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(Original Article)

The Efficiency of Pedigree Line Selection in a Segregating Population (Sakha 3 × Giza 2) of Faba Bean *(Vicia faba L.)*

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Abstract

A single faba bean (*Vicia faba* L.) population derived from the cross Sakha 3 x Giza 2 was subjected to two cycles of pedigree line selection (PSM). Selection criteria included seed yield/ plant (SY/P), number of pods/ plant (NP/P), and seed index (SI). Analysis of variance revealed significant differences among families within the F_3 and F_4 generations for all studied traits, indicating successful selection progress. Notably, mean values for all traits, except days to flowering, increased from cycle 1 to cycle 2. Days to flowering exhibited the opposite trend, with a higher mean value observed in cycle 1. The expected gain from selection **(**EGS%) for SY/P in the F_2 generation was 29.52 and increased in the F_3 and F_4 generations in values of 34.41 and 2.06, respectively. The realized gain from selection **(**RGS%) for SY/P in the F_3 generation was 23.06, then decreased in successive generation which amounted to 9.56 in F_4. Multiple promising faba bean genotypes were identified within Families 1, 2, 13, 56, and 60. These families exhibited superior performance in relative yield traits compared to the better parent, check variety, and bulk samples. Additionally, they displayed favorable values for most characters assessed. These findings suggest their significant potential for incorporation into breeding programs to enhance faba bean yield.

Keywords: *GCV, Heritability, Pedigree selection, PCV, Vicia faba*

Introduction

Faba bean (*Vicia faba* L.) is a critical pulse crop cultivated worldwide, particularly in Egypt and the Mediterranean region. Highly valued for its high protein content and an important source of nutrition for both animals and humans. Additionally, the faba bean is recognized for its exceptional ability to fix atmospheric nitrogen (N_2) through biological N_2-fixation to enhance soil fertility. The cultivated area of broad beans in 2021 reached about 42758 hectares producing 139607.12 tons of seed in Egypt (FAO, 2021). To address the growing demand, increasing faba bean yield has become a primary focus of most breeding programs, achieved through the selection of high-yielding strains. To achieve this target, the breeders should choose a breeding method which facilitates the simultaneous improvement of yield and yield components characters. In the quest for improved faba bean varieties, plant breeders constantly evaluate and refine

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selection methods. Pedigree line selection, a popular approach, has proven effective in enhancing various faba bean traits. Haridy (2017) identified the number of pods/ plant as a promising indirect selection criterion. Additionally, Haridy (2018) demonstrated success with direct selection for seed yield/ plant, achieving a 7.9% yield increase over two selection cycles compared to the better parent. Bakhiet and Metwali (2011) reported that the selection for seed weight/plant after two cycles of pedigree selection increased in population1 by 71.38, 60.91 and 9.94 compared to the best parent, check cultivars and bulk sample, respectively. Born *et al.* (1998) reported high heritability and genetic advance (GA%) for pods/ plant and seed yield/ plant in faba bean, suggesting significant potential for improvement through selection. Building on these findings, the present investigation aimed to estimate key breeding parameters, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and GA%, for seed yield/ plant, number of pods/ plant, and seed index across three generations (F_2, F_3, and F_4) in a cross population derived from Sakha 3 x Giza 2. The purpose of the current study was designed to access the efficiency of pedigree line selection for seed yield and its some components for faba bean.

Material and Methods

This study was conducted at the Faculty of Agriculture's Experimental Farm, Al-Azhar University, Assiut Branch across three consecutive winter seasons of 2021/2022, 2022/2023, and 2023–2024. In this work, two different selection strategies were used to separate segregated generations of a single broad bean population (*Vicia fabe* L.) to determine genetic variability, heritability, and response to selection. The used population was Sakha 3 X Giza 2 through its F_2, F_3, and F_4 generations as the breeding materials for this experiment.

