



## VARIABILITY, SIMILARITY NETWORK AND GENOTYPIC PATH ANALYSIS OF COMMON BEAN YIELD TRAITS

César Pedro<sup>1\*</sup>, Marques Cachisso Bambo Donça<sup>1</sup>, Salva Inácio Somueque<sup>1</sup>,  
 José Eulário Lampi Dique<sup>2</sup>, Edson Candido Bambo<sup>1</sup>, Henriques Victor  
Colial<sup>1</sup>, Diocleciano Calton Alexandre<sup>1</sup>, Sabir Tualibo Gimo<sup>1</sup>, Belarmino  
Amadeu Faife Divage<sup>1</sup>, Delénia Margarida Rodrigues Rico<sup>3</sup>, Ivan de Paiva  
Barbosa<sup>4</sup>, Vivaldo Felizmino<sup>1</sup>, Ramiza Inácio Serrote<sup>1</sup>, Yasser António Alfina  
Moisés<sup>5</sup>, Nikson Rafael Amós<sup>1</sup>

*1 Instituto de investigação Agrária de Moçambique-Centro Zonal Nordeste (CZnd),  
Leguminosas, Av. FPLM. Estrada de Corrane, Km 7, C.P.622. Nampula, Moçambique;*

*2 Instituto de investigação Agrária de Moçambique-Centro Zonal Centro (CZC),  
Leguminosas,; Estrada nacional no 6, C. P. 42.Manica –Mozambique;*

*3 Universidade Federal de Lavras, Nutrição e Saúde, Aqueça Sol, Lavras - MG, CEP37200-  
900, Brasil;*

*4 Universidade Federal de Viçosa, Departamento de Agronomia, Avenida Peter Henry Rolfs,  
s/no, Campus Universitário, CEP 36570- 000 Viçosa, MG, Brazil;*

*5 Universidade Mussa Bin Bique, Nampula, Ciências Agrárias, U/C Mualhaco, Estrada  
Nacional N°:104, km – 10, Nampula - Nametil, Moçambique.*

*\* Corresponding author: César Pedro ([cpedroscentia@gmail.com](mailto:cpedroscentia@gmail.com)).*

**Abstract:** The objective of this research was to evaluate the genetic variability and associations between traits, in order to identify traits that can be used as selection criteria in the development process of high-yielding common bean cultivars in a breeding program. Plant height (PH), primary branches per plant (BP), pod length (POL), seeds per pod (SPO), pods per plant (POP), days to anthesis (DA), days to flowering (DF), days to maturity (DM), 100 seeds mass (SM) and grain yield (Y), were evaluated at Nampula Research Station, Mozambique, an augmented block design with 24 accessions, three checks and four blocks. Analysis of variance, genetic parameters, similarity network and path analysis were performed based on the genetic correlation matrix. The results indicated high heritability for all traits. High genetic variability were shown by PH, Y, POP, SM, SPO and BP. High genotypic correlations were shown by POP, SPO, DM, DA and BP. The POP and SPO additionally showed high positive direct effects and can be used as selection criteria in the development process of high-yielding bean cultivars in a breeding program.

**Keywords:** *Phaseolus vulgaris*, genetic parameters, correlation, heritability.

## Introduction

The common bean (*Phaseolus vulgaris L.*) is an annual species, belonging to the Fabaceae family. It is one of the most important grain legumes for direct human consumption worldwide (ECPGR,2022). In Mozambique, are important staple food and source of dietary protein for rural and urban house holds. In addition, fresh and dry grains represent a major commercial value for small farmers.

Despite the notorious socio-economic importance, the grain yield ( $\text{kg ha}^{-1}$ ) reached by farmers in Mozambique is around 533.8 (MADER, 2021), considered low compared to the average yield of some major producing countries such as China: 1744.1, United Republic of Tanzania: 1343.7, Myanmar: 911.6 (FAOSTAT, 2020) and Brazil: 1.113 (CONAB, 2022). The low yield in Mozambique can be attributed to several factors, such as poor agricultural techniques, abiotic and biotic stresses and the use of varieties with low genetic potential for yield. This last factor can be increased through genetic improvement. However, is a polygenic trait and very influenced by the environment, which makes it difficult to obtain gains in the direct selection process.

