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Morphological and agronomic characterization of fava bean genotypes (*Phaseolus lunatus* L.) cultivated in the state of Ceará[1]

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A B S T R A C T
The fava bean (*Phaseolus lunatus* L.) is a legume cultivated in all regions of Brazil, especially in the Northeast region, where it has higher production. The objective of this research was to identify the morphological and agronomic characters of 15 bean genotypes cultivated in different municipalities of the state of Ceará, Brazil, to obtain information about the descriptors that may contribute to studies of genetic characterization and variability of this crop. The trials were conducted in the experimental area of the Laboratory of Plant Ecophysiology (ECOFISIO) of the State University of Ceará (UECE), in Fortaleza-CE. 38 descriptors were analyzed for the identification and characterization of the genotypes studied. It was observed that the descriptors weight of one hundred seeds, length and width of the seeds were those that most contributed to the genetic variability of the genotypes analyzed. The genotypes BF 304, BF 308 and BF 312 presented higher values for these parameters, becoming promising genotypes for genetic improvement. The botanical aspects that allowed to differentiate the genotypes analyzed were color and shape of the tegument; color of hypocotyl and cotyledons; texture of the forehead; color of the veins and presence of anthocyanins in the primary leaves; color of the leaf; shape of the central foliage; color of the keel and wings in the inflorescence; shape of the apex, curvature and color of the pod. Thus, it is concluded that the analysis of these descriptors is important in the differentiation and determination of cultivars of fava more productive in the state of Ceará, since there is little information about the genetic diversity and agronomic potential of this crop in Brazil.
Keywords: Multivariate analysis, descriptors, genetic variability.

Caracterização morfológica e agronômica de genótipos de fava (*Phaseolus lunatus* L.) cultivadas no estado do Ceará

R E S U M O
A fava (*Phaseolus lunatus* L.) é uma leguminosa cultivada em todas as regiões do Brasil, sobretudo na região Nordeste, em que apresenta maior produção. O objetivo desta pesquisa foi realizar a identificação dos caracteres morfológicos e agronômicos de 15 genótipos de fava cultivados em diferentes municípios do estado do Ceará, para obtenção de informações sobre os descritores que possam contribuir para estudos de caracterização e variabilidade genética desta cultura. Os ensaios foram conduzidos na área experimental do Laboratório de Ecofisiologia Vegetal (ECOFISIO) da Universidade Estadual do Ceará (UECE), em Fortaleza–CE. Analisaram-se 38 descritores para identificação e caracterização dos genótipos estudados. Observou-se que os descritores peso de cem sementes, comprimento e largura das sementes foram os que mais contribuíram para a variabilidade genética dos genótipos analisados. Os genótipos BF 304, BF 308 e BF 312 foram os que apresentaram maiores valores para estes parâmetros, tornando-se os genótipos promissores para o melhoramento genético. Os aspectos botânicos que permitiram diferenciar os genótipos analisados foram cor e forma do tegumento; cor do hipocótilo e dos cotilédones; textura da testa; cor das nervuras e presença de antocianinas das folhas primárias; cor da folha; forma do folíolo central; cor da quilha e das asas na inflorescência; forma do ápice, curvatura e cor da vagem. Desta forma, conclui-se que a análise destes descritores é importante na diferenciação e determinação de cultivares de fava mais produtivas no estado do Ceará, visto que há informações escassas sobre a diversidade genética e o potencial agronômico desta cultura no Brasil.
Palavras-chave: Análise multivariada, descritores, variabilidade genética.

Introduction

The fava bean (*Phaseolus lunatus* L.), also known as the bean-leaf or lima-bean or broad bean, is a legume of the Fabaceae family that is one of the sources of proteins, carbohydrates, fats, fibers and mineral salts for the population of the Northeast region of Brazil, who usually consume it in the form of green, ripe and dry grains (Gomes et al., 2016; Machado et al., 2022).

Of the genus *Phaseolus*, it is the second economically most important species, with production of approximately 12 thousand tons of grain in Brazil by 2022 (IBGE, 2022). The Northeast region is responsible for 99.6% of this production, with highlighting the states of Paraíba, Ceará, Pernambuco and Rio Grande do Norte (Nunes et al., 2023). The state of Paraíba is the largest national producer of fava beans with an average yield of approximately 200 Kg/ha/year (Granja et al., 2019).

This low productivity, especially in the Northeast region, comes from the absence of technologies that assist in the management of the crop, as well as in planting in consortium with other crops, such as corn (*Zea mays* L.); and the climate uncertainties resulting from precipitation fluctuations in the planting regions (Nunes et al., 2023; Santos et al., 2002).

According to Santos et al. (2002), although the fava bean has a relatively lower consumption compared to common beans (*Phaseolus vulgaris* L.), it has the advantage of having high genetic variability and a greater adaptive capacity to environmental stresses. It grows best in wet and hot tropics, and sandy and clay soils (with a pH range ranging from 5.6 to 6.8) with greater tolerance to drought (Oliveira et al., 2014). Its socio-economic importance for family farming is linked to the self-consumption of this legume within the communities in which it is inserted; it is also a source of income due to the marketing of the surplus of production to intermediaries and at local/regional fairs (Barbosa & Arriel, 2018).

The little attention paid to this culture by researchers, research and extension bodies has contributed to a limited knowledge of the morphological and agronomic characteristics of the crop. The morphological study of fava genotypes is relevant, as it promotes a greater ease in the registration of identification characters of this culture, helping in the search and choice of plants that have better responses as to their productivity associated with cultivation in different environmental conditions (Santos et al., 2002).

In view of this, the objective of this work was to identify the morphological and agronomic characteristics of 15 fava beans (*Phaseolus lunatus* L.) genotypes from different municipalities in the state of Ceará and grown in Fortaleza-CE, to obtain information about the descriptors that can contribute to studies of characterization and genetic variability of this culture.

Material and methods

Location of the Experimental Area

The trials were conducted in the experimental area of the Laboratory of Vegetal Ecophysiology belonging to the Centre of Health Sciences/Course of Biological Sciences of the State University of Ceará-UECE, located in the Campus of Itaperi (latitude 3°47'22.2"S and longitude 38°33'19.8"W) in Fortaleza–CE, in the period February to December/2022.

Climate Characterization

According to the Institute of Research and Economic Strategy of Ceará (IPECE, 2022), the predominant climate in the city of Fortaleza-CE is of the type ‘Tropical hot subhumid’ (with summer-autumn precipitation) and average annual temperature around 26 to 28ºC, with average annual rainfall of 1,378 mm. The rainy season is concentrated in the months of January to May; and the relative humidity of the air holds an average history of 77% (IPECE, 2022; Magalhães & Zanella, 2015). Climate data for the region during the experiment period are shown in Figure 1.

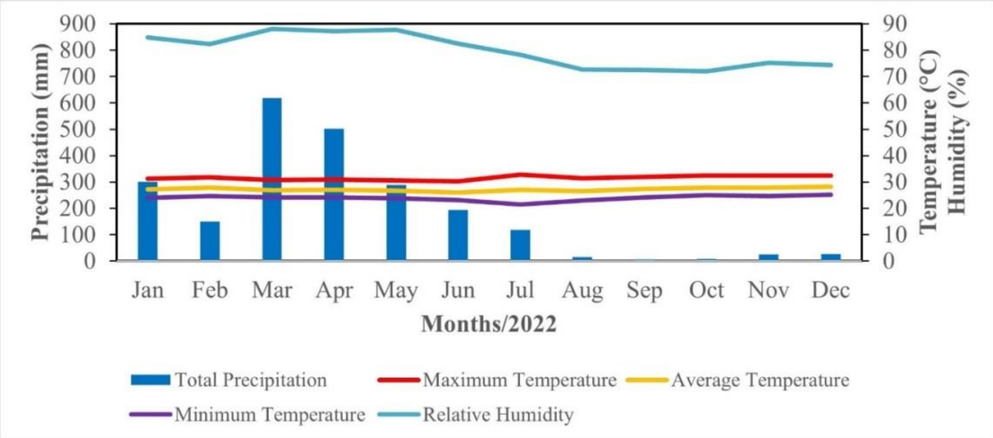

Figure 1. Climatological data for the period of preparation and conduct of the experiment for the municipality of Fortaleza-CE. Source: INMET (2022); FUNCEME (2022).

