

Research Article

# Correlation and Path Coefficient Analysis of Yield and Yield Components in Faba Bean (*Vicia faba* L.) Genotypes

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## Abstract

Through the use of path coefficient analysis and correlation, crop breeders can improve complex traits like grain yield through indirect selection. The current study set out to quantify the relationship between yield and traits related to yield as well as pinpoint critical features for indirect selection aimed at enhancing the grain yield of faba bean. The objective of the current study was to identify key characteristics for indirect selection targeted at increasing the grain yield of faba beans as well as quantify the relationship between yield and variables related to yield. The study was conducted at Fogera National Rice Research and Training Center at the Debre Tabor research site used a 7x7 simple lattice design with two replications to evaluate 49 faba bean genotypes during the rainy cropping season of 2022. The study found a significant positive correlation between grain yield, plant height, pod number, biomass yield, 100-seed mass, and harvest index. The study found that biomass yield and harvest index significantly impact grain yield, suggesting they can be used as indirect selection criteria to enhance faba bean grain yield.

## Keywords

Biomass Yield, Indirect Selection, Grain Yield, Harvest Index

## 1. Introduction

Due to its high seed protein content, the faba bean (*Vicia faba* L.,  $2n = 12$ ) is a significant cool-season grain legume (pulse) crop that is farmed all over the world for the production of human and animal feed [13]. Ethiopia, after China, is the world's second-largest producer of fababeans. The country's total cultivated fababean area was 504,569.99 hectares, and its total production was 10,706,365.38 quintals, with an average national yield of 21.22 quintals per hectare [1].

It is crucial to have knowledge about the relationships between yield attributes and how they affect grain yield both directly and indirectly. Path analysis combined with correlation would provide a more comprehensive understanding of the causal relationships between various character pairs. Understanding the relationship between yield and its component traits in detail is essential before starting any successful selection program [3] to improve faba beans further. By doing this, the likelihood of getting a correlated response

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in the intended direction would increase.

The yield is a complex and highly variable character and is a result of the cumulative effect of its component characters; therefore, direct selection for yield may not be very effective. Understanding the degree and kind of relationships between traits facilitates the creation of effective multiple trait selection systems. Therefore, study on phenotypic and genotypic correlation on crop among traits of crop are important in planning, evaluating and setting out a selection criteria for desired traits in breeding program [10]. Phenotypic correlation, the observable correlation between two variables, which includes both genotypic and environmental effects, and genotypic correlation, the inherent association between two variables were estimated using the standard procedure suggested by [11].

When more traits are considered in correlation studies, correlations of traits become more complex; therefore, correlation study followed by path analysis will help to identify yield attributing traits. Path coefficient analysis is a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated. It is used in plant breeding programs to determine the nature of the relationships between yield and yield components that are useful as selection criteria to improve the crop yield. Path coefficient analysis was carried out using the phenotypic correlation coefficients as well as genotypic correlation coefficients to determine the direct and indirect effects of the yield components and other morphological characters on seed yield [7]. Therefore, the present study was conducted with the objectives of determining the relationship between grain yield and yield components, and their direct and indirect effects of contributing characters to seed yield in faba bean.

## 2. Material and Methods

### 2.1. Description of the Study Area

The field experiment was conducted in 2022 main cropping season, under rain-fed condition at Fogera National Rice Research and Training Center in Debre Tabor research site, northwestern Ethiopia. The experimental location represent the highland areas of major faba bean growing area of south Gondar and located about 660 km Northwest of Addis Ababa, about 103 km from Bahir Dar town. The latitude and longitude of the experimental site is 11° 88' N and 37° 98' E, respectively, and an elevation of 2706 masl. The experimental site receives high amount of rainfall and an average annual rainfall of 1500.9 mm with maximum and minimum temperatures of 29 and 16 °C, respectively. The soil type of experimental area was characterized by nitisols.

### 2.2. Treatments, Experimental Design and Procedures

Forty nine faba bean genotypes were used for this study (Table 1). The tested forty nine faba bean genotypes were obtained from collection and crossed which were obtained from Holeta Agricultural Research Center. The experiment was arranged in simple lattice design with two replications. The experimental areas was 780 m<sup>2</sup> (30 m \* 26 m) with experimental plot area 3.6 m<sup>2</sup> (3 m \* 1.2 m) having three rows and thirty plants per row. Spacing between replication, incomplete block, plots, rows, and plants was 2m, 1.5m, 0.6m, 0.4m, and 0.1m, respectively. NPS fertilizer was applied at planting time in the rate of 121kg/ha. Weeding practice was applied uniformly for all treatments for two times at seedling stage and after flowering stage.

