



Agronomic behavior of broad bean genotypes for the Colombian high andean zone

Comportamiento agronómico de genotipos de haba para la zona altoandina colombiana

David-E Álvarez-Sánchez¹; Benjamin Sañudo²; Claudia Salazar-González³; Carlos Betancourth⁴

ARTICLE DATA

¹ Research professor, Ph.D, Universidad de Nariño, San Juan de Pasto, Nariño, Colombia, daevalvarezsa@udenar.edu.co, <https://orcid.org/0000-0003-3563-2529>

² Researcher professor, Agronomist Engineer, Universidad de Nariño, San Juan de Pasto, Nariño, Colombia, benjaminsañudo@udenar.edu.co, <https://orcid.org/0000-0001-9943-5650>

³ Research professor, Ph.D, Universidad de Nariño, San Juan de Pasto, Nariño, Colombia, claudiasalazarg@udenar.edu.co, <https://orcid.org/0000-0002-5461-2761>

⁴ Research professor, Ph.D, Universidad de Nariño, San Juan de Pasto, Nariño, Colombia, cbet70@udenar.edu.co, <https://orcid.org/0000-0001-6573-4230>

Cite: Álvarez-Sánchez, D.; Sañudo, B.; Salazar-González, C.; Betancourth, C. (2022). Agronomic behavior of broad bean genotypes for the Colombian high Andean zone. *Revista de Ciencias Agrícolas*. 39(2): 175-185. doi: <https://doi.org/10.22267/rcia.223902.190>

Received: June 27 2022.

Accepted: November 26 2022.



ABSTRACT

Broad bean cultivation is considered a productive strategy and a component of food sovereignty in Southern Colombia. Therefore, this study was carried out in order to evaluate twelve promising genotypes and two commercial controls, to expand the improved varieties supply of this legume in the future. For this, an experimental assay was established with 14 treatments and four repetitions. Where, 13 agronomic traits and the reaction to the pathogen *Botrytis fabae* were estimated. The information was analyzed by a simple ANOVA test. Also, a Principal Component Analysis (PCA) was developed with the traits with the highest coefficient of variation. Results showed genetic diversity, with promising genotypes in relation to the controls. The number of stems, flowering days, pod formation days, pods per plant, weight of one hundred seeds, and yield allowed three groups to be identified by PCA. The first one was made up of two controls, the second group characterized by higher yields, and a third group represented by an intermediate yield added to an earliness condition. These results allow the recognition of candidate genotypes to be included into breeding programs and contribute to the crop protection.

Keywords: *Vicia faba* L; *Botrytis fabae* Sard; legumes; diseases; family farming; yield.

RESUMEN

El cultivo de haba en el sur de Colombia es considerado una estrategia productiva y un componente de soberanía alimentaria. Por tanto, esta investigación buscó evaluar doce genotipos promisorios y dos testigos comerciales, para ampliar en el futuro la oferta de variedades mejoradas en esta leguminosa. Para esto, se estableció un cultivo experimental con 14 tratamientos y cuatro repeticiones. En donde, se estimaron 13 variables agronómicas y la reacción al patógeno *Botrytis fabae*. La información de las variables fue analizada mediante ANDEVA simple y se desarrolló un Análisis de Componentes Principales con las variables de mayor

coeficiente de variación. Los resultados evidenciaron diversidad genética, sobresaliendo los genotipos promisorios respecto a los testigos. Las variables número de tallos, días a floración, días a formación de vainas, vainas por planta, peso de cien semillas y el rendimiento, permitieron identificar mediante ACP tres grupos. El primero conformado por los dos testigos, un segundo grupo caracterizado por presentar mayor rendimiento y el tercero caracterizado por un rendimiento intermedio sumado a una condición de precocidad. Estos resultados permiten reconocer materiales candidatos para ser integrados a programas de mejoramiento y contribuir a la protección del cultivo.

Palabras clave: *Vicia faba* L; *Botrytis fabae* Sard; leguminosas; enfermedades; agricultura familiar; rendimiento.

INTRODUCTION

The broad bean is considered one of the first domesticated plant species, and its origin is related to the tenth millennium BC (Babay *et al.*, 2020). One of the distinctive characters of this species is partial allogamy that can vary widely depending on environmental conditions with exogamy rates ranging from 4 to 72% (Brünjes & Link, 2021).

The Near East is its center of origin, from there this crop spread over time to various regions of the world. Where it was adopted under different climatic, edaphic and management conditions, generating genetic variability (Babay *et al.*, 2020; Horque, 2004).

This legume has a protein content between 27 to 34% based on dry matter (Kumar & Kaushik, 2020), and is a source of mineral nutrients, vitamins, and bioactive compounds (Bodner *et al.*, 2018; Salazar *et al.*, 2019).

