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## Selection of lima bean accessions for fresh and dry production<sup>1</sup>

### Seleção de acessos de feijão-fava nos estádios verde e seco

Loren R. Damas<sup>2\*</sup>, Priscila A. Barroso<sup>3</sup>, Wilson V. de Assunção Neto<sup>4</sup>, Angela C. de A. Lopes<sup>4</sup>,  
José V. da Silva Junior<sup>3</sup>, Regina L. F. Gomes<sup>4</sup> & Artur M. Medeiros<sup>3</sup>

<sup>1</sup> Research developed at Bom Jesus, Piauí, Brazil

<sup>2</sup> Universidade Federal do Piauí/Graduação em Engenharia Agrônoma/ Campus Professora Cinobelina Elvas, Bom Jesus, PI, Brazil

<sup>3</sup> Universidade Federal do Piauí/Campus Professora Cinobelina Elvas, Bom Jesus, PI, Brazil

<sup>4</sup> Universidade Federal do Piauí/Centro de Ciências Agrárias/Departamento de Fitotecnia, Teresina, PI, Brazil

#### HIGHLIGHTS:

*There is genetic variability in bean germplasm for production components.*

*Lima bean accessions should be selected independently for fresh and dry lima bean production.*

*Dry lima beans showed an inverse relationship between the traits associated with pod production and number of pods.*

**ABSTRACT:** The selection of lima bean accessions in the fresh and dry stages is an excellent tool to increase crop yield in Brazil and ensure a source of vegetable protein for the population. Principal component analysis and nonparametric indices can be used to identify promising accessions based on the desired agronomic variables. The aim of the present study was to select accessions from traditional lima bean varieties in the fresh and dry stages using principal component analysis and nonparametric selection indices. The experiment consisted of a randomized block design, evaluating 13 treatments in four replicates. The experimental plot contained 20 plants in its study area. The first two principal components for the two stages explained more than 80% of the variation found among the accessions. The Mulamba & Mock and Genotype-Ideotype selection indices were efficient in classifying promising varieties for breeding programs. The UFPI 1111 accession can be used in fresh lima bean production, and its UFPI 1248 and 1294 counterparts in lima bean breeding programs.

**Key words:** *Phaseolus lunatus* L., heirloom varieties, breeding programs

**RESUMO:** A seleção de acessos de feijão-fava nos estádios verde e seco é uma excelente ferramenta para aumentar a produtividade da cultura no país e garantir uma fonte de proteína vegetal para a população. O uso de componentes principais e índices de seleção não-paramétricos podem ser utilizados para identificar acessos promissores com base em características agrônomicas desejáveis. O objetivo do presente estudo foi selecionar acessos de variedades crioulas de feijão-fava nos estádios frescos e secos utilizando componentes principais e índices de seleção não paramétricos. O experimento foi disposto em delineamento em blocos casualizados, sendo avaliados 13 tratamentos em quatro repetições. A parcela experimental conteve 20 plantas em sua área útil. Os dois primeiros componentes principais, para os dois estádios, explicaram mais de 80% da variação encontrada entre os acessos. Os índices de seleção de Mulamba & Mock e Genótipo-Ideótipo foram eficientes na classificação de variedades promissoras para programas de melhoramento. O acesso UFPI 1111 pode ser direcionado para a produção de fava verde, e os acessos UFPI 1248 e UFPI 1294 podem ser utilizados para programas de melhoramento de fava seca.

**Palavras-chave:** *Phaseolus lunatus* L., variedades crioulas, programas de melhoramento



## INTRODUCTION

Lima bean (*Phaseolus lunatus* L.) is one of the most commercially exploited species of the genus *Phaseolus* (Ormeño-Orrillo et al., 2015). It is versatile and can be consumed fresh or dried, is rich in protein, fiber, carbohydrates, vitamin B6, riboflavin and niacin and low in fat (Farinde et al., 2018). In 2020, Brazil produced approximately 16,000 tons of dry lima beans, with an average yield of 448 kg ha<sup>-1</sup> (IBGE, 2021). No data were collected on the *in natura* production of lima beans, a niche market to be explored. The productive potential of the species has not yet been determined in comparison with large producing regions.

