P	23.91	53.06	204.40	6.82	233.53	2747.32	1891.86	6724.14	248.44	624.88	1803.82
σ^2_G	22.91	51.91	179.00	6.17	226.53	2691.50	1854.41	6528.30	233.81	568.16	1773.67
H %	95.82	97.83	87.57	90.47	97.00	97.97	98.02	97.09	94.11	90.92	98.33

Table 4. Descriptive statistics of the base population II and its parents as well as heritability in broad sense in the F3 generation

Variable	FD	MD	PH	BN	PN	PW	SN	BY	HI	SI	SY
Base population 2											
Mean	42.44	136.39	93.04	7.55	27.98	88.70	80.35	184.39	35.44	79.93	65.43
SE	0.33	0.35	0.81	0.15	0.91	3.11	2.75	4.53	0.91	1.49	2.44
Variance	31.91	35.38	191.30	6.96	241.25	2850.45	2219.10	6022.60	244.09	655.69	1748.33
Minimum	34.00	127.00	45.00	2.00	2.00	2.70	4.00	32.50	1.07	11.00	2.54
Maximum	83.00	151.00	130.00	18.00	84.00	266.70	243.00	441.15	59.92	115.29	198.40
C.V. %	13.31	4.36	14.87	34.95	55.52	60.19	58.63	42.09	44.09	32.04	63.90
Misr1 (P1)											
Mean	44.00	139.60	107.00	5.40	42.40	139.00	125.80	201.00	52.56	83.93	105.56
SE	0.45	0.40	3.39	0.24	2.50	4.85	2.15	4.30	1.20	1.80	2.68
Variance	1.00	0.80	57.50	0.30	31.30	117.50	23.20	92.50	7.23	16.26	35.96
Minimum	43.00	138.00	95.00	5.00	34.00	125.00	122.00	185.00	47.80	80.33	98.00
Maximum	45.00	140.00	115.00	6.00	48.00	150.00	132.00	210.00	54.36	90.85	111.75
C.V. %	2.27	0.64	7.09	10.14	13.19	7.80	3.83	4.78	5.12	4.80	5.68
RenaMora (P2)											
Mean	36.40	126.40	65.00	7.00	15.40	94.39	55.20	142.41	52.58	135.54	74.62
SE	0.51	0.51	2.74	0.45	1.47	1.28	1.77	5.48	1.63	4.40	1.97
Variance	1.30	1.30	37.50	1.00	10.80	8.17	15.70	150.24	13.24	96.85	19.37
Minimum	35.00	125.00	55.00	6.00	10.00	91.60	51.00	127.00	48.73	126.43	69.00
Maximum	38.00	128.00	70.00	8.00	18.00	98.56	61.00	159.11	56.88	151.33	78.80
C.V. %	3.13	0.90	9.42	14.29	21.34	3.03	7.18	8.61	6.92	7.26	5.90
σ^2_E	1.15	1.05	47.50	0.65	21.05	62.83	19.45	121.37	10.23	56.56	27.67
σ^2_P	31.91	35.38	191.30	6.96	241.25	2850.45	2219.10	6022.60	244.09	655.69	1748.33
σ^2_G	30.76	34.33	143.80	6.31	220.20	2787.62	2199.65	5901.23	233.85	599.13	1720.66
H %	96.40	97.03	75.17	90.66	91.27	97.80	99.12	97.98	95.81	91.37	98.42

B. Broad sense heritability

High heritability estimates were obtained at the F3 generation in both populations. Where the heritability values ranged between 87.57% (PH) and 98.33% (SY/P) in Pop. I, while it ranged between 75.17% (PH) and 99.12% (SN/P) in the Pop. II. The higher estimates of heritability may be due mainly to the high estimates of the genetic variance compared to the environmental variance (the environmental variance was computed from the two parent's variances for each population). Bakheit and Metwali (2011) obtained high estimates of heritability for number of pods/main stem and seed weight/plant (g)

in both populations. Ahmad (2016) found high heritability estimates for seed yield/plant and 100-seed weight in F4 that were 82.10 and 83.53 in population1 and 65.81 and 81.01 in population 2, respectively.

2. Analysis of variance in the F4 and F5 generations and means

The analysis of variance for each trait of each population was performed twice, the first for the selected families to calculate *pcv*, *gcv* and heritability, and the second one for the selected families, parents and bulk sample to compare their means. The analysis of variance (Table 5) reveals highly significant differences among families as well as among en-

tries for all studied traits in both populations at F4 and F5 generations. Moreover, the variation among families exceeded the variation among entries in most studied traits in both populations, indicating the transgressive segregation. Tables 6 and 7 show some summary statistics of the selected families, their parents and bulk along with genotypic and phenotypic variances, coefficient of variations and heritability in broad sense in the F4 and F5 generations of the Pop. I and Pop. II, respectively. Several investigators have reported on the variability present among selected families such as Alghamdi 2007; Ahmed *et al.*, 2008; Bakheit and Metwali 2011; Soliman *et al.*, 2012; Muluaem *et al.*, 2013 and Ahmad 2016.

3. The first cycle of pedigree selection for seed yield/plant

3.1. Means

In population I (Tables 6 and 7), the mean of F4 families was superior the mid-parents mean for the most investigated traits. For example, the mean values of SY/P (66.62 g), SI (89.09 g), BY (178.01 g), SN (76.19 g), PW (88.84 g), PN/P (26.35) and BN/P (6.55) exceeded the means of the mid-parents of the same traits, but they were lower than the better parent. Nevertheless, the selected families were late in flowering and maturity and lower in harvest index than both mid- or better parents. A slight

different scenario was observed in the Pop. II, that values of the F4 families' mean were higher than those of mid-parents and better parent in seed yield and its attributes except HI and SI. Since, the mean value of SY/P (74.22 g), SI (95.43 g), BY (197.35 g), SN (78.65 g), PW (97.61 g), PN/P (27.19) and BN/P (6.92) exceeded the means of the better parents of these traits. In general, the Pop II was superior than Pop I in seed yield/plant and its attributes in this cycle of selection. In the first cycle of selection of 16.5 % superior plants in both populations, the selection was effective in isolating superior families compared to bulk's mean and mid-parents in most of investigated traits of the Pop II. Since, the selected families had high SY/P, heavier SI, had high HI, heavier BY/P, high PW/P and taller plants by values 8.79 g, 15.50 g, 2.38%, 12.96 g, 8.91 g and 32.21 cm than the mean values of the same traits in the previous generation. The same trend was observed in the selected families of the Pop I but with slight effective selection in F4 generation. The selected families in both populations were late in flowering and maturity than their base population. These results are in accordance with those obtained by Alghamdi 2007; Ahmed *et al* 2008; Bakheit and Metwali 2011; Mohamed and Abdelhaleem 2011; Muluaem *et al.*, 2013 and Ahmad 2016.