**Table 1.** List of 49 faba bean genotypes used in the study.

Genotypes			Genotypes
1	Cool-0030	26	EH011029-2
2	EK 01002-1-1	27	EK05024-2
3	Cool-0025	28	EH011049-2
4	EH011070-1	29	ET 07013-1
5	EH011040-1	30	EK 01006-7-1
6	EH011001-1	31	EK 01015-1-1
7	EH011093-2	32	EH011037-2
8	Cool-0031	33	EK 05023-1
9	EK 01001-5-1	34	EH 06007-2
10	Cool-0018	35	Coll 155/00-3
11	Cool-0035	36	EK05005-4
12	Cool-0024	37	EH01048-1
13	EK 01001-8-1	38	Gora(S.C)
14	EK 05014-3	39	EH99051-3
15	EK05027-5	40	EK 01004-2-1
16	EK 01001-9-2	41	EH 06028-1
17	EK 01001-10-5	42	EH95073-1
18	EH96009-1	43	EK 01019-7-5
19	EH95078-6	44	EH00102-4-1
20	EK 01007-2-6	45	R-878-3
21	CSR02010-4-3	46	EK 01024-1-1
22	CSR02012-2-3	47	EH96049-2
23	EH011089-3	48	EK 01021-4-1
24	EK 01019-2-1	49	ET 07005-1
25	Numan (S.C)		

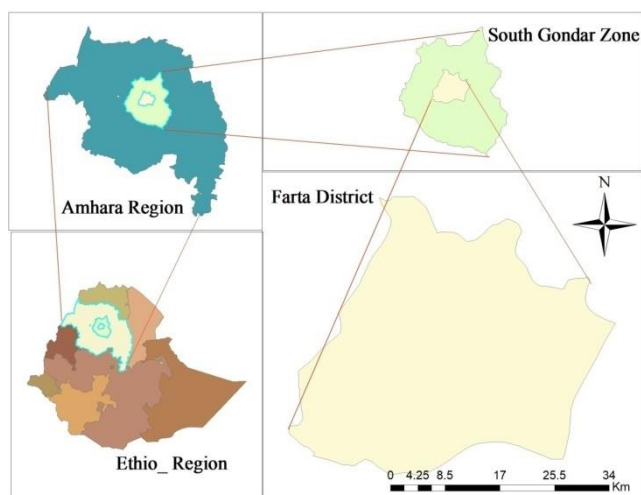


Figure 1. Map of the study area.

## 2.3. Data Analysis

### 2.3.1. Estimation of Correlation Coefficients

Correlation between the traits was estimated using R software (R version 4.1.0, 2021) package “Variability” version 0.1.0. Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by [11] from corresponding variance.

$$\text{Phenotypic correlation coefficient } (r_{p_{xy}}) = \frac{\sigma_{p_{xy}}}{\sqrt{\sigma_{p_x}^2 * \sigma_{p_y}^2}}$$

Where,  $r_{p_{xy}}$  = phenotypic correlation coefficient between character x and y

$$\text{Genotypic correlation coefficient } (r_{g_{xy}}) = \frac{\sigma_{g_{xy}}}{\sqrt{\sigma_{g_x}^2 * \sigma_{g_y}^2}}$$

$r_{g_{xy}}$  = genotypic correlation coefficients between character x and y

Phenotypic correlation coefficient was tested for their significance using the formula suggested by [12].

$$t = \frac{r}{\sqrt{\frac{1-r^2}{n-2}}}$$

Genotypic correlation coefficient was tested with the following formula suggested by Robertson (1959)

$$t = \frac{r_{g_{xy}}}{SEr_{g_{xy}}} \text{ where, } SEr_{g_{xy}} = \sqrt{\frac{1-r_{g_{xy}}^2}{2h_x^2 * h_y^2}}$$

$SEr_{g_{xy}}$  = Standard error of genotypic correlation coefficient between character X and Y

$h^2_x$  = heritability for character X

$h^2_y$  = heritability for character y

The calculated absolute t value was test against the tabulated t- value at g-2 degree of freedom for both phenotypic and genotypic correlations. Environmental correlation coefficients was tested at  $\{(g-1)(r-1) - 1\}$  degree of freedom. Where g is the number of genotypes and r is number of replication.

### 2.3.2. Path Coefficient Analysis for Traits Subjected for Analysis

By using R software path coefficient analysis was performed as suggested in [7] with phenotypic and genotypic correlation coefficients to know the direct and indirect effect of yield components on grain yield using the general formula of by considering grain yield per hectare as dependent variable.

$$R_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where,  $R_{ij}$  = Mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients.  $P_{ij}$  = Components of direct effects of the independent character (i) as measured by the path coefficients and  $\sum r_{ik} P_{kj}$  = summation of components of indirect of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown factor will measure as the residual factor ( $P_R$ ), which was calculated as:  $P_R = \sqrt{1 - \sum r_{ij} p_{ij}}$  the magnitude of  $P_R$  indicates how best the causal factors account for the variability of the dependent factor. That is, if  $P_R$  value is small (for instance, nearly zero) the dependent trait considered (grain yield) is fully explained by the variability in the independent characters, whereas higher  $P_R$  value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield).

## 3. Result and Discussions

Estimates of genotypic and phenotypic correlation coefficients were calculated among all quantitative traits studied (Table 2). The study found that the genotypic correlation coefficient had higher values than the phenotypic correlation coefficient for most studied traits, indicating a strong inherent relationship.

### 3.1. Correlation of Traits

Estimates of genotypic and phenotypic correlation coefficients were calculated among all quantitative traits studied (Table 2). The study found that the genotypic correlation coefficient had higher values than the phenotypic correlation

coefficient for most studied traits, indicating a strong inherent relationship.