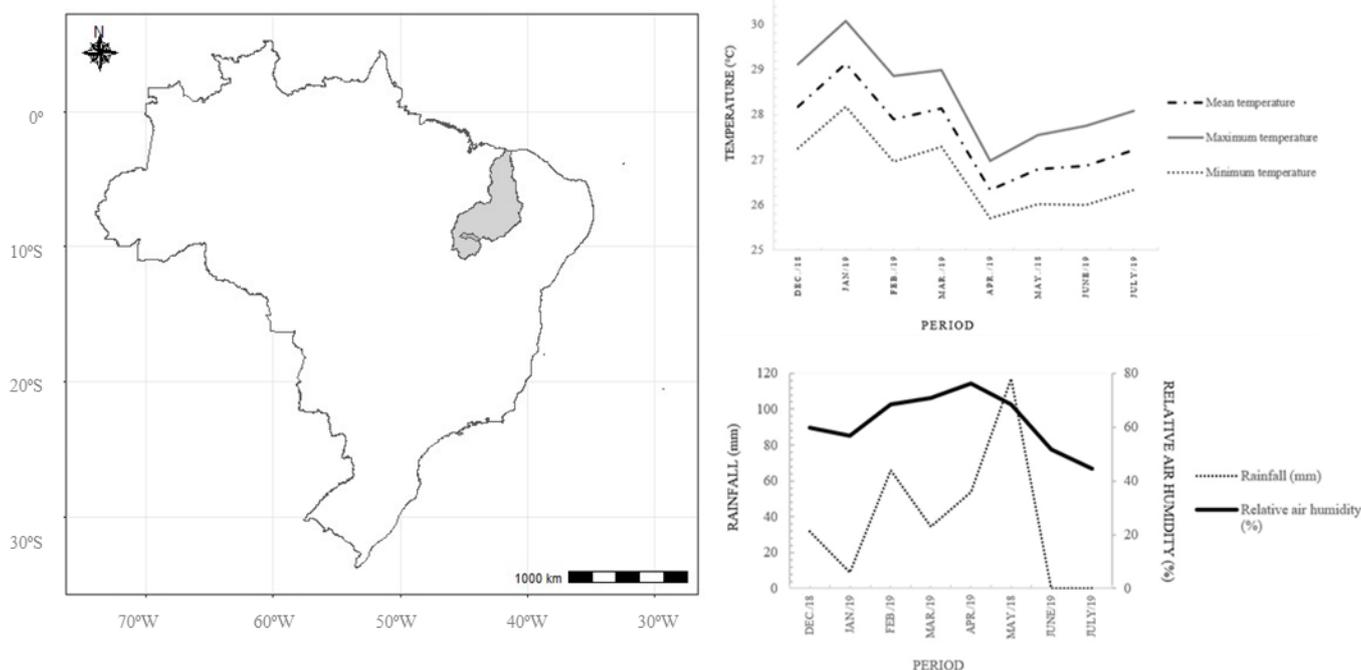
In Brazil, there is only one lima bean variety registered in the Ministry of Agriculture, Livestock and Supply and none in the National Registry of Seeds and Seedlings. It is essential to identify traditional lima bean varieties in the fresh and dry phases that meet the needs of the market. Lima bean breeding programs have identified accessions with greater productive potential (Almeida et al., 2021; Sousa et al., 2022). However, all are focused on dry beans. It is unknown whether accessions with productive potential for dried lima beans can

also be selected for the fresh lima bean market (Kurihara et al., 2013; Souza et al., 2019).

In this context, where a set of variables of interest is analyzed, the use of principal component analysis (PCA) is an alternative. PCA reduces the number of variables, disregarding the components that exhibit a small variance (Hongyu et al., 2016). The use of selection indices can also guide the choice of accessions (Buzzelo et al., 2015) through the efficient combination of several traits and their simultaneous selection. The aim of the present study was to select traditional lima bean accessions in the fresh and dry stages using principal component analysis (PCA) and non-parametric selection indices.