Season 2021/2022, F_2, generation

The 1000 plants F_2 of the aforementioned population and its parents were sowed on November 5th in spaced plants for the first season of 2021/2022. Plants were spaced 25 cm apart from one another and 60 cm apart between rows. Every slope had a single plant and the recommended agricultural practices were applied for faba bean. 600 randomly guarded plants were used to capture the data, and 10% of one population was chosen at harvest based on seed yield/plant, the number of pods per plant, and the seed weight (100).

Season 2022/2023, F_3- generation

During the fifth of November, 60 families from the basic population were sowed alongside the bulk sample and a local check (Giza 402). A randomized block design with three replications was employed. The plot was 4 meters long, with hills spaced 60 centimeters apart and 30 centimeters apart inside the row. Seedlings were trimmed to one plant per hill when emergence concluded. Throughout the entire growth season, the suggested cultural practices were followed. Three selection criteria *i.e.* (seed yield/plant (SY/P), number of pods/plant (NP/P), and seed index (SI) for the top 20 families (selection intensity=30%) were identified, and the best plant from each family was preserved for a subsequent selection cycles.

To create the population for seed bulk population, a small number of seeds (five seeds) from each chosen F_2 plants were bulked for bulk population and grown in the same way.

Season 2023/2024, F_4- generation

The best three plants in SY/P (self-seeds) were planted to represent the F4 family where the second cycle of selection was used to raise the F4 generation. Using PSM (pedigree selection method), the best three plants from each row were mixed and grown as a population by bulk method in the F4 generation. The F4 generation which contain 20 families was tested at selection 30%, respectively.

The following characters were recorded on each plant

1-Seed yield/plant, g (SY/P), number of branches/plant (NB/P), Number of pods/plant (NP/P), Seed index in grams (SI) or 100-weight seed, and days to first flower (DFF).

Statistical analysis

Table 1. The analysis of variance and expected mean squares

S.O.V.	D.F	M.S	Expected mean square	
			Variance	Covariance
Replications	r–1	M_3	$\sigma^2e + g\sigma^2r$	
Genotypes	g-1	M_2	$\sigma^2e + r\sigma^2g$	Cov.e + r Cov.g
Error	(r-1)(g-1)	M_1	σ^2e	Cov.e

Where, g and r stand for the number of genotypes and replications, respectively. Error variance and covariance are represented by σ^2e and Cov.e, respectively, while genetic variance and covariance are represented by σ^2g and Cov.g.

Moreover, the heritability in general was calculate as

Heritability in F2 (H) = [VF2-((VP1+ VP2) /2)) / VF2] X 100

Heritability in F3 and F4 (H) = (σ2g / σ2p) X 100

Phenotypic and genotypic variance

The Burton (1952) genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as:

$$PCV = \sqrt{(VP/\bar{X})} * 100 \; ; \; GCV = \sqrt{(VG/\bar{X})} * 100 \; ,$$

where the PCV and GCV are phenotypic and genotypic coefficients of variation, respectively, and $\bar{X}$ is the population mean. The relative values of these two types of coefficients provide insight into the amount of variability found in a population.

Expected gain from selection (EGS%)

The expected genetic advance (GA) expressed as a percentage of the mean value with an assumed 5% intensity of selection pressure was computed by the formula given by Allard (1960) as EGS $= k.\ \mathrm{H}\sqrt{\sigma^2 P}$

Where: k = 1.75 and 1.16 constant for 10 and 30% selection intensity (*i.e.* the highest-performing 10 and 30% are selected), respectively.

H is the broad-sense heritability and $\sigma^2 P$ is the Phenotypic variance of the population.

Realized gain from selection (RGS%)

RGS% $= (\overline{X}_0 - \overline{XP}) \times 100 / \overline{XP}$

Where: RGS% RG the realized advance in one generation of selection, $\overline{X}_0$ is the mean phenotype of the offspring of selected parents, $\overline{XP}$ the phenotype mean of the whole parental generation.

Results and Discussion

1-Evaluation of the base population

Two cycles of pedigree selection were achieved is one population of faba bean (*Vicia faba* L.) derived from cross breeding between (Sakha 3 X Giza 2) in generations F_2, F_3 and F_4. Direct pedigree selection was applied to the seed yield/plant, the number of pods per plant, and the seed weight (100). Description of the base population (F_2 generation); means, ranges, variation and heritability in broad sense are presented in Table 2.