3.2. Variability and heritability estimates

The huge genetic variation among the F4 families led to high estimates of broad sense heritability coupled with high or moderate σ^2_p in both populations (Tables 6 and 7). Since, the quantitative traits such as seed yield/ plant and its attributes showed high estimates of σ^2_p and ranged between 41.41 (PN) and 2583.17 (BY) in Pop. I, while it ranged from 108.02 (HI) to 5547.90 (BY) in Pop II. While, the other traits exhibited σ^2_p ranged between (2.95 and 3.79) for BN/P and (136.60 and 94.85) for PH in Pop. I and Pop. II, respectively. BY/P showed the maximum percentage of GCV % and scored 28.26% followed by SY/P (27.17%) in Pop. I, while SN exhibited the highest percentage of GCV and recorded 44.87% followed by PN/P (43.53%) in Pop. II. High estimates of broad sense heritability were observed for all investigated traits in both populations in F4 generation, especially Pop II. H% estimates ranged between 88.65 (SI) and 98.80 (FD) in Pop. I, while it ranged from 90.05 (HI) to 99.88 (SN) in Pop. II. These results are in accordance with those obtained by Alghamdi 2007; Ahmed *et al.*, 2008; Bakheit and Metwali 2011; Mohamed and Abdelhaleem 2011; Mulualem *et al.*, 2013 and Ahmad 2016.

4. The second cycle of pedigree selection for seed yield/plant

4.1. Means

A relatively different picture was observed in the second cycle of selection of seed yield/plant for both populations. Since, the mean values of the investigated traits were lower

in this generation than those of the same traits in the previous generation except HI (Table 6). The mean values of SY/P (54.39 g), SI (81.56 g), HI (41.12 %) and PN/P (24.79) of the selected families surpassed the mid-parents, bulk's mean and better parent in some cases. Meanwhile, the selected families were late in flowering (45.56 day) compared to better parent, mid-parents and bulk's mean, but they matured early (131.47 day) than better parent. The selected families were shorter (123.51 cm) than their parents and bulk's mean. The response to selection was negative for all studied traits except PH and HI, and ranged from -46.87 (BY/P) to -0.89 (FD). The pedigree selection in the second cycle of Pop II was better effective than in Pop I. Despite of the reduction in response to selection in F5 generation, the seed yield/plant (73.69 g), SI (80.93 g), BY/P (175.17 g), SN/P (90.46), PN/P (27.58), BN/P (4.65) and PW/P (105.15 g) were higher than those of mid-parents and sometimes than better parent and bulk's mean. These results are similar with those found by Alghamdi 2007; Ahmed *et al.*, 2008; Bakheit and Metwali, 2011; Mohamed and Abdelhaleem, 2011; Mulualem *et al.*, 2013 and Ahmad, 2016.

4.2. Variability and heritability estimates

The genetic variation among the selected families for all investigated traits in both populations was decreased in the F5 generation compared to the previous generation and this may due to the low number of selected families (ten families out of 50 family) and increasing the percentage of the homozygosity than in

F4 generation. The σ^2_G and σ^2_P ranged from (0.57 and 0.63) for BN/P to (633.68 and 725.35) for BY/P in the Pop I, respectively. While they ranged from (0.46 and 0.53) for BN/P to (567.80 and 670.47) for BY/P in Pop. II, respectively. In Pop. I, PW/P showed the maximum percentage of GCV and PCV and scored 22.16 and 24.29 %, respectively. While MD showed the minimum percentage of GCV and PCV and scored 2.05 and 2.15%, respectively. In Pop II, SY/P exhibited the highest percentage of GCV and PCV and recorded 27.22 and 29.65%, respectively. While, MD

showed the minimum percentage of GCV and PCV and recorded 1.08 and 1.42%, respectively. Moderate to high estimates of broad sense heritability were observed in the F5 generation of both populations. The H% estimates ranged between 49.34 (SY/P) and 96.66 (PH) in Pop I, while it ranged from 57.70 (MD) to 92.05 (PN/P) in Pop II. These results are in accordance with those obtained by Alghamdi 2007; Ahmed *et al* 2008; Bakheit and Metwali, 2011; Mohamed and Abdelhaleem, 2011; Mulalem *et al.* 2013 and Ahmad, 2016.

Table 6. Summary statistics of the selected families, bulk, and parents of the population I in the F4 and F5 generations along with genotypic, phenotypic variances, coefficients of variation and heritability in broad sense for the studied traits.

