

Genetic analysis of *Vicia faba* L.: Advancements, hereditary traits, and correlations in ‘Sakha 3’ × ‘Nubaria 3’

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Abstract: Genetic diversity, heritability, and genetic advance are crucial considerations in the field of plant breeding. This research aimed to evaluate these factors for traits related to yield in faba bean (*Vicia faba* L.), specifically focusing on the F3 and F4 generations resulting from the cross between ‘Sakha 3’ and ‘Nubaria 3’. In the initial season (2021/2022), 200 families from each F3 population were cultivated with specific spacing, and selection criteria included seed yield per plant (SYP) and the number of pods per plant (NPP). Top-performing plants were identified for the second cycle of pedigree selection. In the following season (2022/2023), the F4 families were arranged in a randomised complete block design. Traits like the number of branches per plant (NBP), NPP, SYP, and seed index (SI) showed substantial phenotypic and genotypic coefficients of variation, indicating their noteworthy variation. Phenotypic and genotypic correlation analyses showed positive associations between SYP and the NBP and NPP. Additionally, path coefficient analysis indicated that these traits had high positive direct effects on SYP. This research provides valuable insights into the genetic variability, heritability, and selection parameters for yield-related traits in faba bean, offering a foundation for future breeding programs aimed at improving yield and productivity.

Keywords: broad bean, correlation, genetic advance, genetic variability, path coefficient

INTRODUCTION

Faba beans are a valuable legume crop that is important for both humans and animals (Mínguez and Rubiales, 2021). Faba beans are a nutritious crop that is high in carbohydrates, protein, minerals, and bioactive compounds (Lizarazo *et al.*, 2015;

Karkanis *et al.*, 2018). In any agricultural setting, the cultivation of broad beans has the potential to enhance soil fertility and promote biological activity owing to their mutually beneficial association with *Rhizobium* bacteria. This partnership enhances the process of biological nitrogen fixation, as demonstrated by previous studies (Karkanis *et al.*, 2018; Etemadi *et al.*, 2019).

In the year 2021, Egypt recorded a cultivated area of approximately 26,513 ha dedicated to broad beans, resulting in seed production of 86,566.34 Mg, as reported by Eliw (2021).

Enhancing crop yield stands as a primary objective within global faba bean breeding initiatives. Breeders leverage genetic reservoirs to craft cultivars attuned to the evolving demands of society. They are constantly looking for more effective and efficient selection methods (Hoisington *et al.*, 1999). Plant breeders are always looking for better ways to select the traits they want in their crops. In the realm of faba bean breeding, diverse selection techniques have been employed to enhance various traits, with pedigree selection emerging as the prevailing choice. Haridy (2017) highlighted the efficacy of the number of pods per plant (*NPP*) as a valuable trait for indirect selection aimed at yield improvement. Haridy (2018) discovered that when directly selecting for seed yield per plant (*SYP*), there was a 7.9% increase in yield after two selection cycles, calculated as a deviation from the means of the superior parent. High heritability estimates followed by substantial genetic advancement percentages (*GA%*) for number of pods per plant (*NPP*) and *SYP* indicated the potential for enhancement through selective breeding, as highlighted by Gupta *et al.* (1998). Path coefficient analysis facilitates the differentiation between direct and indirect effects, offering a more realistic understanding of the relationships between traits and aiding in effective selection, as explored by Kumar *et al.* (2017), Esho and Salih (2021), and Abo-Hegazy (2022). Path coefficients represent the breakdown of genotypic correlation coefficients for individual traits with respect to seed yield. Investigating path coefficients enables breeders to focus on the trait with the most significant direct impact on seed yield, ultimately streamlining the selection process by concentrating on one or a few key traits (Dewey and Lu, 1959). Path coefficient analysis has been used by many workers, such as Kumar *et al.* (2017), Dewangan *et al.* (2019), Esho and Salih (2021), and Singh *et al.* (2021).

The aim of this study is to comprehensively investigate genetic advancements, heritability patterns, correlations, and pathway analyses within a specific population originating from the crossbreeding of 'Sakha 3' and 'Nubaria 3' in broad beans (*Vicia faba* L.). We hypothesise significant genetic variability within the studied population, evidenced by the assessment of genetic advancements and heritability estimates for various agronomic traits. We expect certain traits to exhibit substantial correlations with *SYP*, influencing the overall productivity of the broad bean population. Additionally, we anticipate that pathway analysis will reveal the direct and indirect effects of individual traits on *SYP*, elucidating key factors contributing to improved yield. We also hypothesise that the study will provide valuable insights into the potential for selective breeding and trait improvement, ultimately contributing to enhanced broad bean crop productivity.