Table 2. The range and mean values in the F_2 population and parents for all studied traits in one faba bean population during season of 2021/2022

Families		DFF	NB/P	NP/P	SY/P	SI
Pop1	Rang	40-61	2-11	18-77	50.09-167.58	55.18-114
	Mean	49.24	5.09	41.99	93.24	84.56
	Variance	24.778	3.033	166.592	766.929	179.603
	CV%	10.11	34.20	30.73	29.69	15.84
	H	87.23	48.93	72.39	96.77	88.66
Sakha3 (P_1)	Mean	45.15	4,27	39.83	107.97	91.95
Giza2 (P_2)	Mean	44.77	4.25	37.97	81.53	89.28
	CV% P_1	4.25	10.24	13.65	4.60	5.70
	CV% P_2	3.62	13.25	12.06	6.59	4,063

DFF: days to first flower; NB/P: Number of branch per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; SI: seed index. CV%: coefficient of variation; H: Broad sense heritability.

The range index of variability was comparatively wider in the F_2 generation as compared with the next generations for studied characters (Table 2) indicating a sufficient coefficient of variability in the F_2 population (29.69) in the criterion of selection *i.e.* SY/P. The results showed a sufficient coefficient of variability in the F_2 population (30.73) in NP/P criterion of selection and reported a sufficient CV% in F_2 pop. I (15.84) for SI. The CV% of the other traits ranged from 10.11 to 34.20% for DFF and number of branches/plant; respectively. Forever, the CV of all traits except branches/plant (10.24 and 13.25) and number of pods/plant (13.65 and 12.06) and low CV% for other traits in the two parents, respectively.

Similar results were found by Yassien *et al* (2012), Tadle *et al* (2019)، Waly *et al* (2021), Prateek and Mishra *(*2022) and Hiywotu *et al* (2022).

Heritability in broad sense estimates were higher for all traits except number of branches/plant in the base population. Also, Ibrahim *et al* (2015) estimated that the heritability was high in DFF, NB/P, NP/P and SY/P.

2- Pedigree line selection in F3 and F4 generation

According to the analysis of variance, the genotypic and phenotypic variances for DFF, NB/P, SY/P, and SI and phenotypic variance for NP/P variance were highly significant (**) among the F_3 and F_4 families (Table 3). This result revealed to the available variance for future selection in the current population of faba bean.

Table 3. Mean squares estimates for all traits in F3 and F4 generations of a single population

			F_3			
S.O.V.	DF	DFF	NB/P	NP/P	SY/P	SI
REP.	2	3.77	0.81	5.4	3.68	8.80
Genotypes	59	44.19**	6.45**	449.25**	1677.64**	398.18**
Error.	118	1.18	0.32	6.33	2.450	2.00
			F_4			
REP.	2	0.500	1.01	11.3	8.77	1.51
Genotypes	19	38.69**	7.13**	389.09**	1612.65**	266.90**
Error.	38	0.79	0.98	4.49	21.22	1.244

DFF: days to first flower; NB/P: Number of branch per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; SI: seed index. S.O.V.: source of variation; REP: Replications.
** significant at 0.01 levels of probability.

A- Seed yield/ plant (SY/P)

The averages for SY/P, NP/P, and SI in the F_3 and F_4 generations of the current population are displayed in Table (4). Their averages of the selected families were greater in the F_4 than F_3 generation. Otherwise, for DFF average was earlier in the F_4 than F_3 generation. This result is good to have superior selections in yield and early flowering.

The F_3 generation's average for SY/P (120.67 g). It was evident that the sufficient differences across families within the current population were found and support the possibility to effective selection for seed yield. Moreover, it is clear result that the averages of the selected families for seed yield/plant, number of pods/plant, number of branches/plant and seed index were higher in F4 than F_3 generations by 9.64, 18.62, 14.74 and 6.89%, respectively, revealing to effectiveness of pedigree line selection in faba bean (Table 4).