	Item	FD	MD	PH	BN	PN	PW	SN	BY	HI	SI	SY
Cycle 1	F4 family's mean	43.19	141.67	122.54	6.55	26.35	88.84	76.19	178.01	38.98	89.09	66.62
	Minimum	33.00	129.00	90.00	3.00	11.50	22.61	36.61	99.20	14.09	36.09	26.86
	Maximum	59.00	151.00	156.60	12.00	42.44	153.26	130.00	320.73	56.57	192.38	122.49
	Bulk's mean	30.17	139.83	106.67	7.12	21.78	87.63	65.33	162.98	43.45	109.37	70.80
	Nubariah2 (P1)	46.89	136.89	124.32	7.69	30.26	88.79	90.94	210.22	32.59	75.30	68.49
	RenaMora (P2)	37.11	131.22	123.78	4.79	18.94	77.21	64.00	120.90	52.94	100.00	63.97
	Mid-parents	42.00	134.06	124.05	6.24	24.60	83.00	77.47	165.56	42.77	87.65	66.23
	Error variance	0.39	1.00	3.93	0.13	1.60	45.21	24.72	74.59	2.94	35.42	23.57
	σ^2_G	32.56	19.91	132.68	2.82	39.81	519.02	377.24	2508.58	105.90	276.61	328.32
	σ^2_P	32.96	20.91	136.60	2.95	41.41	564.23	401.96	2583.17	108.85	312.03	351.89
	GCV %	13.30	3.16	9.42	25.66	24.09	25.72	25.55	28.26	26.25	18.60	27.17
	PCV %	13.38	3.24	9.56	26.25	24.57	26.81	26.37	28.67	26.61	19.76	28.13
	H %	98.80	95.22	97.12	95.57	96.13	91.99	93.85	97.11	97.30	88.65	93.30
	Response to selection	1.19	6.75	33.56	-0.28	-1.37	6.29	2.42	16.03	2.82	12.90	7.27
Cycle 2	F5 family's mean	42.30	131.47	123.51	3.82	24.79	76.18	67.37	131.14	41.12	81.56	54.39
	Minimum	34.33	127.67	103.83	2.80	17.10	49.50	50.10	106.60	31.07	64.67	33.70
	Maximum	56.00	136.33	146.97	5.10	34.40	100.60	87.33	170.60	50.93	110.73	70.10
	Bulk's mean	39.89	135.89	142.00	4.59	25.44	67.73	71.36	143.47	35.70	71.75	51.20
	Nubariah (P1)	45.56	135.78	125.10	5.38	23.98	63.03	71.70	199.90	23.92	66.68	47.81
	RenaMora (P2)	33.67	131.67	124.22	4.46	19.22	117.74	78.76	163.33	33.67	69.83	55.03
	Mid-parents	39.61	133.72	124.66	4.92	21.60	90.39	75.23	181.62	28.79	68.25	51.42
	Error variance	5.89	0.75	4.20	0.06	2.37	59.94	48.55	91.67	11.07	62.54	55.06
	σ^2_G	43.10	7.33	121.66	0.57	29.10	296.51	66.40	633.68	47.90	115.66	53.62
	σ^2_P	48.99	8.08	125.86	0.63	31.47	356.45	114.95	725.35	58.97	178.19	108.67
	GCV %	15.74	2.05	8.82	18.74	22.15	22.16	11.83	18.00	17.84	13.66	13.64
	PCV %	16.79	2.15	8.97	19.64	23.04	24.29	15.56	19.26	19.79	16.95	19.42
	H %	87.97	90.68	96.66	91.10	92.48	83.18	57.76	87.36	81.22	64.90	49.34
	Response to selection	-0.89	-10.20	0.97	-2.73	-1.56	-12.66	-8.82	-46.87	2.14	-7.53	-12.23

Table 7. Summary statistics of the selected families, bulk, and parents of the population II in the F4 and F5 generations along with genotypic, phenotypic variances, coefficients of variation and heritability in broad sense for the studied traits.

	Item	FD	MD	PH	BN	PN	PW	SN	BY	HI	SI	SY
Cycle 1	F4 family's mean	44.03	143.66	125.25	6.92	27.19	97.61	78.65	197.35	37.82	95.43	74.22
	Minimum	32.00	131.00	60.00	3.00	7.00	11.80	7.00	49.20	4.09	35.71	7.00
	Maximum	66.00	153.00	156.30	12.60	80.60	284.50	264.50	438.90	65.43	184.34	242.29
	Bulk's mean	43.00	145.17	128.33	5.83	17.67	74.85	53.37	207.00	26.00	100.89	53.87
	Misr1 (P1)	44.00	130.67	143.46	3.86	24.93	73.38	74.90	150.27	35.06	70.33	52.68
	RenaMora (P2)	37.11	131.22	123.78	4.79	18.94	77.21	64.00	120.90	52.94	100.00	63.97
	Mid-parents	40.56	130.95	133.62	4.33	21.94	75.30	69.45	135.59	44.00	85.17	58.33
	Error variance	0.99	0.24	4.88	0.08	0.74	13.42	5.46	285.54	10.75	0.79	6.15
	σ^2_G	23.62	37.83	89.97	3.72	403.84	4298.15	4392.04	5262.36	97.27	560.79	3004.14
	σ^2_P	24.61	38.07	94.85	3.79	404.58	4311.57	4397.51	5547.90	108.02	561.57	3010.29
	GCV %	11.48	4.35	7.24	27.09	43.53	38.07	44.87	27.95	18.92	24.39	39.75
	PCV %	11.72	4.37	7.43	27.37	43.57	38.13	44.90	28.70	19.94	24.40	39.79
	H %	95.98	99.38	94.86	97.95	99.82	99.69	99.88	94.85	90.05	99.86	99.80
	Response to selection	1.58	7.27	32.21	-0.63	-0.79	8.91	-1.69	12.96	2.39	15.51	8.79
Cycle 2	F5 family's mean	43.13	132.57	130.37	4.65	27.58	105.15	90.46	175.17	41.62	80.93	73.69
	Minimum	37.00	128.00	105.00	3.40	17.80	70.80	55.00	114.80	21.88	43.94	37.20
	Maximum	59.00	140.00	158.00	6.20	43.80	161.50	176.20	243.70	55.56	117.76	128.60
	Bulk's mean	36.11	130.44	124.44	3.50	26.56	92.73	92.96	156.11	44.78	75.08	69.79
	Misr1 (P1)	45.00	131.33	142.02	3.79	25.22	68.90	76.07	166.46	30.17	66.03	50.22
	RenaMora (P2)	33.67	131.67	124.22	4.46	19.22	117.74	78.76	163.33	33.67	69.83	55.03
	Mid-parents	39.33	131.50	133.12	4.12	22.22	93.32	77.41	164.89	31.92	67.93	52.63
	Error variance	4.89	1.50	15.25	0.08	2.61	99.60	71.76	102.66	9.96	20.01	68.01
	σ^2_G	18.97	2.05	126.90	0.46	30.25	453.05	277.36	567.80	55.11	156.94	364.61
	σ^2_P	23.85	3.55	142.15	0.53	32.86	552.65	349.12	670.47	65.07	176.95	432.62
	GCV %	10.37	1.08	8.64	15.10	20.62	20.79	18.79	13.84	18.39	15.96	27.22
	PCV %	11.63	1.42	9.15	16.29	21.49	22.96	21.08	15.04	19.98	16.95	29.65
	H %	79.51	57.70	89.27	85.92	92.05	81.98	79.45	84.69	84.70	88.69	84.28
	Response to selection	-0.89	-11.09	5.11	-2.26	0.39	7.54	11.81	-22.19	3.79	-14.51	-0.53