### 3.1.1. Correlation of Grain Yield and Other Traits

In this finding, seed yield had a significant positive genotypic correlation with plant height ( $r_g = 0.69^{**}$ ,  $r_p = 0.62^{**}$ ), pod per plant ( $r_g = 0.85^{**}$ ,  $r_p = 0.78^{**}$ ), above-ground biomass ( $r_g = 0.73^{**}$ ,  $r_p = 0.63^{**}$ ), harvest index ( $r_g = 0.83^{**}$ ,  $r_p = 0.76^{**}$ ), and hundred seed weight ( $r_g = 0.39^{**}$ ,  $r_p = 0.37^{**}$ ) (Table 2). Based on the finding, the present study genotypes with high plant height, pod per plant, above ground biomass, harvest index and hundred seed weight produce high seed yield. In agreement with these result, [6] reported that seed yield had a positive and significant association with pod per plant and hundred seed weight both at the phenotypic and genotypic level. Likewise, [8] reported similar results between the genotypic correlations of pod per plant, plant height, number of branches per plant, and above-ground biomass with seed yield. The finding of [9] showed that pod per plant and seed per pod had a significant positive correlation with seed yield. Similarly, [5] reported consistent findings with current findings for above-ground biomass, harvest index, pod per plant, and hundred seed weight, both at genotypic and phenotypic levels. Based on this study, seed yield had a significant positive correlation with seed per pod at both genotypic and phenotypic levels ( $r_g = 0.35^*$ ,  $r_p = 0.24^*$ ). A similar finding was reported for seed per pod, which had a significant positive correlation with seed yield at the genotypic level [8]. Likewise [2] suggested that, seed yield had a highly significant and positive correlation with plant height, number of branch per plant, pod per plant, above ground biomass, hundred seed weight and harvest index for both genotypic and phenotypic correlations. Likewise, [4] reported a high and positive correlation between seed yield with plant height, pod per plant, seed per pod, number of branches at Girar Jerse, and thousand seed weights at Degem in 2018. The study indicates a strong positive correlation between certain traits and seed yield, suggesting that any enhancement in these traits could potentially enhance the seed yield of faba beans.

On the other hand, seed yield showed a negative and significant association with days to flowering ( $r_g = -0.28^*$ ,  $r_p = -0.25^*$ ) both at genotypic and phenotypic levels, including grain filling period at the phenotypic level. As shown in Table 2, seed yield also showed a non-significant negative correlation with days to maturity, both at genotypic and phenotypic levels, and grain filling period only at the genotypic level. In the present study, seed yield had a negative significant correlation with grain filling period ( $r_p = -0.23^*$ ) at the phenotypic level, and days to maturity had a negative non-significant correlation with seed yield both at the genotypic and phenotypic levels ( $r_g = -0.15$ ,  $r_p = -0.14$ ), which is similar to the report of [4] only in days to maturity, which showed a non-significant correlation with seed yield. The chocolate spot showed a negative and highly significant correlation with grain yield at both the genotypic and phenotypic

levels. This is in disagreement with the finding of Gizachew Yilma *et al.* (2022), who reported a non-significant and negative correlation between seed yield and chocolate spot. Generally, based on the correlation analysis, seed yield had positive and significant association with pod per plant, harvest index, above ground biomass and plant height.

### 3.1.2. Correlation Between Traits

In the study, days to 50% flowering had a significant positive correlation with days to maturity ( $r_g = 0.3^*$ ) and grain filling period ( $r_g = 0.33^*$ ) at the genotypic level. This indicated that increasing days to 50% flowering would increase days to maturity and the grain filling period. It showed a significant negative correlation with plant height ( $r_g = -0.45^{**}$ ) and biomass yield ( $r_g = -0.39^{**}$ ) at the genotypic level, which indicates that genotypes with the lowest days to flowering had the highest plant height and biomass yield. Days to flowering had a positive, non-significant correlation with traits such as seed per pod ( $r_g = 0.08$ ), hundred seed weight ( $r_g = 0.18$ ), and chocolate spot ( $r_g = 0.25$ ). It also showed a non-significant negative correlation with the number of branches ( $r_g = -0.22$ ), pods per plant ( $r_g = -0.17$ ), and harvest index ( $r_g = -0.13$ ).

At the phenotypic level, days to 50% flowering had a significant positive correlation with days to maturity ( $r_p = 0.24^*$ ) and chocolate spot ( $r_p = 0.21^*$ ), and it showed a highly significant positive correlation with grain filling period ( $r_p = 0.29^{**}$ ). (Dubey *et al.*, 2022) reported there was a significant phenotypic correlation coefficient ( $p < 0.01\%$ ) between days to flowering and days to maturity. [5] reported days to flowering and days to maturity ( $p < 0.05$ ). As represented in Table 2, the days to flowering showed a highly negative and significant correlation with plant height and above-ground biomass yield with  $r_p$  values of  $0.36^{**}$  and  $0.31^{**}$ , respectively. It also had a significant negative correlation with the number of branches ( $r_p = -0.24^*$ ) and seed yield ( $r_p = -0.25^*$ ). [5] reported a significant negative correlation between days to flowering and grain yield. On the contrary, days to flowering exhibited a positive, non-significant correlation with seed per pod and hundred seed weight, as well as a negative, non-significant correlation with the trait pod per plant and harvest index (Table 2).

There was also observed a highly significant positive genotypic correlation between days to maturity and grain-filling period ( $r_g = 0.55^{**}$ ). Days to maturity showed a significant negative correlation with plant height ( $r_g = -0.29^*$ ), while it showed a non-significant negative correlation with pod per plant, seed per pod, above ground biomass, seed weight, and grain yield. On the other hand, it showed a positive non-significant correlation with number of branches, harvest index, and chocolate spot.