The coupled PCV% and GCV% for SY/P in the F3 selected families were 19.58 and 19.56% and reduced to 17.52 and 17.40 in F4, respectively (Table 4). This diversity raises the possibility the selection foe seed yield/plant within the F3 families. Waly *et al*. (2021), Haridy *et al*. (2021), and Hiywotu *et al*. (2022) concluded the similar outcomes. Waly *et al*. (2021) reported additive gene influence SY/P with higher heritability and high genetic advance (GA%) as a percentage of the average.

Table 4. Means, PCV, GCV and heritability estimates (H%) for all characters in f$_3$ and f$_4$ generations of the one population faba bean

Treat.	DFF		NB/P		NP/P		SY/P		SI	
Generations	**F$_3$ Fam.**	**F$_4$ Fam.**	**F$_3$ Fam.**	**F$_4$ Fam.**	**F$_3$ Fam.**	**F$_4$ Fam.**	**F$_3$ Fam.**	**F$_4$ Fam.**	**F$_3$ Fam.**	**F$_4$ Fam.**
Mean± S.E	49.44± 0.63	48.58± 0.51	5.63± 0.69	6.46± 0.57	44.9± 1.45	53.26± 1.22	120.67± 0.90	132.30± 2.65	98.75± 0.81	105.56± 0.64
σ2p	14.73**	12.89**	2.51**	2.37**	149.75**	129.69**	559.21**	537.55**	132.72**	88.96**
σ^2g	14.33**	12.63**	2.04**	2.05**	147.64**	128.19**	558.39**	530.47**	132.05**	88.55**
P.C.V.%	7.68	7.39	26.03	23.85	27.25	21.37	19.58	17.52	11.66	8.93
G.C.V.%	7.58	7.31	25.37	22.15	27.06	21.25	19.56	17.4	11.63	8.91
H %	97.31	97.93	94.96	86.42	98.59	98.84	99.85	98.68	99.49	99.53
Mean of parents										
Sakha 3	51.66	46.18	4.3	4.46	39.3	38.96	101.24	102.11	100.48	88.93
Giza 2	44.16	45.55	4.35	4.09	37.75	35.2	82.25	83.04	93.03	87.19

DFF, days to first flower; NB/P, Number of branch per plant; NP/P, number of pods per plant; SY/P, seed yield per plant; SI, seed index. SE: standard error; σ2p: Phenotypic variance; σ2g: Genotypic variance; PCV%: Coefficient of phenotypic variance; GCV%: coefficient of genotypic variance; H: Broad sense heritability.

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

In general, GCV% was less than PCV%. Ahmad (2013), Sheelmary and Shivania (2015)، and Chaurasia *et al.* (2022) discovered similar outcomes. Abo-Elwafa *et al.* (2022) and Ahmad (2016) discovered similar outcomes for the results of seed yield/plant. However, Abdel-Aziz *et al.* (2015) observed that the SY/P indicated that selection is unsuccessful in increasing seed yield due to the moderate heritability and genetic advance (GA%).

Robinson *et al.* (1949) classified heritability levels as low (0–30%), moderate (30–60%), and high (60–plus). The high estimates of heritability were recorded and accounted 99.85 and 98.68% in F$_3$ and F$_4$, respectively. The high values of (H) generally revealed to the effects of the environment were smaller than the influences of heredity. These findings are consistent with those of Parteek and Mishra (2022), Bakhiet *et al*. (2015), and Hiywotu *et al*. (2022). Conversely, Haridy *et al*. (2021) found that for cycle 1 and cycle 2, seed yield/plant had strong heredity in the narrow sense (≤ 50%), while the remaining features had heritability ranging from low to medium. Moreover, Bakhiet *et al.* (2015) found that high PCV for the number of branches/plant, in all seasons.