Experimental Area Preparation, Chemical Characterization and Soil Fertilization

The experimental area for the planting of the fava beans genotypes was divided into 15 beds, of approximately 5 m^2 each. Before planting, the area was fenced for the removal of vegetation that was inside and around the beds. Then 20 soil samples from 15 beds, at a depth of 20 cm, were randomly collected and homogenized in a suitable container, as directed by Melém Junior and Batista (2012). Approximately 500 g of this material was packaged in a plastic bag and sent to the Soil Laboratory of Embrapa Agroindústria Tropical. The result of the soil analysis is available in Table 1.

Table 1. Chemical characteristics, units/values and interpretation of soil analysis.

Chemical Characteristics	**Units/values**		**Interpretation**[1]
pH in Water – soil:water ratio of 1:2:5	-	6.5	Weak acidity
Ca^{2+} (KCl 1M)	$mmol_c/dm^3$	35	Average
Mg^{2+} (KCl 1M)	$mmol_c/dm^3$	10	Average
Na^+ (Mehlich 1)	$mmol_c/dm^3$	1.0	Low
K^+ (Mehlich 1)	$mmol_c/dm^3$	2.9	Low
Al^{3+} (KCl 1M)	$mmol_c/dm^3$	0.0	Not detected
$H^+ + Al^{3+}$ $(CH_3COO)_2Ca \cdot H_2O$ 0.5 M pH 7.1-7.2	$mmol_c/dm^3$	17	Low
Sum of Bases (SB) ($K^+ + Ca^{2+} + Mg^{2+} + Na^+$)	$mmol_c/dm^3$	49	Average
CEC – Cation Exchange Capacity (SB +(H+Al))	$mmol_c/dm^3$	65	Average
Saturation Index by Bases (V) (SB/CEC)*100	%	75	High
Aluminium Saturation Index (m) (Al^{3+}/SB+ Al^{3+})*100	%	0.0	Low
Zn	mg/dm^3	4.7	High
Cu	mg/dm^3	0.6	Low
Fe	mg/dm^3	29	Average
Mn	mg/dm^3	8.3	Average
Organic matter – MO (Walkley-Black)	g/Kg	10.9	Low
Assimilable Phosphorus (P) (Mehlich 1)	mg/dm^3	35.3	Average

[1]Interpretation according to Prezotti e Guarçoni M. (2013).

After interpreting the chemical analysis of the soil, fertilization of each bed was carried out using bovine debris and NPK according to recommendations for the crop (20 t/ha of bovine dust and NPC in the ratio of 9:6:4) and the addition of the micronutrient FTEBR-12 in the proportion of 50 Kg/ha. The calculations were made on the basis of the guidelines for the kidney bean (*Phaseolus vulgaris* L.), since the literature consulted for the state of Ceará does not contain information for the fava bean (*Phaseolus lunatus* L.) (UFC, 1993).

The cultivated fava bean seeds were obtained through the Material Transfer Agreement (ATM) promoted between the Laboratory of Vegetal Ecophysiology of the State University of Ceará (ECOFISIO/UECE) and Embrapa Genetic Resources and Biotechnology (CENARGEN), establishing the exchange of seeds between the institutions. The genotypes used in this research and their collection municipality are described in Figure 2.

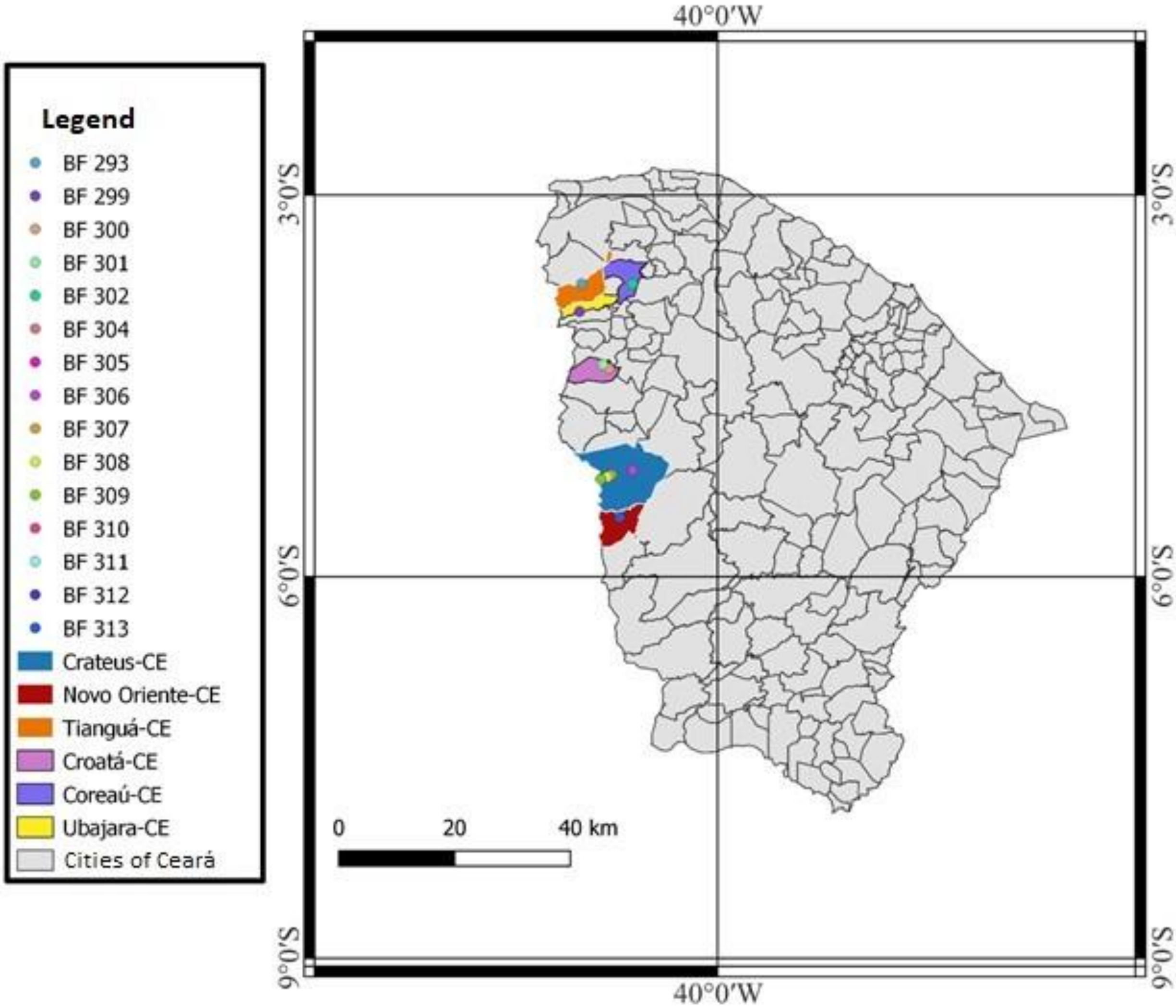

Figure 2. Localization of the fava genotypes of this study.

