

Pedigree selection in one population of faba bean (*Vicia faba* L.).

M. H. Haridy, I. N. Abd El-Zaher and M. A. A. El-Said

Agronomy Department, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt.

Abstract: Two cycles of pedigree selection for one faba bean cross population i.e. Giza 429 x Giza 3 were done from F₄ to F₆ generations during three successive seasons, 2011/2012, 2012/2013 and 2013/2014. The obtained results showed significant differences among families at both cycles of selection. The overall families means exceeded significantly the best parent for seed yield/plant in the first cycle as well as, number of branches/plant, number of pods/plant and 100-seed yield/plant in the second cycle. The C1 families possessed considerable amount of genotypic and phenotypic variability for all studied traits. Consequently, high estimates of heritability were obtained. The variability between C2 families decreased rapidly for all studied traits. Positive significant genotypic and phenotypic correlations were detected between most pairs of traits at both cycles of selection. However, strong positive significant genotypic and phenotypic correlations were found between seed yield/plant and number of pods/plant at both cycles of selection, indicated number of pods/plant is a good selection criterion to improve seed yield/plant. The actual response to selection was higher than the expected response for all studied traits at the two cycles of selection.

INTRODUCTION

Faba bean (*Vicia faba* L.) is an important source of protein for human and animal nutrition. In addition, as other seed legumes, faba bean provides nitrogen fixation and has a major role in crop rotation in many regions of the world (Alan and Ceren 2007). Plant breeders are for continuously searching for more effective and efficient selection procedures for crops improvement. Pedigree selection method is a preferable method for improvement yielding ability in faba bean (Ahmed *et al* 2008). Heritability estimates provide values of relative importance of genetic components to

phenotypic variation and is useful in predicting the expected genetic advance from selection in segregating populations. Correlation between traits can be useful in developing selection criteria (Kloth, 1998). Falconer, 1989 reported that if two traits are associated and one is easier to assess and select, selection pressures should be applied to this trait to improve the other. Genotypic and phenotypic correlations are widely used to standard the nature of complex interrelationships among traits and to identify the source of variation. This investigation was aimed to study the efficiency of pedigree selection to improve seed yield of 220 F₄ families at two cycles of selection.

MATERIALS AND METHODS

Two cycles (C1 and C2) of pedigree selection for one faba bean cross population i.e. Giza 429 x Giza 3 were done from F₄ to F₆ generations during three successive seasons, 2011/2012, 2012/2013 and 2013/2014 at Experimental Farm, Faculty of Agriculture, Al-Azhar University, Assiut Branch, Egypt, to study the efficiency of pedigree selection to improve seed yield. The basic materials used in this study consisted of 220 F₄ families which traced back to F₃ families from cross Giza 429 x Giza 3. The parents Giza 429 and Giza 3 were obtained from Legume Crops Section, Field Crops Research Institute, Agriculture Research Center, Giza, Egypt.

In 2011/2012 growing season, 220 individual F₄ families were grown in non-replicate experiment, seeds hills spaced 20 cm apart and one plant was left per hill. The best 60 plants were selected by seed yield/plant criterion to obtain F₅ families.

In 2012/2013 growing season, the 60 families with parents, check cultivar (Misr 1) and F₅ bulk random sample (a mixture of equal number of seeds from each plant) were sown in a randomized complete block design with three replications. Each family, bulk sample, parents and check cultivar were represented in each replicate by one ridge, 3 m long, 60 cm apart and 20 cm between hills. The best 10 families were selected by seed yield/plant criterion to obtain F₆ families.

In 2013/2014 growing season, the 10 families with parents, check cultivar and F₆ bulk sample were sown on 20th October in a randomized complete block design with three replications. Each family, bulk sample, parents and check cultivar were represented in each replicate by one ridge, 3 m long, 60 cm apart and 20 cm between hills.

The recommended cultural practices for faba bean production were applied at the proper time. Data were collected on ten random plants from each family, parents, bulk and the check for plant height, number of branches/plant, number of pods/plant, 100-seed weight and seed yield/plant.

Statistical Analysis: Analysis of mean squares with a randomized complete block design to compute the significance for genotypes (Table 1) was made according to **Snedecor and Cochran 1980**. The least significant difference (L.S.D) test at 0.05 and 0.01 levels of probabilities was used to compare among means according to **Steel and Torrie 1980**.

Table 1: Analysis of variance and expected mean squares.