## MATERIAL AND METHODS

The experiment was conducted, from December 2018 to July 2019, on a farm in Lagoa do Barro located in the municipality of Bom Jesus, PI, Brazil, at 09° 04' 28" S and 44° 21' 31" W, and average altitude of 277 m (Figure 1 and Table 1). The soil in the region is classified as Quartzipsamments (United States, 2014), which corresponds to a Neossolo Quartzarênico (EMBRAPA, 2018). The climate is classified as



Source: <http://www.inmet.gov.br/portal/index.php?r=bdmep/bdmep>

**Figure 1.** Location and meteorological characteristics of the region where lima bean accessions and temperature, rainfall and relative air humidity data were assessed for the region from December 2018 to July 2019

**Table 1.** Chemical characterization of soil samples in the experimental area: pH in water, hydrogen + aluminum (H+Al), aluminum (Al), calcium (Ca), magnesium (Mg), potential CTC (T), phosphorus (P), potassium (K), sum of bases (SB), base saturation (V), aluminum saturation (m) and organic matter (OM) content

Soil	pH H <sub>2</sub> O	H + Al	Al	Ca	Mg	SB	T	P	K	V	m	OM	Clay	Silt	Sand
Clay Lagoon (0-20 cm)	6.2	0.91	0.00	0.70	0.10	0.87	1.79	23.6	28	48.8	0.00	1.20	62	52	885
Clay Lagoon (20-40 cm)	6.2	0.78	0.00	0.50	0.30	0.93	1.71	13.0	49	54.3	0.00	1.20	85	68	847

P and K - Mehlich extractor1; Ca, Mg and Al - KCl Extractor - 1 mol L<sup>-1</sup>; H + Al - Calcium Acetate Extractor up to pH 7.0; Organic Matter (OM) - Walkley-Black method; SB - Sum of Exchangeable Bases; CEC (T) - Cation Exchange Capacity at pH 7.0; V = Base Saturation Index; m = Aluminum Saturation Index

Aw (humid with dry winters), according to the Köppen climate classification system.

A total of 13 lima bean accessions belonging to the Active Germplasm Bank of the Federal University of Piauí (BGP-UFPI), Brazil, were analyzed (Table 2). The experiment used a randomized block design involving 13 treatments (accessions) in four replicates. The experimental plots consisted of four 3.5-m-long rows containing five plants each. The rows and plants were spaced 0.8 × 0.7 m apart. The study area of the experimental plot contained 20 plants. Three heirloom seeds per furrow were also sown, serving as a support crop for a lima bean. Thinning was performed 15 days after germination, leaving one plant per furrow. During the entire cycle, the experimental plots were kept weed-free by hand weeding to avoid competition and facilitate evaluation and monitoring of the experiment. This method was selected because there are no herbicides registered for lima bean weed control. Lima beans are cultivated mainly by family farmers, who either do not use an irrigation system, or irrigate only for supplementation without any water supply criteria. A non-technological sprinkler irrigation system, commonly called wetting, was adopted. In this system, family farmers supply enough water to moisten the plots during periods of drought. No fertilizer was applied in the area.

The pods were evaluated in the fresh and dry lima bean stages, using five pods per plot for the former and 20 pods for the latter. The samples were gradually collected when the pods contained totally formed beans. The following traits were assessed based on the *Phaseolus lunatus* descriptors proposed by the IPGRI (2001) in the 13 lima bean accessions in the fresh and dry stages:

- Pod length (CV): measured with a digital pachymeter (mm);
- Pod weight (PW): for fresh lima bean, the weight of five randomly selected pods was measured; for dry lima bean, the mean weight of 20 randomly selected ripe pods was used;
- Number of beans per pod (NBP): for fresh lima beans, five randomly collected pods were weighed; for dry lima bean, the mean weight of 20 randomly selected ripe pods was calculated;
- Pod/bean weight (P/BW): the bean weight of five fresh and 20 randomly collected ripe pods was taken;

**Table 2.** Accessions from the lima bean active germplasm bank of the Federal University of Piauí (BAG-UFPI), Brazil, with their common names and origin