Genetic improvement through direct selection in yield is generally not efficient, with the need to practice indirect selection in its easily measured traits, with high variability, heritability, correlation and direct effect. However, the study of correlations between traits does not allow, *per se*, to show conclusions about cause and effect relationships, that is, the correlation is just a measure of linear association between two traits. The estimated correlation may not represent the true association between two traits, since a high or low association may occur under the influence of a third trait or set of traits (Cruz et al.,2014).

The similarity or correlation network is a multivariate technique that makes it possible to visually explore, through graphs, relationships that occur simultaneously between multiple traits and clusters of correlated traits (Ursem et al., 2008; Epskamp et al., 2012; Leme et al., 2020). In this work, it was used to identify clusters of

traits correlated with each other and with yield, allowing to discard those that are redundant and to increase the selection efficiency in the common bean breeding program. Similar studies carried out and published in Mozambique are scarce, however, several studies in the world, such as Ejara et al. (2017), Oliveira et al. (2018), AlBallat and Al-Araby (2019), Sharma et al. (2019), Medianeira Giroletta dos Santos et al.(2020),Yohannes et al. (2020) and Basavaraja et al. (2021) showed the importance identifying traits of interest that improve the yield of common bean. Studying the variability and relationships between traits is one of the most important steps in the initial genetic improvement program aimed at developing high-yielding varieties. Thus, the objective was to evaluate the genetic variability and associations between traits, in order to identify traits that can be used as selection criteria in the development process of high-yielding common bean cultivars in a breeding program.

## Material and methods

The trial was carried at Nampula Research Station (PAN) ( $15^{\circ}09'01.8''\text{S}$   $39^{\circ}18'47.0''\text{W}$ ) under Mozambique Agricultural Research Institute (IIAM), in the Northeast Zonal Center (CZnd).

Twenty-seven common bean genotypes were evaluated, being 24 accessions and three checks (Table 1) in an experiment with Augmented Block Design (Federer, 1956), with four blocks, through which the following traits were evaluated: plant height (PH), primary branches per plant (BP), seeds per pod (SPO), pods per plant (POP), days to anthesis (DA), days to flowering (DF), days to maturity (DM), 100 seeds mass (DM) and grain yield (Y), according to the methodology of IPGRI (2001).

Sowing was carried out on 25/02/2021, with a density of 10 seeds per linear meter in plots of two meters in length and two rows, spaced 0.5 meters apart. The agronomic management consisted of two weedings, carried out 15 and 30 days after plant emergence. Two foliar fertilization with codafol NPK liquid fertilizer (7-21-7) and two applications of the insecticide

Cypermethrin (Hitcel 44EC) for pest control were carried out at phenological stages V3 and V6. In each plot, the operations of harvesting, drying, threshing and seed selection were carried

out, followed by weighing the 100 seeds mass (SM) in grams and the seed weight converted into grain yield (Y) in kilograms per hectare. All activities were performed manually.

**Table 1.** Twenty-seven (27) common bean genotypes (24 accessions and three checks) from Nampula, Centro Zonal Nordeste (CZnd), Mozambique.

ID	ACCESSES	ID	ACCESSES	ID	ACCESSES	ID	ACCESSES
1	CZnd01	8	CZnd08	15	CZnd17	22	CZnd26
2	CZnd02	9	CZnd09	16	CZnd18	23	CZnd27
3	CZnd03	10	CZnd11	17	CZnd20	24	CZnd29
4	CZnd04	11	CZnd12	18	CZnd21	25	Check1-MAG
5	CZnd05	12	CZnd13	19	CZnd22	26	Check2-CATAR
6	CZnd06	13	CZnd14	20	CZnd23	27	Check3-BRAN
7	CZnd07	14	CZnd16	21	CZnd24	-	-

ID = identification; - = Absent.

To verify the existence of variability in the traits, analysis of variance was performed considering the genotypes as random to obtain the mathematical hopes of the mean squares and estimation of the variance components to obtain the genetic parameters and correlations between traits according to Cruz et al. (2012) and Ramalho et al. (2012).

The significance of the estimates of genotypic correlations was done by t-test at 1 and 5% probability, later they were represented in Heat map to facilitate the reading of the direction and intensity of negative and positive correlations between the traits.