The inclusion of rotation systems improves soil fertility by symbiosis with *Rhizobium* sp. that allow the fixation of atmospheric nitrogen, and the incorporation of crop residues increases organic matter (Alghamdi *et al.*, 2017; Horque, 2004).

Broad bean is currently grown on all continents, with an estimated area of 2.6 million hectares and a production of 5.4

million tons (FAO, 2020). Colombia produces approximately 7304 tons in 1084 hectares, and Nariño is the department with the largest broad bean area (58%) and production (79%) (MADR, 2021).

In Nariño, broad bean crops are established under different systems, from monoculture in greater extensions to management in miscellaneous arrangements associated with peasant and indigenous populations. The inclusion of this species offers a productive strategy for areas with cold climates and a component of food sovereignty (Álvarez *et al.*, 2021).

Unfortunately, in recent years in Colombia there has been a considerable reduction in the area dedicated to this legume. This is possibly due to the decrease in crop yield levels and a greater incidence and aggressiveness of phytosanitary problems, especially the “chocolate spot”, caused by *Botrytis fabae* Sard. (Olle & Sooväli, 2020; Alharbi & Adhikari, 2020; Álvarez *et al.*, 2021).

In the department of Nariño, for example, in the last decade, the area planted with broad beans was reduced by a third, going from 956ha in 2009 to 630ha in 2019 (MADR, 2021).

Collect and preserving local broad bean resources are necessary to evaluate the

existing genetic variability and the presence of morphological, physiological, health and quality traits of the seed and so to meet the needs of both, the producer, and the market (Salazar *et al.*, 2019; Kumar & Kaushik, 2020).

Therefore, this research was carried out to evaluate twelve promising broad bean genotypes from the working collection of the Plant Health Research Group of the University of Nariño in order to: a) Determine their agronomic behavior; b) Estimate their reaction to the pathogen *B. fabae* and, c) Establish possible groups for future selection.

MATERIALS AND METHODS

This research was developed from October 2020 to May 2021 in the Chaves village of the municipality of Pasto (Nariño-Colombia) at 2473 meters above sea level, located at the coordinates 01°10'20" Latitude N and 77°16'53" West Longitude; with an average temperature of 13°C, average rainfall of 803 mm year⁻¹ and relative humidity 82% (IDEAM, 2021).

The evaluated genotypes corresponded to twelve variants of the Argentina variety (commercial cultivars), from the work collection of the Plant Health Research Group. These genotypes were collected in different municipalities of the department of Nariño since 2017 and recurrently selected for four generations according to their agronomic aptitude and earliness. The regional broad bean varieties Blanca Común and Alpargata were used as controls.

In an area of 1064 m², a Completely Randomized Block design with four repetitions and 14 broad bean genotypes was established.

Each experimental plot had 16 m² and the rows were 4m long. The distance between rows and between plants was 1m and 0.45m, respectively. The useful area per plot corresponded to the two central rows without considering the plants at the ends.

The 13 agronomic traits were evaluated on six plants previously marked in the usable plot. These were flowering period (FD) from sowing until 50% of plants with flowers; number of flower nodes (FN) in the central axis of each plant; flowers per node (FIN); plant height in cm (PH) at pod formation; number of stems per plant (SP); pod formation days (PD) from sowing until pods were visible in 50% of plants; days to harvest maturity (DHM) for which the commercial maturity index of Balderrama *et al.* (2001) was used as a reference; number of pods per plant (PP); pod length (PL) in cm (average of five pods per plant); number of seeds per pod (SEP); fresh yield (FY): harvesting all the plants from the first central row of the useful plot, determining the weight and extrapolating the result to t ha⁻¹; dry yield (DY): harvesting all the plants from the second central row of the useful plot when the seed presented 15% moisture and extrapolating the result to t ha⁻¹; seed length (SL) in cm and weight of 100 grains (W100) in g.

Additionally, after the flowering stage in the last repetition, the chemical control applications of the *Botrytis fabae* were eliminated (active ingredient Carbendazim and Benomyl), evaluating the disease severity on three times on ten plants using the scale proposed by Elwakil *et al.* (2016); where: 0 = no visible infection (0%), 1 = small spots (1 - 15%), 2 = increased number of spots and spread (15 - 30%), 3 = coalescing spots (30 - 45%) and 4 = more than half of necrotic leaf (45 - 100%).

Genotypes were evaluated by simple analysis of variance ($\alpha = 0.05$). If statistical differences were found, and after checking the assumptions, a Tukey mean comparison test was carried out ($\alpha = 0.05$).

In addition, a genotype matrix was constructed with the traits that presented a higher value of variation coefficient, operating the multivariate analysis of Principal Components to group the materials according to their similarity and affinity with the traits studied. The statistical processes were carried out using the R v.4.2 programming language, *Agricolae* and *Factoextra* libraries.