S.O.V	d.f	M.S	E.M.S
Replications	r-1	m ₃	$\frac{\sigma^2 e + g\sigma^2}{r}$
Genotypes	g-1	m ₂	$\frac{\sigma^2 e + r\sigma^2}{g}$
Error	(r-1)(g-1)	m ₁	$\sigma^2 e$

Estimates of phenotypic and genotypic variances (σ^2_{ph} and σ^2_g) and heritability estimates were calculated from partitioning mean squares expectation (E.M.S) of variance components of the selected families (Table 1) according to **Al-Jibouri et al (1958)** as follows:

- The phenotypic variance $\sigma^2_{ph} = \sigma^2_g + \sigma^2_e$
Where $\sigma^2_e = m_1/r$
- The genotypic variance $\sigma^2_g = (m_2 - m_1)/r$

Broad sense heritability (H^2b) was calculated as the ratio of genotypic variance (σ^2g) to the phenotypic variance (σ^2ph) according to **Fehr 1987** as follows:

$$H^2b = (\sigma^2g/\sigma^2 p) \times 100$$

The phenotypic (P.C.V %) and genotypic (G.C.V %) coefficients of variability were estimated according to **Burton 1952** as follows:

- P.C.V % = $(\sigma p/\bar{x})100$

- G.C.V % = $(\sigma g/\bar{x})100$

Where: σp and σg are the phenotypic and genotypic standard deviations of the family mean and \bar{x} is the family mean for a given trait.

The predicted response to selection in seed yield/plant was calculated from C1 and C2 families as follows:

$$\Delta g = i\sigma ph^2$$

Where: i = intensity of selection, σp = standard deviation of phenotypic value and h^2 = narrow sense heritability. Whereas, response to selection of the 10%.

The phenotypic ($r_{p_{xy}}$) and genotypic ($r_{g_{xy}}$) correlations were estimated according to **Johanson et al 1955** as follows:

$$r_{p_{xy}} = \text{Cov}_{p_{xy}} / (\sigma_{p_x} \cdot \sigma_{p_y})$$

$$r_{g_{xy}} = \text{Cov}_{g_{xy}} / (\sigma_{g_x} \cdot \sigma_{g_y}).$$

where: $\text{Cov}_{p_{xy}}$ is the phenotypic covariance of two variable x and y .

$\text{Cov}_{g_{xy}}$ is the genotypic covariance of two variables x and y .

RESULTS AND DISCUSSION

Two cycles (C1 and C2) of pedigree selection method were achievement from F_4 to F_6 generations of one faba bean population (*Vicia faba* L.) stemmed from the cross between Giza 429 x Giza 3.

Variability among families: Mean squares of families for all studied traits at both cycles of selection are presented in Table 2. The obtained

results revealed significant differences among families for all studied traits at the two cycles of selection. This result was in agreement with these obtained by **Abd-El-Haleem and Mohamed 2011** and **Yassien *et al* 2012**.

Table 2: mean squares of the selected families for all studied traits at the two cycles of selection.

S.O.V		Plant height	No. of branches/plant	No. of pods/plant	100-seed weight	Seed yield/plant
Reps.	C1	25.22	0.18	23.83	0.38	20.12
	C2	18.80	0.12	9.30	0.47	21.25
Families	C1	170.75**	0.88**	16.20**	97.65**	53.53**
	C2	146.12**	0.36*	13.90**	29.40**	32.35**
Error	C1	20.55	0.63	7.44	14.19	9.55
	C2	30.52	0.25	7.50	6.25	10.05

* and ** are significant at 0.05 and 0.01 level of probability, respectively.

Means of the families, bulk population, two parents and the check cultivar for all studied traits at the two cycles of selection are presented in Table 3. The obtained results revealed that overall families means exceeded significantly the best parent for seed yield/plant in the first cycle as well as, number of branches/plant, number of pods/plant and 100-seed weight in the second cycle.

Table 3: Means of families, bulk population, two parents and check variety for all studied traits at the two cycles of selection.

Item		Plant height(cm)	No. of branches/plant	No. of pods/plant	100-seed weight(g)	seed yield/plant(g)
C1	Families	127.12	3.70	17.90	26.93	60.40
	Bulk	124.60	3.60	16.00	25.02	58.00
	Parent 1	121.23	2.98	14.25	23.99	50.12
	Parent 2	117.97	3.05	13.12	19.89	47.25
	Check	127.65	3.90	18.05	28.55	61.22
	L.S.D 0.05	7.32	1.28	4.41	6.09	4.99
	L.S.D 0.01	9.69	1.70	5.83	8.05	6.60
C2	Families	129.25	4.04	21.55	31.68	62.45
	Bulk	125.00	3.90	17.11	26.16	60.97
	Parent 1	122.55	3.11	15.66	24.06	59.00
	Parent 2	118.96	3.03	14.22	20.44	51.09
	Check	127.77	3.95	18.66	28.77	61.55
	L.S.D 0.05	9.48	0.86	4.70	4.29	5.43
	L.S.D 0.01	12.98	1.17	6.43	5.87	7.45

Means of seed yield/plant of 60 selected families, bulk population, parents and check cultivar at the first cycle of selection (Table 4) showed that 12 and 18 families out of 60 surpassed significantly bulk population and the best parent, respectively. On the other hand, only family (number 27) surpassed significantly check cultivar (Misr 1).