Days to maturity showed a positive significant phenotypic correlation coefficient with grain filling period ( $r_p = 0.41^{**}$ ) and a negative significant correlation with plant height and above-ground biomass yield ( $r_p = -0.25^*$ ,  $r_p = -0.2^*$ ) in re-

spective order. On the contrary, days to maturity showed that there was a non-significant negative phenotypic correlation with plant height, pod per plant, seed per pod, harvest index, and seed yield, whereas the number of branches and chocolate spot had a positive, non-significant correlation with days to maturity (Table 2). As the result revealed, the number of branches had a non-significant positive correlation with traits such as days to maturity, plant height, pod per plant, seed per pod, above-ground biomass, harvest index, and hundred seed weight both at genotypic and phenotypic levels, but it had a significant positive correlation with above-ground biomass at the phenotypic level ( $r_p = 0.22^*$ ). It showed a negative significant correlation with days to flowering ( $r_p = -0.24^*$ ) at the phenotypic level and a highly negative significant correlation with chocolate spot, both at the phenotypic level ( $r_p = -0.308^{**}$ ), whereas there was a negative significant correlation with chocolate spot at the genotypic level ( $r_g = -0.33^*$ ). On the other hand, the number of branches had a non-significant negative correlation with days to flowering and grain filling period at the genotypic level, whereas at the phenotypic level, only the grain filling period had a non-significant negative correlation with the number of branches, as represented in (Table 2).

Grain filling period had significant positive genotypic correlation with days to flowering and days to maturity ( $r_g = 0.33^*$ ,  $r_g = 0.55^{**}$ ), respectively. There were a negative significant association between grain filling period and above ground biomass yield ( $r_g = -0.32^*$ ). On the other hand, it had non-significant negative correlation coefficient with number of branch, plant height, pod per plant, seed per pod, harvest index, and hundred seed weight at genotypic level, while it showed a positive non-significant correlation with chocolate spot (Table 2).

At the phenotypic level, the grain filling period had a highly significant correlation coefficient with days to flowering ( $r_p = 0.29^{**}$ ) and days to maturity ( $r_p = 0.41^{**}$ ). As a result of this study, grain filling period had a highly significant negative correlation with above-ground biomass at  $p < 0.01$  ( $r_p = -0.28^{**}$ ) and a significant negative correlation with hundred seed weight at  $p < 0.05$  ( $r_p = -0.24^*$ ). On the contrary, grain filling period had a non-significant negative phenotypic correlation with number of branches, plant height, pod per plant, seed per pod, and harvest index. It also showed a positive, non-significant correlation with the chocolate spot (Table 2).

Plant height showed positive significant correlation with pod per plant, biomass yield and seed yield with  $r_g$  value  $0.7^{**}$ ,  $0.87^{**}$ , and  $0.69^{**}$ , respectively at genotypic level which implies that increase in plant height leads to increase pod per plant, biomass yield and seed yield. Plant height also showed positive and significant correlation with seed per pod ( $r_g = 0.31^*$ ) and harvest index ( $r_g = 0.3^*$ ) at genotypic level. This indicated that genotypes with high plant height had high seed yield and harvest index. The result is inconformity with result obtained by [2] revealed plant height had positive and highly significant correlation with pod per plant, number of

branch per plant, above ground biomass and hundred seed weight. On the other hand, it was also showed that negative and highly significant correlation with days to flowering ( $r_g = -0.45^{**}$ ) and chocolate spot ( $r_g = -0.38^{**}$ ) and negative significant correlation with days to maturity at  $P < 0.05$  ( $r_g = -0.29^*$ ). [2] reported similar finding for the correlation coefficient of plant height and chocolate spot. On the other hand, plant height showed non-significant positive genotypic correlation with number of branch and hundred seed weight and also non-significant negative correlation with grain filling period (Table 2). At phenotypic level, plant height showed positive and highly significant correlation with pod per plant ( $r_p = 0.6^{**}$ ), biomass yield ( $r_p = 0.71^{**}$ ) and grain yield ( $r_p = 0.62^{**}$ ). It also showed that negative and highly significant correlation with days to flowering ( $r_g = -0.36^{**}$ ) and chocolate spot ( $r_g = -0.34^{**}$ ) and negative significant correlation with days to maturity at  $P < 0.05$  ( $r_g = -0.25^*$ ). On the other hand, it showed non-significant positive phenotypic correlation coefficient with number of branch seed per pod, harvest index and hundred seed weight whereas it showed non-significant negative correlation with grain filling period (Table 2).

Pod per plant showed positive and highly significant genotypic correlation with plant height ( $r_g = 0.7^{**}$ ), above ground biomass ( $r_g = 0.83^{**}$ ), harvest index ( $r_g = 0.6^{**}$ ), hundred seed weight ( $r_g = 0.45^{**}$ ) and grain yield ( $r_g = 0.85^{**}$ ). [2] reported similar finding for above ground biomass. Pod per plant showed positive and significant correlation with seed per pod ( $r_g = 0.31^*$ ). Similar result was reported for the correlation coefficient between pod per plant and seed per pod [1]. On the other hand, pod per plant had non-significant and negative association with days to flowering, days to maturity and grain filling period and also it showed positive non-significant association with number of branch as represented in (Table 2). At phenotypic level, pod per plant showed positive and highly significant correlation with plant height ( $r_p = 0.6^{**}$ ), above ground biomass ( $r_p = 0.64^{**}$ ), harvest index ( $r_p = 0.52^{**}$ ), hundred seed weight ( $r_p = 0.4^{**}$ ) and grain yield ( $r_p = 0.78^{**}$ ). Pod per plant showed positive and significant phenotypic correlation with seed per pod ( $r_g = 0.21^*$ ). It also had a negative and highly significant correlation with chocolate spot ( $r_p = -0.41^*$ ). In the otherwise, pod per plant had negative non-significant association with days to flowering, days to maturity and grain filling period and also it showed positive non-significant association with number of branch as represented in (Table 2).