MATERIALS AND METHODS

PLANT MATERIALS AND EXPERIMENTAL DESIGN

The current study was carried out at the Experimental Farm of the Faculty of Agriculture, Al-Azhar University (Assiut branch), Assiut Governorate, Egypt (27°12'16.67" N and 31°09'36.86" E) during two consecutive winter seasons, covering the period from

2021/2022 to 2022/2023. The average weather of two growing seasons (2021/2022 and 2022/2023) is shown in Figure S1. Three dosages of fertilisation treatments were applied: the first following germination, the second a month later, and the third at the blooming stage. The Egyptian Ministry of Agriculture states that before soil preparation, 357 kg·ha⁻¹ of mono superphosphate fertilisers (15.5% P = 55.34 kg P₂O₅) and 107.5 kg·ha⁻¹ of ammonium nitrate (36 kg N) were administered as a stimulatory dosage. After thirty days from germination, 119 kg·ha⁻¹ of potassium sulphate was added. Irrigation was provided according to the plants' needs and weather fluctuations. Some properties of the experimental site are listed in Table S1.

The genetic materials employed in this study consisted of the F3 and F4 generations, which were derived from the cross between 'Sakha 3' and 'Nubaria 3'. In the initial season, 2021/2022, the F4 generation of the aforementioned population, along with the parent plants, was sown on 5 November, with spaced plants. Specifically, 200 families from each F3 population were cultivated. The rows were spaced 60 cm apart, with a 20 cm distance between individual plants. One plant per hill was maintained, and consistent agricultural practices were applied throughout the broad bean experiment, following the recommended cultural practices for the entire growing season. Upon harvest, 20% of one population was selected based on seed yield per plant (*SYP* in g) and the number of pods per plant (*NPP*). The best-performing plants from the top families in terms of seed yield per plant were chosen to initiate the second cycle of pedigree selection. In the subsequent season, 2022/2023, all the selfed seeds from the best-performing plants of each population represented the F4 families. These families were arranged in a randomised complete block design with three replications for each family in both the *SYP* and *NPP* groups.

MORPHOLOGICAL PARAMETERS

These parameters provide valuable information about the plant's performance and characteristics. Days to 50% flowering (*DFP*) represent the number of days it takes for a faba bean plant to reach the stage at which 50% of its flowers have bloomed. Days to maturity (*DM*) indicate the number of days required for a faba bean plant to reach full maturity from the time of planting. Number of branches per plant (*NBP*) measures the total number of branches that develop on a single faba bean plant. Number of pods per plant (*NPP*) quantifies the total number of pods that are produced by an individual faba bean plant. Seed index (*SI*) or 100-seed weight is a measure of the weight of a specific number of seeds (often 100 seeds). Seed yield per plant (*SYP*) represents the total weight of seeds per plant (in g) produced by a single faba bean plant.

HERITABILITY IN A BROAD SENSE

Heritability in a broad sense (H_b^2) for traits observed in the F3 and F4 generations of a population was calculated using the equation according to Falconer and Mackay (1996):

$$H_b^2\% = (\sigma^2_g / \sigma^2_p) 100 \quad (1)$$

where: $H_b^2\%$ = percentage of heritability in a broad sense, σ^2_g (genetic variance) = variance due to genetic factors, it quantifies

how much of the total variation in the trait is caused by genetic differences among individuals in the population; $\sigma^2 p$ (phenotypic variance) = total variance in the trait within the population, including both genetic and environmental factors, it quantifies the overall variability observed in the trait across all individuals.

EXPECTED GAIN FROM SELECTION

The genetic advance (GA), which represents the expected gain from selection (EGS – concept used in genetics and breeding programs to estimate the improvement that can be achieved by selecting the best individuals from a population based on certain traits) cycle, was calculated as a percentage of the average value, assuming a 5% selection intensity. This calculation was based on the formula proposed by Singh (1985), represented as:

$$EGS = kH_b^2 \sqrt{\sigma^2 p} \cdot 100 \quad (2)$$

where: EGS = expected gain from selection, k = constant set to 1.40 in constant for 20% selection intensity (i.e. the highest-performing 20% are selected), H_b^2 = broad-sense heritability, encompassing all genetic factors contributing to trait variation.

Additionally, the genetic advance as a percentage of the mean value ($\Delta G\%$) is estimated according to Miller *et al.* (1958) and is calculated using the formula:

$$\Delta G = 100(\Delta G/\bar{X}) \quad (3)$$

where: ΔG = genetic advance, which indicates the improvement expected through selective breeding, \bar{X} = signifies the average value of the trait under consideration.

REALISED GAIN FROM SELECTION

The calculation for realised gain from selection (RGS in %), realised genetic advance in one generation of selection, is expressed as follows:

$$RGS = (\bar{X}_0 - \bar{X}_P)/\bar{X}_1 \cdot 100 \quad (4)$$

where: \bar{X}_0 = average trait value in the chosen parents, \bar{X}_P = the average trait value in the parental generation, \bar{X}_1 = average trait value in the offspring generation.

This equation determines the anticipated proportional increase in a particular characteristic of the offspring of chosen parents compared to their predecessors. It is determined by taking \bar{X}_0 and \bar{X}_P , and then dividing this difference by the average trait value in the offspring generation (\bar{X}_1).

THE PHENOTYPIC AND GENOTYPIC COEFFICIENTS OF VARIATION

The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), computed according to Burton (1952), provide insights into the extent of variability within a population:

$$PCV = \frac{\sqrt{VP}}{\bar{X}} \cdot 100 \quad (5)$$

$$GCV = \frac{\sqrt{VG}}{\bar{X}} \cdot 100 \quad (6)$$

where: VP = phenotypic variance, VG = genotypic variance, \bar{X} = mean.

