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Morphoagronomic diversity in *Butia capitata* progenies (Arecaceae)

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Abstract *Butia capitata*, coquinho azedo, is a palm tree endemic to the Brazilian Cerrado, ecologically important and with great economic potential, related to the agro-industrial use of its fruits. As a subsidy to the conservation actions and management strategies of the species, the objective was to characterize the relative importance of the morphoagronomic characters and the diversity of half-sib progenies, using different multivariate approaches. Twenty-three quantitative and 33 qualitative traits were evaluated in 18 half-sib progenies of *Butia capitata* 6-year-old progenies. Phenotypic variability among progenies was evaluated using descriptive statistics, analysis of canonical variables and clustering using dendrograms. The relative importance of the characters was determined. The progenies showed significant diversity, based on 11 quantitative characters. The highest phenotypic correlation r_p value was observed between fruit weight (WFR) and bunch weight (WBU) (r_p = 0.99); there was also a significant correlation between leaf length and production traits (bunches and fruits number and weight). The first and second canonical variables accounted for 72% of the total variation. The length and width of the leaves, the ratio of the length and width of the fruits, the flavor and color of the fruit were the characteristics that most contributed to explain the variation between individuals. The 11 quantitative descriptors allowed grouping the 18 progenies into four distinct groups. This study provides important information on the characterization of diversity among *B. capitata* progenies, considering both the univariate and multivariate approaches. In addition, traits of agronomic importance that should be prioritized in breeding programs for this promising neotropical fruit tree were defined.

Keywords Palm · Cerrado · Phenotypic variability · Half-sib · Breeding · Morphological descriptors

Introduction

In recent decades, tropical savannas around the world have been among the most affected biomes due to the suppression of native vegetation (Hofmann et al. 2021). The Brazilian Cerrado, also called the Neotropical Savannah, is a global biodiversity hotspot that has already lost more than 46% of its native vegetation cover (Strassburg et al. 2017). Endemic trees are increasingly threatened,

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even before their full potential has been exploited (Hofmann et al. 2021). In this scenario, we find *Butia capitata* (Mart.) Becc., a palm tree native to the Brazilian Cerrado (Lorenzi et al. 2010). Its pulp is rich in carbohydrates, oil, dietary fiber, provitamin A, carotenoids, vitamin C, phenolic compounds (catechin, tannic acid) and potassium (Aguiar et al. 2014; Vieira et al. 2016; Ventura et al. 2022) and widely used both in natura and processed. The commercialization of its fruits is carried out in regional markets, which generates an important source of income for the populations. In addition, due to the peculiar taste of the fruit, there is potential for this species to reach the national and international markets (Dias et al. 2022), which would further increase the demand for these. However, the supply of fruits is done exclusively through extractivism (Sá et al. 2018), contributing to classify it as vulnerable to extinction (CNCFlora 2012; Silva and Scariot 2013),

Knowledge of genetic diversity is the first step towards developing effective conservation and management strategies for plant species (Khadivi et al. 2020). Morphological characters have been widely used in this diversity characterization. In Arecaceae species, such as *Acrocomia aculeata* (macaúba), *Cocos nucifera* (coconut tree) and *Euterpe oleracea* (açaí palm), plant height, rachis length, number of rachillae, fruit circumference and mass, number of bunches, fruit yield per bunch and the mass of 100 fruits have contributed to the characterization of dissimilarity within groups (Domiciano et al. 2015; Elsafy et al. 2015; Sousa et al. 2017; Sobral et al. 2018). However, several factors are involved in determining which characteristics have the greatest discriminating effect, among these, mainly, the species and the environmental conditions in which the population is established (Oliveira et al. 2007a; Sobral et al. 2018).

Selection based on morphological characters resulted in obtaining current commercial varieties in Arecaceae. For the *Elaeis guineensis* Jacq. (oil palm), the Brazilian breeding program, in the 1980s, showed that selection using morphological characters led to an increase in oil production, as a result of the greater number and weight of bunches, in addition to the reduction in the size of the plant, which facilitates handling (Nunes 1996). As for *E. oleracea*, the breeding program, from the mid-1990s, resulted in the release of the first cultivar in 2004 (Oliveira and Neto 2004), which presents off-season production and smaller fruits with higher pulp yields.

Biometric methods, associated with multivariate statistics, favor obtaining objective information about the study population and have proven to be efficient for defining associations between characters and for directing the selection. Canonical variable analyzis and hierarchical grouping methods are widely used in the characterization of genetic diversity. Both techniques were useful and agreed in the assessment of genetic divergence in *C. nucifera* (Ribeiro et al. 1999; Sobral et al. 2018, 2019). The canonical variables analysis also allows identifying the characters of greater relative importance in the characterization of diversity. Cluster analysis using the UPGMA method (Unweighted Pair-Group Method using Arithmetic Averages) is widely used in palm trees (Oliveira et al. 2007b; Nunes et al. 2008; Manfio et al. 2012; Magalhães et al. 2015; Sousa et al. 2017). This type of analysis allows the evaluation of quantitative and qualitative variables, both separately and together (Domiciano et al. 2015; Cortes et al. 2017; Andrade et al. 2017; El Kadri et al. 2019).