Seed per pod showed positive and significant correlation with plant height ( $r_g = 0.31^*$ ), pod per plant ( $r_g = 0.31^*$ ), harvest index ( $r_g = 0.34^*$ ) and seed yield ( $r_g = 0.35^*$ ) at genotypic and negative and significant correlation with chocolate spot ( $r_g = -0.35^*$ ). Seed per pod had positive highly significant phenotypic correlation with harvest index ( $r_p = 0.27^{**}$ ) and similarly, it had positive and significant correlation with pod per plant and grain yield ( $r_p = 0.21^*$ ,  $0.24^*$ ), respectively whereas chocolate spot had negative and significant correla-

tion with seed per pod ( $rp=-0.25^*$ ). As the result showed, seed per pod had positive and non-significant phenotypic correlation with days to flowering, number of branch, plant height, above ground biomass yield and hundred seed weight and also it had negative and non-significant correlation with days to maturity and grain filling period.

Above ground biomass showed positive and highly significant genotypic correlation with plant height ( $rg=0.87^{**}$ ), pod per plant ( $rg=0.83^{**}$ ), hundred seed weight ( $rg=0.37^{**}$ ) and grain yield ( $rg=0.73$ ) and it showed negative and highly significant association with days to flowering ( $rg=-0.39^{**}$ ) and chocolate spot ( $rg=-0.46$ ). It also had negative and significant association with grain filling period ( $rg=-0.32^*$ ). On the other hand, above ground biomass had positive and non-significant phenotypic correlation with number of branch, seed per pod and harvest index and also it had negative correlation with days to maturity non-significantly (Table 2).

At the phenotypic level, above ground biomass showed positive and significant phenotypic correlation with plant height ( $rp=0.71^{**}$ ), pod per plant ( $rp=0.64^{**}$ ), hundred seed weight ( $rp=0.33^{**}$ ) and seed yield ( $rp=0.63$ ) and it showed negative and highly significant association with days to flowering ( $rp=-0.31^{**}$ ), grain filling period ( $rp=-0.28^{**}$ ) and chocolate spot ( $rp=-0.36^{**}$ ). It also had negative and significant association with grain days to maturity ( $rp=-0.2^*$ ). On the other hand, above ground biomass had positive and non-significant phenotypic correlation with seed per pod and harvest index. Harvest index showed positive and highly significant genotypic correlation with pod per plant ( $rg=0.6^{**}$ ) and seed yield ( $rg=0.83^{**}$ ) and it had positive significant correlation with plant height and seed per pod ( $rg=0.3^*$ ,  $0.34^*$ ), respectively. As the result indicated, harvest index had negative significant correlation with chocolate spot ( $rg=-0.35^*$ ). On the other hand, it showed positive and non-significant correlation with days to maturity, number of branch, above ground biomass and hundred seed weight and also negative and non-significant correlation with days to flowering and grain filling period.

Harvest index had positive and highly significant phenotypic correlation with pod per plant ( $0.52^{**}$ ), seed per pod ( $0.27^{**}$ ) and grain yield ( $rp=0.76^{**}$ ) however it had negative and highly significant correlation with chocolate spot ( $rp=-0.29^{**}$ ). It also had positive significant correlation with hundred seed weight ( $rp=0.2^*$ ). In the contrary, harvest index had negative and non-significant phenotypic correlation with traits such as days to flowering, days to maturity and grain

filling period whereas plant height, seed per pod and above ground biomass had positive non-significant correlation with harvest index (Table 2).

Hundred seed weight had positive and highly significant correlation with pod per plant ( $rg=0.45^{**}$ ), biomass yield ( $rg=0.37^{**}$ ) and seed yield ( $rg=0.39^{**}$ ) and it also had negative and significant with chocolate spot ( $rg=-0.34^*$ ) at genotypic level. Disease significantly reduces yield, while hundred seed weight positively correlates with traits like days to flowering, number of branches, plant height, seed per pod, harvest index, and grain filling period (Table 2). In phenotypic correlation coefficient, hundred seed weight had positive significant correlation with pod per plant ( $rp=0.4^{**}$ ), biomass yield ( $rp=0.33^{**}$ ) and seed yield ( $rp=0.37^{**}$ ) and positive significant correlation with harvest index ( $rp=0.2^*$ ) and it also had negative and highly significant association with chocolate spot ( $rp=-0.31^*$ ) but had significant correlation with grain filling period negatively. Oppositely, hundred seed weight had positive non-significant correlation coefficient with days to flowering, number of branch, plant height and seed per pod but it had negative non-significant correlation with days to maturity.

