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Research Article

Genetic Variability, Heritability and Path Coefficient Analyses of Some Agronomic traits in Faba Bean (*Vicia faba* L.)

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Abstract

Background and Objective: Heritability, correlation and path coefficient analyses are essential tools in selection experiments. They are used to determine direct and indirect relationships between yield and certain plant characters. The present investigation aims to study the genetic diversity of nine faba bean (*Vicia faba* L.) genotypes and to determine some selection criteria for plant breeding to enhance seed yield and production. **Materials and Methods:** The study was carried out during the 2018/19 and 2019/20 growing seasons to estimate the genetic parameters of 10 faba bean genotypes grown at the Experimental Farm of the Faculty of Agriculture, Cairo University, Giza, Egypt. The experiment was laid out as a Randomized Complete Blocks Design (RCBD) with 3 replications. **Results:** The performance of the studied genotypes significantly differed for all studied traits in each season. Combined analysis of variance elucidates that years had a significant effect on pods plant⁻¹, seeds pod⁻¹, seeds plant⁻¹ and seed yield plant⁻¹. Season x genotype interaction was not significant for all studied traits, except for harvest index. The highest estimates of heritability (h^2_B) were obtained for the seed index in the 1st and 2nd seasons. Significant positive correlations were detected between seed yield plant⁻¹ and all studied traits. Path analysis exhibited that number of seeds plant⁻¹ had the highest positive direct effects on seed yield plant⁻¹. **Conclusion:** Indirect selection for any character with a significantly positive association with yield would improve the productivity, seeds plant⁻¹ is the principal yield component and selection for this trait may be useful in improving the yield of faba bean crop.

Key words: Faba bean, genotypes, genetic variability, broad-sense heritability, path coefficient analysis, genetic advances, seed yield

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most extensively cultivated pulses in Egypt and other Mediterranean basins. The total cultivated area was approached 33 million hectares with 28.9 million tons of seed yield production in the world and 28460 hectares with 132130 tons of seed yield production in Egypt (FAOSTAT, 2019). Faba bean ($2n = 12$) has attracted the attention of geneticists and plant breeders to improve the average yield per area unit, due to its value for both human and animal nutrition. An important objective of the Egyptian Government is consequently to reduce the dependence on imported faba beans by enhancing seed yield and production. Egypt governorates have different and unstable weather conditions, under which the variability among locations, years and seasons can severely affect the yield of faba bean. Increasing faba bean productivity is a national target in Egypt to fill the gap between faba bean consumption and production. The yield of faba bean can be increased in 2 ways, i.e., either by bringing more land area under cultivation or by increasing its yield productivity per unit area. Currently, it is not possible to increase the area of faba bean due to other competitive winter crops especially wheat and Egyptian clover. The only alternative is to obtain a higher yield per area unit by growing new high-yielding varieties and better crop management.

To develop elite genotypes, knowledge on interrelationships between yield and its component traits and direct and indirect contribution towards yield are important. Before initiating any breeding program, it is essential to obtain information regarding the interrelationship between various yield attributed traits with seed yield.

Seed yield is a complex trait and is highly influenced by many genetic factors and environmental fluctuations that are quantitatively inherited with low heritability values^{1,2}. The low heritability and consequent limited genetic advance for yield in response to selection had led many scientists to search for characters that are associated with yield but which are more highly heritable^{3,4}. Selection for seed yield can only be effective if the desired genetic variability is present in the genetic stock. In-plant breeding programs, direct selection for seed yield as such could be misleading. A successful selection depends upon the information of the genetic variability and association of morpho-agronomic characters with seed yield. Knowledge of the association between yield and its components will serve to make the simultaneous selection for more characters.

