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Improvement the yield and its components as response to selection in early generations of two crosses of Faba bean.

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THE PRESENT investigation was carried out at the experimental farm of Sakha Agricultural Research Station, Kafer El-sheikh- Agriculture Research Centre, Egypt, during four successive winter seasons i.e., 2019 / 2020, 2020 / 2021, 2021/2022 and 2022 / 2023 growing seasons. The objective of this investigation was to study the effectiveness of pedigree selection in early segregating population for improvement of seed yield / plant and its components in two faba bean crosses; (Misr1×Sakha4) and (Misr1×Giza843) through the F3, F4, and F5 generations. The obtained results could be summarized as follows; the mean squares of F3, F4 and F5 showed si Heritability broad and narrow senses values increased from F3 to F5 for all traits of selection for seed yield/plant significant differences among both crosses as well as the selected families for all the studied traits in both crosses . In the first cross (Misr1×Sakha4) all selected families in F5 generation surpassed the better parent for number of pods / plant, number of seeds / plant, 100 seeds weight and seed yield / plant., while the selected families number 3, 4, 20, 31, 35, 36 and 40 were earlier in flowering date compared to the earliest parent., With respect to the second cross (Misr 1 × Giza 843), all selected families in F5 generation out yielded the better parent for number of pods / plant, number of seeds / plant, 100 seeds weight and seed yield / plant, while the selected families number; 2,4, 5 and 8 were earlier in flowering date compared to the earliest parent, also they surpassed the better parent for number of branches / plant. It could be concluded that the pedigree selection method was efficient and could be used in breeding for improving seed yield and its components of faba bean.

Keywords: Faba bean, selection for seed yield and its components, heritability .and correlation.

Introduction

Faba bean (*Vicia faba* L.) is one of the most important legume crops in Egypt (**Salman *et al.*, 2024**). The total production of faba bean in Egypt in 2024 was about 200.000 tons obtained from 52.08 hectares, which covers about 33 % of our consumption **(E.A.S, 2024).** It had high nutritive values and protein content (about 25-26 %), and it is consider as good and cheap alternative protein compared to the expensive animal, poultry and fish productions (**Mahmoud 2018 and Abdelaal 2023).** The cultivated area with faba bean in Egypt was decreasing therefore, it is necessary to find ways to increase the productivity of feddan so, breeding programs with estimating of genetic variation are important to obtain the best results **(Ramadan *et al.*, 2024).** Great efforts from plant breeders in continuously searching for more effective and efficient method to improve yield of the field crops. Selection method can be used to improve yield and its attributes in faba bean in Egypt **(Ahmed *et al*, 2008 and Ahmad, 2016.)** The success of a plant-breeding program depends on the choice of populations able to produce 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, may give promising results in improving faba bean performance (**Ahmed *et al*., 2008; Ahmad, 2016). Bakheit and Metwali (2011)** reported that the selection for seed weight/plant after two cycles of pedigree selection increased the criterion of selection in population1 by 9.94, 60.91 and 71.38% compared to the bulk sample, check cultivar and the best parent, respectively.

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High heritability estimates followed by high genetic advance for number of pods per plant and seed yield per plant, indicating 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 present investigation was to study the effectiveness of pedigree selection method for seed yield /plant in isolating high yielding lines or families in two crosses of faba bean crop.

2. Materials and Methods

The present investigation was carried out at the experimental farm of Sakha Agricultural Research Station, Kafrelsheikh Governorate, Agriculture Research Center, Egypt, during three successive winter seasons i.e., 2019/2020, 2020 /2021,2021 /*2022* and 2022/2023 growing seasons. Tow crosses; i. e. cross 1 (Misr × Sakha4) and cross 2 (Misr 1×Giza 843) Included in this study were obtained from the best selected crosses, which had high desirable specific combining ability of yield and its components from the practical part of master of agriculture sciences thesis of the candidate **Abd El-Rahaman 2017/2018.** the pedigree for used parental varieties of faba bean (*Vicia faba* L.) was shown in Table 1.

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

Cultivar name	Origin	Pedigree
Misr1	Egypt	Single cross (Giza 3 × A123/45/76)
Sakha4	Egypt	Sakha 1 x Giza 3
Giza 843	Egypt	X 461/845/8561/2076/85

In the first growing season 2019 /2020, 300 plant of the F2 generation from each cross with their original parents were sown in non-replicated rows. Each row 2-meter-long 60cm., wide and 20 cm., between hills on one side of the ridge with one seed per hill. All recommended cultural practices for faba bean production were applied at the proper time. At flowering time and harvest, the best 100 plants were selected based on seed yield / plant and saved to give F3 generation.

In the next season 2020 /2021 F3(100plants) with the original parents were sown in a randomized complete block design with three replications, two-meter-long 60cm wide and 20 cm between hills on one side of the ridge with one seed per hill. The best 40 families were selected based on seed yield / plant and saved to the next generation.

In the third growing season of 2021 /2022, The 40 selected F4-families from each population with the original parents were sown at 15th November in separate experiments in a randomized complete block design with three replications, each family was represented by one row – long, 60 cm wide and 20 cm between hills on one side of the ridge with one seed per hill. The best 20 families were selected based on seed yield/plant and saved for the next generation.

In the fourth growing season of 2022/2023, the 20 selected F4- families from each cross with the original parents were sown in a randomized complete block design with three replications, each family was represented by one row – long, 60 cm wide and 20 cm between hills on one side of the ridge with one seed per hill. The best 10 families were selected based on seed yield / plant from each cross was chosen as the F5 lines. Data were recorded on: days to Flowering, no. of branches/ plant, no. of pods/ plant, no. of seeds / pod, 100- seed weight and seed yield / plant.

Statistical analysis: Analysis of variance for each cross according, **Steel and Torrie (1960).**, as shown and presented in Table 2

Table 2a. The analysis of variance and expected mean squares.