These estimates were used in the construction of the similarity network according to Epskamp et al. (2012) to identify clusters of correlated traits. For better visualization and interpretation, the traits were partitioned into clusters of growth, reproduction, production components and their relationship with the main trait (yield). Negative correlations were represented by red lines, positive correlations were represented by green lines, and line thickness is proportional to the magnitude of the correlation. The lines showed a correlation in modulus greater than 0.3 (cutoff point: 0.3).

The diagnosis of multicollinearity in the matrix of genotypic correlations was made by the method of (Montgomery et al. (2012) to perform the path analysis developed by WRIGHT (1921) which

consists of standardized multiple linear regression, considering a casual chain model. The genotypic correlations were decomposed into a set of coefficients that indicate the direct and indirect effect of the explanatory traits considered as a cause on the main trait (yield), considered as an effect. All analysis were performed using the Genes software (Cruz, 2016).

## Results and discussion

Statistical differences were observed at the level of 0.1, 1 and 5% for all traits (Table 2) inferring the existence of genetic variability and the possibility of selection of common bean accessions with desirable traits for genetic improvement.

For the checks, no variability was observed for the traits BP, DA, DF and SPO. The accessions were different in relation to the checks in the traits BP, DA, DF, DM, SPO and Y and similar in PH, POP and SM. Except for DF, all traits were non-significant with adjusted block variation, indicating homogeneity. The coefficient of variation (CV) for the traits ranged from 1.34% to 15.52% for days to maturity and plant height, respectively, indicating good experimental precision according to PIMENTEL-GOMES (2009).

The genetic parameters of traits that exhibited genetic variability in the material evaluated showed heritability above 80%, which indicates a greater association between phenotypic and genotypic values, while the highest estimates of

GCV were observed in PH, POP, Y and SM, followed by SPO and BP, which indicates greater genetic variability and the possibility of genetic gain in these traits. Similar results were observed

by Basavaraja et al. (2021) who reported high GCV for PH, POP, Y and SM followed by BP and SPO, and high  $h^2$  for PH, DM, DF, SM, Y, POP and SPO.

**Table 2.** Analysis of variance and genetic parameters of nine traits evaluated in 27 common bean (*Phaseolus vulgaris*) genotypes (24 accesses and three checks), in Nampula Research Station, Mozambique, 2021.

Sources of variation	DF <sup>#</sup>	Mean squares								
		PH (cm)	BP	DA	DF	DM	POP	SPO	SM (g)	Y (kg ha <sup>-1</sup> )
Blocks	3	486 <sup>1</sup>	0.42 <sup>1</sup>	9.61	15.45 <sup>2</sup>	12.99 <sup>2</sup>	18.87 <sup>2</sup>	1.02 <sup>2</sup>	86.27 <sup>2</sup>	345164 <sup>2</sup>
Genotypes <sup>+</sup>	26	2344 <sup>3</sup>	0.298 <sup>1</sup>	6.52	6.80 <sup>2</sup>	32.17 <sup>3</sup>	17.87 <sup>2</sup>	0.31 <sup>1</sup>	73.59 <sup>3</sup>	452600 <sup>3</sup>
Checks	2	11538 <sup>3</sup>	0.08	1.08	2.08	82.58 <sup>3</sup>	15.63 <sup>2</sup>	0.02	32.89 <sup>1</sup>	173201 <sup>1</sup>
T and T vs. Checks	24	1578 <sup>3</sup>	0.32 <sup>1</sup>	6.98	7.19 <sup>2</sup>	27.97 <sup>3</sup>	18.05 <sup>2</sup>	0.33 <sup>2</sup>	76.98 <sup>3</sup>	475883 <sup>3</sup>
Blocks <sup>+</sup>	3	185	0.24	1.78	3.67 <sup>1</sup>	0.75	1.66	0.07	3.96	43751
Genotypes	26	2379 <sup>3</sup>	0.32 <sup>1</sup>	7.43	8.16 <sup>2</sup>	33.59 <sup>3</sup>	19.85 <sup>2</sup>	0.42 <sup>2</sup>	83.09 <sup>3</sup>	487379 <sup>3</sup>
Test (T)	23	1682 <sup>3</sup>	0.31 <sup>1</sup>	6.41	8.03 <sup>2</sup>	23.35 <sup>3</sup>	21.06 <sup>3</sup>	0.43 <sup>2</sup>	79.74 <sup>3</sup>	498834 <sup>3</sup>
Test vs. Checks	1	78	0.94 <sup>2</sup>	53.56	23.35 <sup>2</sup>	171.13 <sup>3</sup>	0.49	0.91 <sup>2</sup>	260.41	852252 <sup>2</sup>
Error	6	90	0.064	0.86	0.75	0.92	1.20	0.04	4.02	25804
Overall mean	-	62.51	3.95	25.51	27.92	72.61	10.22	3.91	45.02	1447.15
CV (%)	-	15.17	6.26	3.73	3.17	1.34	10.96	5.52	4.32	11.52
$h^2$ (%)	-	94.83	81.04	85.09	90.49	96.03	94.1	87.29	95.05	94.63
GCV (%)	-	64.02	13.26	8.64	9.58	6.45	43.25	14.17	19.73	44.84
GCV/CV	-	4.28	2.07	2.39	3.08	4.92	3.98	2.62	4.38	4.2