Genotypic and phenotypic correlations are important in determining the degree to which various yield contributing characters are associated. The increase in seed yield can be possible if the existing genetic resources and information are properly utilized. Knowledge of the correlation between different traits is necessary for plant breeding programs. Correlation coefficients are useful if the indirect selection of a secondary character is to be used for improving the primary character of interest. Correlation studies along with path analysis provide a better understanding of the association of different characters with seed yield^{3,5}. Yield character was closely correlated with the number of pods plant⁻¹, the number of seeds plant⁻¹ and seed yield plant⁻¹ traits in faba bean^{1,6-7}. A significant and positive correlation was found between seed yield and the number of seeds pod⁻¹, seed yield plant⁻¹^{7,8}.

The present investigation was conducted to derive information on heritability, variance components, phenotypic correlation, genetic advance, direct and indirect effects of yield components and genotype x year interactions for seed yield traits determined on 10 faba bean genotypes to employ the most successful genotype (s) for the improvement of new faba bean cultivars. This may help faba bean breeders in reshaping and improving future faba bean breeding strategies.

MATERIALS AND METHODS

Experiment and plant material: This study was carried out during the 2 successive growing seasons, 2018/19 and 2019/20 at the experimental farm of the Faculty of Agriculture, Giza, Cairo University, Egypt (30°02'N Latitude and 31°13' E Longitude, Altitude 22.50 m). The experimental material comprised of 10 Egyptian faba bean genotypes, namely, Sakha 3, Sakha 4, Nubaria 1, Giza-843, Cairo-4, Cairo-5, Cairo-25, Line 24 H, Line 36 and Line 379 (Table 1). They were used as treatments and evaluated in the investigation.

Experimental design and cultivation practices: The experiment was carried out as Randomized Complete Blocks Design (RCBD) with 3 replications. Each genotype was represented in each replicate by 3 ridges, 4 m long with 60 cm apart (plot size = 7.2 m²). Seeds were sown as 2 seeds hill⁻¹, spaced 20 cm at one side of the ridge. Faba bean plants were provided with normal irrigation. The plants were subjected to a recommended package of agronomic and plant protection practices to obtain a healthy crop. At harvest, 10 guarded faba

Table 1: Origins of the faba bean genotypes

Genotype names	Pedigree	Origin	Remarks
Line 24 H	Developed via single seed descent were derived from <i>Orobanche</i> tolerant landraces	AD, FA, CU	Line
Line 36	Developed via single seed descent were derived from <i>Orobanche</i> tolerant landraces	AD, FA, CU	Line
Line 379	Developed via single seed descent were derived from <i>Orobanche</i> tolerant landraces	AD, FA, CU	Line
Cairo-4	Egyptian local selection " <i>Orobanche</i> tolerant variety"	AD, FA, CU	Variety
Cairo-5	Egyptian local selection " <i>Orobanche</i> tolerant variety"	AD, FA, CU	Variety
Cairo-25	Egyptian local selection " <i>Orobanche</i> tolerant variety"	AD, FA, CU	Variety
Sakha 3	Promising line 716/402/2001 derived from cross 716 (Giza 461/842/83 × 503/453/83)	FCRI	Variety
Sakha 4	Sakha 1 × Giza 3	FCRI	Variety
Nubaria 1	Individual plant selection from Rena Blanka	FCRI	Variety
Giza-843	(BPL710 × R.S.P.S line to <i>Orobanche</i> from Giza 429)	FCRI	Variety

FCRI: Field crops research institute, AD: Agronomy department, FA: Faculty of agriculture and CU: Cairo university

Table 2: The expectation of mean squares (MS) for the analysis of variance for separate and combined analysis

Source of variations	df	MS	Expectation of M.S
Separate			
Replications (r)	(r-1)	MS _r	
Genotypes (G)	(a-1)	MS _a	$\delta_e^2 + r \delta_g^2$
Error	(r-1) × (a-1)	MS _e	δ_e^2
Combined			
Season (S)	(a-1)		
Reps/season	a (r-1)		
Genotypes (G)	(b-1)	MS _a	$\delta_e^2 + r \delta_{ga}^2 + ra \delta_g^2$
G × S	(a-1) (b-1)	MS _{as}	$\delta_e^2 + r \delta_{ga}^2$
Error	a (r-1) (b-1)	MS _e	δ_e^2

bean plants were randomly taken from each plot to measure yield and its components.