Chocolate spot had negative and highly significant genotypic association with plant height ( $rg=-0.38^{**}$ ), pod per plant ( $rg=-0.49^{**}$ ), biomass yield ( $rg=-0.46^{**}$ ) and seed yield ( $rg=-0.53^{**}$ ) and significant negative genotypic correlation with number of branch ( $rg=-0.33^*$ ), seed per pod ( $rg=-0.35^*$ ), harvest index ( $rg=-0.35^*$ ) and hundred seed weight ( $rg=-0.34^*$ ) while there was a positive non-significant correlation between chocolate spot and days to flowering, days to maturity and grain filling period at genotypic level. Where as in the case of phenotypic correlation, chocolate spot had a negative and highly significant correlation coefficient with number of branch ( $rp=-0.30^{**}$ ), plant height ( $rp=-0.34^{**}$ ), pod per plant ( $rp=-0.41^{**}$ ), biomass yield ( $rp=-0.36^{**}$ ), harvest index ( $rp=-0.29^{**}$ ), hundred seed weight ( $rp=-0.32^{**}$ ), and seed yield ( $rp=-0.48^{**}$ ) and also had negative and positive significant correlation with seed per pod and days to flowering ( $rp=-0.25^*$ ) and ( $rp=0.21^*$ ) respectively. Chocolate spot had positive non-significant correlation with days to maturity and grain filling period.

Generally, from the result of correlation study positive correlations between traits such as plant height, pod per plant, biomass yield, harvest index, seed weight, and seed per pod indicate that enhancing one trait can lead to enhancing others.

**Table 2.** Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for 12 traits of 49 faba bean genotypes.

Traits	DF	DM	NB	GFP	PH	PPP	SPP	BY	HI	HSW	CS	GY
DF	1	0.33 *	-0.22	0.33*	-0.45 **	-0.17	0.08	0.39 **	-0.13	0.18	0.25	-0.28*
DM	0.24*	1	0.11	0.55 **	-0.29*	-0.16	-0.16	-0.27	0.04	-0.2	0.12	-15
NB	-0.24*	0.11	1	-0.07	0.19	0.13	0.08	0.26	0.2	0.05	-0.33*	0.29 *

Traits	DF	DM	NB	GFP	PH	PPP	SPP	BY	HI	HSW	CS	GY
GFP	0.29 **	0.41 **	-0.07	1	-0.14	-0.23	-0.15	-0.32*	-0.14	-0.25	0.12	-0.23
PH	-0.36**	-0.25*	0.17	-0.12	1	0.7**	0.31 *	0.8**	0.3*	0.24	-0.38**	0.69**
PPP	-0.12	-0.1	0.11	-0.18	0.6**	1	0.31*	0.8**	0.6**	0.45**	-0.49**	0.85**
SPP	0.05	-0.15	0.05	-0.08	0.15	0.21*	1	0.18	0.34*	0.04	-0.35*	0.35*
BY	-0.31**	-0.2*	0.22*	-0.28**	0.71**	0.64**	0.04	1	0.25	0.37**	-0.46**	0.73**
HI	-0.09	-0.02	0.17	-0.12	0.17	0.52**	0.27**	0.06	1	0.23	-0.35*	0.83**
HSW	0.17	-0.19	0.04	-0.24*	0.19	0.4**	0.04	0.33**	0.2*	1	-0.34*	0.39**
CS	0.21 *	0.08	-0.3**	0.13	-0.34**	-0.41**	-0.25*	-0.36 **	-0.29**	-0.3**	1	-0.53**
GY	-0.25*	-0.14	0.27**	-0.23*	0.62**	0.78**	0.24*	0.63**	0.76**	0.37**	-0.48**	1

\*And\*\* indicates significant at 0.05% and 0.01%, respectively

DF =days to flowering; DM = days to maturity; NB= number of branch; GFP= grain filling period; PH = plant height; PPP=pod per plant; SPP=Seed per pod; BY=above ground biomass yield; HI= harvest index; HSW= hundred seed weight; and CS= chocolate spo.

## 3.2. Path Coefficient Analysis

The phenotypic and genotypic correlation coefficients were divided into the corresponding direct and indirect effects through path coefficient analyses. Tables 3 and 4 show the direct and indirect effects of various traits on seed yield that are caused by genotype and phenotypic factors, respectively.

### 3.2.1. Phenotypic Path Coefficient Analysis

In the present study, number of branch, grain filling period, plant height, seed per pod, biomass yield, harvest index and hundred seed weight showed positive direct effect on seed yield at phenotypic level. However, biomass yield and harvest index exerted the maximum positive direct effect (0.705) and (0.695) on grain yield (Tables 3 and 4), respectively. This is in line with this result; Chaurasia *et al.* [5] reported similar results for biomass yield and harvest index. Similarly, [2] observed that traits such as plant height, number of branch per plant, pod per plant, above ground biomass and harvest index had a positive direct effect on seed yield. These highest direct effects of above ground biomass and harvest index on yield suggest a true relationship, and selection based on these traits may give better response for improvement of grain yield in faba bean.

Plant height (0.438), pod per plant (0.369), hundred seed weight (0.18) and number of branch (0.125) exerted a mod-

erate to high indirect effect via above ground biomass and negligible direct effect on grain yield (Table 3). This indicates that the significant positive correlation of these traits with the grain yield at phenotypic levels was due to the indirect effects of these traits on grain yield via biomass yield. The traits days to flowering, days to maturity, pod per plant and chocolate spot had negative direct effects on grain yield but pod per plant had a highly significant positive correlation with grain yield via its indirect effect through biomass yield (0.369) and harvest index (0.362).