RESULTS AND DISCUSSION

Results showed statistical differences in all agronomic traits, suggesting genetic variability between genotypes. This condition would allow the plant material selection with desirable traits within the collection, raising the possibility of increasing the production and quality of this legume in the future within a region (Kumar & Kaushik, 2020).

Regarding the flowering period (FD) in genotypes 18-L1, 18-L3, 18-L9, 18-L9, 19-L1b and 20-L3, a range from 52 to 59 days was determined, showing a statistical difference with a decrease of 40.4 days in relation to the statistical group in which the two controls were placed and genotypes 18-L2, 20-L4 and 20-L8, corroborating a favorable behavior for this trait within the collection (Table 1).

Flowering is considered one of the most important phenological stages as it establishes the transition from

the vegetative phase to the reproductive phase; therefore, the search for earliness to reduce the crop exposure to different stress conditions is favorable (Alharbi and Adhikari, 2020; Bodner *et al.*, 2018). More so, when high heritability has been reported with the preponderance of additive gene action in controlling earliness characters (El-Abssi *et al.*, 2019).

Worldwide reports expose FD values in European and Asian materials from 47 to 126 days (Alghamdi *et al.*, 2017; Bodner *et al.*, 2018) and in the case of South American varieties, Balderrama *et al.* (2001) and Horque (2004) reported a range between 67 to 111 days, slightly higher to that found in this research.

Associated with the previous trait, in Table 1, materials 18-L1, 18-L2, 18-L3, 19-L1, 20-L4 and 20-L8 showed a statistically higher yield in the number of floral nodes (FN) with a value between 7.2 at 7.7. On the other hand, the number of flowers per node (FPN) was smaller for all the genotypes in relation to the control "Blanca Comun" with an average of 5.8 flowers.

Contrasting the results with Salazar *et al.* (2019), who evaluated 39 broad bean materials collected in Mexico, it was possible to establish that although a higher number of FN was reported with an average of 10.3, there was also a low number of FN with 4.5, which together slightly surpassed the genotypes evaluated in Nariño. At the same time, similarity was found with values obtained by Sozen & Karadavut (2016) in a collection of broad beans from the Mediterranean, region where an average FN of 7.4 and FN of 5.7 were reported.

Table 1. Agronomic traits evaluated in twelve promising broad bean genotypes and commercial controls

Gen.	FD	FN	FPN	PH	SP	PD	DHM
18-L1	54.0 d	7.5 a	5.2 de	1.2 cd	3.8 g	88.0 f	145.0 fg
18-L2	96.2 ab	7.5 a	5.4 bcd	1.2 cd	5.8 b	127.0 b	171.5 b
18-L3	52.0 d	7.2 a	4.8 e	1.1 cd	4.2 fg	81.7 f	144.0 g
18-L4	79.0 c	6.0 bc	4.8 e	0.98 e	4.2 fg	109.7 e	143.5 g
18-L9	59.0 d	6.7 bc	4.3 f	1.2 cd	4.4 ef	87.0 f	147.0 f
19-L1	88.0 bc	7.7 a	5.6 bc	0.96 e	5.2 cd	110.7 e	157.0 e
19-L1b	54.0 d	7.1 ab	4.9 e	1.1 d	3.8 g	81.7 f	143.0 g
19-L7	90.8 b	7.1 ab	5.7 bc	1.2 c	4.9 de	119.2 cd	171.5 b
20-L3	55.7 d	5.6 c	4.5 e	1.1 d	4.7 def	88.0 f	143.0 g
20-L4	94.3 ab	7.5 a	5.3 cd	1.3 b	5.6 bc	128.5 ab	163.0 d
20-L5	88.5 bc	6.7 bc	4.9 e	1.1 cd	6.0 b	123.2 bc	156.0 e
20-L8	91.7 ab	7.4 a	5.2 d	1.1 cd	6.2 a	116.7 d	162.0 d
Alp	101.8 a	5.8 c	5.5 bcd	1.6 a	4.7 def	134.2 a	188.5 a
BCom	92.5 ab	6.8 bc	5.8 a	1.1 cd	4.6 ef	125.0 bc	175.5 c
	78.39	6.92	5.15	1.2	4.87	108.3	157.6
CV (%)	24.0	9.1	8.8	12.5	37.4	17.5	7.5
<i>P</i>	**	**	*	**	**	**	**

In each column, the values followed by different letters are significantly different, according to the Tukey test ($P \leq 0.05$). FD = flowering period; FN = flower nodes; FPN= flowers per node; PH= plant height; SP= stems per plant; PD= pod formation days; DHM= days of harvest maturity; * = $P < 0,05$; ** = $P < 0,01$.

These estimates confirm the broad bean ability for the formation of reproductive structures, which under the conditions of this research presented an average of 139.2 flowers per plant and 1.9 million flowers per hectare; for this reason, the ability to attract pollinating insects in crop establishment areas has recently been assessed.