BAG code	Common name	Origin
UFPI 1111	Fava branca	São Domingos-MA
UFPI 1112	Branca	São Domingos-MA
UFPI 1235	Fava branca	Buriti Bravo-MA
UFPI 1237	Fava mulatinha	Farias Brito-CE
UFPI 1245	Branquinha	Balsas-MA
UFPI 1247	Chumbinho	Miguel Alves-PI
UFPI 1248	Branca	Tianguá-CE
UFPI 1249	Fava branquinha	Tianguá-CE
UFPI 1250	Fava branca	São Benedito-CE
UFPI 1266	Fava branca	Araípe-CE
UFPI 1294	Fava raio de sol	Cariaiaçu-CE
UFPI 1297	Boca de moça	Varjota Assaré-CE
UFPI 1299	Fava marrom	Bom Jesus-PI

- 100-seed weight (100 SW): determined by weighing 100 beans from each treatment in each block;
- Number of pods (NP): average number of randomly collected fresh and dry pods;
- Bean yield (YLD): the total bean weight in the study in grams, transformed into kg ha<sup>-1</sup>.

Pod length was obtained using a digital pachymeter with 0.01 mm accuracy. Bean weight was measured on a digital scale with an accuracy of 0.0001 g.

The data were submitted to PCA with standardized data, where  $x_{ij}$  is the standardized mean of the  $j$ th character ( $j = 1, 2, \dots, v$ ) evaluated in the  $i$ -th accession ( $i = 1, 2, \dots, g$ ), processed using the original variable covariance matrix, obtaining the eigenvalues that constructed the eigenvectors. When obtaining the principal components, the following properties were considered:

- If  $y_{ij}$  is a principal component, then:  $Y_{ij} = a_1 x_{i1} + a_2 x_{i2} + \dots + a_p x_{ip}$
- If  $y_{ij'}$  is another principal component, a new linear combination is expressed by  $y_{ij'} = b_1 x_{i1} + b_2 x_{i2} + \dots + b_p x_{ip}$
- Among the principal components,  $y_{i1}$  has the largest variance,  $y_{i2}$  the second largest, and so on.

The parameters associated with the principal components are estimated by solving the system of equations:  $(R - \lambda_j I) a_j = 0$ , where  $\lambda_j$  are the characteristic roots or eigenvalues of the matrix of correlations between the original variables or covariances between standardized variables. There are  $p$  eigenvalues corresponding to the variances of each of the  $p$  principal components;  $a_j$  is the characteristic vector or eigenvector, representing the set of orthogonal transformations by which the original standardized variables must be multiplied to produce the transformed variables;  $I$  the identity matrix of dimension  $p \times p$ ; and  $R$  the matrix of phenotypic correlations between pairs of original variables. The relative importance of each component ( $IR_j$ ) was evaluated by the percentage of total variance that it explains, i.e.:

$$IR_j = \frac{V(y_{ij})}{\text{Trace of } R}$$

where:

$V(Y_{ij})$  - variance of the component  $ij$  and  $V(Y_{i1}) + V(Y_{i2}) + \dots + V(Y_{ip})$  the Trace of  $R$ , in which  $V(Y_{i1})$  is the variance of component 1,  $V(Y_{i2})$  the variance of component 2 ... and  $V(Y_{ip})$  the variance of component  $p$ .

The accessions were plotted on a biplot graph for the first two principal components. Accessions were classified using the Mulamba & Mock (1978) and Genotype-Ideotype selection indices (Schwarzbach, 1972). The rank sum index (Mulamba & Mock, 1978) was computed by the expression:

$$I_{MMi} = \sum n_{ij}$$

where:

- $I_{MMi}$  - classification index; and
- $n_{ij}$  - classification number of genotype  $i$  with respect to trait  $j$ .

In the genotype-ideotype distance index (Schwarzbach, 1972), the Euclidean distance was adopted.

$$D_{ij} = \sqrt{\sum d^2_{ij}}$$

where:

$D_{ij}$  - Euclidean distance between genotype  $i$  and ideotype  $I$ ; and,

$d_{ij}$  - standardized deviation between the mean of trait  $j$ , measured in genotype  $i$  ( $x_{ij}$ ), and the value assigned to the ideotype of that trait ( $x_j$ ), that is,  $d_{ij} = (x_{ij} - x_j)/\sigma_j$ .