5. The expected genetic gain from selection

Data in Table 8 represent the expected genetic gain (ΔG) estimated based on the proportion of the selected families in both populations after carrying two cycles of pedigree selection. Moderate and high estimates of broad sense heritability coupled with high or moderate σ^2_p gave high estimates of expected genetic gain from selection of 16.5 % and 20% superior plants of both populations in the F4 and F5 generations, respectively. The estimates of expected genetic gain from selection of

16.5% superior plants were higher for seed yield/plant and its attributes in Pop. II than those of Pop. I. This result reflects the extent of variability in both populations. While the estimates of the expected genetic gain from selection of 20% superior plants in the F5 generation were higher in Pop II for seed yield/plant along with some traits than those of Pop. I. The gain from selection in the first cycle ranged from (2.68 and 2.43 for BN/P) to (80.45 and 88.79 for BY/P) in Pop. I and II, respectively. While, the gain from selection in the second cycle ranged from (0.99 and 0.86 for BN/P)

to (32.23 and 30.04 for BY/P) in Pop. I and II, respectively. With respect to the expected genetic gain from selection in relation to bulk's mean and better parents, the data revealed high percentage of the expected genetic gain in relation to better parents in most studied traits especially in the second cycle of selection of Pop. II. Since, SY/P showed highest estimate of ΔG /better parent (43.64 %) in the second cycle in Pop II. These results indicate the success of pedigree selection to isolate high productivity plants.

Judging by the values of σ^2_G , σ^2_P , GCV %, PCV % and H % for each trait in both cycles of selection and in both populations (Tables 6 and 7), it is quite obvious that these parameters were depleted from cycle 1 to cycle 2 of pedigree line selection for seed yield/plant and its attributes. This depletion may due to the number of the selected families that was 50 families in cycle 1 and 10 families in cycle 2. Furthermore, the genetic variation among the 50 selected families was higher than the genetic variation among the 10 selected families. Beside this the impact of the environment on the behavior of the selected families. This result may indicate that the pedigree selection in the early generations is enough in faba bean populations. El-shimy *et al.* (2005) and Mahdy *et al.* (2015) found that great depletion of genetic coefficient of variability after two cycles of pedigree selection for seed yield in sesame. Ahmad (2016) reported that broad sense heritability values of all studied characters were reduced from filial to filial according to pedigree

selection which increases of homogeneity of plants.

6. Observed direct and correlated responses after applying two cycles of pedigree selection for seed yield/plant (SY/P).

Tables 9 and 10 show the means (observed direct) of the best 10 families selected according to the selection criterion "seed yield/plant" and correlated responses after carrying two cycles of pedigree selection in F5 generation in Pop I and II, respectively. The correlated response was estimated as percentage from bulk's mean, better parent and mid-parents in both populations. The pedigree selection succeeded to isolate superior genotypes in seed yield/plant with one or more effective attributed traits such as seed index and harvest index in both populations.

Days to first flower (FD)

Flowering in faba bean is an important trait and depends on the time of sowing, moisture, climatic factors and geographic location, but only 13-64% of flowers produce pods (Suso, *et al.*, 1996). In Pop I, families number F187, F10, F245 and F101 were insignificantly earlier in flowering than bulk's mean and mid-parents and recorded 34.33, 36.00, 36.00 and 36.33 days, respectively (Table 9). Also, these families were insignificantly late than the earliest parent (33.67 days). The same scenario was observed in Pop II, since all selected families were late in flowering than the earlier parent and bulk's mean. Families F177 and F026 were close to the earlier parent and recorded 37.67 and 38.67 days, respectively (Table 10).

Days to maturity (MD)

In Pop I, most of the selected F5 families were early in seed maturity compared to bulk sample and mid-parents. Eight families out of ten were significantly earlier than bulk's mean, and six families were earlier than mid-parents. In addition, families number F141 and F040 were significantly earlier in maturity than the earliest parent (RenaMora) and recorded 127.67 and 128.33 days, respectively (Table 9). In Pop II, all families were close to the bulk's

mean, better parent and mid parent values except the family no. F174 was significantly late. Families no. F008 and F111 were earlier in maturity than better parent Misr1 (Table 10). Flowering and fruit setting are affected by genetic makeup and environmental factors. Further, the environmental factors affecting fruit setting are mainly related to change in temperature and rainfall (Nanda *et al.*, 1988).

Table 8. Expected genetic advance (ΔG) of the base population and as percentage from bulk's mean and better parent at F4 (cycle 1) and F5 (cycle 2) generation in both populations.

Population	Generation	Expected gain	FD	MD	PH	BN	PN	PW	SN	BY	HI	SI	SY
Population I	F4 generation	ΔG	9.25	7.10	18.50	2.68	10.08	35.62	30.67	80.45	16.55	25.52	28.53
		ΔG /bulk's mean	30.65	5.08	17.35	37.59	46.30	40.64	46.95	49.36	38.08	23.34	40.29
		ΔG /better parent	24.91	5.41	14.95	34.80	33.32	40.11	33.73	38.27	31.25	25.52	41.65
	F5 generation	ΔG	8.44	3.53	14.86	0.99	7.11	21.52	8.48	32.23	8.55	11.87	7.05
		ΔG /bulk's mean	21.15	2.60	10.46	21.61	27.93	31.77	11.89	22.47	23.94	16.54	13.76
		ΔG /better parent	25.06	2.68	11.96	18.44	29.64	18.27	10.77	16.13	25.38	17.00	12.80
Population II	F4 generation	ΔG	8.10	6.68	19.83	2.43	13.44	64.11	46.25	88.79	19.13	41.66	52.80
		ΔG /bulk's mean	18.83	4.60	15.46	41.69	76.08	85.64	86.66	42.89	73.57	41.29	98.02
		ΔG /better parent	21.82	5.11	16.02	50.78	53.91	83.03	61.75	59.09	36.13	41.66	82.54
	F5 generation	ΔG	5.32	1.49	14.58	0.86	7.23	26.40	20.34	30.04	9.36	16.16	24.02
		ΔG /bulk's mean	14.73	1.14	11.72	24.58	27.22	28.47	21.88	19.24	20.90	21.53	34.41
		ΔG /better parent	15.80	1.13	11.74	19.30	28.66	22.42	25.82	18.05	27.80	23.15	43.64