On the other hand, related to the genotype architecture, the collection showed a plant height (PH) between 0.96 to 1.60m, a range similar to that referred to in Bolivian and Peruvian broad bean materials with values between 1.0 to 2.0 m (Balderrama *et al.*, 2001; Horque, 2004). Genotypes 18-L4 and 19-L1 stand out with a height of less than 1 m, forming an independent statistical group and where

all the materials presented differences with respect to the “Alpargata” control (Table 1).

The above can be explained by the fact that the collection is the product of a recurrent selection through which it was possible to concentrate favorable genes. This made it possible to achieve low-growth genotypes, with an adequate size for mechanical harvesting and with a low risk of overturning.

No clear relationship was found between the plant height and the stems number (SN), as suggested by Alharbi & Adhikari (2020), but high variability was evidenced for this last trait, as reported in different collections (Bodner *et al.*, 2018; Skovbjerg *et al.*, 2020). In Table 1, materials 18-L1, 18-L3, 18-L4 and

19-L1b presented a range between 3.8 to 4.2 stems, statistically outperforming most genotypes, while material 20-L8 with an average of 6.2 stems was established as the most prominent.

However, this trait showed a low value in relation to other reports, where plants with 6 to 10 stems stand out, this possibly has to do with the broad bean adaptation in the Andean region that contrasts with research conducted in locations with a temperate climate (Sozen & Karadavut, 2016; Alharbi & Adhikari, 2020).

It was also determined that in the Argentina variety, on average, 30 days after flowering and 49.3 days later, pod formation (PD) and fresh harvest maturity (DHM) respectively occur, depending of the genotype. Genotypes 18-L1, 18-L3, 18-L9, 19-Lb and 20-L3 showed statistical differences in (PD) with a shorter time compared to the rest of the trial with an average of 85.3 days, highlighting the reduction of 39 and 48 days in relation to the controls Blanca Comun and Alpargata (Table 1).

Genotype 18-L4 in DHM was attached to the previous group, again establishing statistical differences by registering the earliest time for fresh harvest with a reduction of 31 and 44 days compared to Blanca Comun and Alpargata controls (Table 1). This result can be complemented with the Horque (2004) classification, where it is reported that early materials can be harvest in less than 160 days, as occurs in eight genotypes, where two are classified as semi-early with 160 to 170 days. Finally, the controls, together with two genotypes from the collection with a value above 170 days, are classified as late.

The existence of genetic diversity associated with FD, PD and DHM suggests future research opportunities for adapting the earliest and most productive genotypes to the conditions of the second semester in southern Colombia, in order to expand the productive supply and rotation in cold climate zones.

In addition, to analyze number of pods per plant (PP), it was evidenced that this species presents a high level of floral abortion, going from 5.1 flowers to 1.6 pods, which represents an estimated 31% of fruit set. That is why Bodner *et al.* (2018) and Kumar & Kaushik (2020), with similar results, refer to PP as a decisive yield component.

The controls were statistically outperformed by all the promising materials of the Argentina variety. The 18-L2 and 20-L5 genotypes presented statistical differences, with an increase of 40% in relation to the rest of the trial (Table 2). The potential for the selection of productive broad bean materials within the collection was identified by comparing this result with the maximum value of PP reported by other authors, 32.1 (Sozen & Karadavut, 2016), 45.3 (Alghamdi *et al.*, 2017) and 48.2 (Salazar *et al.*, 2019).

On the contrary, no significative difference was observed in relation to the pod length (PL), with a variation between the promising materials of 2.9 cm, with genotype 18-L9 standing out statistically with a length of 13.9 cm (Table 2). Associated with this trait, the number of seeds per pod (SEP) was found to be between 2 to 3 grains, in which again there were statistical differences in genotype 18-L9, with pods providing up to four seeds of adequate commercial size when fresh (Table 2).

Table 2. Agronomic traits evaluated in twelve promising broad bean genotypes and commercial controls (continued).