Recorded data: Data on yield and yield components were recorded on plants randomly selected from the middle row. Observations were recorded on 10 randomly selected plants in each genotype per replication for the characters number of pods plant⁻¹, number of seeds plant⁻¹, number of seeds pod⁻¹, 100-seed weight "Seed Index" (SI), Harvest Index (HI) and seed yield plant⁻¹.

Statistical analysis: A combined analysis of variance across seasons was carried out⁹. Broad sense heritability (h²) was estimated by using the variance components method¹⁰ as shown in Table 2.

The genotypic and phenotypic variances (δ_g^2 and δ_{ph}^2) were calculated from the partitioned mean squares expectation (Table 2) as follows:

$$\delta_g^2 = \frac{MS_a - MS_e}{r}$$

$$\delta_{ph}^2 = \frac{\delta_g^2 - \delta_e^2}{r}$$

Where:

$$\delta_e^2 = MS_e$$

However, those over seasons are calculated from the pertinent mean squares expectation (Table 2) as follows:

$$\delta_g^2 = \frac{MS_a - MS_{as}}{ra}$$

$$\delta_{ph}^2 = \frac{\delta_g^2 + \delta_{ga}^2}{r + \delta_e^2 / rs}$$

Where:

$$\delta_e^2 = MS_e$$

Broad sense heritability (h²_B) was calculated as follows:

$$h^2_B = \frac{\delta_g^2}{\delta_{ph}^2} \times 100$$

The simple correlation coefficients estimates were computed between seed yield plant⁻¹ and other studied characters previously¹¹.

The expected Genetic Advance (GA) from selection was calculated with the suggested method¹².

$$GA = K \cdot \delta_{ph} \cdot h^2_B$$

Where:

GA = Genetic advance

K = Constant = 2.06 at 5% selection intensity

δ_{ph} = Square root of phenotypic variance

h_B^2 = Heritability in the broad sense

$$\text{GA as (\% of mean (GAM))} = \frac{\text{GA}}{\text{Mean value}} \times 100$$

Path coefficient analysis: Path coefficient analysis was used to partition the correlation coefficients and to determine the direct and indirect effects¹³ of:

- Number of pods plant⁻¹
- Number of seeds pod⁻¹
- Number of seeds plant⁻¹
- Seed index (SI)
- Harvest index (HI)
- Seed yield plant⁻¹ (g)

The path coefficient analysis (direct effects) of the 5 characters on seed yield plant⁻¹, were determined. They were acquired by solving the following simultaneous Eq.:

$$r_{16} = P_{16} + r_{12} P_{26} + r_{13} P_{36} + r_{14} P_{46} + r_{15} P_{56} \quad (1)$$

$$r_{26} = r_{21} P_{16} + P_{26} + r_{23} P_{36} + r_{24} P_{46} + r_{25} P_{56} \quad (2)$$

$$r_{36} = r_{31} P_{16} + r_{32} P_{26} + P_{36} + r_{34} P_{46} + r_{35} P_{56} \quad (3)$$

$$r_{46} = r_{41} P_{16} + r_{42} P_{26} + r_{43} P_{36} + P_{46} + r_{45} P_{56} \quad (4)$$

$$r_{56} = r_{51} P_{16} + r_{52} P_{26} + r_{53} P_{36} + r_{54} P_{46} + P_{56} \quad (5)$$

where, r_{16} , r_{26} , r_{36} , r_{46} and r_{56} are the simple correlation coefficients of the 5 traits involved in the model with seed yield plant⁻¹ (6), respectively.