Table 4: Mean of seed yield/plant of 60 families, bulk population, parents and check cultivar for all studied traits at the first cycle of selection.

Family No.	Seed yield (g)	Family No.	Seed yield (g)	Family No.	Seed yield (g)	Family No.	Seed yield (g)	Family No.	Seed yield (g)	Family No.	Seed yield (g)
1	28.04	12	24.50	23	28.25	34	31.00	45	31.00	56	24.50
2	27.22	13	30.58	24	27.80	35	29.22	46	28.10	57	25.35
3	25.01	14	25.00	25	29.50	36	32.99	47	27.16	58	31.25
4	33.50	15	23.22	26	30.11	37	25.55	48	28.19	59	26.20
5	31.37	16	28.11	27	34.22	38	22.19	49	30.50	60	28.50
6	25.23	17	26.44	28	22.80	39	26.60	50	25.50	Bulk	25.02
7	21.01	18	26.22	29	23.15	40	30.19	51	33.12	Parent 1	23.99
8	23.44	19	25.35	30	26.12	41	20.16	52	27.25	Parent 2	19.89
9	24.06	20	29.33	31	25.00	42	30.60	53	26.00	Check	28.55
10	19.55	21	31.50	32	27.12	43	23.12	54	29.50	L.S.D 0.05	4.99
11	22.55	22	23.00	33	18.01	44	28.80	55	27.05	L.S.D 0.01	6.60

Means of seed yield/plant of 10 selected families and their percentage of the bulk population, the best parent and check cultivar at the second cycle of selection (Table 5) showed that 5 and 8 families out of 10 surpassed significantly bulk population and the best parent, respectively. On the other hand, only family (number 36) surpassed significantly check cultivar by 118.87 %. These results are in general agreement with those reported by Bakheit and Mahdy 1988b, Abdelmula and Abuanja 2004, Abd-El-Haleem and Mohamed 2011 and Yassien *et al* 2012.

Table 5: Means of seed yield/plant of 10 families and their percentage of bulk population, the best parent and check cultivar at the second cycle of selection.

No. of family	Family mean (g)	Mean percentage from		
		Bulk	Best parent	Check
4	32.90	125.76	136.74	114.36
5	31.88	121.87	132.50	110.81
13	28.88	110.40	120.03	100.38
21	33.89	129.55	140.86	117.80
27	31.50	120.41	130.92	109.49
34	31.66	121.02	131.59	110.04
36	34.20	130.73	142.14	118.87
42	28.86	110.32	119.95	100.31
45	31.50	120.41	130.92	109.49
58	31.55	120.60	131.13	109.66
Bulk	26.16			
Best parent	24.06			
Check	28.77			
L.S.D 0.05	5.43			

Table 6: Genotypic (σ^2_g) and phenotypic variance (σ^2_p), genotypic (GCV %) and phenotypic (PCV %) coefficients of variability and heritability in broad sense (H.B.S %) at the two cycles of selection.

Traits	σ^2_g	G.C.V%	σ^2_p	PCV%	H.B.S%		Means
Plant height	C1	50.07	5.57	56.92	5.94	87.97	127.12
	C2	38.53	4.80	48.70	5.40	79.12	129.25
Number of branches/plant	C1	0.08	7.80	0.29	14.64	30.56	3.70
	C2	0.04	4.74	0.12	8.58	28.41	4.04
Number of pods/plant	C1	2.92	9.55	5.40	12.98	54.07	17.90
	C2	2.13	6.78	4.63	9.99	46.04	21.55
100-seed weight	C1	27.82	8.73	32.55	9.45	85.47	60.40
	C2	7.72	4.45	9.80	5.01	78.74	62.45
Seed yield/plant	C1	14.66	14.22	17.84	15.69	82.16	26.93
	C2	7.43	8.61	10.78	10.37	68.93	31.68

Genetic parameters: Phenotypic (PCV %) and genotypic (GCV %) coefficients of variability and heritability in broad sense (H.B.S %) at the two cycles of selection are presented in Table 6. The obtained results revealed that values of phenotypic and genotypic coefficients of variability among the selected families showed small differences for all studied traits at the two cycles of selection, revealing that the environment has not a major role to influence variation among families. As well as, values of phenotypic and genotypic coefficients of variability decreased in cycle 2 than cycle 1 for all studied traits. Broad sense heritability values decreased in cycle 2 than cycle 1 for all studied traits. This result was expected because of low number of selected families (10) which were superior in seed yield/plant. These results are supported with the findings of **Bakheit**

and Mahdy 1987, Bakheit and Mahdy 1988a, El-Shazly 1993, Yamani 2003, Abd-El-Haleem and Mohamed 2011 and Yassien *et al* 2012.