Both $RGS\%$ and PCV/GCV are important measures for breeders to consider when selecting parents for the next generation. $RGS\%$ provides an estimate of the genetic improvement that can be achieved in one generation of selection, while PCV/GCV provides insights into the extent of genetic variability within the population.

PHENOTYPIC AND GENOTYPIC CORRELATION

Determining phenotypic (RP) and genotypic (RG) correlations involves the need for estimates of related variances and covariances, as outlined by Walker (1960) as follows:

$$RP = \frac{\text{Cov } pxy}{spx \cdot spy} \quad (7)$$

$$RG = \frac{\text{Cov } gxy}{sgx \cdot sgy} \quad (8)$$

where: RP = phenotypic correlation between traits x and y , $\text{Cov } pxy$ = covariance between traits x and y due to phenotypic factors, spx and spy = standard deviations of traits x and y due to phenotypic factors, respectively, RG = genotypic correlation between traits x and y , $\text{Cov } gxy$ = covariance between traits x and y due to genetic factors, sgx and sgy = standard deviations of traits x and y due to genetic factors, respectively.

PATH-COEFFICIENT ANALYSIS

The path-coefficient analysis of various traits was carried out following the approach pioneered by Wright (1921) and elaborated upon by Dewey and Lu (1959) using the genotypic correlation coefficient to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$$r_{ij} = P_{ij} + \sum (r_{ik} p_{kj}) \quad (9)$$

where: r_{ij} = mutual association between the independent trait (i) and dependent trait (j), seed yield as measured by the correlation coefficients, p_{ij} = components of direct effects of the independent trait (i) as measured by path-coefficients, $\sum (r_{ik} p_{kj})$ = summation of components of indirect effects of a given independent trait (i) on a given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor is measured as the residual effect. Residual effect (h) is calculated using the formula given by Dewey and Lu (1959).

$$h = \sqrt{1 - R^2} \quad (10)$$

where: $R = \sum (r_{ij} p_{ij})$.

STATISTICAL ANALYSIS

The analysis of variance (ANOVA) and expected mean squares were computed to understand the variability attributable to different sources, including replications, genotypes, and errors.

Table 1 presents the sources of variance, degrees of freedom (DF), mean squares (MS), and the expected mean squares for the analysis.

Table 1. The analysis of variance and expected mean squares

Source of variance	DF	MS	Expected mean square	
			variance	covariance
Replications	$r-1$	M_3	$\sigma^2 e + g\sigma^2 r$	–
Genotypes	$g-1$	M_2	$\sigma^2 e + r\sigma^2 g$	$\text{Cov}(E) + r \text{Cov}(G)$
Error	$(r-1)(g-1)$	M_1	$\sigma^2 e$	$\text{Cov}(E)$

Explanations: DF = degrees of freedom, MS = mean squares, $g\sigma^2 r$ = the difference between the genetic variance (V_g) and the environmental variance (V_e), M_3 = mean square for replications, M_2 = mean square for genotypes, M_1 = mean square for error, $r\sigma^2 g$ = residual variance of the trait, r = number of replications, g = number of genotypes, $\sigma^2 e$ = error variance, which quantifies the variability in data attributable to random errors or non-genetic factors, $\text{Cov}(E)$ = covariance of errors, measuring how errors in data are related, $\sigma^2 g$ = genetic variance, which quantifies the variability in data attributed to genetic factors, $\text{Cov}(G)$ = covariance of genetic effects, which describes how genetic effects in data are related. Sources: own study.

Covariance of errors ($\text{Cov}(E)$) was calculated using the following formula:

$$\text{Cov}(E) = \Sigma(X_{Ei} - X_{E\bar{i}})(Y_{Ei} - Y_{E\bar{i}})/n \quad (11)$$

where: X_{Ei} and Y_{Ei} = observed values of the two variables, respectively, $X_{E\bar{i}}$ and $Y_{E\bar{i}}$ = mean values of the two variables, respectively, n = number of observations.

Covariance of genetic effects ($\text{Cov}(G)$) was calculated using the following formula:

$$\text{Cov}(G) = \Sigma(X_{Gi} - X_{G\bar{i}})(Y_{Gi} - Y_{G\bar{i}})/n \quad (12)$$

where: X_{Gi} and Y_{Gi} = observed values of the two genetic traits, respectively, $X_{G\bar{i}}$ and $Y_{G\bar{i}}$ = mean values of the two genetic traits, respectively.

Error variance ($\sigma^2 e$) was calculated using the following formula:

$$\sigma^2 e = \Sigma(Y_i - Y\bar{i})^2/n \quad (13)$$

where: Y_i = observed value of the variable, $Y\bar{i}$ = expected value of the variable under the model.

The difference between the genetic variance and the environmental variance ($g\sigma^2 r$) was calculated using the following formula:

$$g\sigma^2 r = V_g - V_e \quad (14)$$

where: V_g = genetic variance of the trait, V_e = environmental variance of the trait.