Sov	Df	MS	E M S
Rep	r-1	M3	$\sigma^2e + F\sigma^2r$
Families	F-1	M2	$\sigma^2e + r\sigma^2f$
Error	(r-1)(f-1)	M1	σ^2e
Total			

Where: r and f = number of replications and families, respectively. σ^2e and σ^2f = error variance and genetic variance, respectively.

Based on expected mean squares, the estimates of genotypic(σ2g) and phenotypic (σ2p) variances among family averages and their parents for each cross were calculated as given by **Al-Jibouri *et al* (1958)**.

The phenotypic variance $\sigma^2p = \sigma^2 + \sigma^2e / r$. **The genotypic variance** $\sigma^2g = (M2–M1)/r$.

Heritability in broad-sense; $H2 = (\sigma^2g / \sigma^2p) \times 100$

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

Phenotypic coefficient of variability (PCV %) : $PCV\ \% = \sigma p\ /\ X \times 100$ **Genotypic coefficient of variability** (GCV %) : $GCV\ \% = \sigma g\ /\ X\ x\ 100$ Where: σp and σg are the phenotypic *and* genotypic standard deviations of the family means, espectively, and X is a family mean for a given trait.

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 : $GA = k.H^2_b\, \sigma p$, Where: k =1.50 and 1.37 constants for nearly 16.5 and 20% selection intensity (i.e.the highest-performing are selected), Hb = broad-sense heritability, and σP = Phenotypic standard deviation of the population. The observed response to selection was measured as the deviation percentage of the mean of the selected families from better parent and grand mean. Comparing the observed response to selection was calculated using L.S.D.

To calculate the additive variance (VA) and dominance variance (VD) in F3, F4 and F5 generations.

Analysis for all corresponding characters was conducted according **Kearsey and Pooni (1996**) method to estimate $\sigma^2 W$ and $\sigma^2 B$. table 2-b .

Table 2- b The analysis of variance and expected mean squares for families in F3 ,F4 and F5generations.

S o v	D f	M S	E M S	F
Between families	f-1	MSB	$\sigma^2 W + r\sigma^2 B$	
Within families	F(r -1)	MSW	$\sigma^2 W$	
Total				

$\sigma^2 B = (MSB - MSW) / r$, $\sigma^2 W = MSW$, $VA = \sigma^2 B$, $\frac{3}{4} D = 2\ \sigma^2 B - \sigma^2 W$

$VA = (2\times\sigma^2 B) - \sigma^2 B / 0.75$ additive component of genetic variance

$VH = \sigma^2 W - (0.25 \times VD)\ 0.125$ dominant component of genetic variance

3. **Results**

Analysis of variance

Analysis of variance for selected families of the two crosses; (Misr×Sakha4) and (Misr 1 × Giza 843) in F3, F4 and F5 generations are shown in Table 3. Results revealed that, highly significant differences were practiced among families in F3, F4 and F5 generations for all the studied traits in two crosses when the selection based on seed yield / plant and its components. Indicating the presence of genetic variability among selected families, it cleared that, pedigree selection method base on seed yield / plant and its components would be effective for improving seed yield and its components of faba bean. These results are compatible with those obtained by **Bakheit and Metwali (2011)** and **Ahmed et al (2018)** who reported highly significant differences amongF3 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. Also **Bulbul and Sakr (2024)** revealed significant differences among families within the F3 and F4 generations for all studied traits, indicating successful selection progress.

Phenotypic coefficients of variability (p c v) and genotypic coefficients of variability (g c v), as well as, heritability in broad and narrow senses of the two crosses for all the studied traits

Phenotypic coefficients of variability (p c v) and genotypic coefficients of variability (g c v) of the two crosses are presented in Table (4).

Phenotypic and genotypic coefficients of variability varied from one trait to the other. High G C V value of traits suggested the possibility of improving these traits through selection. Data showed that, moderate phenotypic coefficients of variability (p c v) and genotypic coefficients of variability (g c v) were detected for number of branches / plant, number of pods / plant, number of seeds / plant and seed yield / plant, while low values of (p c v) and (g c v) were obtained for days to flowering and 100 seed weight (g.) in F3, F4 and F5 selected families in two crosses. **Hassan (2025)** found that high values of genotypic and phenotypic coefficients of variability indicated presence of variability in the F3 base population sufficient to achieve high response to selection for all traits Also**, El-Said et al. (2020)** found that the phenotypic and genotypic coefficients of variability values were higher in the F3-generation and gradually decreased in the next generations of the studied traits.

Table 3. Mean squares of the F3, F4 and F5 selected families for all the studied traits of the two crosses (Misr 1 × Sakha4) and (Misr 1 × Giza 843).

Cross	So v	df	DF	BR	POD	NS/p	SW	SY/P
			MS	MS	MS	MS	MS	MS
F3								
Misr1 × Sakha 4	Replica	2	4.13	0.16	3.9	25	8.8	16.2
	Family	41	21.4**	0.5**	17.8**	133.4**	41.9*	82**
	Error	82	7.2	0.2	3.8	15.7	18.4	12.9
Misr 1 × Giza843	Replica	2	4.1	0.1	5.8	41.3	23.4	38.3
	Family	41	20.6**	0.8*	16.9**	174.6**	122.2*	165.7**
	Error	82	7.2	0.4	4.4	52.7	125.1	83.6
F4								
Misr1 × Sakha 4	Replica	2	4.00	0.08	3.2	27.4	6.02	16.4
	Family	21	20.7**	0.4	21.9**	167.1**	47.5*	113.5**
	Error	42	5.8	0.6	2.6	10.8	27.7	7.5
Misr 1 × Giza843	Replica	2	4.08	0.2	8.55	39.1	17.07	49.3
	Family	21	23.23**	0.95*	41.6**	209.4**	142.6*	264.1**
	Error	42	2.23	0.47	5.84	31.6	64.95	32.8
F5								
Misr1 × Sakha 4	Replica	2	4.07	0.11	3.05	27.69	4.42	14.84
	Family	11	22.59**	0.76*	25.62**	201.06**	48.88**	142.77**
	Error	22	5.51	0.4	4.08	27.99	8.59	15.05
Misr1 × Giza843	Replica	2	3.83	0.17	6.3	34.7	17.28	47.5
	Family	11	24.41**	1.02*	42.70**	213.34**	158.43*	298.99**
	Error	22	1.66	0.51	2.82	65.23	91.9	41.89