Residual effect was obtained by the following Eq.:

$$P_{ry} = \sqrt{1 - (P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ky} r_{ky})}$$

Where:

P_{ry} = Residual effects

r_{iy} = Correlation coefficient between *i*th independent variable X (yield components) and *g*th dependent variable Y (yield plant⁻¹)

P_{iy} = Direct effect of X on Y

The path coefficient analysis was performed by examining seed yield plant⁻¹ as a dependent variable for major contributors' character to seed yield plant⁻¹ via OpenStat version 30.06.10, a software program¹⁴.

RESULTS AND DISCUSSION

Analysis of variance: Mean square values due to different sources of variability for the studied traits in the separate analysis and the combined one are presented in Table 3. Results showed that the genotypes differed significantly for all studied traits in each season and combined analysis. Combined analysis of variance across seasons elucidates that season mean squares were significant or highly significant for all studied traits, except for SI and HI. Therefore, it could be concluded that environmental factors significantly affected the performance of the investigated faba bean genotypes, except for SI and HI. These results are in agreement with those obtained by previous studies^{15,16}.

Results showed that mean squares due to season x genotype interaction were significant for all studied traits, except for harvest index. This declared that the studied genotypes significantly differed for their ranks from one season to another for all studied traits, except harvest index.

It is worthy to note that the variances due to differences among genotypes were higher than those due to the interaction between genotypes and environments. The ratio between the 2 variances was greatest for harvest index followed by seed index and seed yield plant⁻¹. This ratio reached its minimum for the number of seeds pod⁻¹ followed by the number of seeds plant⁻¹ and number of pods plant⁻¹. These results indicated that most of the variability in the 1st 3 traits was mainly controlled by genetic factors with less influence by environmental effects compared to the latter 3 traits. This means that improvement for the 1st 3 traits group could be achieved by selection. The effectiveness of selection depends on the variability present in germplasm and the extent to which it is heritable. Substantial genetic advance through selection for different yield components needs sufficient genetic variability^{2,17,18}.

Mean performance: The mean performances for the studied traits of 10 faba bean genotypes are presented in Table 4. Combined data across seasons showed that Line 24 H possessed the highest values for the number of pods plant⁻¹, number of seeds pod⁻¹, number of seeds plant⁻¹, harvest index and seed yield plant⁻¹ (23.83, 3.53, 64.23, 54.92% and

Table 3: Mean squares of studied traits in 2018/19, 2019/20 and combined data across years

Trait/S.V	df	Number of pods plant ⁻¹	Number of seeds pod ⁻¹	Number of seeds plant ⁻¹	Seed index (SI)	Harvest index (HI)	Seed yield plant ⁻¹
2018/19							
Genotypes (G)	9	25.776**	0.593**	205.018*	363.473**	98.891**	161.644**
Error	18	5.291	0.137	59.399	12.212	6.755	27.307
2019/20							
Genotypes (G)	9	46.862**	0.435**	225.292*	380.731**	132.322**	161.331**
Error	18	12.685	0.052	60.272	9.254	4.390	27.255
Combined							
Season (S)	1	112.340**	1.441*	77.521*	0.308ns	4.704ns	127.313*
G	9	58.689**	0.986**	262.390**	704.466**	227.617**	280.944**
S×G	9	13.949*	0.242**	67.920*	39.738**	3.596ns	42.031*
Error	36	5.988	0.044	29.835	10.733	5.573	17.281

ns: Not significant, *: Significant at 0.05, **: Significant at 0.01 levels of probability, respectively

Table 4: Mean performance of ten faba bean genotypes for studied traits during 2018/19, 2019/20 and combined data across seasons