Residual variance of the trait ($r\sigma^2 g$) was calculated using the following formula:

$$r\sigma^2 g = V_t - V_g \quad (15)$$

where: V_t = total variance of the trait, V_g = genetic variance of the trait.

RESULTS

DESCRIPTION OF THE BASE POPULATIONS

The initial populations, as presented in Table 2, displayed a high coefficient of variability within the F3 population, particularly for the selection criterion of seed yield per plant (SYP) at 31.56% and

Table 2. Means, variances, coefficients of variation, heritability, and genetic advance for traits in F3 and F4 generations

Trait	Generation	Mean	Parameter studied in both F3 and F4 generations							
			VP	VG	PCV (%)	GCV (%)	H_b^2	GA	EGS (%)	RGS (%)
DFF	F3	49.04	18.22	18.03	8.70	8.65	98.94	6.12	12.48	–
	F4	48.46	7.65	7.08	5.70	5.49	92.54	3.71	7.66	–1.66
DM	F3	151.73	136.80	136.66	7.71	7.70	99.90	16.94	11.16	–
	F4	145.42	42.22	41.95	4.46	4.45	99.30	9.35	6.43	–4.15
NBP	F3	5.09	1.28	0.66	22.24	15.98	51.68	0.90	16.66	–
	F4	5.81	1.53	1.40	21.27	20.31	91.24	1.63	28.14	14.21
NPP	F3	41.89	83.41	81.42	21.80	21.53	97.61	12.92	30.85	–
	F4	44.54	59.55	56.97	17.32	16.94	95.66	10.70	24.03	6.37
SYP	F3	96.69	931.67	930.45	31.56	31.54	99.86	44.20	45.71	–
	F4	128.95	536.30	535.62	17.95	17.93	99.88	33.53	26.00	33.36
SI	F3	84.10	189.98	121.86	16.38	13.11	64.14	12.81	15.24	–
	F4	94.57	126.20	126.13	11.88	11.87	99.94	16.28	17.21	12.46

Explanations: VP = phenotypic variance, VG = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H_b^2 = heritability in a broad sense, GA = genetic advance, EGS = expected gain from selection, RGS = genetic selection percentage, DFF = days to 50% flowering, DM = days to maturity, NBP = number of branches per plant, NPP = number of pods per plant, SYP = seed yield per plant, SI = seed index. Source: own study.

for the number of branches per plant (*NBP*) at 21.80%. These results suggest a promising potential for effective selection of these traits. In contrast, all traits in the two parent plants showed very low coefficients of variation, attributable to the high genetic purity of these parental plants. The performance of the F3 and F4 generations within the population for various traits, including days to 50% flowering (*DFF*), days to maturity (*DM*), *NBP*, number of pods per plant (*NPP*), *SYP*, and seed index (*SI*) was average. These findings suggest that, in general, there was a varying degree of increase in the mean values from one generation to the next. Remarkably, upon comparing the selected families, the F3 generation displayed higher mean values for traits, including *DFF*, *DM*, *NBP*, *NPP*, *SYP*, and *SI* in comparison to the F4 generation within this population.

Traits such as the *NBP*, *NPP*, *SYP*, and *SI* exhibited notable *PCV* and *GCV* values, except for *DFF* to maturity, in both the F3 and F4 generations. Furthermore, the results reveal that *PCV* and *GCV* estimates decreased across successive generations. In general, *PCV* tended to be relatively higher than *GCV*, emphasising the substantial phenotypic variation observed in these traits compared to the genetic variation. Medium *PCV* values were observed for *DM* and the *NPP* across all seasons, while *SYP* exhibited medium *PCV* in the first season. Additionally, moderate *GCV* values were estimated for days to maturity and *NPP* in all seasons, as well as seed weight per plant in one season. Conversely, low *GCV* was noted for *DFF* in the first season, as well as for the *NBP* and seed yield in two seasons. Furthermore, they conducted a genotypic correlation analysis for *SYP* and other yield-related traits, revealing high positive direct effects on *NPP* (0.648) and *NBP* (0.416), with a positive effect of *DM* at 0.171 on seed yield per plant.

In the F3 generation, broad-sense heritability surpassed 50% for all traits, indicating a significant genetic influence. Furthermore, consistently high to moderate broad-sense heritability estimates were noted for most of the studied traits in both the F3 and F4 generations.

The *EGS* for *NPP* in the F3 generation was 30.85% and increased in the F4 generation to 24.03%. Similarly, for the *NBP*, the *EGS* in the F3 generation was 16.66%, and it increased to 28.14% in the F4 generation. Furthermore, in the F3 generation, the *EGS* for *DFF* and *DM* was 12.48% and 11.16%, respectively. These values decreased in the F4 generation to 7.66% for *DFF* and 6.43% for *DM*. Conversely, the *EGS* for *SI* in the F3 generation was 15.24% and increased in the F4 generation to 17.21%.