3; 2; 1= significant at 0.1, 1 and 5% probability, respectively; \* = ignoring Blocks; + = eliminating C vs. C; SV= sources of variation; DF = Degree of freedom; CV = coefficient of variation;  $h^2$  = heritability; GCV = genetic coefficient of variation; - = absent. PH = Plant height, BP = Primary branches per plant, DA= Days to anthesis, DF=Days to flowering, DM= Days to maturity, POP = Pods per plant, SPO = Seeds per pod, SM = 100 seeds mass and Y = Grain yield.

Sharma et al. (2019) observed high GCV for Y, SM, PH, POP, BP, SPO and high  $h^2$  for DF, DM, PH and SM, Y and POP. Medianeira Giroletta dos Santos et al. (2020) observed higher GCV estimates for PH, POP, SPO and SM. Yohannes et al. (2020) observed high GCV for POP, Y and SPO and high  $h^2$  for DM, POP, Y and SM. All traits presented estimates of  $GCV/CV \geq 1.0$ , confirming a favorable situation for the practice of the selection process according to Vencovsky and Barriga (1992) and Cruz et al. (2012).

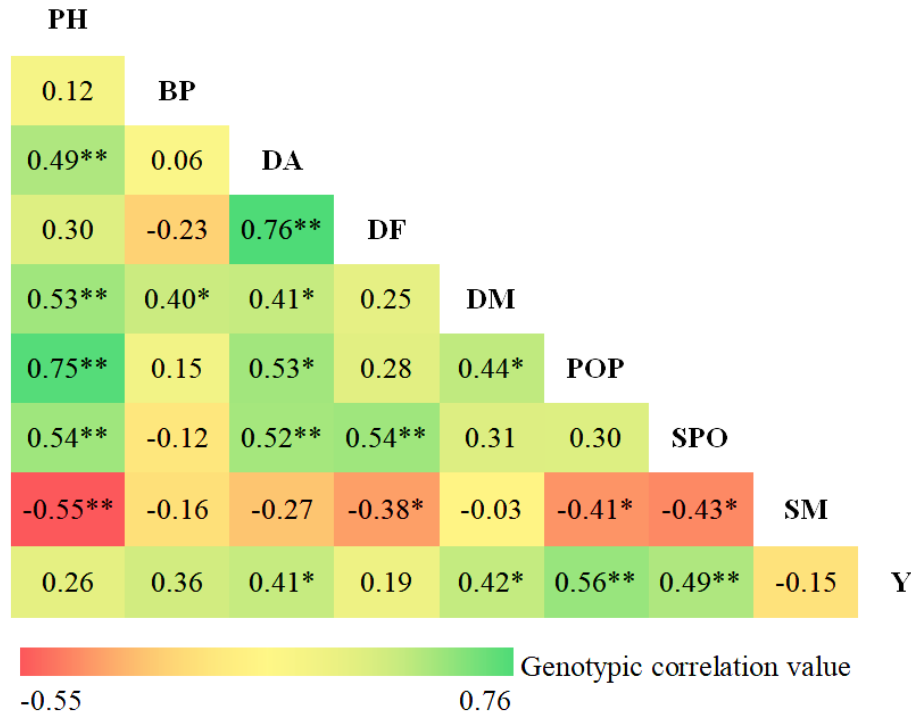
The results of the genotypic correlation between secondary traits and these with yield considered the main trait (Figure1), indicate the traits POP, SPO, DM and DA showed significant positive correlations with Y.