B- Number of pods/plant (NP/P)

The families' average number of pods/ plant varied from 19 to 72, with an average of 44.90. This average increased to 53.26 in F$_{4,}$ which exerted 18.62% above the F$_3$ (Table 4). It was evident that there was sufficient variation among families as done for NP/P.

The values of both coefficients of variability i.e. GCV and PCV were recorded in Table 4 for F$_3$ and F$_4$ generations. The negligible difference exited between PCV and GCV, indicating little influence of the environment on the characters' expression. The coupled PCV% and GCV% for NP/P in the F$_3$ selected families were 27.25 and 27.06% which reduced to 21.37 and 21.25 in F4, respectively (Table 4). These variations imply that selection within the F$_3$ families could result in a shift in the population's average number of pods per plant. PCV% was generally slightly greater than GCV%. According to Prateek and Mishra (2022), the number of pods per plant had modest values for both genotypic and phenotypic coefficients of variability. However, Bakhiet *et al.* (2015) discovered that in two seasons, a medium PCV was noted for the number of bods/plant. High values of heritability were high as 98.59% and 98.84% in F3 and 4 for NP/P. These results are in accordance with those of Waly *et al.*, (2021), Abo-Hegazy (2022), Bakhiet *et al.* (2015) and Ibrahim *et al* (2015).

PCV% was generally comparatively greater than GCV%. Ahmad (2013), Ahmad (2016), and Tadle et al (2019) discovered similar outcomes for both of PCV and GCV. Sheelamary and Shivani (2015) noted a direct and indirect effect of yield components i.e. NP/P on SY/P.

C- Seed index (SI)

The families' mean seed index (SI) increased from 98.75 in F3 to 105.56% in F4 (Table 4). Otherwise, the PCV and GCV% were decreased from11.66 and 11.63% in F3 to 8.93 and 8.91% in F4 under the seed index selection. According to estimates of PCV and GCV%, selection among the F3 families may be the primary cause of the majority of the variability. High heritability estimates were found of 99.49 and 99.53% in F3 and F4, respectively, revealing the high genetic variability for seed index in the current population. The GCV% was not quite as high as the PCV%. Afeta *et al.* (2020) and Waly *et al.* (2021) reported similar findings, that the PCV value was greater than the GCV% and H values for SI. Additive gene influence was reported for SI with high heritability and high GA% as a percentage of the average. These findings are consistent with those of Abo-Hegazy (2022) and Ahmad (2016).

D- Number of branches/plant (NB/P)

The families' average number of branches/ plant increased from 5.63 in F3 to 6.46 in F4, which accounted increase of 14.74 in F4 comparing to F3 (Table 4). It was evident that there was sufficient variation among families as done for NB/P.

The values of both coefficients of variability i.e. PCV and GCV were decreased from 26.03 and 25.37 in F3 to 23.85 and 22.15% in F4 (Table 4), indicating little influence of the environment on the characters' expression. The coupled PCV% and GCV% with high heritability for NB/P in the F3 and F4 for selected families gave chance for future selection for this trait.

The PCV and GCV% in the F3 and F4 families are lower than those of the F2 families (34.20%). According to Salwa Mostafa et al. (2017), Ahmed (2016), Ibrahim (2015), Afeta *et al.* (2020), and Waly *et al.* (2021), the PCV% value was greater than the GCV% and H values that were provided for NB/P. Conversely, Bakhiet *et al.* (2015) found high PCV for the number of branches/plant in all seasons

The PCV and GCV% in the F3 and F4 families are lower than those of the F2 families (10.11%). According to Salwa Mostafa *et al.* (2017), Ahmed (2016), Ibrahim (2015), Afeta *et al.* (2020), and Waly *et al.* (2021), the PCV% value was greater than the GCV% and H values that were provided for FFD. Conversely, Bakhiet *et al*. (2015) found that the high PCV and GCV for DFF were recorded in all seasons, but poor GCV was noted for DFF in the first season.

E- Days to first flowering (FFD)

The average days to first flowering decreased from 49.44 in F3 to 48.58 days in F4, which accounted earliness of 1.70 days in F4 comparing to F3 (Table 4). It was evident that there was sufficient variation among families as done for DFF.