Genotypes	Number of pods plant ⁻¹			Number of seeds plant ⁻¹			Number of seeds pod ⁻¹		
	1st	2nd	Combined	1st	2nd	Combined	1st	2nd	Combined
Line 24 H	22.67	25.00	23.83	60.20	68.27	64.23	3.80	3.27	3.53
Line 36	14.00	21.40	17.70	58.60	53.77	56.18	4.20	2.60	3.40
Line 379	17.33	24.33	20.83	60.57	63.00	61.78	3.60	2.80	3.20
Cairo-4	15.67	16.53	16.10	50.53	52.20	51.37	3.27	3.17	3.22
Cairo-5	18.67	23.33	21.00	54.73	65.03	59.88	2.97	2.80	2.88
Cairo-25	18.33	19.33	18.83	66.73	58.83	62.78	3.63	3.10	3.37
Sakha 3	16.00	17.33	16.67	60.80	56.43	58.62	2.67	2.53	2.60
Sakha 4	16.00	13.33	14.67	50.63	50.60	50.62	3.20	3.80	3.50
Nubaria 1	17.07	18.73	17.90	54.43	59.73	57.08	3.20	3.20	3.20
Giza-843	11.67	15.43	13.55	36.70	48.80	42.75	3.13	3.30	3.22
Range	11.67-22.67	13.33-25.00	13.55-23.83	36.7-66.73	48.8-68.27	42.75-64.23	2.67-4.20	2.53-3.80	2.60-3.53
LSD _{0.05}	3.26	5.04	4.15	9.91	9.99	8.72	0.52	0.32	0.42
Genotypes	Seed index (SI) (g)			Harvest index (HI) (%)			Seed yield plant ⁻¹		
	1st	2nd	Combined	1st	2nd	Combined	1st	2nd	Combined
Line 24 H	68.33	75.00	71.67	54.87	54.97	54.92	50.93	60.33	55.63
Line 36	73.67	77.00	75.33	38.57	39.53	39.05	41.20	44.13	42.67
Line 379	69.00	65.33	67.17	36.60	34.43	35.52	40.17	46.23	43.20
Cairo-4	70.33	62.00	66.17	39.23	38.67	38.95	44.43	40.43	42.43
Cairo-5	65.67	63.67	64.67	41.87	42.13	42.00	37.67	43.30	40.48
Cairo-25	62.67	69.00	65.83	41.63	41.13	41.38	42.67	42.37	42.52
Sakha 3	72.67	69.00	70.83	46.07	46.17	46.12	44.83	41.00	42.92
Sakha 4	73.67	69.00	71.33	34.40	30.13	32.27	38.47	35.70	37.08
Nubaria 1	101.07	101.07	101.07	40.67	41.13	40.90	44.60	46.00	45.30
Giza-843	62.67	67.23	64.95	38.53	38.53	38.53	23.07	32.67	27.87
Range	62.67-101.07	62.00-101.07	64.67-101.07	34.4-54.87	30.13-54.97	32.27-54.92	23.07-50.93	32.67-60.33	27.87-55.63
LSD _{0.05}	4.95	4.31	4.54	3.68	2.97	3.27	6.40	5.39	7.24

55.63 g, respectively). On the other hand, Giza-843 possessed the lowest values for the number of pods plant⁻¹ (13.55) and the number of seeds plant⁻¹ (42.75). For seed index, Nubaria 1 possessed the heaviest seed weight (101.07 g) followed by Line 24 H (71.67 g) among the 10 investigated genotypes. On the other hand, Giza-843 and Cairo-5 showed the lowest values (64.95 and 64.67 g, respectively). Line 24 H exhibited the highest value (55.63g) for seed yield plant⁻¹ followed by 45.30 and 43.20 g for Nubaria 1 and Line 379, respectively. On the other hand, Giza-843 and Sakha 4 showed the lowest values for seed yield plant⁻¹ (27.87 and 37.08 g, respectively).

From the above-mentioned results, it could be concluded that line 24 H exhibited the highest number of pods plant⁻¹, number of seeds pod⁻¹, number of seeds plant⁻¹ and seed yield plant⁻¹. These results reflect that the selection prospects within this genotype to improve the performance through a breeding program.

Variance components, heritability and genetic advance:

Estimates of phenotypic variance (δ^2_{ph}) for seed index was the highest one (115.0), followed by seed yield plant⁻¹ (45.45) across the 2 seasons, while it was low for seeds pod⁻¹ (0.15).