The preservation of the current genetic collection and its efficient use depend on the evaluation of the extent of diversity through the distinction of materials within the species. For this purpose, a germplasm collection of *B. capitata* was established at the Institute of Agricultural Sciences at UFMG, in Montes Claros—MG. The evaluation and characterization of germplasm collections have strategic applications for conservation and breeding research (Nietsche et al. 2015). In this context, we sought to characterize this germplasm, through the evaluation of morphoagronomic characters and the definition of the relative importance of the characters in 18 progenies, using different multivariate approaches.

Materials and methods

Plant material and experimental site

The diversity of 87 individuals comprising 18 half-sib progenies 6-year-old of *Butia capitata* established in the Germplasm Collection of ICA/UFMG, Brazil, was evaluated. The collection was implanted in 2014, in randomized blocks, with three replications

Table 1 Location, collection area, number and criterion used to select the mother plants for fruit collection that originated the of 18 half-sibs

Municipality	Coordinates	Collection area	Number of plants	Selection criteria
Montes Claros	16° 68′ 20″ S; 43° 83′ 96″ W	Experimental orchad	07	More productive plants
Mirabela	16° 26′ 61″ S; 44° 19′ 33″ W	Wild	04	Plants with attractively colored fruits, bunches and large fruits
Bonito de Minas	15° 43′ 34″ S; 44° 69′ 25″ W	Wild	07	Random collection of plants in production

and three plants per plot, spaced 5 m (between rows) × 3 m (within rows). However, due to the difficulty in handling, several plants died, reducing the number of plants per plot. The fruits originate from free pollination of 18 plants selected in the municipalities of Bonito de Minas, Mirabela and Montes Claros, in the north of Minas Gerais, in wild area and experimental orchad with criterion different used to select the mother plants (Table 1). These are the main regions of occurrence of the species in the North of Minas Gerais, based on previous unpublished surveys. The collection is registered in the Sistema Nacional de Gestão do Patrimônio Genético e do Conhecimento Tradicional Associado (SisGen—www.sisgen.gov.br), under number A3AED55, following institutional and national norms, guidelines and legislation.

Qualitative and quantitative descriptors

In the period between June 2019 and May 2021, twenty-three quantitative and thirty-three qualitative descriptors were evaluated in each plant (Table 2) (Mistura et al. 2015). At the beginning and at the end of the study, all plants were evaluated for stem circumference at ground level (mm) and plant height up to insertion of the arrow leaf (mm). The growth in circumference (SCIRC) and in height (TRH) were determined by means of the difference between the evaluated years. In addition, during these 2 years, the issued sheets (EMLE) were evaluated weekly, each new sheet being marked and identified. When the newly issued sheet became the third, the length (LEL) and width (LEW) were measured using a tape measure.

Bunches were harvested when more than 30% of the fruits reached maturity, which was visually defined by the change in color from green to yellow/orange. The number of bunches (NBU) was obtained by adding all the bunches harvested per plant. In each bunch, the length (BUL), the mass of the bunches (stems, rachillae and fruits) and of the fruits and the number of fruits were evaluated. The sum of the mass of bunches (WBU) and fruits (WFR) and the number of fruits (FRN) was determined for each individual. Samples of 20 fruits, randomly collected from each bunch, were used to determine the length (FRL), diameter (FRW) and thickness (FRTH) of the fruits. The time between the emission of the leaf and the harvest of the bunch in the axil of this leaf, called time to ripening (RITI), was also evaluated.

For fruit flavor (FRTT), each bunch was evaluated by three volunteer experimenters who assigned grades from 1 to 5 for one ripe fruit in natura each, five for the best flavor and one for the worst. The pulp was obtained from a sample of ten fruits per plant and it was used for analysis of total soluble solids (TSS), pH and total titratable acidity (TTA) (AOAC 1990; Magalhães et al. 2017).

Qualitative observations were classified according to Mistura et al. (2015), with the addition of the characteristics leaf density and adherence of the fruit to the bunch (Table 2).

Statistical analysis

The average values of each plot (three plants) were considered for the statistical analysis. Mean, minimum value, maximum value, standard deviation (SD) and coefficient of variation (CV%) were evaluated for quantitative characters. A preliminary selection of quantitative descriptors was performed using univariate analysis of variance (ANOVA). Those significant were subjected to multivariate analysis of variance (MANOVA) using the Pillai test with 5% significance.