On the date of planting, each seedbed was divided into two lines containing ten caves each, respecting the space of 50 cm between plants and 80 cm between lines. Each seedbed received only seeds of a single fava genotype, totalling 15 experimental units.

In each of the caves, two corn seeds and two fava bean seeds were added, and one corn plant per cave was cut off 30 days after the sowing-DAS, according to the adapted methodology of the work of Sousa et al. (2020). The irrigation of the crop was performed by micro spraying at a flow of 1.8 L/min for 40 and 60 minutes in the vegetative and reproductive stages, respectively.

Descriptors for morphological identification of Phaseolus lunatus L. *genotypes*

For morphological characterization of the 15 fava beans genotypes that were planted, the descriptors for *Phaseolus lunatus* L. were used as a theoretical reference (IPGRI, 2001), the botanical characterization of wild species of the genus *Phaseolus* L. (Silva & Costa, 2003) and the minimum descriptors indicated for characterizing common bean cultivars/varieties (*Phaseolus vulgaris* L.) (Silva, 2005).

The list of descriptors to be evaluated in this work is in Table 2. The illustrations contained in the Descriptors for *Phaseolus lunatus* L. will be used to determine the Seed Tegument Pattern (STP) and Seed Shape (SS) (IPGRI, 2001), transcribed for this work through Figure 3 and Figure 4, respectively.

The quantitative data were submitted to the variance analysis (ANOVA) and the averages were compared by the Tukey test with a significance level of 5%, with the help of the 'Sisvar' program (Ferreira, 2019). The correlation matrix of quantitative variables was carried out through the software ®Jamovi (Jamovi, 2022) and the multivariate analysis of data and hierarchical grouping through the ®PAST (Palaeontological Statistics) (Hammer et al., 2008). The hierarchical grouping analysis was performed from the genetic distance matrix using the method of unweighted pairs with the arithmetic average (UPGMA), based on their Euclidean distances from all quantitative descriptors described in the linear correlation matrix (Moreira et al., 2009).

Table 2. Descriptors analyzed in the characterization of fava bean genotypes.

Organ of the Plant	Analysed descriptors	Descriptor characterization
Seeds	Background color (BC)	The brightest color of the seed
	Standard color including auréole (SCIA)	If it is bicolor the default color becomes the brightest
	Second default color (SDC)	The darkest color of the pattern
	Seed tegument pattern (STP)	It refers to the different shapes and location of the spots observed on the forehead of the seed
	Seed Shape (SS)	As shown in the descriptor
	Weight of one hundred seeds (WOHS)	Weight of 100 seeds (g) (12-14% moisture)
	Color of the cotyledons (CC)	Verified after emergency
	Hypocotyl color (HC)	Verified after emergency
	Length (L)	Measured with pacemeter (mm)
	Width (W)	Measured with pacemeter (mm)
	Thickness (T)	Measured with pacemeter (mm)
	Coefficient J (CJ)	$LW = \frac{Length}{Width}$
	Coefficient H (CH)	$TW = \frac{Thickness}{Width}$
	Volume (V)	$V = \pi \frac{(L\ x\ W\ x\ T)}{6}$ (mm^3)
	Head texture (HT)	Verified after seed drying
Stem	Pigmentation of the main stem (PMS)	Observed 4–6 weeks after sowing
	Ramification of the stem (RC)	Observed 6 weeks after sowing
	Growth pattern (GP)	Observe whether the plant has a definite or in-definite growth pattern
Leaf	Length of the central follicle (LCF)	Measurement of the 3rd trifoliated leaf (cm) terminal follicle from the base to the tip of the limbo
	Central follicle width (CFW)	Measurement of the 3rd trifoliated leaf (cm) terminal follicle, affixed to the middle part of the limbo
Organ of the Plant	**Analysed descriptors**	**Descriptor characterization**
	Folio shape (LCF/CFW)	Estimated from the ratio between the length and width of the terminal folio of the 3rd trifo-liated leaf

Leaf	Transparent Marks (TM)	Observed along the ribs of the more developed primary leaves
	Primary leaf rib color (PLRC)	Observed on the abaxial side of the leaf
	Presence of anthocyanins pigments in the leaves (PAPL)	Check for purple-colored pigments on the leaves
	Leaf color (LC)	Green Color Intensity
	Leaf Pilosity (LP)	On the inner side of the first leaf expanded from the end
	Leaf Persistence (LP)	Observed when 90% of the pods are ripe
Inflorescence	Quill Color (QC)	End color
	Color of wings (CW)	Open flowers
	Standard color (SC)	Upper part of the banner's interior
	Pilosity of the banner (PB)	Exterior of newly opened flowers
	Opening the wings (OW)	Freshly opened flowers
Fruit	Pod pubescence (PP)	Checked on fully developed immature pods
	Shape of the pod apex (SPA)	Observed in fully developed immature pods
	Pod dehiscence (PD)	Observed in the ripening process - phase R8 of the phenological cycle
	Pod length (PL)	Average (cm) length of 20 mature pods, randomly selected.
	Pod width (PW)	Average (cm) width of 20 mature pods, randomly selected.
	Number of seeds per pod (NSP)	Analyzed when the pods are dry - at stage R_9 of the phenological cycle

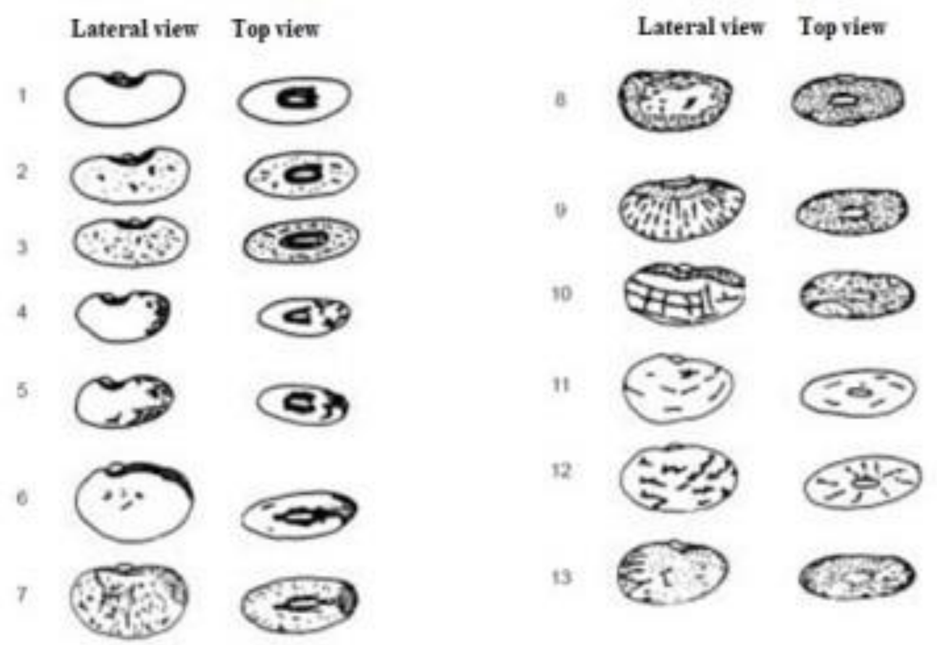

Figure 3: Illustration of the seed coat pattern of *Phaseolus lunatus* L. seeds.
Source: IPGRI (2001).