Non-significant correlations were shown by BP, PH and DF. This indicates that plants that produce many pods, have many seeds per pod,

and have a relatively late period for anthesis and maturation can significantly increase grain yield. This expected effect can also be provided by plants that produce many branches, as they have a relatively higher correlation, although it is not statistically significant. The results agree with the genotypic correlations observed by several authors, such as AlBallat and Al-Araby (2019), Sharma et al. (2019) and Yohannes et al. (2020), who observed a positive and significant correlation of Y with POP, SPO and DM. Ejara et al. (2017) observed a positive and significant correlation of Y with SPO and non-significant with BP, PH and DF. Basavaraja et al. (2021) and Medianeira Giroletta dos Santos et al. (2020) observed positive and significant correlations of Y with POP and SPO and non-significant with PH and DF. The SM trait showed a negative and non-significant correlation with Y, indicating that selection in this trait may not cause noticeable changes in the negative direction for

yield. According to AlBallat and Al-Araby (2019), the SM trait showed a negative and significant correlation with Y. Basavaraja et al. (2021) observed a significant positive correlation with Y and Yohannes et al. (2020) observed a

negative and non-significant correlation with Y. The differences between the different studies may indicate that this trait is highly influenced by genetic and environmental factors of the evaluation conditions.



**Figure 1.** Significant genotypic correlation coefficients at 1% (\*\*) and 5% (\*) probability by t-test, evaluated in common bean (*Phaseolus vulgaris*) genotypes (24 accesses and three checks) in Nampula Research Station, Mozambique, 2021. The intense green to light and red to light orange color gradients represent positive and negative correlations, respectively. The strength of the color is proportional to the strength of the correlation. PH = Plant height, BP = Primary branches per plant, DA= Days to anthesis, DF=Days to flowering, DM= Days to maturity, POP = Pods per plant, SPO = Seeds per pod, P100S = 100 seeds mass and Y = Grain yield.

Positive and significant genotypic correlations were observed between the PH trait with DA, DM, POP and SPO. A significant negative correlation was observed between PH and SM. This means that the practice of selection on tall plants implies the selection of genotypes for late flowering and maturation that also produce many pods and seeds per pod. However, this will imply the selection of genotypes with lower seed mass. Similar results were reported by AlBallat and Al-Araby (2019) who observed positive and significant correlations of PH with POP, SPO and DM and significantly negative with SM. Basavaraja et al. (2021) observed positive and significant correlations of PH with POP and SPO and non-significant negative correlations with SM. Sharma et al. (2019) observed positive and significant correlations of PH with POP, SPO and DM and non-significant negative correlations with SM. These authors

observed significant and non-significant negative correlations between PH and MS.

Positive and non-significant correlations were observed between AP with DF and BP. Ejara et al. (2017) also observed a non-significant positive correlation between PH and BP and Basavaraja et al. (2021) observed a non-significant positive correlation between PH and DF. This indicates that selection on tall plants may not provide notable changes for the increase in primary branches, however, the correlation between PH and DF, although not statistically significant, in biological terms, can cause notable changes for late flowering.

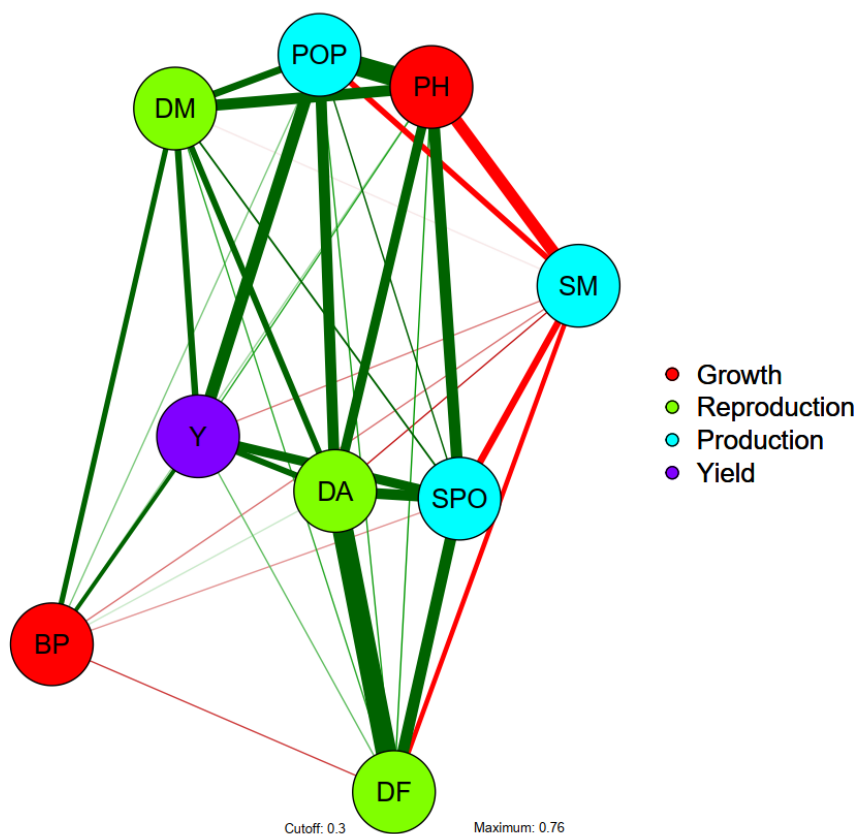
The correlations between BP and DM were significantly positive and between BP with DA and POP were not significant. Negative and non-significant correlations were observed between