Standardization prevents traits measured in larger units from exerting a greater influence than the others on the index value, and consequently, on hybrid classification. Analyses were carried out using R software, version 4.0.2 (R Core Team, 2021).

### RESULTS AND DISCUSSION

The first two main components (PCs) explained 84.50% of the variance between the accessions studied for the seven traits assessed in lima bean in the fresh stage. In the dry stage, the first two principal components explained 82.62% of the data variance (Table 3). The Kaiser criterion (Kaiser, 1958) was used to select principal components that explained most

of the variation in the dataset. This makes it possible to reduce the initial dataset into few PCs without losing information. The first two components of the present study effectively summarize the total variance for the two developmental stages according to Hongyu et al. (2016) can be used to study the dataset.

The variables with the highest eigenvector values in a main component are considered important (Tables 4 and 5). In the first principal component (PC1), for both fresh and dry lima, the traits that contributed most to discriminating accessions were pod/bean weight (P/BW), pod weight (PW), 100-seed weight (100 W) and number of beans per pod (NBP). The first component is therefore represented by weight-related traits, and in the second, yield traits predominate (Tables 4 and 5). In the common bean (*P. vulgaris*), the variables related to pod and bean yield contributed only from the third main component forward (Oliveira et al., 2018). This factor demonstrates greater uniformity between the accessions and *P. vulgaris* for the variables cited, which was not observed for a lima bean in the present study, reinforcing the need to select and explore the available *P. lunatus* germplasm. Brito et al. (2020) found that pod-related descriptors are efficient in differentiating lima bean accessions.

Variables with the same sign act directly on phenotypic expression (Table 4), that is, the highest values of one variable

**Table 3.** Eigenvalue, explained variance ratio (%) and cumulative explained variance ratio (%) of the principal components (PCs) for fresh and dry lima bean grains

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Fresh lima bean							
Eigenvalue	2.09	1.24	0.81	0.54	0.32	0.10	0.08
Explained variance (%)	62.40	22.1	9.46	4.29	1.46	0.16	0.10
Cumulative explained variance (%)	62.40	84.5	93.97	98.26	99.73	99.89	1.00
Dry lima bean							
Eigenvalue	2.06	1.23	0.80	0.68	0.28	0.11	0.03
Explained variance (%)	60.96	21.65	9.29	6.73	1.14	0.19	0.01
Cumulative explained variance (%)	60.96	82.62	91.91	98.64	99.79	99.98	1.00

**Table 4.** Eigenvectors (weighting coefficient) and eigenvalues explained by the principal components (PCs) of the seven fresh lima bean variables analyzed

	Weighting coefficients						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
PL	-0.354	0.348	0.330	0.801	-0.003	0.051	-0.008
PW	-0.429	0.263	0.031	-0.303	0.762	-0.130	0.238
P/BW	-0.452	0.187	-0.201	-0.246	-0.158	0.664	-0.441
NBP	-0.282	-0.354	-0.794	0.366	0.097	-0.127	0.071
NP	-0.313	-0.557	0.359	-0.029	0.118	-0.321	-0.587
100 W	-0.427	-0.305	-0.074	-0.256	-0.572	-0.563	0.099
YLD	-0.356	-0.496	0.290	-0.076	-0.211	0.321	0.624

PL - Pod length; PW - Pod weight; P/BW - Pod/bean weight; NBP - Number of beans per pod; NP - Number of pods; 100 W - 100-seed weight; YLD - Yield

**Table 5.** Eigenvectors (weighting coefficient) explained by the principal components (PCs) of the seven dry lima bean variables analyzed

	Weighting coefficients						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
PL	-0.323	0.318	0.442	0.761	0.108	-0.096	-0.009
PW	-0.467	-0.175	-0.050	0.053	-0.357	0.785	-0.048
P/BW	-0.469	-0.180	-0.091	-0.086	-0.119	-0.326	0.782
NBP	-0.335	-0.561	0.034	-0.034	0.722	-0.005	-0.222
NP	0.268	-0.465	-0.524	0.626	-0.187	-0.106	-0.011
100 W	-0.474	0.013	-0.157	-0.130	-0.391	-0.495	-0.580
YLD	-0.219	0.552	-0.703	0.047	0.371	0.115	-0.023