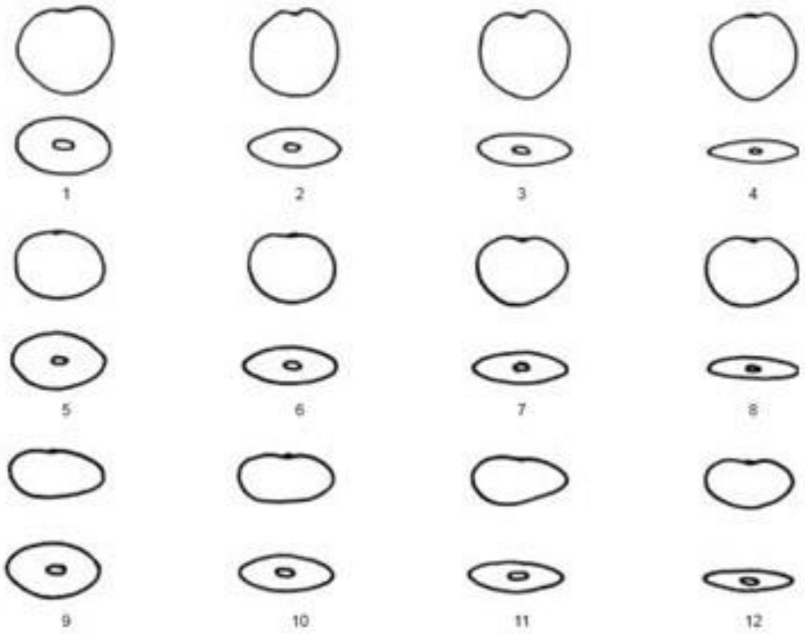

Figure 4: Illustration of the shape of *Phaseolus lunatus* L. seeds.
Source: IPGRI (2001).

Results and discussion

Morphological characterization of the seed

Seed color was measured using the descriptors for *Phaseolus lunatus* L. (IPGRI, 2001). Figure 5 shows an image of the seeds evaluated in this study.

Figure 5: Fava beans seeds used in this study.

Table 3 shows the tegument color of the fava bean seeds. According to Table 1, the majority (40%) of the seeds had a single background color or standard color (lighter color), with a predominance of white color for the genotypes analyzed.

Table 3. Coloration of fava bean seed coat based on botanical descriptors.

Genotype	Standard color or background color (lighter color)	Second standard color (darkest color)
BF 293	White	Absent
BF 299	White	Absent
BF 300	White	Absent
BF 301	Light brown/purple-red	Red-purple/Absent
BF 302	Gray	Black
BF 304	White	Dark brown
BF 305	Brown/light brown	Absent/Absent
BF 306	White	Light brown/orange
BF 307	Gray	Black
BF 308	Grey/red-purple	Red-purple/Absent
BF 309	White	Absent
BF 310	Brown/light brown	Absent/Absent
BF 311	White	Absent
BF 312	Gray	Black
BF 313	White	Absent

These results corroborate the work of Nere et al. (2021), who analyzed the coloring of 70 fava bean cultivars, where around 30% of the genotypes evaluated had white as the only standard color. For genotype BF 301, the presence of seeds with a single standard color (purple-red) and bicolored seeds (light brown and purple-red) was observed. Genotypes BF 305 and BF 310 showed seeds with different colors: some light brown and others brown, without a second standard color.

In the BF 308 fava bean, the seeds were seen to be completely red and gray with red. The BF 312 cultivar has black as a secondary color. In the works by Nobre et al. (2012) and Silva et al. (2015) it is possible to observe a range of colors for the seed coat, namely: white, brown, beige, purple, pink, red, yellow and black; colors compatible with those presented by species of the genus *Phaseolus* (Silva & Costa, 2003).

According to Sandrine et al. (2020) the characteristics of the seeds related to color, shape and size are the ones that most attract the attention of the consumer market, and can be used to differentiate local cultivars. Dantas et al. (2023) states that white and yellowish seeds are more preferred for marketing, as well as cooking fasterand having greater iron availability compared to colored genotypes.

In Brazil, the Ministry of Agriculture, Livestock and Supply (MAPA) classifies beans of the species *Vigna unguiculata* L. Walp. and Phaseolus vulgaris L. as group, class and type based on the color of the integument and the percentage of defects found. These classification standards could serve as a reference for the construction of technical regulations for fava beans (Nere et al., 2021).

As for the pattern of the seed coat (SCP), most of the genotypes had the number 11 (dispersedly marbled body) (Figure 3), and seed shape number nine (Figure 4), as shown in Table 4.

In the research by Chagas et al. (2019), when analyzing the shape of the seeds of ten fava bean genotypes, seed shape number ten was observed for five of the genotypes evaluated. The values five, seven and nine were also present in the study, corroborating the results of this research.

Among the characteristics observed in the plants, it was found that the fava bean seedlings emerged between 4 and 9 days, corroborating the work of Gomes et al. (2016) and had cotyledons and hypocotyls varying in color from green to green and purple, as shown in Table 5.

Table 4. Description of the seed coat pattern (SCP) and Seed Shape (SS) of fava beans.

Genotype	Seed Coat Pattern (SCP)	SCP	SS*
BF 293	Scattered marbling on the body	11	10
BF 299	Scattered marbling on the body	11	11
BF 300	Scattered marbling on the body	11	12
BF 301	Distinct halo with spots on less than 50% of the body	4	5/10
BF 302	Distinct halo with few signs on the body	2	10
BF 304	Distinct halo with spots on less than 50% of the body	4	10
BF 305	Scattered marbling on the body	11	9
BF 306	Pattern only around the aureole	1	9
BF 307	Distinct halo with few signs on the body	2	5
BF 308	Distinct halo with spots on more than 50% of the body	5	9/11
BF 309	Scattered marbling on the body	11	9
BF 310	Scattered marbling on the body	11	9
BF 311	Scattered marbling on the body	11	9
BF 312	Bruised halo in the hilum region and all over the seed	8	9
BF 313	Absent	0	10

Table 5. Morphological characterization of cotyledons, hypocotyls and primary leaves of fava bean genotypes.

Genotype	Color of cotyledons	Hypocotyl color	Forehead texture
BF 293	Green	Green	Moderately wrinkled
BF 299	Green	Green	Flat
BF 300	Green	Green	Flat
BF 301	Green	Green	Flat
BF 302	Green with purple streaks	Purple	Moderately wrinkled
BF 304	Green	Green	Moderately wrinkled
BF 305	Purple/green with purple streaks	Purple	Flat
BF 306	Green/Green with purple streaks	Green and Purple	Moderately wrinkled
BF 307	Green with purple streaks	Purple	Flat
BF 308	Green/Green with purple streaks	Green and Purple	Flat and moderately wrinkled
BF 309	Green	Green	Flat
BF 310	Green with purple streaks	Purple	Moderately wrinkled
BF 311	Green	Green	Moderately wrinkled
BF 312	Green	Green	Moderately wrinkled
BF 313	Green	Green	Flat

Similar results can be observed in the work of Nere et al. (2021) and Frazão et al. (2010) when analyzing fava bean cultivars grown in states in the Northeast region of Brazil. Most of the genotypes analyzed showed a green color for the cotyledons and hypocotyls.

The authors point out that this parameter is relevant in identifying different fava bean genotypes and can influence the color of the inflorescence. For seed texture, the genotypes analyzed ranged from smooth to moderately wrinkled (Table 6). These characteristics were also evaluated in the research by Bria et al. (2019).

The weight of 100 seeds, as well as the biometric parameters of length, width, thickness, volume, J coefficient (CJ), H coefficient (CH) and seed classification (SC), are described in Table 6.