Gen.	PP	PL	SEP	FY	DY	SL	W100
18-L1	33.6 cd	13.0 b	2.7 bc	14.6 bcd	2.1 bc	2.7 bc	233.0 bc
18-L2	58.0 a	12.2 c	2.2 e	23.0 a	2.7 a	2.9 b	223.9 bcd
18-L3	30.0 d	12.9 b	2.9 ab	13.5 bcd	2.0 bc	2.7 bc	220.3 cd
18-L4	39.7 bcd	12.9 b	2.7 abc	12.9 cde	1.7 cd	2.5 e	174.0 f
18-L9	37.1 cd	13.9 a	3.3 a	16.5 bc	2.1 bc	2.7 cd	220.1 cd
19-L1	43.8 bc	11.2 d	2.2 e	17.5 bc	2.2 b	2.8 b	219.3 cd
19-L1b	29.5 d	12.5 bc	2.5 cde	11.4 cde	1.8 cd	2.6 de	202.9 e
19-L7	52.2 ab	12.6 bc	2.3 e	19.7 b	2.0 bc	2.7 bc	211.0 de
20-L3	36.4 cd	12.5 bc	2.63 bcd	8.5 de	1.9 bc	2.6 de	188.1 f
20-L4	46.3 bc	12.4 bc	2.3 de	16.8 bc	2.2 b	2.8 bc	222.4 bcd
20-L5	58.6 a	11.0 d	2.4 de	18.9 b	2.1 bc	2.6 de	223.8 bcd
20-L8	52.2 ab	12.4 bc	2.3 e	15.5 bcd	2.0 bc	2.7 bc	237.5 b
Alp	3.2 e	10.3 e	1.7 f	1.3 f	1.5 d	3.2 a	276.1 a
BCom	13.4 e	12.0 c	2.2 e	5.8 de	1.4 d	2.9 b	226.3 bcd
	38.1	12.3	2.4	12.7	2.0	2.7	220.4
CV (%)	41.8	7.5	16.1	42.7	16.1	7.4	15.0
<i>p</i>	**	*	**	**	**	**	*

In each column, value followed by different letters is significantly different, according to the Tukey test ($P \leq 0.05$). PP= pods per plant; PL= pod length; SEP= seeds per pod; FY= fresh yield; DY= dry yield; SL= seed length; W100= weight of 100 grains; * = $P < 0.05$; ** = $P < 0.01$.

PL and SEP values were similar to reports for this legume, which indicate an average size for the first trait between 10 to 14cm and for the second a recurring value between 1 to 3 seeds (Horque, 2004; Sozen & Karadavut, 2016; Bodner *et al.*, 2018; Salazar *et al.*, 2019); showing an additive genetic effect therefore, a strict phenotypic selection on these characters has been recommended (El-Abssi *et al.*, 2019).

Fresh yield (FY) and dry yield (DY), summarized in Table 2, expressed a potential gain between 60% and 90% in favor of the promising materials compared with the

controls. In addition, 11 of the 12 promising genotypes showed a 39% higher FY behavior compared to the average yield of Nariño (9.0t ha⁻¹) (MADR, 2021).

Genotype 18-L2 was statistically significant with a yield of 23t ha⁻¹, and the group made up of genotypes 19-L7 and 20-L5 with an average of 19.3t ha⁻¹ exceeded five of the materials evaluated, including the controls (Table 2). In addition, the above materials performed satisfactorily when compared to the experimental FY value of Horque (2004) of 16.3t ha⁻¹.

The difference between materials was lower when measuring the yield on a dry basis, where genotype 18-L2 again presented a statistically superior behavior with 2.67t ha⁻¹ but closer to the general average of 2.09t ha⁻¹ in DY (Table 2). Compared with other investigations, the results found were slightly higher than those reported by Horque (2004), Bodner *et al.* (2018) and Salazar *et al.* (2019), with 2.2, 2.0 and 2.1 t ha⁻¹ respectively, but lower than the value indicated by Balderrama *et al.* (2001) of 2.9t.ha⁻¹.

Regarding yield, it is important to express two aspects; the first one linked to the fact that early genotypes were less productive than the late ones within the collection, confirming what was reported by Bodner *et al.* (2018) and Skovbjerg *et al.* (2020); this should be considered in view of the possibility of having two harvests per year with this type of material.

Secondly, it must be considered that this crop shows a notable proportion of yield variation attributed to the genotype by environment interaction (Alghamdi *et al.*, 2017; Skovbjerg *et al.*, 2020; Brünjes & Link, 2021), reason why the genotypes behavior should continue to be evaluated in advanced generations and multienvironmental trials.

Finally, according to the length and weight of one hundred seeds, it was found that the control, Alpargata, presents statistical differences with the rest of the materials, with a value in SL of 3.23cm and of 276.1g in W100 (Table 2), an expected behavior due to the fact that this variety used as a control stands out for having the largest seed size in Nariño.

The rest of the genotypes with an average size showed in SL a range between 2.48 - 2.87cm

and in W100 174.0 - 237.5g, similar to the results obtained by Álvarez *et al.* (2021) in the region for the Argentina variety, establishing a desirable trait for the dry grain market.

Results show that the tested genotypes have favorable traits for the can be used as selection headers or directly as new cultivars, presenting comparative advantages over the controls due to their higher average yield and precocity.

Each trait analyzed made it possible to demonstrate the genetic diversity of this species and the possibility of incorporating tested genotypes in the production system. In addition, it ratifies the commitment of the peasant and indigenous communities of Nariño that contributed to the protection, selection, and exchange of broad bean materials, aware of the value that this legume represents in the diet and agricultural dynamics, developing in situ conservation processes that allow the identification of promising materials (Álvarez *et al.*, 2021).