### 3.2.2. Genotypic Path Coefficient Analysis

Tesfaye Walle *et al.* [14] classified path coefficients (0.00 - 0.09) negligible, (0.10 - 0.19) low, (0.20 - 0.29) moderate, and (0.30 - 0.99) high and more than 1.00 is very high. Genotypic path coefficient analysis revealed that above ground biomass exerted the highest positive direct effect on seed yield ( $r_g=2.05$ ,  $p \leq 0.01$ ), followed by harvest index ( $r_g=1.265$ ,  $p \leq 0.01$ ), which showed a good relationship between these traits and seed yield (Table 4). This result indicates that the positive and significant correlation of biomass yield and harvest index on seed yield at genotypic levels was due to the direct effects of these traits on the seed yield. The study found that pod per plant and plant height had a negative direct effect on seed yield, but also had a positive association due to the influence of other traits like days to flowering, number of branches, grain filling period, and seed weight.

**Table 3.** Estimates of direct (bold diagonal) and indirect effect (off-diagonal) at phenotypic level for different traits on grain yield and yield components of faba bean.

	DF	DM	NB	GFP	PH	PPP	SPP	BY	HI	HSW	CS	rp
DF	-0.00275	-0.00069	-0.00505	0.00475	-0.01615	0.00042	0.00012	-0.1673	-0.06908	0.0075	-0.00467	-0.25*

	DF	DM	NB	GFP	PH	PPP	SPP	BY	HI	HSW	CS	rp
DM	-0.00068	-0.00728	0.00231	0.00681	-0.01105	0.00035	-0.00036	-0.11838	-0.01572	-0.00831	-0.00188	-0.14
NB	0.00067	-0.00031	0.02077	-0.00125	0.00753	-0.00038	0.00012	0.12533	0.11861	0.00174	0.00657	0.27**
GFP	-0.0008	-0.00116	-0.00159	0.01626	-0.00054	0.00061	-0.00019	-0.14264	-0.0839	-0.01017	-0.00289	-0.23*
PH	0.00101	0.0007	0.00355	-0.002	0.04402	-0.00197	0.00036	0.43857	0.12459	0.00817	0.00732	0.62**
PPP	0.00035	0.0003	0.00243	-0.00303	0.02661	-0.00327	0.00049	0.36967	0.36285	0.01706	-0.00894	0.78**
SPP	-0.00014	0.00043	0.00112	-0.00135	0.00681	-0.00069	0.00233	0.03895	0.19297	0.00191	0.00547	0.24*
BY	0.00081	0.00058	0.00457	-0.00407	0.0339	-0.00212	0.00016	0.70589	0.05259	0.01325	0.00842	0.63**
HI	0.00027	0.00006	0.00354	-0.00196	0.00788	-0.0017	0.00064	0.04305	0.69565	0.00875	0.00631	0.76**
HSW	-0.00049	0.00055	0.00086	-0.00392	0.00852	-0.00132	0.00011	0.17868	0.14414	0.04222	0.00666	0.37**
CS	-0.0006	-0.00024	-0.00639	0.0022	-0.01509	-0.00137	-0.00059	-0.22469	-0.20584	-0.01317	-0.02133	-0.48**

Residual effect=0.0289; DF =days to flowering; DM = days to maturity; NB= number of branch; GFP= grain filling period; PH = plant height; PPP=pod per plant; SPP=Seed per pod; BY=above ground biomass yield; HI= harvest index; HSW= hundred seed weight; and CS= chocolate spot

**Table 4.** Estimates of direct (bold diagonal) and indirect effects (off-diagonal) at genotypic level for different traits on grain yield and yield components of faba bean.

	DF	DM	NB	GFP	PH	PPP	SPP	BY	HI	HSW	CS	Rg
DF	0.05791	-0.05804	0.03822	0.12288	0.30259	0.20355	0.01329	-0.8185	-0.1654	0.01171	0.00852	-0.28*
DM	0.01756	-0.19146	-0.01994	0.20369	0.20017	0.18871	-0.02586	-0.57218	0.05239	-0.01371	0.00426	-0.15
NB	-0.0132	-0.02276	-0.1677	-0.02905	-0.13237	-0.15612	0.0126	0.54796	0.26411	0.00327	-0.01152	0.29*
GFP	0.01956	-0.10719	0.01339	0.36384	0.09584	0.26248	-0.02382	-0.66811	-0.18314	-0.01609	0.00424	-0.23
PH	-0.02606	0.057	-0.03301	-0.05186	-0.67243	-0.80252	0.04971	1.78807	0.38815	0.01559	-0.01294	0.69**
PPP	-0.01041	0.03192	-0.02313	-0.08437	-0.47676	-1.13188	0.04901	1.71622	0.07707	0.02813	-0.01685	0.85**
SPP	0.00495	0.03183	-0.01359	-0.0557	-0.21488	-0.35659	0.15556	0.38122	0.43067	0.00262	-0.01205	0.354 *
BY	-0.02311	0.05341	-0.0448	-0.11851	-0.58619	-0.94707	0.02891	2.05113	0.31744	0.02314	-0.01564	0.73**
HI	-0.00757	-0.00793	-0.03501	-0.05267	-0.20629	-0.68951	0.05295	0.51463	1.26519	0.01483	-0.01218	0.83**
HSW	0.01085	0.042	-0.00879	-0.09368	-0.16782	-0.50961	0.00652	0.75966	0.30032	0.06249	0.01153	-0.39**
CS	0.01455	-0.02407	0.05699	0.0455	0.25667	0.56262	-0.05532	-0.94633	-0.45457	-0.02126	-0.03389	-0.53**