From the data in this table, it can be inferred that there was a significant difference between the genotypes according to the Tukey test at 5% probability.

Table 6. Hundred seed weight (HSW), length (L), width (W), thickness (T), seed volume (SV), coefficient J (CJ), coefficient H (CH) and classification of fava bean seeds.

Genotype	HSW (g)	L (mm)	W (mm)	T (mm)	V (mm^3)	CJ	CH	Seed classification
BF 293	47.3153 f	13.14 def	9.76 de	5.22 e	350.21 fg	1.35	0.53	Spher./Flatt.
BF 299	71.2325 c	17.35 a	11.88 a	5.25 e	566.22 bc	1.46	0.44	Ellípt./ Flatt.
BF 300	64.0966 d	15.56 bc	11.04 b	5.67 cde	509.24 cd	1.41	0.51	Spher./Flatt.
BF 301	27.8512 g	10.67 h	8.17 g	5.57 cd	251.49 h	1.31	0.68	Spher./Flatt.
BF 302	63.8370 d	14.37 cd	10.30 cd	6.54 ab	507.74 cd	1.40	0.63	Spher./Flatt.
BF 304	82.7441 b	17.25 a	11.81 a	6.76 a	721.35 a	1.46	0.57	Ellípt./ Flatt.
BF 305	63.0375 d	14.43 cd	10.66 bc	6.37 abc	512.74 cd	1.35	0.60	Spher./Flatt.
BF 306	54.9489 e	12.95 ef	10.67 bc	5.88 bcde	426.00 def	1.21	0.55	Spher./Flatt.
BF 307	43.7952 f	10.89 h	9.03 f	6.29 abc	324.13gh	1.21	0.70	Spher./semif
BF 308	87.5186 a	17.27 a	11.87 a	6.85 a	735.32 a	1.45	0.58	Ellípt./ Flatt.
BF 309	44.5953 f	12.48 g	9.46 ef	5.25 e	325.90 gh	1.32	0.55	Spher./Flatt.
BF 310	46.9010 f	12.58 g	9.26 ef	6.16 abcd	380.78 efg	1.36	0.67	Spher./Flatt.
BF 311	57.3854 e	14.30 cde	10.56 bc	5.99 bcd	473.78 d	1.35	0.57	Spher./Flatt.
BF 312	74.8916 c	16.57 ab	12.25 a	6.18 abdc	656.29 ab	1.35	0.50	Spher./Flatt.
BF 313	57.9968 e	14.53 c	10.79 bc	5.73 cde	469.84 de	1.35	0.53	Spher./Flatt.
Average	59.2098	14.29	10.50	5.98	480.74			
CV(%)	4.23	3.79	2.59	4.64	7.41			

*Means followed by the same letter do not differ at the 5% probability level using Tukey's test; n = 100 seeds. Abbreviations: Spher.: spherical; Flatt.: flattened; ellipt.: elliptical; semif.: semi-full.

For the weight of 100 seeds, genotype BF 308 had the highest value (87.51 g) and BF 301 the lowest (27.85 g), both differing statistically from the other genotypes. Nunes et al. (2023), when assessing the weight of a thousand seeds of fava bean cultivars, obtained a range of 879.90 to 800.3 g. In the study by 879.90 a 800.3 g. Souza et al. (2019), the authors found values of 58.5 a 29.8 g.

Gonçalves et al. (2019) analyzed eight fava bean cultivars from the Active Germplasm Bank of the Federal University of Piauí (UFPI) and obtained a wide range of mass between the cultivars (84.31 to 39.60 g), which is close to the results of this research. The authors state that fava bean cultivars with a 100-seed weight of more than 60 g have a better market preference because they have larger seeds.

For seed length, it was observed that genotypes BF 299, BF 304 and BF 308 showed the highest values (around 17 mm); corroborating the results of Nunes et al. (2023); and genotypes BF 301 and BF 307 the lowest values (approximately 10 mm), as observed for the genotypes studied in the research by Sandrine et al. (2020). With regard to seed width, the highest values were expressed by genotypes BF 299, BF 304, BF 308 and BF 312; while the lowest value was observed for genotype BF 301; with a range of 12.25 to 8.17 mm, respectively. Asanthe et al. (2007) evaluated the seed width of 31 fava bean genotypes and found variations ranging from 12.5 to 7.0 mm, similar to the results of this study.

In terms of seed thickness, genotypes BF 304 and BF 308 stood out (6.85 and 6.76 mm, respectively); BF 293 (5.25 mm), BF 299 and BF 309 (5.22 mm); presenting the highest and lowest values, respectively, similar to what was observed in the work by Advíncula et al. (2015). In terms of seed volume, genotypes BF 304 and BF 308 stood out for having the largest volumes, while genotype BF 301 had the smallest volume. According to Nere et al. (2021), a positive correlation can generally be observed between the weight of a hundred seeds (PCS) and the linear dimensions (length, width, thickness and volume), as can be seen in Figure 6.

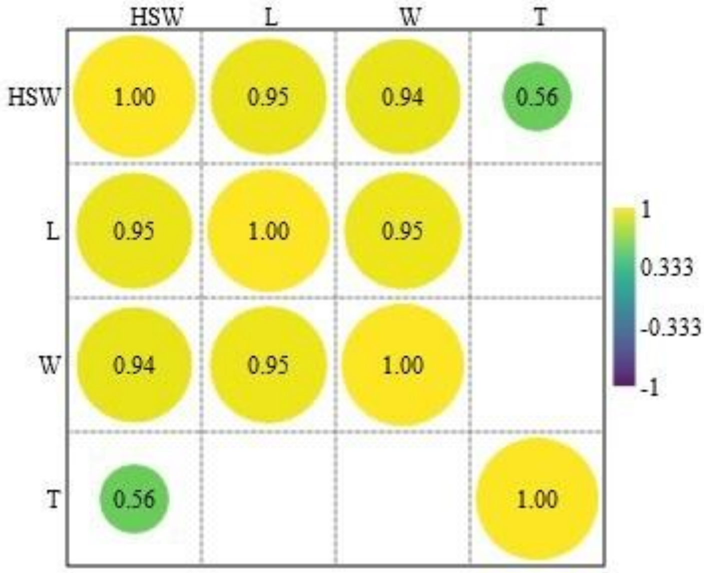

Figure 6. Pearson's correlation between Hundred Seed Weight (HSW) and biometric variables (Length-L; Width-W; Thickness-T).

Asanthe et al. (2007) state that information on the weight of a hundred seeds, as well as linear dimensions, is relevant for distinguishing morphotypes of the *Phaseolus lunatus* L species, making it fundamental in characterization and genetic diversity studies.

By calculating the J coefficient, fava bean seeds can be classified as spherical (1.16-1.42), elliptical (1.43-1.65) and oblong (1.66-2.00). For the H coefficient, they can be classified as flat (<0.69), semi-full (0.70-0.79) and full (>0.80) (Silva, 2005). Most genotypes had spherical and flat seed shapes, corroborating the work of (Silva, 2005). Most genotypes had spherical and flat seed shapes, corroborating the work of Advíncula et al. (2015) and Nere et al. (2021).

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Morphological characterization of the stem

As for the growth pattern, all the fava bean genotypes analyzed had an indeterminate growth pattern of the climbing type, densely branched and with green pigmentation as the predominant color on the stem.

According to Oliveira et al. (2011), plants with a determinate growth habit show complete development of the terminal bud in their inflorescences, causing less growth compared to those with an indeterminate habit, which continue their vegetative development with the opening of new nodes, where new flower buds are emitted, increasing their productivity. Due to these characteristics, fava beans are planted in rainfed conditions in consortium with other crops such as corn, cassava or castor beans, which serve as a support for their growth (Silva et al., 2019).