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

Heritability in broad and narrow senses of the two crosses for all the studied traits

Heritability estimate consider one of the most important parameters to selection response in early generation, indicating the importance of the genetic effects in the inheritance of all the studied traits. Heritability values were estimated from the analysis of variance of the F3, F4 and F5 are presented in Table (4). Low to moderate narrow sense heritability estimates were noted for the studied traits

The obtained results of narrow sense heritability values for flowering date, no of branches / plant, no of pods / plant, no of seeds /plant, 100 seed /plant and seed yield / plant in the first cross were (33.9, 38.3 and 41.0), (13.9, 32.2 and 44.7), (21.1, 33.7, and 42.8), (35.5, 43.9 and 45.0), (18.2, 29.1 and 47.2) and (29.7, 37.6 and 44.1) for families in F3, F4 and F5 generations respectively. Meanwhile, for second cross were (28.2, 37.2 and 43.3), (46.3, 28.1 and 43.8), (9.4 ,27.8, and 44.0), (23.4,38.9 and 47.7), (19.5,29.6 and 37.9)0 and (22.8,35.0 and 37.9) for the same traits families in F3, F4 and F5 generations respectively. The results indicated that the magnitude of heritability in narrow sense in F5 generation was larger than its corresponding one in F3 generation for all the studied traits, revealing the increased contribution of additive gene effects in F5 relative to the F3 generation. This means that the additive gene effects increases in the subsequent generation, which help the breeder to select the best genotypes in this generation. So, the materials used herein can be used successfully in faba bean breading programs. Similar results were obtained by **Abou-Zaid *et al* (2023).**

Table 4. Phenotypic coefficients of variability (p c v) and genotypic coefficients of variability (g c v) as well as heritability in broad and narrow senses for in; F_3, F_4 and F_5 of the two studied crosses for all the studied traits.

Cross	Parameter	**FD**			BR			**POD**			**NS/p**			**SW**			**SY/P**		
		F3	F4	F5	F3	F4	F5	F3	F4	F5	F3	F4	F5	F3	F4	F5	F3	F4	F5
Misr1 × Sakha 1	**σ2A**	8.60	9.24	9.61	0.17	0.17	0.29	5.75	6.68	7.40	53.76	67.56	69.34	11.40	11.41	11.45	30.89	36.55	36.70
	σ^2D	15.86	14.22	13.32	0.98	0.34	0.34	19.76	12.38	9.60	92.64	83.98	82.85	46.65	25.89	12.63	68.16	57.94	45.33
	σ^2E	0.91	0.62	0.46	0.10	0.02	0.01	0.10	0.02	0.01	4.86	2.05	1.69	4.41	1.81	0.15	4.66	2.67	1.08
	σ^2_{ph}	25.37	24.08	23.39	1.25	0.53	0.64	27.26	19.77	17.27	151.3	153.6	153.9	62.46	39.11	24.22	103.7	97.17	83.11
	σ^2_g	24.47	23.46	22.92	1.15	0.51	0.63	25.51	19.06	17.00	146.4	151.5	152.2	58.06	37.29	24.07	99.05	94.50	82.03
	h^2(b) %	96.42	97.42	98.02	91.99	96.05	98.83	93.58	96.40	98.41	96.79	98.66	98.90	92.95	95.37	99.39	95.51	97.25	98.70
	h^2(n)%	33.90	38.38	41.07	13.96	32.21	44.75	21.10	33.78	42.84	35.54	43.99	45.06	18.26	29.17	47.26	29.79	37.62	44.16
	GA	3.52	3.88	4.09	0.32	0.48	0.74	2.27	3.09	3.67	9.01	11.23	11.51	2.97	3.76	4.79	6.25	7.64	8.29
	GA%	7.21	8.09	8.81	8.80	11.70	15.31	9.69	12.33	13.76	13.22	14.89	14.14	3.39	4.23	5.32	10.49	11.45	11.37
	PCV	10.72	10.23	10.42	33.54	17.63	16.61	23.04	17.73	15.60	17.49	16.43	15.23	9.33	7.05	5.47	17.13	14.77	12.50
	GCV	10.52	10.10	10.31	32.17	17.28	16.51	22.28	17.40	15.47	17.20	16.32	15.14	9.00	6.88	5.45	16.74	14.57	12.42
Misr 1 × Giza843	**σ2A**	7.53	9.04	9.36	0.30	0.37	0.43	4.34	15.50	15.55	65.90	89.38	90.12	32.61	32.71	36.32	60.12	105.2	106.59
	σ^2D	17.86	14.57	11.94	0.34	0.88	0.53	37.72	37.42	19.32	199.1	134.6	97.69	122.6	72.81	64.17	186.8	184.7	166.82
	σ^2E	1.29	0.69	0.32	0.01	0.06	0.01	0.01	0.06	0.01	16.65	5.65	0.95	11.25	5.01	3.48	15.83	9.94	7.53
	σ^2_{ph}	26.69	24.30	21.62	0.65	1.31	0.97	46.23	55.66	35.34	281.6	229.6	188.7	166.4	110.5	103.9	262.7	299.8	280.94
	σ^2_g	25.40	23.61	21.30	0.64	1.25	0.96	42.06	52.92	34.87	264.9	224.0	187.8	155.2	105.5	100.4	246.8	289.8	273.41
	h^2(b) %	95.16	97.16	98.51	99.18	95.15	98.64	90.98	95.08	98.67	94.09	97.54	99.50	93.24	95.47	96.65	93.97	96.68	97.32
	h^2(n)%	28.23	37.21	43.30	46.33	28.16	43.88	9.40	27.85	44.00	23.40	38.92	47.74	19.59	29.60	34.93	22.89	35.08	37.94
	GA	3.00	3.78	4.15	0.77	0.66	0.89	1.32	4.28	5.39	8.09	12.15	13.51	5.21	6.41	7.34	7.64	12.51	13.10
	GA%	5.84	7.64	8.69	20.43	17.65	20.61	5.70	17.86	21.11	12.93	17.70	18.34	5.25	6.40	7.25	12.29	18.24	17.60
	PCV	10.00	9.97	9.74	20.14	30.43	22.80	28.73	31.13	23.29	25.69	22.08	18.65	12.54	10.50	10.07	24.25	25.25	22.52
	GCV	9.75	9.83	9.67	20.06	29.68	22.64	27.40	30.35	23.13	24.91	21.81	18.60	12.11	10.26	9.90	23.51	24.82	22.22