Table 5: Estimates of δ^2_{ph} , δ^2_g , h^2_B and GA for studied traits in 2018/19, 2019/20 and combined data across seasons

Trait	2018/19			2019/20			Combined				
	δ^2_{ph}	δ^2_g	h^2_B (%)	δ^2_{ph}	δ^2_g	h^2_B (%)	δ^2_{ph}	δ^2_g	h^2_B (%)	GA	GAM
Pods pL^{-1}	8.59	6.83	79.47	15.62	11.39	72.93	9.34	7.46	79.84	5.03	27.76
Seeds pL^{-1}	68.34	48.54	71.03	75.10	55.01	73.25	41.62	32.41	77.88	10.35	18.31
Seeds pod^{-1}	0.20	0.15	76.90	0.15	0.13	88.05	0.15	0.12	80.87	0.65	20.09
SI	121.16	117.09	96.64	126.91	123.83	97.57	115.80	110.79	95.67	21.21	29.50
HI	32.96	30.71	93.17	44.11	42.64	96.68	38.05	37.34	98.14	12.47	30.44
SY pL^{-1}	53.88	44.78	83.11	53.78	44.69	83.11	45.45	39.82	87.61	12.17	28.96

δ^2_{ph} : Phenotypic variance, δ^2_g : Genotypic variance, h^2_B : Broad sense heritability, GA: Genetic advance and GAM: Genetic advance as percent of mean

Table 6: Phenotypic correlation coefficients among studied traits of ten faba bean genotypes (combined data)

Trait	Seeds pod^{-1}	Seeds pL^{-1}	SI	HI	SY pL^{-1}
Pods pL^{-1}	-0.739**	0.726**	-0.109	0.247*	0.473**
Seeds pod^{-1}		0.760**	0.766**	0.825**	0.682**
Seeds pL^{-1}			0.820**	0.814**	0.924**
SI				0.866**	0.951**
HI					0.860**

*,**Indicate significance at 0.05 and 0.01 levels of probability, respectively

High values of genotypic variance (δ^2_g) were marked for SI (110.79) followed by p SY $plant^{-1}$ (39.82) in the combined 2 seasons (Table 5). The magnitude of δ^2_g recorded the lowest value for seeds pod^{-1} (0.12) across the 2 seasons.

Broad sense heritability (h^2_B) is defined as a ratio of genotypic to phenotypic variance. The estimates of heritability in the broad sense ranged from 71.03-98.14% (Table 5), the highest estimates of broad-sense heritability were recorded for seed harvest index (98.14%), followed by seed index and seed yield $plant^{-1}$ (95.67 and 87.61%, respectively) across the 2 seasons and it was moderate for the others which were least affected by environmental changes and selection based on phenotypic performance could be possible. The higher magnitude of heritability indicated that these traits could be successfully improved by direct selection. These results confirmed previous results of ^{2,3,5,7,16,19}.

The genetic advance as a percent of the mean (GAM) using 5% selection intensity is presented in Table 5. It ranged from 18.31% for the number of seeds $plant^{-1}$ to 30.44% for harvest index. High genetic advance expressed as a percentage of mean was obtained from HI (30.44%), seed index (29.50%), seed yield $plant^{-1}$ (28.96%) and the number of pods $plant^{-1}$ (27.76%) high values of GAM coupled with high values of h^2_B for the number of seeds $plant^{-1}$ and SI indicate that these traits are under the control of additive genes (Table 5). The current observations were in confirmation with the findings of scientists who reported similar results in their study on faba bean genotypes^{1,20}. On the other hand low estimates of genetic advances expressed as a percentage of mean were observed for the number of seeds pod^{-1} (20.09%) and the number of seeds $plant^{-1}$ (18.31%), indicating the existence of low genetic variability for these traits which are also reflected by their respective low genotypic and

phenotypic variances. This in turn showed the importance of genetic variability for the improvement of traits through selection (Table 5).