PL - Pod length; PW - Pod weight; P/BW - Pod/bean weight; NBP - Number of beans per pod; NP - Number of pods; 100 W - 100-seed weight; YLD - Yield

are associated with the highest values of the other. Assessment of PC1, which exhibits the greatest variation (Table 3), shows that all the traits of fresh lima act directly. Thus, the response is favorable to the selection of all the traits when selecting fresh lima bean accessions, which facilitates the breeding program. Assessment of eigenvectors associated with PC1 for dry lima bean revealed that the variables PL, PW, P/BW, NBP, 100 W and YLD act directly and inversely to NP (Table 4), demonstrating that accessions with the largest number of pods have smaller pods that yield less. In common bean, there was also an inverse relationship between the number of pods and 100-seed weight (Oliveira et al., 2018). In “boca de moça” lima bean, this behavior was not observed, and the number of pods was directly associated with bean production and weight (Assunção Filho et al., 2022), reinforcing the hypothesis that this relationship may vary according to genotype by environment interaction.

Accession dispersal in the biplot based on the scores obtained for the first two principal components (Figure 2) makes it possible to visualize the phenotypic diversity in the studied accessions for fresh and dry stages, which favors selection. Heirloom lima bean varieties can grow under different environmental conditions and exhibit large variation in the number of pods, number of beans per pod, bean weight and size, as well as different shapes and colors (Silva et al., 2014; Sánchez-Navarro et al., 2019), important traits in breeding programs because they provide a large source of genetic variability.

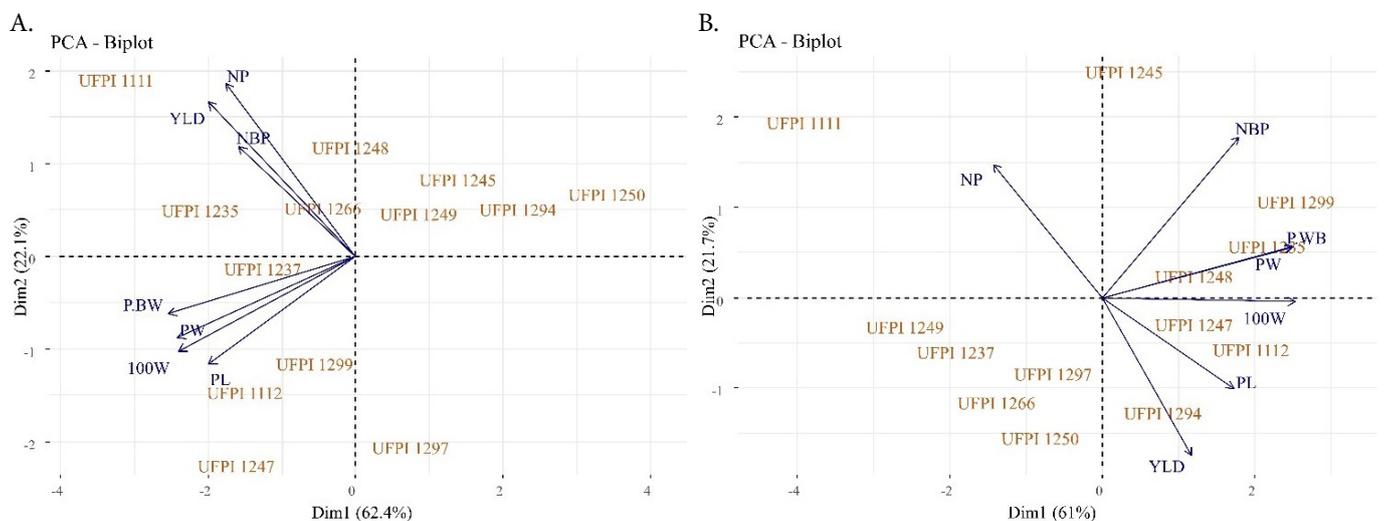
For fresh lima beans (Figure 2A), yield-related variables are concentrated in the upper left quadrant of PC1. In this respect, accessions UFPI 1111, 1235, 1248, 1266 and 1237 show the potential to produce a larger number of pods, number of beans per pod and yield, particularly UFPI 1111. Larger and heavier pods were found in accessions UFPI 1112, 1247 and 1299, although in fewer numbers on the plant, as indicated by the number of vector pods. These accessions could be used in future breeding programs in crosses with more productive accessions. Accessions UFPI 1250 and 1297 obtained the lowest

scores in relation to PC1 and PC2, respectively, exhibiting poor productive performance under the conditions tested, which is not recommended for fresh lima bean production.