In the Northeast region of Brazil, small producers tend to use mainly cultivars with an indeterminate growth habit (Carmo et al., 2015; Guimarães et al., 2007).

Morphological Characterization of the Leaf

The color of the veins of the primary leaves, the presence of anthocyanins, the color and persistence of the leaf are described in Table 7. The color of the veins of the primary leaves was predominantly green, as can be seen in Table 7. However, some genotypes were purple. Genotype BF 306 showed both green and purple coloring. Anthocyanins were found in the primary leaves of genotypes BF 302, BF 305, BF 306, BF 307, BF 308 and BF 310. No transparent marks were observed on the veins of the primary leaves of any of the genotypes analyzed. The color of the leaves was dark green and intermediate green; the leaves were hairless (type of glabrous), corroborating the results presented by Medeiros et al. (2016). For most of the genotypes analyzed in this study, at the end of the pod ripening process, most of the leaves remain on the plant.

Table 7. Color of the vein of primary leaves, presence of anthocyanins, color, and persistence of fava bean leaves.

Genotype	Color of the veins on the primary leaves	Presence of anthocyanins in primary leaves	Leaf color	Leaf Persistence
BF 293	Green	Absent	Intermediate green	Intermediate
BF 299	Green	Absent	Dark green	Most of the leaves remain
BF 300	Green	Absent	Dark green	Most of the leaves remain
BF 301	Green	Absent	Dark green	Most of the leaves remain
BF 302	Purple	Present	Dark green	Most of the leaves remain
BF 304	Green	Absent	Dark green	Most of the leaves remain
BF 305	Purple	Present	Dark green	Intermediate
BF 306	Green and Purple	Present	Dark green	Most of the leaves remain
BF 307	Purple	Present	Dark green	Most of the leaves remain
BF 308	Purple	Present	Dark green	Most of the leaves remain
BF 309	Green	Absent	Dark green	Most of the leaves remain
BF 310	Purple	Present	Dark green	Most of the leaves remain
BF 311	Green	Absent	Dark green	Intermediate
BF 312	Green	Absent	Dark green	Most of the leaves remain
BF 313	Green	Absent	Dark green	Intermediate

Similar results can be observed in the work of Medeiros et al. (2016) when they evaluated the morpho-agronomic characteristics of seven fava bean genotypes, as most of the genotypes evaluated showed a green color for the veins of the primary leaves, an absence of anthocyanins and transparent markings. Leaf color ranged from intermediate green to dark green. The length and width measurements in centimeters and the shape of the central leaflet are described in Table 8.

Table 8. Length, width and shape of the central leaf of fava bean genotypes.

Genotype	CLL (cm)	CLW (cm)	CLL/CLW	Leaf shape
BF 293	8.6	6.4	1.34	Round
BF 299	9.9	7.2	1.38	Round
BF 300	9.8	7.8	1.26	Round
BF 301	8.3	5.4	1.54	Ovate
BF 302	9.8	7.0	1.40	Round
BF 304	10.2	7.4	1.38	Round
BF 305	9.7	7.2	1.35	Round
BF 306	9.2	6.3	1.46	Round
BF 307	9.3	6.6	1.41	Round
BF 308	8.6	6.2	1.39	Round
BF 309	9.7	6.3	1.54	Ovate
BF 310	9.5	6.4	1.48	Round
BF 311	8.9	6.1	1.46	Round
BF 312	9.9	7.2	1.38	Round
BF 313	9.5	6.3	1.51	Ovate
Average	9.4	6.6		
CV(%)	6.0	9.4		

Most of the genotypes analyzed had a rounded leaf shape. Leaf length and width measurements ranged from 8.3 to 10.2 cm and from 5.4 to 7.8 cm, respectively.

These results are in line with research by Nere et al. (2021), where around 30% of the cultivars analyzed had a round leaf shape, with a frequency distribution of over 40% for genotypes with a length of 8.93 cm and 50% for a width of 5.04 cm.

Morphological Characterization of the Flower

Table 9 describes the fava bean genotypes in terms of the following characteristics of the inflorescence: the color of the keel, wings and banner; the hairiness of the banner and the opening of the wings.

Table 9. Color of the keel, wings and banner; hairiness of the banner and wing opening of fava bean genotypes.

Genotype	Keel color	Color of wings	Banner color	Banner Pilosity	Opening the wings
BF 293	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 299	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 300	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 301	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 302	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 304	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 305	Dyed	Purple/Lilac	Green -Yellowish	Absent	Parallel wings
BF 306	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 307	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 308	Dyed	Purple/Lilac	Green -Yellowish	Absent	Parallel wings
BF 309	Dyed	Purple/Lilac	Green -Yellowish	Absent	Parallel wings
BF 310	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 311	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 312	Greenish	White	Green -Yellowish	Absent	Parallel wings
BF 313	Greenish	White	Green -Yellowish	Absent	Parallel wings

Most of the genotypes analyzed had a greenish keel color, white wings and a yellowish-green banner color. The BF 305, BF 308 and BF 309 genotypes showed a tinged pigmentation to the keel, with purple or lilac wings, due to the presence of anthocyanins. These results are in line with research by Frazão et al. (2010), who found that 60% of the cultivars they analyzed had white wings. Nere et al. (2021) found that around 80% of the genotypes analyzed had greenish keels and a yellowish-green standard, corroborating the results of this research. No hairs were observed on the banner, and all the genotypes showed parallel wings, as can be seen in the research by Frazão et al. (2010).

Morphological characterization of the fruit

The fruits of this legume are dehiscent pods with two valves, one dorsal and the other ventral, joined by two sutures (Silva & Costa, 2003).

The length, width and number of seeds per pod are shown in Table 10. For pod length, the genotypes BF 299, BF 304 and BF 308 had the highest values and BF 301 had the lowest, ranging from 9.50 to 5.95 cm, respectively. For this parameter, Nere et al. (2021) found values ranging from 9.98 to 4.95 cm; Guimarães et al. (2007) from 8.95 to 4.86 cm; Chagas et al. (2019) from 7.77 to 4.27 cm; Gonçalves et al. (2019) de 8,06 a 6,99 cm; from 8,06 to 6,99 cm; corroborating the results of this research.

Table 10. Length, width and number of seeds per pod.

Genotypes	Pod length (cm)	Pod width (cm)	Number of seeds per pod
BF 293	7.28 de	1.73 def	2.9 ab
BF 299	9.50 a	2.08 abc	2.8 ab
BF 300	8.05 bcd	2.13 ab	2.8 ab
BF 301	5.95 h	1.60 g	2.9 ab
BF 302	7.25 de	1.78 def	3.3 a
BF 304	9.37 a	1.93 bcde	2.9 ab
BF 305	7.10 def	1.68 ef	2.7 ab
BF 306	6.65 efg	1.83 cdef	2.4 b
BF 307	6.18 fg	1.80 def	3.2 a
BF 308	9.35 a	1.95 abcd	2.8 ab
BF 309	7.00 de	1.73 def	3.0 ab
BF 310	8.20 bcd	1.80 def	3.0 ab
BF 311	7.43 cde	1.70 def	2.5 ab
BF 312	8.55 ab	2.20 a	2.8 ab
BF 313	8.30 bc	1.93 bcde	2.9 ab
Average	7.74	1.86	2.86
CV (%)	14.62	9.41	8.01

For pod width, genotype BF 312 had the highest value and BF 301 the lowest, ranging from 2.20 to 1.60 cm. In this parameter, Oliveira et al. (2011) found values ranging from 1.77 to 1.47 cm for eight fava bean accessions grown in Rio Grande do Norte; Pires et al. (2022)) found values from 1.52 to 1.14 cm and Nere et al. (2021) from 2.14 to 1.39 cm. These studies show the wide genetic variability of fava bean accessions for this parameter.