Correlation analysis: Phenotypic correlation coefficients for all comparisons among the studied faba bean traits are presented in Table 6. The correlations between seed yield $plant^{-1}$ and related components permit researchers to have a clearer idea about the component which should be improved. Significant and positive correlation coefficients were detected between seed yield $plant^{-1}$ (g) and each of number of pods $plant^{-1}$, number of seeds pod^{-1} , number of seeds $plant^{-1}$, SI and HI. These findings indicate that selection for each of the pods $plant^{-1}$ seeds $plant^{-1}$ and seed weight $plant^{-1}$ would be accompanied by high yielding ability under such conditions. Positive and significant correlation coefficients were also between HI and each of number of pods pod^{-1} ($r = 0.247^*$), number of seeds pod^{-1} ($r = 0.825^{**}$), number of seeds $plant^{-1}$ and SI ($r = 0.866^{**}$). SI had a negative correlation with number of pods $plant^{-1}$ ($r = -0.109$) and a positive significant correlation with number of seeds pod^{-1} and number of seeds $plant^{-1}$ ($r = 0.766^{**}$ and 0.820^{**} , respectively). The number of seeds $plant^{-1}$ had a highly significant and positive relationship with each of the number of pods $plant^{-1}$ and number of seeds pod^{-1} ($r = 0.726^{**}$ and 0.760^{**} , respectively). In contrast to this, a highly significant and negative correlation was observed between the number of seeds pod^{-1} and the number of pods $plant^{-1}$ ($r = -0.739$). Overall, an intensive selection for these traits will automatically improve faba bean seed yield. Since the 6 traits are correlated, selection in one of the traits will implicitly result in the improvement of the other traits. Therefore, these characters

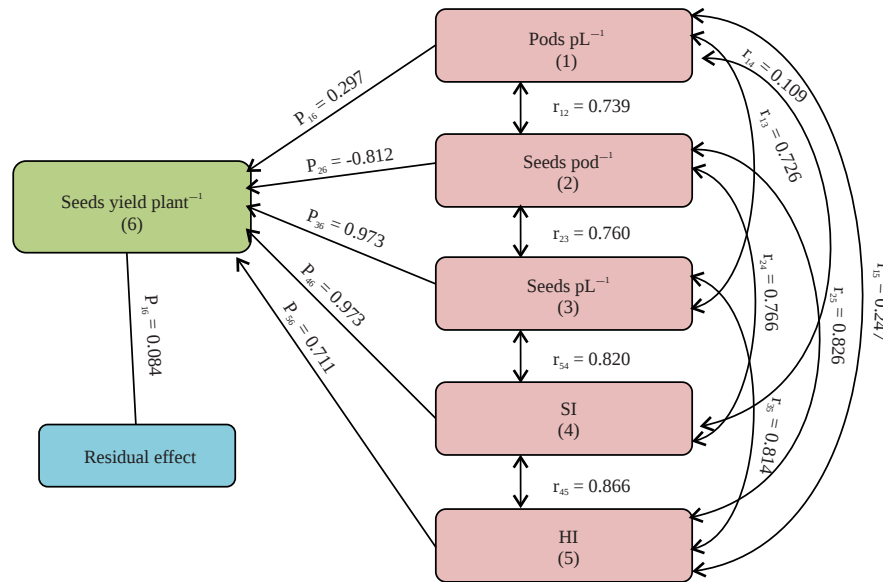


Fig. 1: Diagram of the direct and indirect relationships of seed yield plant⁻¹ with its components, using path coefficient analysis
Single-arrowed lines indicate the path coefficients (direct effect) and doubled-arrowed lines indicate the simple correlations between traits

Table 7: Path coefficient analysis of the direct and indirect effects of five traits and their correlation coefficient with seed yield plant⁻¹ in faba bean
Effect on seed yield plant⁻¹ (g)