Reaction to *Botrytis fabae* Sard. During the research, there was an atypical environmental condition with an average temperature of 16.2°C, relative humidity of 84% and precipitation above 240mm (IDEAM, 2021). This facilitated the disease progression, which affected all the materials. The same happened with Olle & Sooväli (2020), who were able to verify an aggressive spread of *B. fabae* under similar conditions, precipitation was identified as a determining factor in crop damage.

Table 3 shows how ten materials presented an average degree of severity lower than 1, including the commercial control “Alpargata” and “Blanca comun”, with which the farmer is familiar for field management. However,

genotypes 18-L1, 18-L3, 20-L3 and 18-L9 showed greater susceptibility to the disease, reaching 30% damage to the leaflet surface in some repetitions.

Except for genotype 18-L1, high severity values were related to medium or low yield values, in addition to lower seed size and weight. This behavior can be explained by the foliar area reduction during pod filling, affecting the production of photoassimilates and translocation to the pods and seeds in the plant (Olle & Sooväli, 2020).

The earliest genotypes were the most affected by the disease, possibly because the state of highest susceptibility of the plant that is the beginning of flowering and flowering (El-Komy *et al.*, 2015), would coincide with favorable conditions for the pathogen such as high relative humidity and precipitation (El-Abssi *et al.*, 2019; Kumar & Kaushik, 2020), and the suppression of the fungicides that controlled *B. fabae*.

However, it cannot be ruled out that there is susceptibility related to physiological factors of the genotypes. This has been reported by El-Abssi *et al.* (2019), who evaluated broad bean

parentals and hybrids with an early condition, which showed greater susceptibility to the disease than late controls, without further study of this finding.

Despite this, genetic selection to face this biotic stress is considered to be the most cost-effective and environmentally friendly method, with successful cases of partial resistance to chocolate spot in Europe (El-Komy *et al.*, 2015; El-Abssi *et al.*, 2019; Olle & Sooväli, 2020). That being said, it is important to continue evaluating materials, particularly 18-L2, 18-4, 19-L7 and 20-L4, where the severity was lower than the rest of the trial, even with high pressure from nearby treatments.

Principal component analysis. With the use of traits with a coefficient of variation greater than 15%, two components were generated, which explained 91.6% of the total variance. In CP1 (50.23%), were represented the yield components, number of seeds per pod and stems per plant, in addition to the phenological traits that indicated the beginning of the flowering and pod formation phases. On the other hand, CP2 (41.28%) grouped the yield components, number of pods per plant, as well as FY and DY.

Table 3. Average reaction to *Botrytis fabae* in the evaluation of twelve promising bean genotypes and commercial controls.

Genotype	Degree of severity	Genotype	Degree of severity
18-L1	1.33 a	19-L7	0.22 b
18-L2	0.47 b	20-L3	1.03 a
18-L3	1.18 a	20-L4	0.27 b
18-L4	0.27 b	20-L5	0.40 b
18-L9	1.00 a	20-L8	0.40 b
19-L1	0.53 ab	Alp	0.33 b
19-L1b	0.67 ab	BCom	0.33 b

Values followed by different letters are significantly different, according to the Tukey test ($P \leq 0.05$).

In Figure 1, the biplot showed on the four quadrants the relationships between traits and the pattern of arrangement of the broad bean genotypes, indicating a substantial amount of genetic diversity in the collection by presenting dispersion in the materials. Jointly from this methodology, a configuration of three groups represented with different colors was evidenced.

A positive association between FD, PD, W100 and SP was also reported by Bodner *et al.* (2018) and Skovbjerg *et al.* (2020), who identified that the onset of the reproductive phase and pod formation are strongly correlated, and that the prolongation of the reproductive phase is associated with higher seed weight gain. In addition, Alharbi & Adhikari (2020) reported that greater plant branching increases the ability to capture solar radiation, which affects grain production, especially in terms of weight gain.

Same occurred with PP, FY and DY, where there was a positive relationship, similar to the behavior found in other research, which

suggests that the broad bean genotypes with the highest yield are characterized by a high number of pods per node and per plant, considering this trait as significant for early genotype selection (Bodner *et al.*, 2018; Sozen & Karadavut, 2016; Alharbi & Adhikari, 2020).

Finally, SEP generated an inverse relationship with FD and PD, suggesting that in this legume, the shorter the vegetative and flowering period, the more seeds the plant produces, but in turn regulated by the compensation in size. This behavior is supported by Bodner *et al.* (2018) in the plant's ability to decrease sink competition for nutrients and the species' need for increased seed viability.

Now, regarding the broad bean materials disposition, the controls *Alpargata* and *Blanca común* were placed at the upper of the CP1 axis, revealing that they were substantially different from the rest of the genotypes of the Argentina variety. Among other traits the controls, they were the latest, with higher seed weight and low yield, the latter associated with low values in SP, PP and SEP.