Analysis of dispersal accessions for dry lima bean (Figure 2B) reveals that accessions associated with greater yield (UFPI 1294, 1112, and 1247) can be found in the lower right quadrant of PC1. Despite not being in the same quadrant, given that production discrimination power is higher in PC2, accessions UFPI 1250, 1297, 1266 and 1237 also obtained good production scores. UFPI 1299 and 1235 exhibited the highest bean weight per pod, but in smaller numbers, they did not obtain good productive performance. These accessions can be used in future crosses with UFPI 1112 and 1294 accessions, which are more productive but have lower bean weight per pod.

Accessions UFPI 1245 and 1111 showed no productive potential for dry lima bean under the conditions studied. It is important to note the behavior of accession UFPI 1111, considered the most productive for fresh lima bean. When the dry stage variables are analyzed, the accession continues to stand out for the number of pods scored, but dry bean weight (P/BW and 100 W) is poor, resulting in low yield. Bean weight is related to water loss and dry matter accumulation during development until harvest. Moisture content estimates water content directly and bean dry matter indirectly, which can vary between lima bean accessions (Yellavila et al., 2015). The variation obtained in the present study may therefore be related to the genotype, dry matter accumulation during development and the soil and climate conditions in which they were grown (Nachi & Guen, 1996; Yellavila et al., 2015; Souza et al., 2019)

The Mulamba & Mock (1978) and Genotype-Ideotype selection indices were used to identify promising accessions based on agronomic traits. Among the 13 accessions in the fresh and dry stages, the indices indicated accessions UFPI 1111, 1235 and 1237 as the first three in the former stage, with only the order changing in each index (Table 6). These accessions were also identified by PCA, demonstrating the superiority of the accessions, which was confirmed by agreement between the techniques.



PL - Pod length; PW - Pod weight; P/BW - Pod/bean weight; NBP - Number of beans per pod; NP - Number of pods; 100 W - 100-seed weight; YLD - Yield; See Table 2 for lima bean accessions description

**Figure 2.** Dispersion of 13 lima bean accessions from PC1 (Dim 1) and PC2 (Dim 2) obtained from grain production components in the fresh (A) and dry (B) stages

**Table 6.** Ranking using the nonparametric Mulamba & Mock (1978) selection index (MM) and Genotype-Ideotype (GI) distance based on agronomic traits, assessed in 13 lima bean accessions in the fresh stage with agronomic potential in semiarid regions

Accessions	PL	PW	P/BW	NBP	NP	100 W	YLD	MM	GI
UFPI 1111	7.29	5.23	2.96	2.90	1076.00	102.05	2857.24	1°	3°
UFPI 1112	7.27	5.04	2.78	2.75	252.75	100.5	641.75	4°	6°
UFPI 1235	7.36	4.69	2.85	3.20	454.75	101.17	1264.90	2°	1°
UFPI 1237	7.96	4.56	2.30	2.85	499.25	80.50	1067.59	3°	2°
UFPI 1245	6.22	3.98	2.00	2.75	398.25	72.58	648.88	9°	9°
UFPI 1247	7.33	5.44	2.71	2.65	124.00	102.35	300.30	7°	10°
UFPI 1248	6.56	3.93	2.34	3.00	452.75	86.46	1123.19	6°	5°
UFPI 1249	6.4	3.85	2.04	2.80	354.00	72.28	599.12	10°	8°
UFPI 1250	5.52	2.79	1.47	2.65	34.25	54.35	38.61	13°	13°
UFPI 1266	6.93	4.59	2.48	3.05	361.50	81.68	864.51	5°	4°
UFPI 1294	6.35	3.4	1.49	2.65	264.25	57.38	369.84	12°	12°
UFPI 1297	7.67	3.88	2.14	2.50	44.25	87.78	77.98	11°	11°
UFPI 1299	7.09	4.82	2.80	2.90	121.50	95.50	300.33	8°	7°