PHENOTYPIC AND GENOTYPIC CORRELATION COEFFICIENTS

The phenotypic (Fig. 1a) and genotypic (Fig. 1b) correlation coefficients between *SYP* and five other yield components, as well as the correlations among these traits, are presented in Figure 1. Seed yield per plant values demonstrated noteworthy and positive associations with two characteristics: *NBP* (0.264 and 0.369) and *NPP* (0.225 and 0.240). Additionally, *SI* exhibited positive but modest correlations with *SYP* (0.062 and 0.077). On the contrary, *SYP* did not show significant positive correlations with *DFF* (0.139 and 0.141) and *DM* (0.216 and 0.217). The *DFF* parameter displayed significant and positive correlations with four traits: *DM* (0.716 and 0.721), *NBP* (0.294 and 0.409), *NPP* (0.611 and 0.657), and *SI* (0.332 and 0.411). *DM* also displayed a notable and positive correlation with *NPP* (0.423 and 0.453). Additionally,

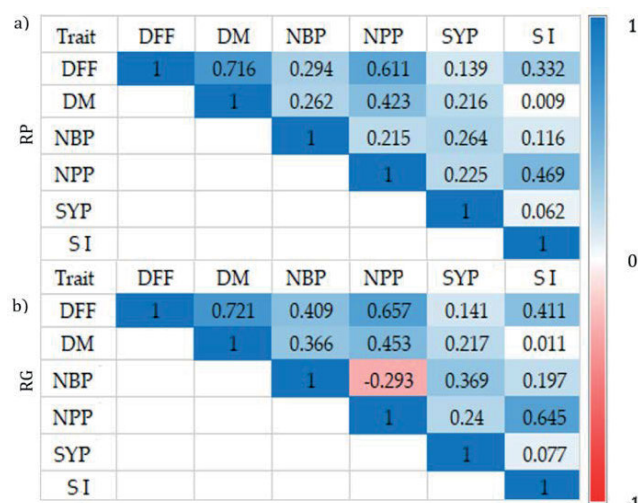


Fig. 1. Estimates of correlation coefficients between all pairs of studied traits in the F3 generation of the population: a) *RP* - phenotypic correlation coefficient, b) *RG* - genotypic correlation coefficient; the correlation coefficients (*r*) range from -1 to 1, with different levels indicating varying strengths of correlation: perfect positive correlation when *r* = 1; strong positive correlation when *r* ∈ [0.7; 0.9]; moderate positive correlation when *r* ∈ [0.4; 0.6]; weak positive correlation when *r* ∈ [0.1; 0.3]; no correlation when *r* = 0; weak negative correlation when *r* ∈ [-0.3; -0.1]; moderate negative correlation when *r* ∈ [-0.4; -0.6]; strong negative correlation when *r* ∈ [-0.7; -0.9]; perfect negative correlation when *r* = -1; *DFF*, *DM*, *NBP*, *NPP*, *SYP*, *SI* as in Tab. 2; source: own study

NPP revealed a significant and positive correlation with 100-seed weight (0.469 and 0.649). However, there was a negative correlation observed between the *NBP* and *NPP* (-0.215 and -0.253).

The results, which detail the phenotypic (Fig. 2a) and genotypic (Fig. 2b) correlation coefficients among *SYP* and the other five yield components, as well as the relationships among the characters, are presented in Figure 2. The trait *SYP* was positively correlated with the *NBP* (0.235 and 0.241), *NPP* (0.282 and 0.285), and *SI* (0.277 and 0.285). However, *SYP* was not positively correlated with *DFF* (0.085 and 0.090) or *DM* (0.153 and 0.158). At

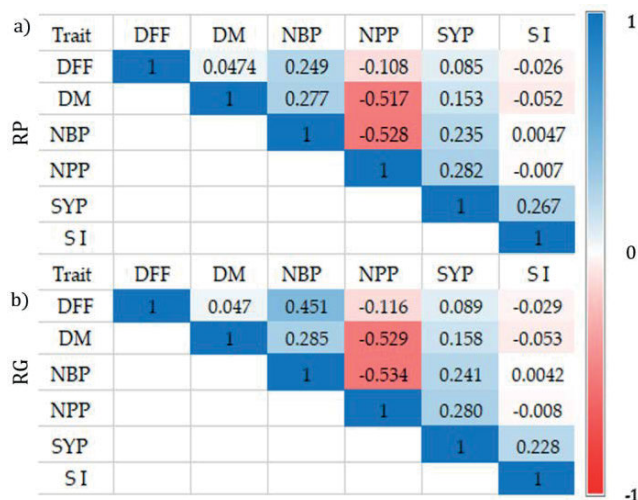


Fig. 2. Estimates of correlation coefficients between all pairs of studied traits in the F4 generation of the population: a) *RP* - phenotypic correlation coefficient, b) *RG* - genotypic correlation coefficient; explanations as in Fig. 1; source: own study

the same time, *DFP* was positively correlated with the *NBP* (0.249 and 0.451); *DM* was positively correlated with the *NBP* (0.277 and 0.285) and *SI*. The trait *NPP* was negatively correlated with itself (–0.517 and –0.529) and *NBP* (–0.528 and –0.534). However, *SI* was not significantly correlated for all traits except *SYP*.