Table 9. Observed direct and correlated responses after two cycles of pedigree selection for seed yield/plant (SY/P) in percentage of the bulk, better parent and mid-parents in Pop I.

Families	Days to flowering				Days to maturity				Plant height			
	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P
F086	50.67	27.02	50.50	27.91	131.00	-3.60	-0.51	-2.04	116.70	-17.82	-6.06	-6.39
F040	42.33	6.13	25.74	6.87	128.33	-5.56	-2.53	-4.03	103.83	-26.88	-16.41	-16.71
F245	36.00	-9.75	6.93	-9.12	132.00	-2.86	0.25	-1.29	123.80	-12.82	-0.34	-0.69
F233	50.00	25.35	48.51	26.23	132.67	-2.37	0.76	-0.79	121.80	-14.23	-1.95	-2.30
F187	34.33	-13.93	1.98	-13.32	130.00	-4.33	-1.27	-2.78	125.20	-11.83	0.79	0.43
F184	56.00	40.39	66.34	41.37	136.33	0.33	3.54	1.95	132.13	-6.95	6.37	5.99
F182	40.00	0.28	18.81	0.98	132.67	-2.37	0.76	-0.79	117.33	-17.37	-5.55	-5.88
F141	41.33	3.62	22.77	4.35	127.67	-6.05	-3.04	-4.53	130.63	-8.00	5.16	4.79
F101	36.33	-8.91	7.92	-8.27	134.33	-1.14	2.03	0.46	146.97	3.50	18.31	17.89
F010	36.00	-9.75	6.93	-9.12	129.67	-4.58	-1.52	-3.03	116.73	-17.79	-6.03	-6.36
Average	42.30	6.04	25.64	6.79	131.47	-3.25	-0.15	-1.69	123.51	-13.02	-0.57	-0.92
Bulk's mean	39.89				135.89				142.00			
Nubariah2 (P1)	45.56				135.78				125.10			
RenaMora (P2)	33.67				131.67				124.22			
Mid-parents	39.61				133.72				124.66			
R.LSD 5% Families	7.83				2.75				6.33			
R.LSD 5% Entries	6.83				2.39				5.33			
Families	Number of branches/plant				Number of Pods/plant				Pods weight/plant			
	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P
F086	3.40	-25.91	-36.78	-30.85	18.60	-26.90	-22.43	-13.89	72.50	7.04	-38.43	-19.79
F040	3.60	-21.55	-33.06	-26.78	23.53	-7.51	-1.85	8.95	66.90	-1.23	-43.18	-25.99
F245	3.73	-18.64	-30.58	-24.07	20.87	-17.99	-12.97	-3.40	57.60	-14.96	-51.08	-36.28
F233	4.13	-9.93	-23.14	-15.93	26.80	5.33	11.77	24.07	100.60	48.52	-14.56	11.30
F187	3.67	-20.10	-31.82	-25.42	34.40	35.20	43.47	59.26	93.17	37.55	-20.87	3.07
F184	2.80	-38.98	-47.93	-43.05	17.90	-29.65	-25.35	-17.13	49.50	-26.92	-57.96	-45.24
F182	5.10	11.14	-5.17	3.73	32.40	27.34	35.13	50.00	74.47	9.94	-36.76	-17.62
F141	2.93	-36.08	-45.45	-40.34	26.00	2.18	8.43	20.37	92.45	36.49	-21.48	2.28
F1010	4.80	4.60	-10.74	-2.37	30.30	19.08	26.37	40.28	80.80	19.29	-31.38	-10.61
F010	4.00	-12.83	-25.62	-18.64	17.10	-32.79	-28.68	-20.83	73.80	8.96	-37.32	-18.35
Average	3.82	-16.83	-29.03	-22.37	24.79	-2.57	3.39	14.77	76.18	12.47	-35.30	-15.72
Bulk's mean	4.59				25.44				67.73			
Nubariah2 (P1)	5.38				23.98				63.03			
RenaMora (P2)	4.46				19.22				117.74			
Mid-parents	4.92				21.60				90.39			
R.LSD 5% Families	0.72				4.60				28.63			
R.LSD 5% Entries	0.65				4.19				22.57			

Table 9: Continued

Families	Number of seeds/plant				Biological yield/plant				Harvest index			
	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P
F086	50.10	-29.79	-36.39	-33.40	119.60	-16.64	-40.17	-34.15	45.80	28.30	36.03	59.07
F040	68.73	-3.67	-12.73	-8.64	116.60	-18.73	-41.67	-35.80	45.16	26.50	34.12	56.84
F245	56.20	-21.24	-28.64	-25.30	106.60	-25.70	-46.67	-41.30	35.55	-0.41	5.59	23.48
F233	79.20	10.99	0.56	5.28	170.60	18.91	-14.66	-6.07	40.83	14.38	21.28	41.82
F187	68.93	-3.39	-12.47	-8.37	132.50	-7.64	-33.72	-27.04	45.34	27.01	34.67	57.47
F184	52.10	-26.99	-33.85	-30.75	108.50	-24.37	-45.72	-40.26	31.07	-12.97	-7.73	7.90
F182	87.33	22.39	10.89	16.09	132.50	-7.64	-33.72	-27.04	46.84	31.21	39.12	62.68
F141	72.30	1.32	-8.20	-3.89	132.85	-7.40	-33.54	-26.85	50.93	42.67	51.27	76.89
F101	72.00	0.90	-8.58	-4.29	158.50	10.48	-20.71	-12.73	34.75	-2.65	3.22	20.70
F010	66.83	-6.34	-15.14	-11.16	133.17	-7.18	-33.38	-26.68	34.89	-2.27	3.62	21.18
Average	67.37	-5.58	-14.45	-10.44	131.14	-8.59	-34.40	-27.79	41.12	15.18	22.12	42.80
Bulk's mean	71.36				143.47				35.70			
Nubariah2 (P1)	71.70				199.90				23.92			
RenaMora (P2)	78.76				163.33				33.67			
Mid-parents	75.23				181.62				28.79			
R.LSD 5% Families	28.30				34.27				12.77			
R.LSD 5% Entries	24.92				27.05				9.85			