Residual effect=0.056; DF =days to flowering; DM = days to maturity; NB= number of branch; GFP= grain filling period; PH = plant height; PPP=pod per plant; SPP=Seed per pod; BY=above ground biomass yield; HI= harvest index; HSW= hundred seed weight; and CS= chocolate spot

The number of branches per plant positively correlates with grain yield due to its indirect effects on above ground biomass and harvest index. The result was in close agreement with the result obtained by [4] who reported number of branch per plant exerted the negative direct effect on seed yield and exhibited significant positive correlation with grain yield due to their positive indirect effect on seed yield through other traits at Jirar Jerse in 2018. Generally, the current finding with respect to path analysis was partly in

agreement with the result reported by [4] (days to flowering and plant height and pod per plant) at Jirar Jerse and in 2018 and 2019, respectively, whereas at Degem he reported pod per plant exerted negative direct effects on grain yield and also had a positive association with seed yield due to its positive indirect effect through other traits. In general, the study highlights the importance of traits like biomass and harvest index in seed yield improvement, suggesting that considering indirect effects may be more effective.

## 4. Conclusion

The phenotypic and genotypic correlation between grain yield and plant height, number of pods per plant, number of branches per plant, biomass yield, 100-seed weight, and harvest index was highly significant ( $p < 0.01$ ). These findings suggested that these traits could be selected to improve grain yield at the same time. According to path coefficient analysis, harvest index and biomass yield had the highest direct effects on yield both at the genotypic and phenotypic levels, indicating the importance of these traits for indirect selection.

## Abbreviations

EIAR Ethiopian Institute of Agricultural Research

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## Author Contributions

**Solomon Sharie Shferaw:** Conceptualization, Resources, Data curation, Software, Formal Analysis, Funding acquisition, Investigation, Methodology, Writing – original draft, Writing – review & editing

**Wossen Tarekegne:** Supervision, Methodology

## Conflicts of Interest

The authors declare no conflicts of interest.

## References

- [1] Alamir Ayenew, Dejen Bikis, Solomon Sharie, Yasin Taye, and Zewdu Addisu. 2023. Participatory variety selection of fababean (*Vicia faba* L.) for yield and yield components in Gunabegemidir District, North Western Ethiopia. 4 (4): 63–70. <https://doi.org/10.11648/j.scidev.20230404.11>
- [2] Andualem Muche Hiwotu, Alemu Abate, and Fisseha Worede. 2023. Correlation and Path coefficient analysis of yield and yield components of some Ethiopian faba bean (*Vicia faba* L.) accessions, 1–11. <https://doi.org/10.14720/aas.2023.119.1.2911>
- [3] Arya, R. K. 2018. Evaluation of faba bean genotypes for seed yield under haryana conditions. Forage Res, 44(1): 60-62.
- [4] Bullo Neda., Tileye Feyissa., Kifle Dagne and Ermias Assefa. 2021. The study of Morphological characteristics and statistics of the phenotypes and correlation in faba bean (*Vicia faba* L.) Germplasm. Plant Breeding and Biotech, 2021(2).
- [5] Chaurasia H., Arya R. K. and Choudhary R. R. 2022. Genetic variability, correlation and path analysis in faba bean (*Vicia faba*) for yield and its attributing traits under semi-arid conditions. 11(4): 530–537.
- [6] Dewangan N. K., Dahiya G. S., Janghel D. K. and Arya R. K. 2019. Correlation and path analysis in exotic and indigenous types of faba bean for yield and its component traits. August 2020.
- [7] Dewey D. R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 5: 515-518.
- [8] Esho K. B. and Salih, M. M. 2021. Correlation and path coefficient analysis in faba bean (*Vicia faba* L.). Plant cell biotechnology and molecular biology, 22(29-30): 53-62.
- [9] Gizachew Yilma., Gebeyaw Achenef and Temesgen Abo. 2022. Genetic variability and character association of faba bean (*Vicia faba* L.) genotypes, southeastern, Ethiopia. Asian Journal of Research in Crop Science, 7(2), 38-47. <https://doi.org/10.9734/AJRCS/2022/v7i230140>
- [10] Johnson H. W., H. F. Robinson and R. E. Comstock. 1955. Estimation of genetic and environmental variability in soybean. Journal, 47(7): 314-318.
- [11] Miller P. A., Williams J. C. and Robinson H. F. 1958. Variety environmental interaction in cotton variety tests. *Agronomy Journal*, 51: 132-134.
- [12] Sharma J. R. 1998. Statistical and biometrical techniques in plant breeding. New age International limited publishers, New Delhi. Pp. 432.
- [13] Skovbjerg C. K., Angra D., Robertson-Shersby-Harvie T., Kreplak J., Keeble-Gagnère G., Kaur, S., Ecker W., Windhorst A., Nielsen L. K., Schiemann A., Knudsen J., Gutierrez N., Tagkouli V., Fechete L. I., Janss L., Stougaard J., Warsame A., Alves S., Khazaei H., Andersen S. U. 2023. Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. Theoretical and Applied Genetics, 136(5): 1–27. <https://doi.org/10.1007/s00122-023-04360-8>
- [14] Tesfaye Walle, Firew Mekbib, Berhanu Amsalu, and Melaku Gedil. 2018. Correlation and path coefficient analyses of cowpea (*Vigna unguiculata* L.) landraces in Ethiopia. American Journal of Plant Sciences 9(13): 2794–2812.