Traits	Direct effect	Indirect effect				
		Pods plant ⁻¹	Seeds pod ⁻¹	Seeds plant ⁻¹	SI	HI
Pods plant ⁻¹	0.297		-0.600	0.706	-0.106	0.176
Seeds pod ⁻¹	-0.812**	0.220		0.739	0.745	0.587
Seeds plant ⁻¹	0.973**	0.216	-0.617		0.798	0.579
SI	0.973**	-0.032	-0.622	0.798		0.616
HI	0.711**	0.073	-0.670	0.792	0.843	

**Indicate significance at 0.01 probability level and Residual effect: -0.084

could be utilized in the breeding programs to improve varieties for higher yield. These results are in agreement with that reported previously^{3,4,6,16,21}.

Path analysis: Path coefficient analysis was used to partition the correlations between seed yield plant⁻¹ and traits related to yield into direct and indirect effects as shown in Table 7 and Fig. 1. The results showed that the number of seeds plant⁻¹ and SI had the highest direct effect (0.973**) for each trait on seed yield plant⁻¹ followed by HI (0.711**), the number of pods plant⁻¹ had the smallest direct effect (0.297). The indirect effect of the number of seeds plant⁻¹ occurred through SI (0.798), HI (0.579) and the number of pods plant⁻¹ (0.216), whereas negative indirect effects occurred through the number of seeds pod⁻¹ (-0.617). While the positive indirect effect of the number of pods plant⁻¹ was followed by the number of seeds plant⁻¹ (0.706), HI (0.176) and the negative indirect effect by SI (-0.106) and the number of

seeds pod⁻¹ (-0.600). Seed index was positively and indirectly affected by the number of pods plant⁻¹ flowering (0.798), HI (0.616) and was negatively and indirectly affected by the number of seeds pod⁻¹ (-0.032) and the number of seeds pod⁻¹ (-0.622).

The high positive direct effects of the number of seeds plant⁻¹, SI and HI in addition to its highly significant coefficient of correlation is evidence that direct selection through these traits would be effective for improving seed yield of faba bean. In contrast, although significant coefficients of correlation were recorded between seed yield plant⁻¹ and seeds pod⁻¹, its direct effect was negligible. These results may be attributed to that path analysis discarded the indirect effects from the simple correlation coefficient. The components of indirect effect were more important than the path of direct effect considering the harvest index and the number of seeds pod⁻¹ and highest values of indirect effect on the number of seed plant⁻¹. From these results, it can be concluded that

faba bean seed yield can be increased by selecting genotypes having more pods plant⁻¹, higher harvest index and higher number of seeds plant⁻¹. The great contribution of these traits on faba bean yield supported their importance as selection criteria in faba bean breeding programs. Results are in agreement with the findings of previous authors²²⁻²⁵. And indirect selection for any trait with a significantly positive association with seed yield would improve the productivity and that seeds plant⁻¹ is the principal yield component and selection for this trait may be useful in breeding programs of a faba bean crop.

CONCLUSION

It is concluded from the present study that a considerable amount of genetic variation and diversity exists among faba bean genotypes for all studied traits in the Egyptian faba bean germplasm used in the present investigation. There is a large extent of simultaneous improvement in seed yield as well as other yield components through selection criteria to improve the seed yield of faba bean. Therefore, selection for seed yield showed to be made through the selection for seeds pl⁻¹, SI, HI and pods pl⁻¹. The results of this investigation should be implemented for improving varieties of faba bean and it would be worthwhile to study more available germplasm over years to identify more different accessions as well as to confirm the importance of the traits identified as predictors of yield.

SIGNIFICANCE STATEMENT

This study has discovered findings that there is a considerable amount of genetic variation and diversity exists among the Egyptian faba bean germplasm that used in the present investigation. This study will assist the breeders in understanding the magnitude of variability present in crop plants and the degree of association between the different agronomic characters of utmost importance as it provides the base for effective selection criteria. Keeping in view the need to develop suitable varieties of faba bean.

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