Families	Seed index				Seed yield/plant			
	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P
F086	110.73	54.33	58.58	62.24	55.05	7.52	0.03	7.05
F040	83.68	16.62	19.83	22.60	52.90	3.32	-3.88	2.87
F245	67.94	-5.31	-2.70	-0.45	39.30	-23.24	-28.59	-23.57
F233	88.90	23.91	27.32	30.26	70.10	36.91	27.38	36.32
F187	86.79	20.96	24.29	27.16	61.10	19.34	11.02	18.82
F184	64.67	-9.87	-7.39	-5.25	33.70	-34.18	-38.76	-34.46
F182	71.37	-0.52	2.22	4.57	62.23	21.55	13.08	21.02
F141	93.64	30.51	34.11	37.20	67.95	32.71	23.47	32.14
F101	76.30	6.34	9.27	11.79	54.95	7.32	-0.15	6.86
F010	71.55	-0.28	2.47	4.83	46.60	-8.98	-15.32	-9.38
Average	81.56	13.67	16.80	19.50	54.39	6.23	-1.17	5.77
Bulk's mean	71.75				51.20			
Nubariah2 (P1)	66.68				47.81			
RenaMora (P2)	69.83				55.03			
Mid-parents	68.25				51.42			
R.LSD 5% Families	30.61				31.47			
R.LSD 5% Entries	26.74				28.14			

Table 10. Observed direct and correlated responses after two cycles of pedigree selection for seed yield/plant (SY/P) in percentage of the bulk, better parent and mid-parents in Pop II.

Families	Days to flowering				Days to maturity				Plant height			
	Mea	Bul	bet-	Mid-	Mea	Bul	bet-	Mid	Mea	Bul	bet-	Mid
F008	41.0	13.5	21.7	4.24	130.	-	-	-	136.	9.82	10.0	2.66
F026	38.6	7.08	14.8	-1.69	133.	2.21	1.52	1.39	119.	-	-	-
F036	45.0	24.6	33.6	14.4	132.	1.70	1.02	0.89	144.	16.2	16.4	8.67
F063	40.3	11.6	19.8	2.54	133.	2.21	1.52	1.39	146.	17.5	17.8	9.92
F076	46.0	27.3	36.6	16.9	132.	1.19	0.51	0.38	139.	12.4	12.6	5.12
F111	39.6	9.85	17.8	0.85	130.	-	-	-	121.	-	-	-
F122	48.0	32.9	42.5	22.0	132.	1.19	0.51	0.38	119.	-	-	-
F174	50.0	38.4	48.5	27.1	137.	5.28	4.57	4.44	143.	15.5	15.7	7.97
F177	37.6	4.31	11.8	-4.24	131.	0.94	0.25	0.13	115.	-	-	-
F203	45.0	24.6	33.6	14.4	133.	1.96	1.27	1.14	117.	-	-	-
Average	43.1	19.4	28.1	9.66	132.	1.63	0.94	0.81	130.	4.76	4.95	-
Bulk's	36.1				130.				124.			
Misr1 (P1)	45.0				131.				142.			
RenaMora	33.6				131.				124.			
Mid-	39.3				131.				133.			
R.LSD 5%	8.06				4.87				12.7			
R.LSD 5%	6.63				4.39				10.8			
Families	Number of branches/plant				Number of Pods/plant				Pods weight/plant			
	Mea	Bul	bet-	Mid-	Mea	Bul	bet-	Mid	Mea	Bul	bet-	Mid
F008	4.77	36.2	6.98	15.6	26.6	0.17	5.46	19.7	82.5	-	-	-
F026	4.40	25.7	-	6.74	26.1	-	3.48	17.4	92.1	-	-	-
F036	4.73	35.3	6.23	14.8	27.0	1.67	7.05	21.5	125.	35.8	6.97	34.9
F063	5.13	46.7	15.2	24.5	19.3	-	-	-	84.6	-	-	-
F076	3.90	11.5	-	-5.39	23.0	-	-	3.50	107.	15.7	-	14.9
F111	3.53	1.02	-	-	39.3	47.9	55.8	76.8	123.	32.6	4.51	31.8
F122	3.80	8.64	-	-7.82	20.6	-	-	-	71.8	-	-	-
F174	5.33	52.4	19.7	29.3	32.0	20.7	27.1	44.3	93.7	1.11	-	0.48
F177	5.40	54.3	21.2	31.0	32.8	23.5	30.0	47.6	125.	34.8	6.16	33.9
F203	5.53	58.2	24.1	34.2	29.0	9.21	14.9	30.5	145.	56.6	23.4	55.7
Average	4.65	33.0	4.44	12.8	27.5	3.85	9.33	24.1	105.	13.3	-	12.6
Bulk's	3.50				26.5				92.7			
Misr1 (P1)	3.79				25.2				68.9			
RenaMora	4.46				19.2				117.			
Mid-	4.12				22.2				93.3			
R.LSD 5%	0.96				5.04				36.2			
R.LSD 5%	0.78				4.42				29.3			