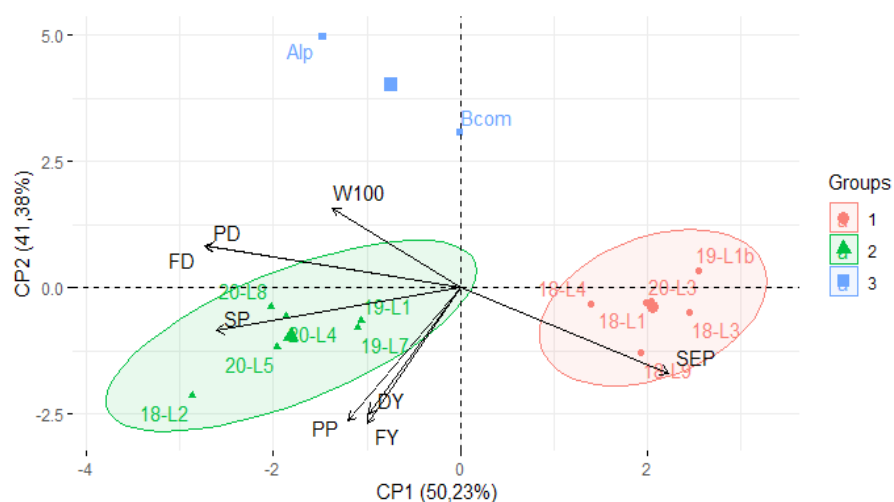


Figure 1. Biplot of bean traits and genotypes in the factorial plane of axes 1 and 2.

In a second group were genotypes 18-L2, 19-L1, 19-L7, 20-L4, 20-L5 and 20-L8, which presented a high number of stems per plant, an intermediate value in flowering time and pod formation and the highest yield within the collection. The reason why these six materials could be considered as candidates to integrate a yield improvement program.

At the right end of CP2 axis, the third group defined by genotypes 18-L1, 18-L3, 18-L4, 18-L9, 19-L1b, and 20-L3 was formed, which had the highest number of seeds per pod, an intermediate value in production, and the identification of genotypes with the shortest period between sowing and flowering is emphasized here. This third group allows selecting candidate materials to integrate an early improvement program, looking for genotypes that can be included in one-semester rotation systems.

These results broaden the knowledge on the genetic diversity associated with the broad bean crops in southern Colombia, suggesting the possibility of obtaining higher yield varieties with better architecture, shorter vegetative time, less affectation to *B. fabae*, with acceptable commercial characteristics. In this way, the availability of broad bean materials used by farmers can generate a local conservation strategy that limits the loss of this important legume in cold climate systems.

CONCLUSIONS

Promising broad bean genotypes showed superior performance in relation to commercial varieties traditionally produced in southern Colombia. Moreover, the formation of two groups due to productivity

(18-L2, 20-L5, 20-L4, 20-L8, 19-L7, 19-L1) and earliness (19-L1b, 20-L3, 18-L3, 18-L4, 18-L1, 18-L9) traits allow the establishment of conservation actions and providing useful germplasm sources for an improvement program in this legume.

A differential reaction to the pathogen *B. fabae* was found within the promising bean genotypes, establishing a lower level of severity in the test for genotypes 19-L7, 18-L4, 20-L4, 18-L2, 20-L5 and 20-L8, which should be further investigated in future research.

ACKNOWLEDGMENTS

The authors thank the “Formación del talento humano de alto nivel para el fortalecimiento de necesidades estratégicas de CTeI del departamento de Nariño” program and CeIBA Foundation.

Conflict of interests: The authors declare that there is no conflict of interest.

BIBLIOGRAPHIC REFERENCES

- Alghamdi, S.S.; Al-Faifi, S.A.; Migdadi, H.M.; Al-Rowaily, S.L.; El-Harty, E.H.; Farooq, M. (2017). Genetic diversity and field performance of mung bean, faba bean and lentil genotypes in the Kingdom of Saudi Arabia. *International Journal of Agriculture and Biology*. 19(4): 689-696. doi: <https://doi.org/10.17957/IJAB/15.0336>
- Alharbi, N.H.; Adhikari, K.N. (2020). Factors of yield determination in faba bean (*Vicia faba*). *Crop and Pasture Science*. 71(4): 305-321. doi: <https://doi.org/10.1071/CP19103>
- Álvarez, D.; González, C.; Sañudo, B.; Betancourth, C. (2021). Evaluación fenotípica de semillas de haba (*Vicia faba* L.) colectadas en Nariño-Colombia. *Rev. U.D.C.A Act. and Div. Cient.* 24(2): 1-30. doi: <https://doi.org/http://doi.org/10.31910/rudca.v24.n2.2021.1874>