The first cross (Misr 1 × Sakha 4).

F3 generation

Analysis of variance of 40 F3 selected families showed highly significant for all the studied traits in the first cross. (Misr1 × Sakha 4). The mean performance of F3 families and their parents; Misr1 and Sakha 4 for all the studied traits are presented in Table (5).

Table 5. Means of the studied families in F_3 for the studied characters in Misr 1 x Sakha4 cross and their parents.

Family	Misr1×Sakha4					
	DF	**BR**	**POD**	**NS/p**	**SW**	**SY/P**
1	52.00	3.67	20.67	70.00	90.12	62.97
2	49.67	3.73	21.33	70.33	90.78	63.80
3	46.33	3.00	23.00	70.33	85.16	59.80
4	51.67	3.33	24.67	74.67	87.95	65.63
5	49.00	3.33	22.33	63.00	85.27	53.73
6	45.00	3.67	26.33	75.67	89.67	67.63
7	51.33	4.33	18.33	60.40	85.58	51.67
8	48.33	4.00	22.00	64.03	88.75	56.67
9	45.33	3.47	25.00	66.23	86.24	56.87
10	52.67	3.67	20.00	56.53	91.78	51.83
11	48.33	3.47	23.00	64.77	90.27	58.47
12	45.00	3.33	20.33	57.50	95.56	54.67
13	52.67	3.17	24.00	62.03	84.69	52.60
14	46.67	3.60	23.33	69.60	88.61	61.67
15	45.33	3.33	25.33	71.23	84.56	60.23
16	51.67	3.67	26.00	72.63	82.65	60.00
17	48.33	4.33	27.00	83.10	82.60	68.63
18	45.00	4.67	21.33	62.50	90.60	56.67
19	52.00	3.33	24.33	67.80	88.19	59.73
20	49.00	3.67	27.00	80.33	85.26	68.47
21	53.00	4.00	20.33	69.00	90.45	62.30
22	51.00	3.73	20.33	69.67	90.62	63.13
23	47.00	3.33	22.67	70.33	84.71	59.47
24	52.33	3.00	24.00	74.00	86.07	63.63
25	48.33	3.67	21.67	62.33	84.62	52.73
26	49.33	4.33	25.67	74.67	89.85	66.97
27	51.67	4.00	19.00	59.73	85.61	51.13
28	48.67	3.67	21.33	63.70	88.07	56.00
29	47.00	3.33	24.67	65.47	83.78	54.83
30	52.67	3.67	19.67	55.50	91.57	50.83
31	49.00	3.67	22.33	64.03	90.51	57.97
32	45.33	3.33	20.67	56.57	96.24	54.00
33	51.67	3.33	23.67	61.33	84.65	51.93
34	47.33	3.33	23.00	68.83	88.15	60.67
35	44.00	3.33	25.00	70.33	84.16	59.20
36	52.33	4.00	25.00	72.00	82.82	59.00
37	47.00	5.00	26.00	82.33	82.93	68.27
38	46.00	4.00	22.00	62.13	90.17	56.00
39	53.00	3.33	24.00	66.33	88.55	58.70
40	47.33	3.50	26.33	79.00	85.72	67.70
Mean	48.98	3.66	23.14	67.75	87.59	59.16
Min	44.00	3.00	18.33	55.50	82.60	50.83
Max	53.00	5.00	27.00	83.10	96.24	68.63
Misr 1	47.8	3.4	19.9	66.9	74.2	48.9
Sakha 4	49.8	5.0	16.8	62.2	95.0	57.7
LSD 5%	1.55	0.51	2.15	3.58	3.41	3.51
LSD 1%	1.60	0.53	2.23	3.71	3.53	3.63

FD = flowering date, BR = no. of branches/plant, POD = no. of pods/plant, NS/p= no. of seeds/plant, SW = 100-seed weight, and SYP = seed yield plant^{-1}.

For days to maturity, the families number 6,9, 12, 15 and 18 showed significant or highly significant for earliness than the early parent (Misr1). The families number 7, 17 and 18 exhibited significant higher number of branches / plant than the better parent. While, the other families showed lower number of branches / plant relative to better parent.