BP with DF and SPO. This indicates that selection on plants with many branches can provide plants with late maturation, however, the days for anthesis, flowering, increased production in pods per plant and the reduction in seeds per pod may not be noticeable. Similar results were observed by Ejara et al. (2017), who observed a positive correlation between BP and POP and a non-significant negative correlation between BP and SPO. Sharma et al. (2019) observed a negative and non-significant correlation between BP and DF.

The correlations between DA and DF, DM, POP and SPO, between DF and SPO, between DM and POP were positive and significant. The correlations between DF and DM and POP, between DM and SPO and between POP and SPO presented non-significant correlations, but with a magnitude that may have biological meaning. The

selection of these traits implies obtaining plants with late flowering and maturation, but which can produce many pods per plant and seeds per pod. These traits showed a negative correlation with SM, which may cause a reduction in seed mass, except for DM and BP, which showed a very low negative correlation with SM. Similar results were observed by Basavaraja et al. (2021) who observed non-significant positive correlations between DF and DM and POP and between DM and SPO. Yohannes et al. (2020) observed positive and significant correlations between DF and SPO and between DM and SPO. These same authors observed a significant positive correlation between POP and SPO.

The genotypic similarity network between traits allows visualizing clusters of traits that are highly correlated with each other and with Y as the main trait (Figure 2).



**Figure 2.** Similarity network based on genotypic correlation between growth (red-colored circles), reproduction (green-colored circles), production (blue-colored circles) and yield (violet-colored circle) traits evaluated in common bean (*Phaseolus vulgaris*) genotypes (24 accesses and three checks), in Nampula Research Station, Mozambique, 2021. Link vectors colored green indicate a positive correlation, and those colored red indicate a negative correlation. The greater thickness of the vectors indicates a greater correlation, and lesser thickness indicates less correlation. PH = Plant height, BP = Primary branches per plant, DA= Days to anthesis, DF=Days to flowering, DM= Days to maturity, POP = Pods per plant, SPO = Seeds per pod, P100S = 100 seeds mass and Y = Grain yield.

The traits PH, DA, DF, DM, SPO and POP formed a cluster positively correlated with each other and with Y, indicating that the selection in one of these traits will represent the other traits in the cluster and will positively influence the improvement of grain yield. However, the traits POP and SPO should be preferred, as they have a greater magnitude of correlation with grain yield.

The traits DM, BP, POP and PH formed the second cluster positively correlated with each other and with Y. Furthermore, the POP trait can be recommended as a selection criterion to be preferred. Depending on the objective of improvement, in the first clustering of traits, it is possible to suggest the discard of DA, which is minimized by the presence of DF, as they are

highly correlated traits, with the maintenance of one of them being representative of the genetic structure of the material studied. According to Cruz et al. (2012), the interest in evaluating a smaller number of traits, saves time and work, in obtaining data in the experiment, in addition to reducing the cost of future analysis.

In Table 3, the results of the direct and indirect effects of the traits are presented. The coefficient of determination was greater than the residual effect, indicating that the set of explanatory traits included in the model satisfactorily explained the variations in the grain yield. This shows the existence of a few important traits that can play a critical role in the genetic improvement of the studied material.