PATH COEFFICIENT ANALYSIS

Path coefficient analysis is employed to concurrently assess the direct and indirect effects of individual component traits on the dependent variable, *SYP*. The genotypic correlation coefficient of *SYP* with the other yield component traits was individually partitioned into direct and indirect effects, and the outcomes are outlined in Table 3. With this connection, high positive direct effects were observed on *NPP* (0.648), *NBP* (0.416), and the positive effect of *DM* (0.171) on *SYP*. The direct effect of *DFP* and seed index *SYP* was negative (–0.529 and –0.389). The indirect effect was a positive one for the *NBP* and *NPP* via *DM* (0.152 and 0.293), respectively, while the indirect effect of *SI* via *NPP* was negative (–0.247). However, the effects for *NBP* and *SI* were negative (–0.917 and –0.125), while the indirect effects of amount *NBP* via the *NPP* were positive (0.190). The residual effect component in the path analysis of yield traits was determined to be –0.112, indicating a lower residual effect. The path analysis also indicated that *SI*, *NPP*, *NBP*, and *DM* had positive and direct effects on *SYP*. However, there were negative but high indirect effects through *DM* and moderate indirect impacts through the *NBP* on *SYP*.

Path coefficient analysis is conducted to assess the combined direct and indirect impacts of individual component traits on the dependent variable, namely *SYP*. The genotypic correlation coefficient of *SYP* with the other yield components characters was individually partitioned into direct and indirect effects and the results are presented in Table 4. With this connection, high positive direct effects were observed on *NBP* (0.599) and *NPP* (0.824) on *SYP*. The direct effect of *DFP* on *SYP* was negative (–0.100), while the effect of *DM* on *SYP* was positive (0.441). The indirect effect was positive for *DFP* via *NBP* (0.270). However, the positive effect for the *NBP* via *DM* was 0.171. The indirect effects through the other three traits (*DFP*, *DM*, and *NBP*) were low positive and negative on the seed index in two seasons, except *NPP* (0.418) in the first season. The residual effect component in the path analysis of yield traits was determined to be 0.003. The smaller residual effect reports that the characters chosen for path analysis were adequate and appropriate.

Table 3. Path analysis coefficient between seed yield per plant (*SYP*) and the studied traits of yield components in F3 generation

Trait	<i>DFP</i>	<i>DM</i>	<i>NBP</i>	<i>NPP</i>	<i>SI</i>	Correlation with <i>SYP</i>
<i>DFP</i>	–0.549	0.123	0.170	0.425	–0.028	0.141
<i>DM</i>	–0.369	0.171	0.152	0.293	–0.030	0.217
<i>NBP</i>	–0.224	–0.063	0.416	0.190	0.050	0.369
<i>NPP</i>	–0.360	0.077	0.122	0.648	–0.247	0.240
<i>SI</i>	–0.042	0.002	0.082	0.418	–0.381	–0.079

Explanations: *DFP*, *DM*, *NBP*, *NPP*, *SYP*, *SI* as in Tab. 2; residual effect = 0.112.

Source: own study.

Table 4. Path analysis coefficient between seed yield per plant (*SYP*) and the studied traits of yield components in F4 generation

Traits	<i>DFP</i>	<i>DM</i>	<i>NBP</i>	<i>NPP</i>	<i>SI</i>	Correlation with <i>SYP</i>
<i>DFP</i>	–0.100	0.021	0.270	–0.096	–0.007	0.088
<i>DM</i>	–0.005	0.441	0.171	–0.436	–0.013	0.158
<i>NBP</i>	–0.045	0.126	0.599	–0.440	0.001	0.241
<i>NPP</i>	0.012	–0.233	–0.320	0.824	–0.002	0.281
<i>SI</i>	0.003	–0.023	0.003	–0.007	0.253	0.229

Explanations: *DFP*, *DM*, *NBP*, *NPP*, *SYP*, *SI* as in Tab. 2; residual effect = 0.003.

Source: own study.

DISCUSSION

DESCRIPTION OF THE BASE POPULATIONS

The variability within the initial populations, as outlined in Table 2, warrants attention. Notably, the F3 population exhibited a remarkably high coefficient of variability, particularly concerning the selection criterion *SYP*, reaching 31.56%. Additionally, the variability in *NBP* was substantial, registering at 21.80%. These results imply that there is a promising prospect for effective selection of these traits. Conversely, all traits in the two parent plants exhibited very low coefficients of variation, which can be ascribed to the high genetic purity of these parental plants. These observations align with similar results reported by Ahmad (2016), Kumar *et al.* (2017), and Abo-Hegazy (2022). Bakhiet *et al.* (2015) observed variations among the tested genotypes for all the studied traits in both seasons, except for *NBP* in the first season. In the study conducted by Hiywotu *et al.* (2022), it was observed that there were highly significant differences ($p \leq 0.01$) among accessions for all traits, except for days to maturity. Moreover, they noted that broad-sense heritability estimates were moderate to high for all traits within a population.