Regarding number of pods / plant, the families number 6,9,15,16,17,20,26,37, and 40 significantly surpassed the better parent (Misr1) for this trait, while the other families showed lower number of pods/ plant relative to better parent. With respect to number of seeds / plant, the families number1, 2, 3, 4 , 6 , 14 , 15 , 16 , 17 , 19 , 20 , 21 , 22 , 23 , 24 , 26 , 34 , 35 , 36 , 37 , and 40 expressed significant higher number of seeds / plant relative to better parent (Misr1) . For 100 seeds / weight, families 1 ,2, 4, 6, 8 , 10,11, 12 , 14 ,18 , 19 , 12 , 22 , 26 , 28 , 30 , 31 , 32 , 38 , and 39 surpassed significantly the grand mean

With respect to seed yield / plant the families number ;1, 2, 3 , 4, 6 , 11 , 14 , 15 , 16 , 17, 19, 20, 21 , 22 , 23 , 24 , 26 , 31 , 34 , 35 , 36 , 37 , 39 , and 40 significantly out yielded the better parent (Sakha4). Generally, the results showed that, some selected families 6,14,16,17,19, and 20 significantly out yielded or surpassed the better parent for most the studied traits. Meaning that selection based on seed yield / plant was effective in improving the studied traits in these materials.

F4 generation.

The mean squares due to F4 selected families were found to be significant for all the studied traits, indicating that the twenty F4 selected families behaved differently from each to other in the first cross. (Misr1 × Sakha 4) The mean performance of twenty families and their parents; Misr1 and Sakha 4 are presented in Table (6).

Table 6. Means of the studied families in F_4 for the studied characters in Misr 1 x Sakha4cross and heir means.

Family	(Misr1 × Sakha 4)					
	FD	**BR**	**POD**	**NS/p**	**SW**	**SY/P**
1	51.20	5.00	23.00	79.67	91.74	73.07
2	47.87	4.00	24.00	81.33	91.00	73.93
3	46.87	4.00	24.33	75.67	89.17	67.40
4	51.33	3.33	24.33	75.33	88.24	66.33
5	48.07	3.67	27.67	80.67	85.28	68.77
6	44.53	4.00	26.67	80.33	89.81	72.10
7	51.20	4.33	20.00	66.63	87.98	58.50
8	46.67	4.33	24.00	70.33	88.70	61.57
9	43.20	3.67	27.00	75.90	84.15	66.67
10	52.20	3.67	21.00	59.27	93.53	55.27
11	47.87	4.67	25.00	70.33	90.37	63.60
12	44.53	4.00	23.00	65.27	95.75	62.47
13	51.20	4.00	26.33	73.33	87.37	64.00
14	47.87	4.00	26.00	79.33	89.23	70.73
15	43.20	4.33	28.67	82.00	85.37	70.00
16	51.20	4.00	26.33	74.33	86.52	62.50
17	47.87	4.33	28.00	86.73	82.91	71.90
18	44.53	4.33	22.00	65.57	92.28	60.37
19	49.53	4.67	25.67	75.17	89.81	67.37
20	48.53	4.33	28.67	91.20	85.43	77.93
Mean	47.97	4.13	25.08	75.42	88.73	66.72
Min	43.20	3.33	20.00	59.27	82.91	55.27
Max	52.20	5.00	28.67	77.93	95.75	77.93
LSD 5%	1.28	0.23	1.37	2.33	2.19	2.66
LSD 1%	1.33	0.24	1.42	2.41	2.26	2.75

Regarding flowering date, the range of the selected families ranged from 43.20 days for family number 18 to 52.20 for family number 19 with an average of 47.97 days. The four families; number 14,18,31 and 38 had earlier of maturity date compared with early parent.

Concerning number of branches / plant four families number; 3,20,31 and 37 expressed significant higher number of branches / plant relative to grand mean. Regarding no. of pods/ plant, the range of selected families varied from 20 pods / plant for families no.15 to 28.67 for families no. 31 and 40 pods / plant. For number of seeds / plant, the range of the selected families varied from 59.27 seeds for family no.19 to86.73seeds for family no. 35. The selected families no. 2,31, 35and 40 had significant superiority than the best parent.

Regarding 100 seed weight, none of the selected families surpassed significantly the best parent, however five families; number 1 ,2,19,21, and36 expressed significant higher 100 seed weight than the grand mean. The family number 21gave the heaviest

100 seed weight followed by family number19 then the family number 36, respectively.

With regard to seed yield / plant seventeen selected families surpassed significantly than the better parent, the range of selected families varied from 55.27 for family no. 19 to 77.93 for family no.40. From the previous results, it is observed that selection based on seed yield / plant was effective for selected superior families.

F5 generation

Analysis of variance of 10 selected familiesF5 were showed highly significant for all the studied traits in the first cross. (Misr1 × Sakha 4) Table 7. The mean performance of 10 families F5 and their parents; Misr1 and Sakha 4 for all the studied traits are presented in Table (7).

Table 7. Means of the studied families in F_5 for the studied traits in Misr 1 x Sakha4 cross and their parents.

Family	(Misr1 × Sakha 4)					
	FD	**BR**	**POD**	**NS/p**	**SW**	**SY/P**
1	50.67	5.47	24.00	83.63	93.82	78.30
3	46.33	5.23	25.33	89.00	91.58	81.50
4	45.67	5.47	29.33	90.77	83.70	75.97
18	49.00	3.37	27.00	84.33	88.66	74.77
20	45.00	5.57	28.33	82.67	87.53	72.20
31	43.83	5.03	27.67	85.00	90.18	76.50
35	45.33	5.03	27.00	82.87	89.66	74.30
36	41.33	4.97	28.67	87.60	88.27	74.00
37	51.33	4.70	30.33	90.30	90.27	81.50
40	46.13	4.23	30.00	96.80	86.53	83.77
Mean	46.26	4.91	27.77	87.30	89.02	77.28
Min	41.33	3.37	24.00	82.67	83.70	72.20
Max	50.67	5.57	30.33	96.80	93.82	83.77
Misr 1	47.8	3.4	19.9	66.9	74.2	48.9
Sakha 4	49.8	5.0	16.8	62.2	95.0	57.7
LSD 5%	1.11	0.14	0.85	2.11	0.62	1.69
LSD 1%	1.15	0.15	0.88	2.19	0.65	1.75