With regard to the number of seeds per pod, this study found a variation of 3.3 to 2.4 seeds. Nere et al. (2021) obtained a wider range for this parameter with values varying from 3.18 to 1.99 seeds, however, Guimarães et al. (2007) in their study identified variations from 2 to 6 seeds per pod. Gonçalves et al. (2019) observed values of 2.92 to 2.30; and Oliveira et al. (2011) found average values of 2 seeds per pod.

The aforementioned results reaffirm that these parameters are important in selecting more productive cultivars, since larger measurements for fruit dimensions are capable of holding a greater number of seeds or heavier seeds (Nere et al. 2021; Dadther-Huaman et al., 2023). The qualitative parameters of apex shape, curvature and pod color are described in Table 11.

Table 11. Apex shape, curvature and pod color of fava bean genotypes.

Genotypes	Pod apex shape	Curvature of the pod	Pod color
BF 293	Thick apex	Slightly curved	Brown
BF 299	Thick apex	Slightly curved	Brown with red
BF 300	Thick apex	Slightly curved	Brown
BF 301	Short apex	Slightly curved	Brown with red
BF 302	Thick apex	Slightly curved	Brown with red
BF 304	Thick apex	Right	Brown with red
BF 305	Thick apex	Slightly curved	Brown with red
BF 306	Thick apex	Slightly curved	Brown
BF 307	Short apex	Slightly curved	Brown with red
BF 308	Thick apex	Right	Brown with red
BF 309	Thick apex	Slightly curved	Brown with red
BF 310	Thick apex	Right	Brown
BF 311	Short apex	Right	Brown
BF 312	Long apex	Slightly curved	Brown with red
BF 313	Short apex	Right	Brown

Most of the genotypes evaluated in this study had a thick apex and slightly curved pods, corroborating the results of Nere et al. (2021) and Dadther-Huaman et al. (2023). The authors state that there are Peruvian fava bean genotypes that can have a medium or long apex shape with a curved pod. No hairs were observed on the genotypes evaluated (glabrous) and all the pods are dehiscent.

According to Table 12, most of the quantitative variables presented in this article showed a significant correlation at the 0.1, 1 and 5% significance levels. It can be seen that the weight of one hundred seeds (WHS) shows a high correlation (>0.80) with the variables: length, width and volume of the seeds; width of the central leaflet and length of the pod.

Guimarães et al. (2007) state that there is greater fixation of atmospheric nitrogen, production of nodules and dry matter of the aerial part in plants developed from seeds that are larger.

Nunes et al. (2023) confirm this information by stating that the size of the seeds influences their physiological quality due to the greater amount of energy reserves produced, helping to develop more vigorous plants. Oliveira et al. (2011) and Pires et al. (2022) state that WHS is one of the most important traits when selecting more productive fava bean genotypes, i.e., those with a higher seed yield.

Table 12. Linear correlation matrix between the quantitative variables analyzed in this study.

Variables	WHS	L	W	T	VS	CLL	CLW	PL	PW
L	0.949^{***}	-	-	-	-	-	-	-	-
W	0.942^{***}	0.955^{***}	-	-	-	-	-	-	-
T	0.556^{*}	0.318^{ns}	0.321^{ns}	-	-	-	-	-	-
VS	0.987^{***}	0.941^{***}	0.927^{***}	0.599^{*}	-	-	-	-	-
CLL	0.450^{ns}	0.463^{ns}	0.483^{ns}	0.166^{ns}	0.419^{ns}	-	-	-	-
CLW	0.599^{*}	0.612^{*}	0.613^{*}	0.208^{ns}	0.553^{*}	0.817^{***}	-	-	-
PL	0.831^{***}	0.904^{***}	0.812^{***}	0.251^{ns}	0.830^{***}	0.423^{ns}	0.471^{ns}	-	-
PW	0.667^{**}	0.727^{**}	0.773^{***}	0.074^{ns}	0.653^{**}	0.528^{*}	0.652^{**}	0.710^{**}	-
NSP	-0.185^{ns}	-0.235^{ns}	-0.365^{ns}	0.133^{ns}	-0.198^{ns}	0.191^{ns}	0.086^{ns}	-0.094^{ns}	$-0{,}084^{ns}$

[1]Hundred seed weight (HSW); Length (L); Width (W); Thickness (T); Seed volume (SV); Central leaflet length (CLL); Central leaflet width (CLW); Pod length (PL); Pod width (PW); Number of seeds per pod (NSP). *, **, *** Significant, respectively, at 5, 1 and 0.1% probability levels using the t-test; ns-not significant.

The Principal Component Analysis (PCA) showed that the WHS (component 1) explained 61.93% of the variance in the data analyzed, followed by the L (component 2) and W (component 3) of the seeds with values of 14.37 and 11.7%, respectively, with eigenvalues greater than 1.0, which are considered significant (Table 13).

Table 13. Linear correlation matrix between the quantitative variables analyzed in this study.

Main Component	Autovalue	Variance (%)
Component 1 (HSW)	6,1928	61,93
Component 2 (L)	1,4368	14,37
Component 3 (W)	1,1663	11,66
Component 4 (T)	0,6175	6,18
Component 5 (VS)	0,2816	2,82
Component 6 (CLL)	0,1813	1,81
Component 7 (CLW)	0,0988	0,99
Other components	0,1236	0,24

Figure 7 shows how the fava bean genotypes are distributed in relation to the first two components of the PCA. An analysis of Figure 7 shows that the genotypes located to the right and left of the x-axis (component 1) have the highest and lowest HSW, respectively.

On the other hand, those located higher up on the y-axis have higher C values, differentiating themselves in this respect from the lower genotypes. Based on the information extracted from the PCA, these genotypes can be grouped into two groups using Hierarchical Cluster Analysis (HCA), as shown in Figure 8.

The first group represents the genotypes with the highest HSW, L, W and T values. The second group is made up of two sub-groups: the first from top to bottom is made up of the cultivars with the lowest HSW, L, W and VS values, and the other is made up of the genotypes with intermediate values for these characteristics and higher values for T.

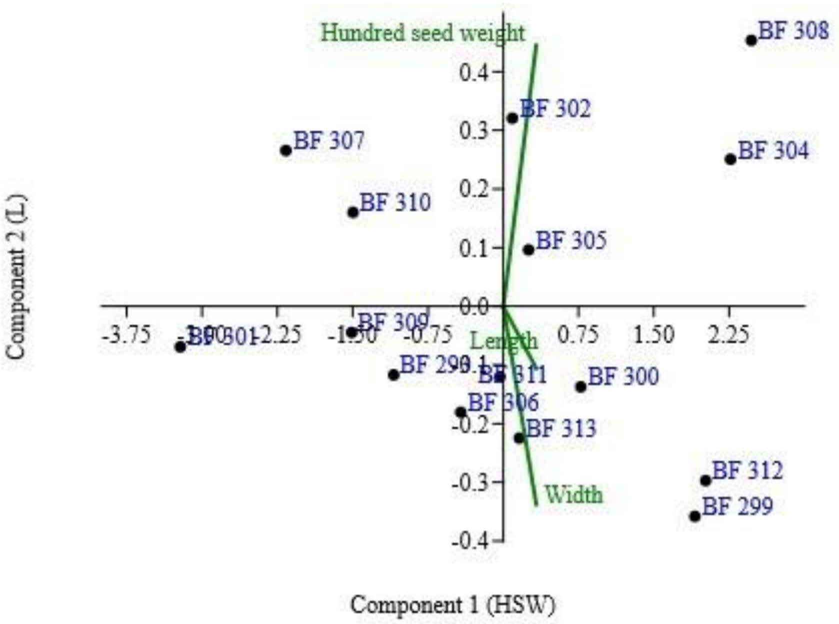

Figure 7. Distribution of the bean genotypes in relation to the main significant components.