Table 2 outlines the average performance of F3 and F4 generations for various traits. F3 generally displayed higher mean values compared to F4, indicating potential selection advantages. Traits like *NBP*, *NPP*, *SYP*, and *SI* exhibited notable variation, with *PCV* higher than *GCV*, emphasising substantial phenotypic variation. The findings of this study are in agreement with those reported by Ahmad (2016), El-Said, Haridy and Abd-El-Zaher (2020), and Hiywotu *et al.* (2022), who observed substantial phenotypic and genotypic coefficients of variability (*PCV* and *GCV*) for traits such as 100-seed weight (*PCV* = 24.02% and *GCV* = 20.29%), seed yield plant (*SYP*) (*PCV* = 31.32% and *GCV* = 30.77%), number of branches per plant (*NBP*) (*PCV* = 36.81% and *GCV* = 27.52%), and number of pods per plant (*PCV* = 43.66% and *GCV* = 37.60%). These high *PCV* and *GCV* values suggest that there is substantial genetic variation within the studied accessions, implying that these traits can be effectively improved through direct selection. Bakhiet *et al.* (2015) undertook a study to explore the variability in various plant traits. They discovered a high *PCV* and *GCV* for *DFP* in the second season. Medium *PCV* values were observed for *DM* and the *NPP* across all seasons, while seed weight per plant exhibited medium

PCV in the first season. Additionally, moderate GCV values were estimated for DM and the NPP in all seasons, as well as seed weight per plant in one season. Conversely, low GCV was noted for DFF in the first season, as well as for the NBP and seed yield in two seasons. Furthermore, they conducted a genotypic correlation analysis for SYP and other yield-related traits, revealing high positive direct effects on NPP (0.648) and NBP (0.416), with a positive effect of DM at 0.171 on SYP.

The heritability values were categorised as low (0–30%), moderate (30–60%), and high (60% and above) according to Robinson, Comstock and Harvey (1949). In the F3 generation, broad-sense heritability exceeded 50% for all traits, indicating a significant genetic influence. Additionally, high to moderate broad-sense heritability estimates were consistently observed for most studied traits in both the F3 and F4 generations. These elevated heritability values underscore the substantial impact of genetic factors in shaping these traits, suggesting minimal influence from environmental factors in their determination. These results are in accordance with Abo-Hegazy (2022) and Bakhiet *et al.* (2015). On the contrary, Helal and El-Hefnawy (2017) documented low heritability for the NBP and high heritability for the NPP and 100-seed weight. Zeinab and Helal (2014) indicated consistently high heritability estimates in both broad and narrow senses for all the studied traits. Specifically, heritability in the narrow sense was notably high for NPP (76.42%), 100-seed weight (75.53%), and the NBP (62.00%). However, it was comparatively low for SYP. These results suggest that genetic elements play a significant role in determining traits, with the level of genetic influence varying depending on the specific trait under consideration. The research carried out by Sheelamary and Shivani (2015), observed elevated broad-sense heritability values for all characteristics, with the exception of the NBP and NPP. Interestingly, most of the characters exhibited improved broad-sense heritability estimates as the study progressed from the F3 to the F4 generations. The enhancement was ascribed to an increased proportion of genetic variance in comparison to the overall variance. This shift resulted from concealed or cryptic genetic alterations induced by two rounds of selection.

According to Johnson, Robinson and Comstock (1955), the genetic advance as a percentage of the mean is classified as low (<10%), moderate (10–20%), and high (>20%). In the F3 generation, the expected gain from selection (EGS in %) for SYP was 45.71, and it increased to 26.00 in the F4 generation, respectively. These results are in accordance with those of Ahmad (2016), Helal and El-Hefnawy (2017), Mishra *et al.* (2021), Abo El-Wafa *et al.* (2022), Abo-Hegazy (2022), and Hiywotu *et al.* (2022), who identified the maximum predicted genetic advance for all traits. Conversely, Abdel Aziz and Osman (2015) reported that the moderate heritability and low genetic advance observed in SYP suggest that selection is not very effective in enhancing seed yield.

The expected gain from selection (EGS) for NPP in the F3 generation increased in the F4 generation. Similarly, for the NBP, the EGS (in %) increases from the F3 to the F4 generation. This observed pattern aligns with the findings of Mishra *et al.* (2021), who reported the highest heritability and predicted genetic advances for all traits except the NBP and NPP across all genotypes. In the study conducted by Abo-Hegazy (2022), it was observed that high genetic advances, expressed as a percentage of

the mean, were obtained for traits such as 100-seed weight (29.50%), SYP (28.96%), and the NPP (27.76%). Furthermore, high genetic advance (GA) percentage values and broad-sense heritability suggest additive gene control of seed index. Comparing relative genetic selection (RGS) percentage estimates for key traits in the F4 generation reveals their respective progress through selective breeding: SYP (33.36%), NBP (14.21%), NPP (6.37%), and SI (12.46%). Ahmad (2016) found that the RGS (in %) estimates for SYP and 100-seed weight in F4 for hybrid 1 (cross between 'Looza' and 'Assiut 98'), hybrid 2 (cross between 'Misr 1' and 'Giza 40') and hybrid 3 (cross between 'Lozza' and 'Giza 429'), were 53.25, 12.94; 48.81, 13.66; and 28.52, 7.29, respectively.