Table 10. Continued

Families	Number of seeds/plant				Biological yield/plant				Harvest index			
	Mea	Bul	bet-	Mid-	Mea	Bul	bet-	Mid	Mea	Bul	bet-	Mid
F008	66.07	-	-	-	176.	13.0	6.05	7.06	24.6	-	-	-
F026	73.60	-	-	-4.92	155.	-	-	-	36.2	-	7.55	13.4
F036	85.60	-	8.69	10.5	185.	19.1	11.7	12.7	38.3	-	13.7	20.0
F063	81.10	-	2.98	4.77	177.	13.7	6.70	7.71	36.9	-	9.68	15.6
F076	81.10	-	2.98	4.77	166.	6.65	0.03	0.97	50.5	12.9	50.2	58.4
F111	129.1	38.8	63.9	66.7	205.	31.4	23.3	24.4	44.0	-	30.7	37.9
F122	69.40	-	-	-	115.	-	-	-	42.3	-	25.7	32.6
F174	106.0	14.1	34.6	37.0	158.	1.70	-	-	41.9	-	24.6	31.4
F177	98.50	5.96	25.0	27.2	189.	21.5	14.0	15.1	49.8	11.2	47.9	56.0
F203	114.1	22.7	44.8	47.3	220.	41.2	32.4	33.7	51.3	14.6	52.4	60.8
Average	90.46	-	14.8	16.8	175.	12.2	5.23	6.23	41.6	-	23.6	30.3
Bulk's	92.96				156.				44.7			
Misr1 (P1)	76.07				166.				30.1			
RenaMora	78.76				163.				33.6			
Mid-	77.41				164.				31.9			
R.LSD 5%	29.45				34.4				10.7			
R.LSD 5%	25.41				29.2				9.09			
Families	Seed index				Seed yield/plant							
	Mean	Bulk	better P	Mid-P	Mean	Bulk	better P	Mid-P				
F008	66.79	-11.04	-4.35	-1.68	43.73	-37.33	-20.53	-16.90				
F026	76.11	1.38	9.00	12.05	56.05	-19.69	1.85	6.50				
F036	80.74	7.54	15.63	18.87	69.20	-0.84	25.74	31.49				
F063	80.96	7.83	15.94	19.19	66.00	-5.43	19.93	25.41				
F076	103.78	38.23	48.63	52.78	85.15	22.01	54.72	61.80				
F111	71.41	-4.89	2.26	5.12	92.75	32.90	68.53	76.24				
F122	70.43	-6.19	0.86	3.68	49.00	-29.79	-10.96	-6.89				
F174	63.51	-15.41	-9.05	-6.51	67.20	-3.71	22.11	27.69				
F177	96.25	28.20	37.84	41.70	94.50	35.41	71.71	79.56				
F203	99.30	32.26	42.21	46.18	113.35	62.42	105.97	115.38				
Average	80.93	7.79	15.90	19.14	73.69	5.59	33.91	40.03				
Bulk's	75.08				69.79							
Misr1 (P1)	66.03				50.22							
RenaMora	69.83				55.03							
Mid-	67.93				52.63							
R.LSD 5%	15.01				28.38							
R.LSD 5%	12.52				23.84							

Plant height (PH)

Plant height of the selected families of Pop. I ranged between 103.83 cm (F040) and 146.97 cm (F101). Nine and six families out of ten were significantly shorter than the bulk's mean and the shortest parent, respectively (Table 9). In Pop II, plant height of the selected families ranged from 115.60 cm (F177) to 146.33 cm (F063). Five families were insignificantly shorter than both of bulk's mean and shortest parent (Table 10).

Number of branches/ plant (BN)

Number of branches per plant of the selected families of Pop I ranged between 2.80 (F184) and 5.10 branches (F182). All families had lower number of branches per plant than the bulk's mean and better parent except only two families number F182 and F101 were insignificantly higher in number of branches/plant than the bulk's mean. A different scenario was observed in the Pop II, arguably, most of the selected families were significantly higher in num-

ber of branches per plant than both of bulk sample and better parent. The best family was F203 that increased bulk sample and better parent by percentage 58.20 and 24.19%, respectively.

Number of Pods/plant (PN)

Number of pods/plant of the ten selected families in the F5- generation after two cycles of selection in Pop I ranged from 17.7 and 34.4 with an average of 24.79. Furthermore, families no. F187, F182 and F101 were significantly increased both bulk sample and better parent by percentages (35.20 and 43.47%), (27.34 and 35.13%) and (19.08 and 26.37%), respectively. The same trend was observed in Pop II, since the number of pods/plant ranged between 19.30 and 39.30 pods. In addition, families no. F111, F177 and F174 were significantly surpassed the bulk sample and better parent by percentages (47.99 and 55.81%), (23.51 and 30.04%) and (20.75 and 27.14%), respectively.

Pods weight/plant (PW)

Pods weight/plant of the ten selected families of the Pop I ranged between 49.50 and 100.60 g with an average of 76.18 g. The best families in pod weight were F233, F187, F141 and F101 which significantly surpassed the bulk's mean by percentages 48.53, 37.56, 36.49 and 19.30, respectively. No families surpassed the better parent 'Rena Mora'. Different trend was observed in Pop II, since the pods weight of the selected families ranged from 71.85 to 145.30 with an average of 105.15 g. Families no. F203, F036, F177 and F111 were significantly surpassed bulk's mean and insignificantly higher than better parent.

Number of seeds/plant (SN)

Number of seeds per plant of the selected families of Pop I ranged between 50.10 (F086) and 87.33 seeds (F182). Four families had insignificantly higher number of seeds per plant than the bulk's mean, and two families were insignificantly higher than better parent. A different scenario was observed in the Pop II, three of the selected families (F111, F203 and F174) were significantly higher in number of seeds per plant than better parent and one family significantly increased the bulk's mean by 38.88%. The best family was F111 that increased bulk sample and better parent by percentage 38.88 and 63.92%, respectively.

Biological yield/plant (BY)

The biological yield of the ten selected families of the Pop. I ranged between 106.60 and 170.60 g with an average of 131.14 g. The family F233 was higher than the other family in biological yield which significantly surpassed the bulk's mean by 18.91%. No families increased the better parent 'Nubariah'. Different trend was observed in Pop II, since the biological yield of the selected families ranged from 115.65 to 220.50 with an average of 175.17 g. Families no. F203 and F111 were the best families and significantly surpassed bulk's mean and better parent. They recorded (41.25 and 32.04%) and (31.48 and 23.30%) increase in biological yield than both bulk sample and better parent, respectively.