For maturity date**,** the families number 3,4,20,31,35, 36 and40 expressed significantly for earliness than the earliest parent. The selected families ranged from 41.33 for family no. 36 to 51.33 days for family no. 37. Concerning number of branches / plant the range of the selected families varied from 3.37 for family no. 18 to 5.57for family no.20, however all selected families except of family no. 18 surpassed the best parent**.**

Regarding no. of pods/ plant, the range of selected families varied from 24 pods / plant for family no. 1 to 30.33 for family no. 37 pods / plant. All selected families surpassed the better parent for this trait. The family

number one gave the lowest one (24pds/plant). With respect to number of seeds / plant, results showed that, all selected families expressed significant higher numbers of seeds / plant compared to better parent. The families no.40 had the largest number of seeds / plant (96.80) followed by family no.4 (90.77) respectively. Regarding 100 seed weight (g) only five selected families;1,3,31, 35 and 37 surpassed significantly than the grand mean, meanwhile the other families exhibited light 100 seed weight, relative to grand mean.

For seed yield / plant, the range of selected families varied from 72.20 for family no.20 to 83.77(g)for family no.40, All selected families exhibited significant higher values of seed yield / plant than the better parent Sakha 4.

Second cross (Misr1 × Giza 843)

F3 Generation

The mean squares associated with F3, F4 and F5 selected families were found to be significant for all the studied traits in the second cross (Misr1 × Giza 843) Table 4.

The mean performance of F3 selected families and their parents; Misr1 and Giza 843for all the studied traits are presented in Table (8)

For maturity date, the range of the selected families ranged from 47.22 to 56.67 with an average of 51.51 days, however the selected families; 4, 5, 8, 12 ,13, 16, 20, 24, 25, 28, 32, 34, 36 and 40 had earlier and significant differences compared with the grand mean.

Regarding number of branches / plant, the results showed that, the range of selected families varied from 3.33 to 5.37 with an average of 3.75. The five families 5, 14, 15, 25 and 35 surpassed significantly the best parent. Concerning number of pod/ plant, all selected families had significant superiority than the best parent except of selected families number 2, 3, 6, 7, 8, 10, 11, 12, 17, 20, 26, 32, 33, 36 and 38. The range of selected families varied from 18 for family number 7 to 27.67 for family number 31.

With respect to number of seeds / plant, data showed that, eight selected families; 2, 4, 5, 14, 15, 22, 34 and 35 had significant superiority than the best parent. The mean values of selected families ranged from 52.67 for family number 17 to 77.67 for family number 34. With regard to 100-seed weight (g) fifteen selected families; 2, 8, 9, 10, 11, 13, 18, 22, 23, 27, 29, 30, 31, 33 and 40 surpassed significant than the best parent. The range of selected families varied from 82.49 for family number 24 to 105.53 for family number 10. Regarding seed yield / plant, the range of selected families varied from 52.27 for family number 37 to 80.00 for family number 22. The selected families; 2, 4, 5, 13, 14, 15, 22, 23, 25, 31, 33, 34 and 35 exhibited significant higher values of seed yield / plant than the better parent Giza 843

Table 8. Means of the studied families in F_3 for the studied characters in Misr 1 x Giza843 cross and their parents.

Family	(Misr1 × Giza 843)					
	FD	**BR**	**POD**	**NS/p**	**SW**	**SYP**
1	52.33	3.67	20.00	60.00	99.74	59.67
2	53.33	4.00	26.33	74.67	102.98	76.70
3	53.33	3.13	23.00	68.67	92.35	63.17
4	47.33	4.33	26.00	76.00	93.93	71.77
5	48.67	5.33	27.00	75.00	98.47	73.77
6	50.03	3.67	21.33	55.67	100.47	54.33
7	51.47	3.33	18.00	53.33	92.98	52.67
8	48.33	3.67	22.00	53.00	100.78	52.67
9	52.33	3.67	25.33	59.67	105.10	62.33
10	51.67	3.33	20.00	53.00	105.53	58.07
11	53.33	3.33	22.93	62.67	104.37	64.60
12	49.33	3.33	20.30	60.33	96.78	58.33
13	49.00	3.13	24.00	64.33	101.45	65.27
14	52.83	5.37	26.00	77.00	97.44	75.10
15	53.50	4.33	25.33	75.67	94.30	71.33
16	49.33	3.80	23.33	54.00	99.38	52.33
17	52.33	3.13	21.00	52.67	99.03	52.60
18	53.33	3.67	22.67	58.33	101.91	58.33
19	58.67	3.67	24.33	60.00	97.47	59.00
20	48.50	3.37	23.00	57.00	99.56	61.00
21	51.67	4.00	21.50	63.33	93.51	59.00
22	56.67	4.00	27.00	77.33	103.45	80.00
23	51.67	4.00	23.67	65.33	102.86	66.83
24	48.33	3.57	24.67	72.33	82.49	60.50
25	48.33	4.33	26.33	73.67	99.99	73.67
26	50.00	3.67	22.33	63.33	82.70	52.33
27	51.23	3.67	24.00	59.00	101.18	59.67
28	48.33	3.40	23.67	58.33	95.67	55.60
29	51.67	3.67	25.33	60.00	104.52	63.00
30	53.33	3.93	26.00	59.00	105.09	61.80
31	54.00	4.00	27.67	70.33	102.35	71.80
32	48.67	3.00	21.67	59.33	97.78	58.00
33	53.33	3.50	23.00	64.00	104.56	66.87
34	48.67	3.33	24.00	77.67	86.66	65.27
35	53.50	4.50	27.00	75.33	94.51	71.17
36	49.33	3.47	22.33	60.67	95.34	57.73
37	51.67	3.87	24.67	56.67	92.33	52.27
38	56.33	3.67	21.67	60.00	97.92	58.00
39	55.33	3.67	25.67	57.33	98.17	53.87
40	49.50	3.33	25.33	59.33	104.88	62.00
Mean	51.51	3.75	23.74	63.58	98.25	62.31
Min	47.33	3.00	18.00	52.67	82.49	52.27
Max	58.67	5.37	27.67	77.67	105.53	80.00
Misr 1	47.8	3.4	19.9	66.9	74.2	48.9
Giza843	49.8	5.0	16.8	62.2	95.0	57.7
LSD 5%	1.85	0.12	3.32	6.63	5.45	6.46
LSD 1%	1.91	0.12	3.44	6.86	5.64	6.69

FD = flowering date, BR = no. of branches/plant, POD = no. of pods/plant, NS/p = no. of seeds/plant, SW = 100-seed weight, and SYP = seed yield $plant^{-1}$.