PL - Pod length; PW - Pod weight; P/BW - Pod/bean weight; NBP - Number of beans per pod; NP - Number of pods; 100 W - 100-seed weight; YLD - Yield; See Table 2 for lima bean accessions description

**Table 7.** Ranking using the nonparametric Mulamba & Mock (1978) selection index (MM) and Genotype-Ideotype (GI) distance based on agronomic traits, assessed in 13 lima bean accessions in the dry stage with agronomic potential in semiarid regions

Accessions	PL	PW	P/BW	NBP	NP	100 W	YLD	MM	GI
UFPI 1111	5.14	1.37	0.86	2.55	1076.00	33.85	256.04	13°	13°
UFPI 1112	6.68	2.10	1.51	2.60	252.75	57.69	466.41	4°	3°
UFPI 1235	7.22	2.41	1.66	2.78	454.75	58.94	426.65	1°	1°
UFPI 1237	5.89	1.71	1.13	2.40	499.25	46.33	428.14	9°	7°
UFPI 1245	4.87	2.09	1.50	2.80	398.25	52.87	269.75	7°	5°
UFPI 1247	6.10	2.13	1.50	2.69	124.00	56.53	446.63	5°	4°
UFPI 1248	6.86	2.15	1.54	2.63	452.75	58.41	427.86	3°	2°
UFPI 1249	6.30	1.66	1.05	2.45	354.00	43.11	318.41	12°	10°
UFPI 1250	7.23	1.72	1.10	2.35	34.25	46.35	357.62	10°	11°
UFPI 1266	6.04	1.77	1.17	2.40	361.50	48.80	434.2	8°	8°
UFPI 1294	6.91	1.93	1.34	2.58	264.25	52.11	491.03	6°	6°
UFPI 1297	6.09	1.66	1.21	2.50	44.25	47.83	394.04	11°	9°
UFPI 1299	8.03	2.42	1.72	2.88	121.50	59.76	330.46	2°	12°

PL - Pod length; PW - Pod weight; P/BW - Pod/bean weight; NBP - Number of beans per pod; NP - Number of pods; 100 W - 100-seed weight; YLD - Yield; See Table 2 for lima bean accessions description

For lima bean in the dry stage, according to the Mulamba & Mock (1978) Index, the first three accessions were UFPI 1235, 1299 and 1248 (Table 7), and UFPI 1235, 1248 and 1112 according to the Genotype-Ideotype, with a difference between the 2<sup>nd</sup> and 3<sup>rd</sup>, but with accessions UFPI 1235 and 1248 appearing in both indices. The aforementioned accessions also obtained good scores for the production components when principal component analysis (PCA) dispersion was evaluated (Figure 2), with greater relevance for UFPI 1112, which obtained a high production score for PCA and was well ranked in the Genotype-Ideotype index. Even using the weights of different variables, the techniques agree and should be used to complement accession selection for the breeding program.

The use of selection indices makes it possible to combine information, which allows selection based on a set of variables with several attributes of interest for the crop (Freitas et al., 2012; Sousa et al., 2021). The indices showed that accession UFPI 1235 can be used to commercialize fresh and dry lima bean, which was not evident in the biplot scores using PCA. Silva et al. (2014) reported that several multivariate techniques are required to make robust inferences about phenotypic variability. However, some accessions can be used in breeding programs with different objectives, namely, fresh lima bean (accession UFPI 1111) and its dry counterparts (accessions UFPI 1248 and 1294).

## CONCLUSIONS

1. The first two principal components for the two stages explained more than 80% of the variation found between the accessions.
2. The Mulamba & Mock and genotype-ideotype selection indices were efficient in classifying promising varieties for breeding programs.
3. The UFPI 1111 accession can be used in fresh lima bean production, and its UFPI 1248 and 1294 counterparts in lima bean breeding programs.

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