The values of both coefficients of variability i.e. PCV and GCV were decreased from 7.68 and 7.58 in F3 to 7.39 and 7.31% in F4 (Table 3). The coupled PCV% and GCV% with high heritability for FFD in the F3 (97.31) and F4 (97.93%) for selected families gave chance for future selection for this trait.

Actual (RGS%) and predicted (EGS%) gains from selection

The actual (RGS%) and predicted (EGS%) gains from selection are presented in Table (5). The expected (EGS%) and realized (RGS%) gain from selection as Johnson *et al.*, (1955) defined genetic advance of low (<10%), moderate (10–20%), and high (>20%) as a percentage of the mean. The EGS% for DFF in the current population if faba bean in the F2 generation was 20.70, then was dropped to 13.61 and 8.39 in the F3 and F4 generations, respectively. In the F2 generation, the EGS% for the number of branches/plant was 70.53, which decreased to 43.51 and 23.86 in F3 and F4, respectively. Ahmad (2016) discovered that for all characters under study, the highest GA and RG values were helpful and declined with sequence generations.

Table 5. The EGS% and RGS% estimates for studied traits in F2, F3 and F4 generations of the current of population faba bean

Treats	**generations**	**Pedigree selection population 1**	
		EGS%	**RGS%**
DFF	F_2	20.70	---------
	F_3	13.61	1.41
	F_4	8.39	-2.71
NB/P	F_2	70.53	------------
	F_3	43.51	10.67
	F_4	23.86	14.79
NP/P	F_2	62.94	……….
	F_3	47.29	6.93
	F_4	24.51	18.63
SY/P	F_2	29.52	------------
	F_3	34.41	23.06
	F_4	20.06	9.56
SI	F_2	32.45	-------------
	F_3	20.43	16.77
	F_4	10.31	6.91

DFF: days to first flower; NB/P: Number of branch per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; SI: seed index. EGS%: expected genetic advance %; RGS%: realized gain from selection.

For number of pods/plant, the EGS% of F2 was 62.94, however it dropped to 47.29 and 24.51% in the F3 and F4 generations. According to Prateek and

Mishra (2022), all of the traits showing the slight influence of environment on the expression of the trait had strong heritability and high genetic progress as a percentage of average for seed index, seed yield/plant, days to 50% flowering, and the number of pods/plant. or every feature showing a small environmental influence on the expression of these traits, which could be controlled via additive gene action. Moreover, Mishra *et al*., (2021) reported high heritability and GA% for all characteristics with the exception of pods/plant. Moreover, the EGS% in F2 for seed yield/plant was 29.52 and increased to 34.41 and 20.06% in the F3 and F4 generations, respectively. The EGS% in F2 for SI was 32.45 and dropped to 20.43 and 10.31% in the F3 and F4, respectively. The outcomes of Tadele *et al*. (2019), Afeta *et al*. (2020), and Abo-Hegazy (2022) are consistent with this one

The realized gain for selection (RGS%) were 1.41 and -2.71; 10.71 and 14.79; 6.93 and 18.63; 23.06 and 9.56; and 16.77 and6.91% for DFF; NB/P; NP/P; SY/P and SI in the F3 and F4, respectively (Table 5). This outcome agrees with the findings of Ahmad (2016) and Mishra *et al*. (2021).

Table 6. The means of best-selected families of faba bean population (Sakha 3 X Giza 2) based on seed yield/plant, pods/plant and seed index in F4 generation