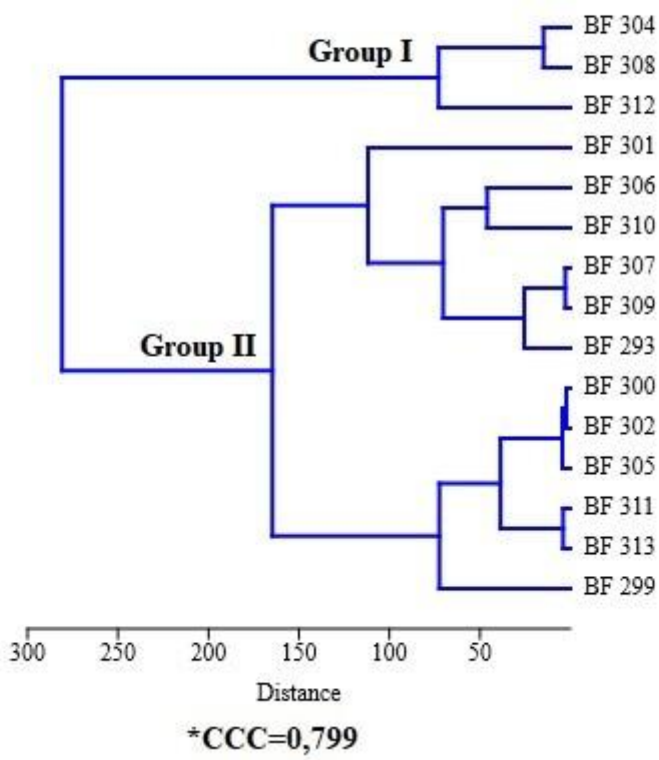

Figure 8. Hierarchical cluster analysis of fava bean genotypes based on quantitative descriptors.

The similarities shown in Figure 8 are correlated with the HSW, L and W variables of the seeds, since these parameters explain more than 80% of the variance in the data, according to the PCA. Genotypes BF 304 and BF 308, which belong to Group I, are in the same subgroup because they have the highest HSW, L, W, T and VS values, differing from genotype BF 312 in the HSW criterion.

In group II, genotype BF 301 (belonging to the first subgroup from top to bottom) is the one with the lowest values for most of the parameters analyzed, with the exception of T, accompanied by genotypes BF 306, BF 310, BF 307, BF309 and BF 293. The second subgroup includes the genotypes with the highest HSW, L, W and T values. It is worth noting that the clustering method used was adequate, since the cophenetic correlation coefficient (CCC) was greater than 0,7 (Gobo et al., 2018).

Taking into account the analysis of the morphological and agronomic variables used to draw up the dendrogram, it can be seen that the fava bean genotypes are similar to each other due to the distance between the two main groups and the high genetic variability, as can be seen in the studies carried out with fava beans in Indonesia (Purwanti & Fauzi, 2019); Peru (Dadther-Huaman et al., 2023); and in different locations in Brazil, namely: Ceará (CE), Pernambuco (PE) and Paraíba (PB) (Guimarães et al., 2007); Goiás (GO), São Paulo (SP), Minas Gerais (MG), Mato Grosso (MT), Espirito Santo (ES) (Pires et al., 2022), Piauí (PI) and Maranhão (MA) (Silva et al., 2015).

Research that takes into account the morpho-agronomic characteristics of crops, such as: morphological aspects of the seeds (color, L, W, T, VS and shape of the seeds) and productivity (HSW, NSP) is relevant in the selection of more productive genotypes; in studies investigating consumer preference, and in the processes of processing and standardizing these creole seeds for marketing purposes (Nere et al., 2021). In order to select promising genotypes, it is necessary to combine multivariate analysis techniques between different morphological and agronomic descriptors in order to genetically improve the crop and select genitors with dissimilarities (Barili et al., 2011).

Amorim et al. (2019) highlight that fava beans, as a legume, are capable of symbiotic interactions with diazotrophic bacteria, promoting greater biological nitrogen fixation and making it available to the plant. The authors concluded that the bacterial diversity found in different genotypes contributed to the crop's adaptation to soils with high aridity, such as soils in the Northeast region that experience periods of moisture scarcity and high temperatures.

Pereira Filho et al. (2020) observed that fava bean genotypes subjected to water and saline stress conditions show a decrease in their initial growth as a morphophysiological response. The researchers state that the reduction in the plant's vegetative growth allows it to maintain, even partially, its physiological activity and water extraction in low proportions from the soil, seeking to develop mechanisms of adaptation to drought.

Another study related to environmental sciences states that broad bean genotypes are drought tolerant because they maintain high levels of photosynthesis, even in conditions of moderate and severe water deficit, keeping their transpiration levels reduced due to greater efficiency in water use (Jacinto Junior et al., 2019).

Uebersax et al. (2022) highlight the importance of planting beans as an alternative to achieving agricultural sustainability, as they have a low carbon footprint associated with a short cultivation cycle, facilitating crop diversification. This contributes to the widespread use of beans of the *Phaseolus* genus in crop rotation processes, with a reduction in the incidence of pests and diseases resulting from a long cultivation period, and the growth in the use of cover cropping practices before or after the harvests of these cultivars.

The fight against hunger in regions suffering from food insecurity, especially in developing countries like Brazil, requires knowledge of the genetic diversity that exists among cultivable plants, since this makes it possible to develop cultivars that are more resistant to unfavorable environmental conditions (aridity, soil erosion and impoverishment, low rainfall, high temperatures, low air humidity, among others) and pests, leading to greater seed production and increased yields. The main custodians of creole seeds in Brazil have been traditional communities through family farming (Klepka et al., 2021).

It is known that fava beans are cultivated in most states of Brazil, especially in the Northeast, with creole germplasm mostly obtained from family producers who do not have the technology to improve their cultivation practices. More research is therefore needed to find genotypes with characteristics that contribute to the genetic diversity of fava beans (*Phaseolus lunatus* L.) and to their genetic improvement, with a view to increasing production yields and combating food shortages, especially when planted in rainfed conditions (Lopes et al., 2017; Pires et al., 2022).

Conclusions

In this study, the genetic variability of fava bean genotypes is explained by the quantitative descriptors: hundred-seed weight, seed length and seed width. The fava bean genotypes BF 304, BF 308 and BF 312 showed the highest values for these parameters, making them promising genotypes for plant breeding.

Characters related to seed coat color, shape and size are relevant to the standardization of fava bean seeds for marketing purposes and are requirements that influence consumer preference. The botanical aspects that made it possible to differentiate the genotypes analyzed were: the color and shape of the seed coat; the color of the hypocotyl and cotyledons; the texture of the forehead; the color of the veins and the presence of anthocyanins in the primary leaves; the color of the leaf; the shape of the central leaflet; the color of the keel and wings in the inflorescence; the shape of the apex, curvature and color of the pod.

The analysis of these descriptors is important in differentiating and determining improved fava bean cultivars in Ceará, since there is little information on the genetic diversity and agronomic potential of this crop in Brazil.

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