Harvest index (HI)

Harvest index of the selected families of Pop I ranged between 31.07 (F184) and 50.93% (F141) with an average of 41.12%. Three and five

families out of ten had higher significantly percentages of harvest index than the bulk's mean and the better parent (RenaMora), respectively (Table 9). In Pop II, harvest index of the selected families ranged from 24.08 (F008) to 51.33% (F203) with an average of 41.62%. Four families were significantly higher in HI than the better parent (Table 10).

Seed index (SI)

The seed index of the ten selected families of the Pop I ranged between 64.67 and 110.73 g with an average of 81.56 g. The family F086 was significantly heavy in 100-seeds weight than both of bulk sample and better parent and recorded 43.98 and 58.57, respectively. Five families insignificantly increased both bulk sample and better parent 'RenaMora'. The same trend was observed in Pop II, since the seed index of the selected families ranged from 63.51 to 103.78 g with an average of 80.93 g. Families no. F076, F203 and F177 were the best families and significantly surpassed bulk's mean and better parent. They recorded (38.23 and 48.63%), (32.26 and 42.21%) and (28.20 and 37.84%) increase in seed index than both bulk sample and better parent, respectively.

Seed yield/plant (SY/P)

The seed yield of the ten selected families of the Pop I ranged between 33.70 and 70.10 g with an average of 54.39 g. Seven families out of ten were insignificantly higher in seed yield per plant than bulk sample and better parent. The family F233 was the best family and recorded 36.91 and 27.39% increase in seed yield than bulk's mean and better parent, respectively. The same

scenario was observed in Pop II, since the seed yield of the selected families ranged from 43.73 to 113.35 g with an average of 73.69 g. Two families (F203 and F177) were the best families and significantly surpassed bulk's mean and better parent. They recorded (62.42 and 105.98%) and (35.41 and 71.71) increase in seed yield than both bulk sample and better parent, respectively. Also, families no. F111 and F076 yielded more seed than the better parent (RenaMora) and recorded 68.53 and 54.72% increase in seed yield than the better parent. Several researchers indicated that pedigree selection method proved to be superior in mean values of the selected populations (El-shimy *et al.* 2005; Ahmed *et al.* 2008; Abdelhaleem and Mohamed 2011; Mohamed and Abdelhaleem 2011; Mahdy *et al.* 2015; Khames *et al.* 2017).

Conclusion

Remarkable variations among families of the both base populations as well as the selected families in cycle 1 and cycle 2 of pedigree line selection were observed for all studied traits. Judging by the range and C.V. for each trait, it is quite obvious that Pop I showed more genetic variation than Pop II in most of studied traits. In addition, the range of both populations fill outside the range of the two parents that formed the population. This result reflects the presence of transgressive segregation among the F3 families of the two populations. Therefore, this genetic variation is sufficient for pedigree selection.

In pedigree line selection, the breeder concerned with the performance of individual selected families.

This may be due to that the overall mean masked the individual family means. Means of the selected families after two cycles of pedigree selection for all studied traits for both populations were reduced from cycle 1 to cycle 2 compared to bulk sample and better parent. Traits days to flowering and maturity showed desirable trend of selection, since most of the selected families after two cycles of selection were early. Comparison among means of the selected families showed that more progress in improving seed yield/plant in both populations could be achieved from pedigree selection in early generations. In Pop. I, families no. F233, F141, F182, F187 and F086 were the best families in most studied traits and out yielded both parents and bulk's mean after two cycles of pedigree selection. In Pop II, families no. F203, F177, F111, F076 and F036 were the best families and surpassed both bulk sample and better parent. The selected families of Pop II were higher in seed weight, higher seed index, higher biological yield, higher pod weight, higher pods number than the selected families of Pop I. Accordingly, the pedigree selection would be reasonably effective for selecting the superior genotypes for each trait.

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الانتخاب المنسب لتحسين محصول البذرة في عشيرتين انعزالتين من الفول البلدي

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الملخص

نفذت هذه التجربة في محطة بحوث المطاعنة بمحافظة الأقصر، مصر خلال ثلاث مواسم هي ٢٠١٣/٢٠١٤، ٢٠١٤/٢٠١٥ و ٢٠١٥/٢٠١٦. تهدف هذه الدراسة الي تحقيق وانجاز دورتين من الانتخاب المنسب لتحسين صفة محصول البذرة للنبات الفردي في عشيرتين انعزالتين من الفول البلدي في الجيلين الرابع والخامس. أظهرت التحليلات الاحصائية وجود اختلافات عالية المعنوية بين العائلات في كلا من العشيرتين القاعديتين وأيضاً بين العائلات المنتخبة في الدورتين الأولى والثانية من الانتخاب المنسب لكل الصفات المدروسة. أظهرت مقارنة متوسطات العائلات المنتخبة وجود تقدم ملحوظ في تحسين صفة محصول البذرة للنبات الفردي في كلتا العشيرتين نتيجة الانتخاب المنسب في الأجيال المبكرة. في العشيرة الأولى، كانت العائلات ٢٣٣، ١٤١، ١٨٢، ١٨٧، ٨٦ أفضل العائلات في معظم الصفات المدروسة وفاقته في محصولها الأباء ومتوسط البلك بعد دورتين من الانتخاب المنسب. في العشيرة الثانية، تفوقت العائلات ٢٠٣، ١٧٧، ١١١، ٧٦، ٣٦ في المحصول البذري أفضل الأباء وكذلك البلك. العائلات المنتخبة من العشيرة الثانية كانت أعلى في محصول النبات الفردي ووزن الـ ١٠٠ بذرة والمحصول البيولوجي ووزن وعدد القرون للنبات من العائلات المنتخبة من العشيرة الأولى. هذه العائلات تعتبر تراكيب وراثية واعدة لزيادة المحصول البذري. وبالتالي، تعتبر طريقة الانتخاب المنسب فعالة في الانتخاب لتراكيب وراثية متفوقة في المحصول.