Superior families	DFF	NB/P	NP/P	SY/P	SI
1	45.00**	6.33**	54.00**	153.40**	100.10**
2	47.00	4.67	35.67	160.67**	121.37**
3	48.33	4.00	39.33	138.78	101.52**
9	50.67	5.00	35.33	139.67	118.09**
12	46.33**	6.33**	57.33**	152.44**	96.90**
13	46.33**	8.67**	64.33**	156.34**	96.42**
15	49.00	6.33**	48.67	152.54**	87.15
55	50.00	4.67	73.33**	173.22**	115.71**
56	58.33	6.00**	62.67**	140.64**	114.44**
60	48.58	7.33**	51.33**	141.31**	95.06**
16	49.03	5.00	55.67**	137.44	112.53**
Generation mean F$_4$	48.58	6.46	53.26	132.30	105.56
Mean of the 11 fam.	49.03	5.76	52.52	149.67	105.39
Point start (M.F$_2$)	49.24	5.09	41.99	93.24	84.56
Better parent (Sakha 3)	46.18	4,46	38.96	102.11	88.93
Check variety (Giza 402)	51.22	4.68	36.18	79.49	84.18
Bulk	49.18	4.22	42.22	87.16	86.18
LSD 5%	1.47	1.32	3.49	7.60	1.67
LSD 1%	1.48	1.96	4.19	9.11	1.96
Act. (MF$_4$-M.F$_2$)	-0.66	1.37	11.27	39.06	21.00

DFF: days to first flower; NB/P: Number of branch per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; SI, seed index; LSD 5%: least significant difference at 5%; LSD 1%: least significant difference at 1%; Act.: Actual genetic advance.
** significant at 0.01 levels of probability.

Superior selections after two cycles of pedigree line selection

The means of the 11 superior selected-families out yielded in F4 generation families, bulk sample and check (Giza 402) exacted in Table 6. The highest values for the majority of the qualities that were evaluated and were comparable to the better parent (Sakha 93). In terms of relative yield features, the top families were 1,2,12, 13, 55,56, 60 and 16. These families provided the best values for the majority of studied characters and outperformed the superior parent, check variety, and bulk samples. In breeding initiatives designed to increase faba bean yield, the breeder might take advantage of these families. These findings concur with those published by Abo Elwafa *et al*. (2022) and Ahmad *et al*. (2018).

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كفاءة الانتخاب المنسب في عشيرة انعزالية من الفول البلدي (سخا 3 × جيزة 2)

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الملخص

أجرى هذا البحث في ثلاثة مواسم من2021/2022, 2022/2023, 2023/2024 في مزرعة تجارب كلية الزراعة- جامعة الازهر - فرع اسيوط وكانت المواد المستخدمة عبارة عن عشيرة قاعدية في الجيل الثاني ناتجة من التهجين بين صنفين من الفول البلدي وهي العشيرة (سخا 3 × جيزة 2) وكان الهدف من هذا البحث هو تقدير التقدم في الانتخاب ومعامل الاختلاف المظهري والوراثي.

أهم النتائج المتحصل عليها يمكن عرضها كالتالي

أظهر تحليل التباين وجود اختلافات عالية المعنوية بين العائلات المنتخبة لصفة محصول البذور للنبات (جم) في هذه العشيرة مما يدل على أن الانتخاب داخل العشيرة يكون فعالاً. كما أظهرت النتائج أن متوسط القيم في الدورة الانتخابية الثانية (الجيل الرابع) أعلى من المتوسطات في الدورة الانتخابية الأولى (الجيل الثالث) لجميع الصفات المدروسة ما عدا صفة الأيام حتى التزهير كان متوسط القيم في الدورة الانتخابية الأولى أعلى من الدورة الانتخابية الثانية. وكان التقدم المتوقع للانتخاب لصفة محصول البذور على النبات (جم) مرتفعا في الأجيال الثلاثة وكانت القيم 29.52، 34.41، 30.43 على الترتيب، بينما كانت هناك قيم ملحوظة من التقدم الفعلي لصفة محصول البذور على النبات في الجيلين الثالث والرابع وكانت القيم 23.06، 9.56 على الترتيب. وقد أمكن الحصول في الجيل الرابع على أفضل العائلات وهي 1، 2، 13، 56، 60 في الصفات المدروسة وتفوقت هذه العائلات عن الصنف القياسي جيزة 402 والأب الأفضل سخا 3 والعينة المجمعة، ويمكن استغلال هذه العائلات في برامج التربية التي تستخدم في تحسين محصول الفول البلدي.