Correlation among traits: Genotypic and phenotypic correlation between pairs of traits at C1 and C2 are listed in Table 7. The obtained results cleared that positive significant genotypic and phenotypic correlation was detected between most pairs of traits at both cycles of selection. However, strong positive significant genotypic and phenotypic correlation was found between seed yield/plant and number of pods/plant at both cycles of selection, indicated that number of pods/plant is a good selection criterion to improve seed yield/plant. These results were in agreement with those obtained by *Antoun et al* 1991, *Singh et al* 1998, *Abo-Elwafa et al* 1999, *Nageeb* 2002, *Alghamdi* 2007 and *Yassien et al* 2012.

Table 7: Genotypic (above diagonal) and Phenotypic (below diagonal) correlation between pairs of studied traits at two cycles of selection.

Traits		Plant height	Number of branches/plant	Number of pods/plant	100-seed weight	Seed yield/plant
Plant height	C1	-	0.525**	0.431**	0.138**	0.415**
	C2	-	0.309**	0.553**	0.883**	0.919**
Number of branches/plant	C1	0.175**	-	0.125**	0.251**	0.767**
	C2	0.233*	-	0.173	0.673**	0.403**
Number of pods/plant	C1	0.335**	0.549**	-	0.458**	0.875**
	C2	0.537**	0.275**	-	0.253*	0.703**
100-seed weight	C1	0.147**	0.181**	0.139**	-	0.235**
	C2	0.285**	0.271**	0.245*	-	0.199
Seed yield/plant	C1	0.357**	0.916**	0.759**	0.158**	-
	C2	0.488**	0.566**	0.862**	0.146	-

Expected and actual response to selection: Expected and actual response to selection for seed yield/plant at the two cycles of selection is

presented in Table 8. The obtained results cleared that the actual response was higher than the expected response for all studied traits at the two cycles of selection. This result is in general with this reported by **Bora et al 1998, Alghmadi 2007 and Yassien et al 2012.**

Table 8: Expected and actual response to selection for all studied traits at the two cycles of selection.

Traits		Expected response	Actual response
Plant height	C1	1.92	2.52
	C2	3.15	4.25
Number of branches/plant	C1	0.05	0.10
	C2	0.09	0.14
Number of pods/plant	C1	1.20	1.90
	C2	3.95	4.44
100-seed weight	C1	1.14	2.40
	C2	1.22	1.48
Seed yield/plant	C1	1.80	1.91
	C2	3.85	5.52

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الملخص العربي

انتخاب النسب لعشيرته من الفول البلدى

مختار حسن هريدى - ابراهيم نجاح عبد الظاهر - محمد عبد العزيز أحمد السيد

جامعه الأزهر - كليه الزراعة- قسم المحاصيل- فرع اسيوط

أجريت هذه الدراسة خلال الثلاث مواسم ٢٠١١/٢٠١٢-٢٠١٢/٢٠١٣-٢٠١٣/٢٠١٤ بمزرعه كليه الزراعة بجامعة الأزهر بأسيوط لتحسين محصول النبات لعشيرته من الفول البلدى مكونه من ٢٢٠ عائله فى الجيل الرابع والمنتخبه من العشيره (جيزه ٤٢٩ x جيزه ٣) عن طريق الانتخاب المنسب لدورتين انتخابيتين.

الصفات التى تم دراستها

طول النبات، عدد الأفرع/نبات، عدد القرون/نبات، وزن الـ ١٠٠ بذره ومحصول البذور/نبات

اهم النتائج المتحصل عليها

اظهر تحليل التباين وجود اختلافات معنويه بين العائلات المنتخبه لكل الصفات المدروسه فى الدورتين الانتخابيتين وقد اتصفت دوره الانتخابيه الاولى بوجود تنوع وراثى وظاهرى اكبر من دوره الانتخابيه الثانيه لجميع الصفات المدروسه وبالتالى كانت القابليه للتوريث عاليه . اظهرت قيم الارتباط الوراثى والمظهري ان عدد قرون النبات كانت الصفه شديده الارتباط بمحصول النبات.