- Babay, E.; Khamassi, K.; Sabetta, W.; Miazzi, M.M.; Montemurro, C.; Pignone, D.; Danzi, D.; Finettisialer, M.M.; Mangini, G. (2020). Serendipitous in situ conservation of faba bean landraces in Tunisia: A case study. *Genes*. 11(2): 1-12. doi: <https://doi.org/10.3390/genes11020236>
- Balderrama, F.; Iriate, V.; Barea, O.; Iporre, G.; Carrasco, E. (2001). Cadena Agroalimentaria del Haba de Altura para Exportacion. Recuperado de <https://www.proinpa.org/web/download/cadena-agroalimentaria-del-haba-de-altura-para-exportacion/>
- Bodner, G.; Kronberga, A.; Lapse, L.; Olle, M.; Vågen, I.M.; Rabante, L.; Fernández, J.A.; Ntatsi, G.; Balliu, A.; Rewald, B. (2018). Trait identification of faba bean ideotypes for Northern European environments. *European Journal of Agronomy*. 96: 1-12. doi: <https://doi.org/10.1016/j.eja.2018.02.008>
- Brünjes, L. and Link, W. (2021). Paternal outcrossing success differs among faba bean genotypes and impacts breeding of synthetic cultivars. *Theoretical and Applied Genetics*. (134): 2411-2427. doi: <https://doi.org/10.1007/s00122-021-03832-z>
- El-Abssi, M.; Rabie, H.; Awaad, H.; Qabil, N. (2019). Combining ability of earliness, yield, quality and chocolate spot disease for faba bean. *Bioscience Research*. 16(4): 3584-3594.
- El-Komy, M.; Saleh, A.; Molan, Y. (2015). Resistance/susceptibility of faba bean to *Botrytis fabae*: The causal agent of Chocolate spot with respect to leaf position. *International Journal of Agriculture & Biology*. 17(4): 691-701. doi: <https://doi.org/10.17957/IJAB/14.0021>
- Elwakil, M.A.; Abass, M.A.; El-Metwally, M.A.; Mohamed, M.S. (2016). Green chemistry for inducing resistance against chocolate spots disease of faba bean. *Journal of Environmental Science and Technology*. 9(1): 170-187. doi: <https://doi.org/10.3923/JEST.2016.170.187>
- FAO-Food and Agriculture Organization. (2020). Crops and livestock products. Retrieved from <https://www.fao.org/faostat/en/#data/QCL/visualize>
- Horque, R. (2004). Cultivo del haba. Retrieved from http://pgc-snia.inia.gob.pe:8080/jspui/bitstream/inia/740/1/Horque-Cultivo_del_Haba.pdf
- IDEAM-Instituto de Hidrología, Meteorología y Estudios Ambientales. ambientales. (2021). Carta climatológica: Medidas mensuales Pasto, Nariño, Colombia. Retrieved from <http://bart.ideam.gov.co/cliciu/pasto/temperatura.htm>
- Kumar, P.; Kaushik, P. (2020). Evaluation of genetic diversity in cultivated and exotic germplasm sources of faba bean using important morphological traits. *BioRxiv*. January (1): 1-9. <https://doi.org/https://doi.org/10.1101/2020.01.24.918284>
- MADR-Ministerio de Agricultura y Desarrollo Rural. (2021). Participación Departamental en la Producción y en el Área Cosechada de haba. Retrieved from <https://www.agronet.gov.co/estadistica/Paginas/home.aspx?cod=2>
- Olle, M.; Sooväli, P. (2020). The severity of diseases of faba bean depending on sowing rate and variety. *Acta Agriculturae Scandinavica*. 70(7): 572-577. doi: <https://doi.org/10.1080/09064710.2020.1814402>
- Salazar, M.; Pérez, D.; González, A.; Vázquez, L. (2019). Variabilidad fenotípica en colectas de haba provenientes del Valle Toluca-Atlaconulco, México. *Revista Mexicana de Ciencias Agrícolas*. 10(3): 713-727. doi: <https://doi.org/https://doi.org/10.29312/remexca.v10i3.1758>
- Skovbjerg, C.K.; Knudsen, J.N.; Füchtbauer, W.; Stougaard, J.; Stoddard, F.L.; Janss, L.; Andersen, S.U. (2020). Evaluation of yield, yield stability, and yield-protein relationship in 17 commercial faba bean cultivars. *Legume Science*. 2(3): e39. doi: <https://doi.org/10.1002/leg3.39>
- Sozen, O.; Karadavut, U. (2016). Determination of Morphological and Phenological Properties of Faba Beans Grown in Eastern Mediterranean Region of Turkey. *Tarla Bitkileri Merkez Araştırma Enstitüsü Dergisi*. 25(2): 209-217. doi: <https://doi.org/10.21566/tarbitderg.281344>