F4 Generation

The mean squares due to F4 selected families were found to be significant for all the studied traits, indicating that the twenty F4 selected families behaved differently from each to other in the second cross. (Misr1 ×Giza 843) Table 9 the mean performance of twenty families and their parents; Misr1 and Giza843 are presented in table (9).

Table 9. Means of the studied families in F_4 for the studied characters in Misr 1 x Giza843 cross and their means.

Family	(Misr1 × Giza 843)					
	FD	**BR**	**POD**	**NSD**	**SW**	**SYP**
1	50.13	4.03	24.77	80.67	102.44	82.67
2	48.50	4.80	27.00	81.00	103.65	83.97
3	52.50	3.00	23.33	73.67	93.08	68.43
4	43.50	4.97	35.00	85.00	100.31	85.23
5	43.20	3.67	26.00	78.00	100.86	78.53
6	49.77	3.23	21.93	64.30	92.93	59.77
7	48.83	3.73	21.00	58.50	102.33	59.77
8	43.50	3.30	22.00	57.17	100.84	57.67
9	51.83	3.13	20.67	60.67	108.84	66.00
10	49.17	3.70	22.67	69.00	109.13	75.00
11	51.83	4.00	22.67	65.67	104.56	68.47
12	48.50	3.70	27.00	71.67	99.40	67.17
13	51.83	4.57	23.67	66.00	102.76	67.90
14	48.50	4.75	30.33	79.33	100.92	79.90
15	53.50	3.83	26.00	77.33	95.98	73.97
16	48.50	3.33	23.33	59.67	99.17	59.13
17	50.83	3.37	21.67	59.33	86.27	50.93
18	48.50	3.50	21.33	60.00	102.57	61.23
19	54.17	3.33	20.33	61.67	102.68	63.40
20	48.50	3.33	18.67	64.00	93.56	62.57
Mean	49.43	3.76	23.97	68.63	100.11	68.59
Min	43.50	3.00	18.67	57.17	86.27	50.93
Max	54.17	4.97	35.00	85.23	109.13	85.23
LSD 5%	1.35	0.41	2.69	3.86	3.64	5.12
LSD 1%	1.40	0.42	2.78	4.00	3.77	5.30

For maturity date, three selected families; 4, 5 and 8 in the F4 generation had earlier and significant differences compared with the earlier parent. Concerning number of branches / plant, the results showed that, the range of selected families varied from 3.00 to 5.80 with an average of 3.76 branches/ plant. The five families 1,2,20,22and 26 surpassed significantly the best parent Giza 843. With respect to number of pod/ plant, five selected families; 2, 4, 21, 26 and 31 had significant superiority than the best parent. The range of selected families varied from 18.67 for family number40 to34.00 for family number 31.

With respect to number of seeds / plant, data showed that, six selected families;1,2,4,6,26and24 had significant superiority than the best parent. The mean values of selected families ranged from 52.17 for family number 16 to 80.67 for family number 1. with an average value of 61.00 seeds / plant. With regard to 100-seed weight (g) seven selected families;1, 2,15,19,2, 36 and 37 surpassed significant than the best parent. The range of selected families varied from 86.27 for family number 35 to 109.25 for family number 1. Regarding seed yield / plant, the range of selected families varied from 50.93 to65.23. The selected families; 1,2, 4, 6,19, 26 and 31 exhibited significant higher values of seed yield / plant than the better parent Giza 843.

F5 generation

The mean squares due to F5 selected families were found to be significant for all the studied traits, indicating that the ten F5 selected families behaved differently from each to other in the second cross. (Misr1 ×Giza 843). The mean performance of ten families and their parents; Misr1 and Giza 843 are presented in Table (10).

Table 10. Means of the studied families in F_5 for the studied characters in Misr 1 x Giza843 cross and their parents.

Family	(Misr1 × Giza 843)					
	FD	**BR**	**POD**	**NSD**	**SW**	**SY/P**
1	49.37	4.27	26.27	84.90	103.07	87.43
2	43.80	5.83	28.83	85.20	104.07	88.63
3	48.80	3.90	23.70	78.67	94.41	74.23
4	43.00	5.57	36.63	88.00	101.55	89.33
5	46.03	4.13	27.27	82.00	102.42	83.83
6	48.00	4.03	28.00	77.00	100.39	76.37
7	48.10	4.03	22.70	78.33	102.43	80.23
8	48.27	5.27	31.13	82.33	101.47	84.23
9	48.53	4.03	26.70	79.33	96.38	76.00
10	47.00	3.87	24.00	74.33	110.65	81.97
Mean	47.18	4.45	27.52	81.01	101.68	82.23
Min	43.00	3.87	22.70	74.33	94.41	74.23
Max	49.37	5.83	36.63	88.00	110.65	89.33
Misr 1	47.8	3.4	19.9	66.9	74.2	48.9
Giza843	49.8	5.0	16.8	62.2	95.0	57.7
LSD 5%	0.92	0.19	1.12	1.58	3.03	4.46
LSD 1%	0.95	0.21	1.15	1.64	3.14	4.62

For maturity date, four selected families; 2, 4 ,5 and 8 in the F5 generation had earlier and significant differences compared with the earlier parent. With respect number of branches / plant, the results showed that, the range of selected families varied from 3.87 to 5.83 with an average of 4.45 branches / plant. The three families 2, 4 and8 surpassed significantly the best parent Giza 843.