PHENOTYPIC AND GENOTYPIC CORRELATION COEFFICIENTS

Noteworthy associations between traits were observed. The SYP showed positive correlations with NBP and NPP. The SI exhibited modest positive correlations with seed yield. Days to 50% flowering displayed significant positive correlations with DM, NBP, NPP, and SI. Days to maturity also showed notable positive correlations with NPP. Additionally, NPP revealed significant positive correlations with 100-seed weight, but a negative correlation with NBP. This is in line with the findings of Bakhiet *et al.* (2015), Kumar *et al.* (2017), Abo-Hegazy (2022), Chaurasia *et al.* (2022) and Haridy *et al.* (2022).

PATH COEFFICIENT ANALYSIS

Path coefficient analysis evaluates the direct and indirect effects of component traits on SYP in F3 generation. High positive direct effects were seen for NPP and NBP, with DM also positively influencing SYP. The DFF and SI had negative direct effects. Indirect effects were noted for NBP and NPP via DM, while the indirect effect of SI via NPP was negative. Additionally, pod weight and SI showed negative effects, with a positive indirect effect of NBP via NPP. The residual effect was minimal, indicating suitability of traits chosen for analysis. Overall, SI, NPP, NBP, and DM directly affected SYP, with negative indirect effects through DM and moderate effects through NBP on SYP. In line with these findings, Kumar *et al.* (2017) and Abo-Hegazy (2022) have demonstrated in their studies that in path analysis, SI exhibited a high direct impact (0.973) on SYP, while NPP had the smallest direct effect (0.297). Interestingly, SI was positively and indirectly influenced by NPP (0.798). Path coefficient analysis evaluates the direct and indirect impacts of component traits on SYP in F4 generation. High direct effects were seen for NBP and NPP on seed yield. However, DFF had a negative direct effect, while DM had a positive one. Indirect effects included a positive effect for DFF via NBP and a positive effect for NBP via DM. The residual effect was minimal, indicating the suitability of traits for analysis. Abo-Hegazy (2022) showed that the path analysis, SI, had a high direct impact (0.973) for each trait of SYP, NPP had the smallest direct effect (0.297), but SI was positively and indirectly affected by NPP (0.798).

Overall, the findings highlight the promising potential for genetic improvement in this plant population, paving the way for developing high-yielding varieties with enhanced agronomic characteristics.

CONCLUSIONS

This study sheds light on the genetic characteristics and interrelationships of various traits within broad bean (*Vicia faba*) populations, specifically focusing on the F3 and F4 generations. The F3 generation displayed significant variability in traits like seed yield per plant (*SYP*) and the number of branches per plant (*NBP*), indicating the potential for effective selection to enhance these traits. Conversely, the parental plants exhibited low variability due to their genetic purity. Broad-sense heritability estimates consistently exceeded 50% for all traits in the F3 generation, underscoring the strong genetic influence on these traits, with limited impact from environmental factors. Expected genetic advances varied between generations for traits such as *SYP*, number of pods per plant (*NPP*), and the *NBP*, signifying opportunities for genetic improvement through selective breeding. Phenotypic (*RP*) and genotypic (*RG*) correlation coefficients revealed significant positive associations between *SYP* and traits like *NBP* and *NPP*. However, traits like days to flowering and days to maturity (*DM*) exhibited weaker correlations with *SYP*, guiding trait selection in breeding programs. Path coefficient analysis unveiled direct and indirect trait effects on *SYP*. Traits like *NPP*, *NBP*, and *DM* had substantial positive direct effects on *SYP*, while days to flowering and seed index (*SI*) showed negative direct effects, clarifying their relative importance. Breeding programs targeting the enhancement of *Vicia faba* populations can prioritise traits with high heritability, significant genetic advances, and positive correlations with seed yield, such as *NPP* and *NBP*. This research contributes valuable insights for the improvement of *Vicia faba* populations. It highlights traits ripe for selection and provides a foundation for future breeding endeavours aimed at increasing the yield and overall performance of broad beans. These findings hold promise for the development of improved cultivars to meet the rising demand for this important leguminous crop.

SUPPLEMENTARY MATERIAL

Supplementary material to this article can be found online at https://www.jwld.pl/files/Supplementary_material_Ahmed.pdf

AUTHOR CONTRIBUTIONS

1st Author (contribution – 25%): study design, data collection, statistical analysis, data interpretation, manuscript preparation, literature search. 2nd Author (contribution – 15%): data interpretation, manuscript preparation, literature search. 3rd Author (contribution – 10%): study design, data collection. 4th Author (contribution – 10%): data interpretation, manuscript preparation. 5th Author (contribution – 10%): manuscript preparation, literature search. 6th Author (contribution – 20%): study design, data collection, statistical analysis, data interpretation, manuscript preparation, literature search. 7th Author (contribution – 10%) – manuscript preparation, literature search).

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CONFLICT OF INTERESTS

All authors declare that they have no conflict of interests.

INSTITUTIONAL REVIEW BOARD STATEMENT

This article does not contain any studies of human participants or animals performed by any of the authors.

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