**Table 3.** Path analysis based on genotypic correlation ( $r_g$ ) of nine traits evaluated in 27 common bean (*Phaseolus vulgaris*) genotypes (24 accesses and three checks), in Nampula Research Station, Mozambique, 2021.

Traits	Direct effect on		Indirect effect through							
	Y (Kg ha <sup>-1</sup> )	PH (cm)	BP	DA	DF	DM	POP	SPO	SM(g)	$r_g$
PH	-0.95		0.04	0.01	-0.06	0.09	0.72	0.44	-0.03	0.26
BP	0.32	-0.11		0.00	0.05	0.07	0.15	-0.10	-0.01	0.36
DA	0.02	-0.47	0.02		-0.15	0.07	0.51	0.43	-0.01	0.41
DF	-0.20	-0.28	-0.07	0.02		0.04	0.26	0.44	-0.02	0.19
DM	0.17	-0.50	0.13	0.01	-0.05		0.42	0.25	0.00	0.42
POP	0.96	-0.71	0.05	0.01	-0.06	0.07		0.25	-0.02	0.56
SPO	0.82	-0.51	-0.04	0.01	-0.11	0.05	0.29		-0.02	0.49
SM	0.05	0.52	-0.05	-0.01	0.08	0.00	-0.39	-0.35		-0.15

$R^2=0.84$ ;  $\epsilon=0.40$

$R^2$  = Coefficient of determination.  $\epsilon$  = Residual variation. PH = Plant height, BP = Primary branches per plant, DA = Days to anthesis, DF = Days to flowering, DM = Days to maturity, POP = Pods per plant, SPO = Seeds per pod, P100S = 100 seeds mass and Y = Grain yield.

The traits POP and SPO, followed by BP, showed positive direct effects of high magnitude on grain yield along with high correlation, indicating a true genetic relationship to increase grain yield. The traits DA and DM had less positive direct effects and high correlation on grain yield, indicating that direct selection may not provide satisfactory yield gains, however, DA had greater positive indirect effects on yield through POP and SPO and DM through POP. Thus, the simultaneous selection of these traits could provide greater yield gains. According to Cruz et al. (2012) traits with high favorable correlation, but with low direct effect, indicate that direct selection in the auxiliary trait may not provide satisfactory gains in the main trait. In this

case, the best strategy should be the simultaneous selection of these traits, with those whose indirect effects are significant. These results agree with Ejara et al. (2017) who observed greater direct effects on grain yield through SPO, POP and BP. AlBallat and Al-Araby (2019) observed a greater direct effect through SPO and DM and a positive indirect effect through DM. Sharma et al. (2019) observed greater direct effects through POP and BP and a positive indirect effect through DM. Although the PH and DF traits showed a positive correlation with yield, they had greater direct negative effects on grain yield, indicating that these traits are not the main determinants of yield increase and that direct selection based only on these traits can

reduce the grain yield. However, these traits had greater positive indirect effects through POP and SPO, traits of which are highly and positively correlated. Thus, it is recommended to select plants with many pods and many seeds per pod to improve yield. Similar results were observed by AlBallat and Al-Araby (2019) who reported a direct negative effect of DF. Ejara et al. (2017) and Sharma et al. (2019) observed a direct negative effect of PH on grain yield.

Greater negative indirect effects were showed by POP, SPO, DM and DA through PH, indicating that the cause of the greatest indirect negative effect on yield is due to the high positive correlation that these traits have with PH, which in turn has a high direct effect negative on grain yield. Therefore, selection based only on these traits can provide an increase in grain yield and simultaneous selection with PH is not recommended, as it can reduce grain yield. SM had very low positive direct effect and negative correlation, but negative indirect effects through POP and SPO were greater on grain yield. The high magnitude positive indirect effect was exerted through PH. Selection in SM for this material is not recommended to obtain gains in yield, because SM presented a high negative correlation with POP and SPO, which are important traits for increasing yield. Ejara et al. (2017) and AlBallat & Al-Araby (2019) observed a negative indirect

effect of SM. Sharma et al. (2019) observed negative indirect effects of POP and SPO. In general, for the genetic improvement of the yield of the studied material, it is recommended that the selection criteria be based on the direct selection of the POP, SPO and BP traits.

## Conclusion

The traits POP and SPO showed high variability, heritability, correlation and positive direct genotypic effect to be used as selection criteria in the development process of high-yielding common bean cultivars in a breeding program.

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