With respect to number of pod/ plant, all selected families had significant superiority than the best parent. The range of selected families varied from 22.70 to 36.63 with an average of 27.52 pods / plant. Concerning number of seeds / plant, data showed that, all selected families had significant superiority than the best parent. The mean values of selected families ranged from 74.33 to 88.00, with an average valueof81.01seeds/plant. With regard to 100-seed weight (g) with the exception of families number 3 and 9,all selected families surpassed significant than the best parent. The range of selected families varied from 94.41for family number 3 to 110.65 for family number 10.

Regarding seed yield / plant, the range of selected families varied from 74.23 to 89.33. All selected families exhibited significant higher values of seed yield / plant than the better parent Giza 843.

Phenotypic correlation coefficients of F5 generation for all the studied traits.

Estimates of correlation coefficients among all the studied traits in the F5 generation of the two crosses are presented in Table 11.

Table 11. Phenotypic correlation coefficients among all the studied traits in F_5 generation of the two crosses Misr 1 x Sakha4 and Misr 1 x Giza843.

Character	**FD**	**BR**	**POD**	**NSD**	**100 SW**	**SY/P**
	F5 generation (Misr 1 × Sakha4)					
FD	1	-0.13	-0.13**	-0.08	-0.18	-0.32*
BR		1	0.62**	0.38**	-0.37**	0.44**
POD			1	0.75**	-0.66**	0.60**
NS/p				1	-0.65**	0.93**
SW					1	0.35**
SYP						1
	F5 generation (Misr 1 × Giza 843)					
FD	1	-0.30**	-0.42**	-0.28*	-0.17	-0.33**
BR		1	0.68**	0.40**	0.27*	0.47**
POD			1	0.65**	0.18	0.66**
NS/p				1	-0.03	0.92**
SW					1	0.37**
SYP						1

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

The values indicating varying strengths of correlation among the different studied traits. The phenotypic correlation coefficients were highly significant and negative among maturity date and all the studied traits in two crosses, while it was negative and insignificant for the traits, number of branches /

plant, number of seeds / plant and 100 seed weight in cross 1 (Misr 1×Sakha 4) and 100 seed weight in cross 2 (Misr1×Giza 843). Moreover, number of branches / plant highly significant, positively correlated with number of pods / plant, number of seeds / plant and seed yield / plant in both crosses. Highly significant and positive estimates of phenotypic correlation coefficients were found between number of pods /plant and each of number of seeds/ plant and seed yield / plant in both crosses, while it was significant negative and insignificant positive correlation with 100 seed weight in cross 1 and cross 2, respectively. The phenotypic correlation coefficients values were positive and highly significant among seed yield / plant and each of number of seeds / plant and 100 seeds weight, while it was negative and significant between seed yield and maturity date in both crosses in F5 generation, indicating that the selection of these traits considered as indirect selection for seed yield / plant.

4. Discussion

The phenotypic and genotypic coefficients of variability showed higher values in F3 families and decreased gradually in the F4 and F5 families for all the studied traits and this may be due to increasing of the homozygosity of plants .and the selection will be effective in advanced generation. Similar results were obtained by **Ahmed *et al* (2018) Haridy (2018)**. Small differences were observed between P C V and G C V for all the studied traits, indicating little environment effect on the expression of these traits and the genetic effects were important in the inheritance of these traits in two crosses. similar results were obtained by **Ahmed, (2016)**, **Haridy (2018)**.and **Ibrahim *et al* (2023). Falconer (1997)** stated that selection reduces genotypes variance of the following generation. The results of the present study, proved that, the selection for seed yield / plant method was effective in improving the studied traits in these materials of faba bean.

These results are in agreement with those obtained by **Tadesse *et al* (2011)** who found that, phenotypic correlation coefficients were negative and significant between days to maturity and each of plant height, as well as, seed yield / plant, while it was positive and significant among seed yield / plant and each of number of branches / plant, number of pods / plant and 100seed weight. Similar results were obtained by **Solieman and Ragheb (2014), Bakhiet *et al* (2015), Abo- Hegzy (2022) Chaurasia *et al* (2022), Haridy *et al* (2022) and El-Refay *et al* (2023).**

In selected families the mean values of all the studied traits recorded lower values in F3 and increased gradually in the next F4 and F5 for all traits except, mean values of days to maturity which recorded higher values in F3 and decreased gradually in the next generations for selection of seed yield / plant in the two crosses. The phenotypic and genotypic coefficients of variability showed higher values in F3 families and decreased gradually in the F4 and F5 families for all the studied traits. The phenotypic correlation coefficients were highly significant and negative among days to maturity and all the studied traits in two crosses, while it was negative and insignificant for the traits, number of branches / plant, number of seeds / plant and 100 seed weight in cross 1 (Misr 1×Sakha 4) and 100 seed weight in cross 2 (Misr1×Giza 843). Positive and significant phenotypic correlation coefficients were obtained among seed yield / plant and each of number of branches / plant, number of pods/ plant, number of seeds / plant and 100 seed weight. The results indicated that the magnitude of heritability in narrow sense in F5 generation was larger than its corresponding one in F3 generation for all the studied traits, revealing the increased contribution of additive gene effects in F5 relative to the F3 generation, indicating the effectiveness of selection in this materials for this trait. These families could be continued to further generation as breeding for improving seed yield of faba bean genotypes.

5. Conclusion

From the results of the present study, it can concluded that the families no. 3, 4, 20, 31, 35, 36 and 40 in the first cross and the families no. 2,4, 5 and 8 in the second cross were earlier in flowering date and surpassed the better parent and could be used for breeding programs in faba bean.

Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest

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