The selected quantitative characters were submitted to simple correlation by Pearson's correlation coefficient. Then the analysis of canonical variables

Table 2 Evaluations of quantitative (1–23) and qualitative (24–56) descriptors in *B. capitata* progenies

N	Trait	Abbreviations	Un	*N*	Trait	Abbreviations	Un
1	Emited leafs	EMLE	Number	29	Ovoid fruit	OVFR	Code
2	Stem circumference	SCIRC	cm	30	Oblong fruit	OGFR	Code
3	Tree height	TRH	mm	31	Uniform maturation	UFM	Code
4	Leaf length	LEL	mm	32	Intermediate maturation	IM	Code
5	Leaf width	LEW	mm	33	Uneven maturation	UVM	Code
6	Ratio leaf length/leaf width	LEL/LEW	mm	34	Yellow male flowers	YMF	Code
7	Leaf number	LEN	Number	35	Pink male flowers	PKMF	Code
8	Bunch length	BUL	mm	36	Purple male flowers	PPMF	Code
9	Number of bunches	NBU	Number	37	Yelow rachillae	YRCH	Code
10	Weight of bunches	WBU	kg	38	Green rachillae	GRCH	Code
11	Weight of fruits	WFR	kg	39	Cream fruit	CRFR	Code
12	Fruit number	FRN	Number	40	Yellow fruit	YFR	Code
13	Weight per fruit	WPFR	kg	41	Orange fruit	OFR	Code
14	Fruit length	FRL	mm	42	Reddish-orange fruit	ROFR	Code
15	Fruit width	FRW	mm	43	Red fruit	RFR	Code
16	Fruit thickness	FRTH	mm	44	Purple fruit	PPFR	Code
17	Ratio fruit length/fruit width	FRL/FRW	Ratio	45	Tree growth habit-intermediate	TRGH2	Code
18	Total soluble solids	TSS	%	46	Tree growth habit-prostrate	TRGH3	Code
19	pH	pH	Number	47	Tree growth habit-erect	TRGH1	Code
20	Total titratable acidity	TTA	%	48	Canopy density-intermediate	CPD2	Code
21	Ratio TSS/TTA	TSS/TTA	Ratio	49	Canopy density-low	CPD3	Code
22	Ripening time	RITI	Days	50	Canopy density-high	CPD1	Code
23	Fruit taste	FRTT	Scale	51	Leaf growth habit-intermediate	LEGH2	Code
24	High fruit adherence	HFRA	Code	52	Leaf growth habit-prostrate	LEGH3	Code
25	Intermediate fruit adherence	IFRA	Code	53	Leaf growth habit-erect	LEGH1	Code
26	Low fruit adherence	LFRA	Code	54	Leaf color-light Green	LEC2	Code
27	Roundish fruit	RUFR	Code	55	Leaf color-dark Green	LEC3	Code
28	Oblate fruit	OTFR	Code	56	Leaf color-greyish	LEC1	Code

(CV) was performed to investigate the relationship and determine the main effective characters in the discrimination between the progenies. The first and second canonical variables (CV1/CV2) were used to create a scatterplot.

In determining the relative importance of both quantitative and qualitative characters, the criterion proposed by Singh (1981) was used, based on the Mahalanobis distance. Additionally, cluster analysis, the UPGMA method, and the Mahalanobis distance were applied to measure dissimilarity.

In the qualitative observations, the occurrence of each classifier was transformed into a percentage matrix of occurrence of each note (Cruz et al. 2012). To calculate the genetic dissimilarity (dii,) between genotypes i and i' (i = 1,2,3… 18 genotypes) the estimator, it was used:

$$d_{ii} = \sqrt{\sum_{j=1}^{j}}\left[\frac{\sum_{k=1}^{k}\left(F_{ijk} - F_{i'jk}\right)^{2}}{jk}\right]$$

where F_{ijk} is the frequency at which genotype i (i = 1, 2, 3…18) received for descriptor j (j = 1, 2…0.33) the score associated with its class k, with F_{ijk} values ranging from 0 to 1; K refers to the number of descriptor classes; J is the number of descriptors (33). After obtaining this matrix, a dendrogram was created by using the UPGMA method.

In order to study the set of dissimilarities (quantitative and qualitative characteristics), the two matrices were standardized in order to have their values varying between 0 and 1, by the equation:

$$Vn = \frac{[1 + (Vobs - Vmax)]}{Vmax}$$

where V*n* is the standardized value; V*obs* the observed value and V*max* is the maximum value of the array. Subsequently, the weighted average was calculated by considering the number of descriptors evaluated in each matrix. To be complementing this, another dendogram was created by using the UPGMA method.

The cut-off point of the dendrograms was established according to Mojena (1977). The cophenetic correlation was determined for each dendrogram. The correlation between the three dissimilarity matrices was estimated by using the Mantel significance test with 1,000 simulations. A graphical representation of the phenotypic values for each progeny was also obtained. All statistical analyzes were performed by using the R software (R Core Team 2016), for multivariate analyzes the Multivariate Analysis package was used.

Results

The progenies showed significant diversity ($p \leq 0.05$), considering 11 quantitative characters by the F test in ANOVA. These characters also allowed to discriminate the progenies by the Pillay test in the MANOVA ($p < 0.01$). Variability is confirmed for quantitative characters such as number of fruits in the bunch and fruit size, as well as for some qualitative characters such as rachis color and fruit color and shape (Fig. 1). Quantitative variables related to production, such as number and mass of bunches and fruits, showed the highest CV values (Table 3). The smallest CVs, below 3.66%, were obtained for leaf length and width (LEL/LEW), fruit length and width ratio (FRL/FRW) and fruit width (FRW). Fruit characteristics, total titratable acidity and fruit flavor/acceptance showed intermediate CV (Table 3).

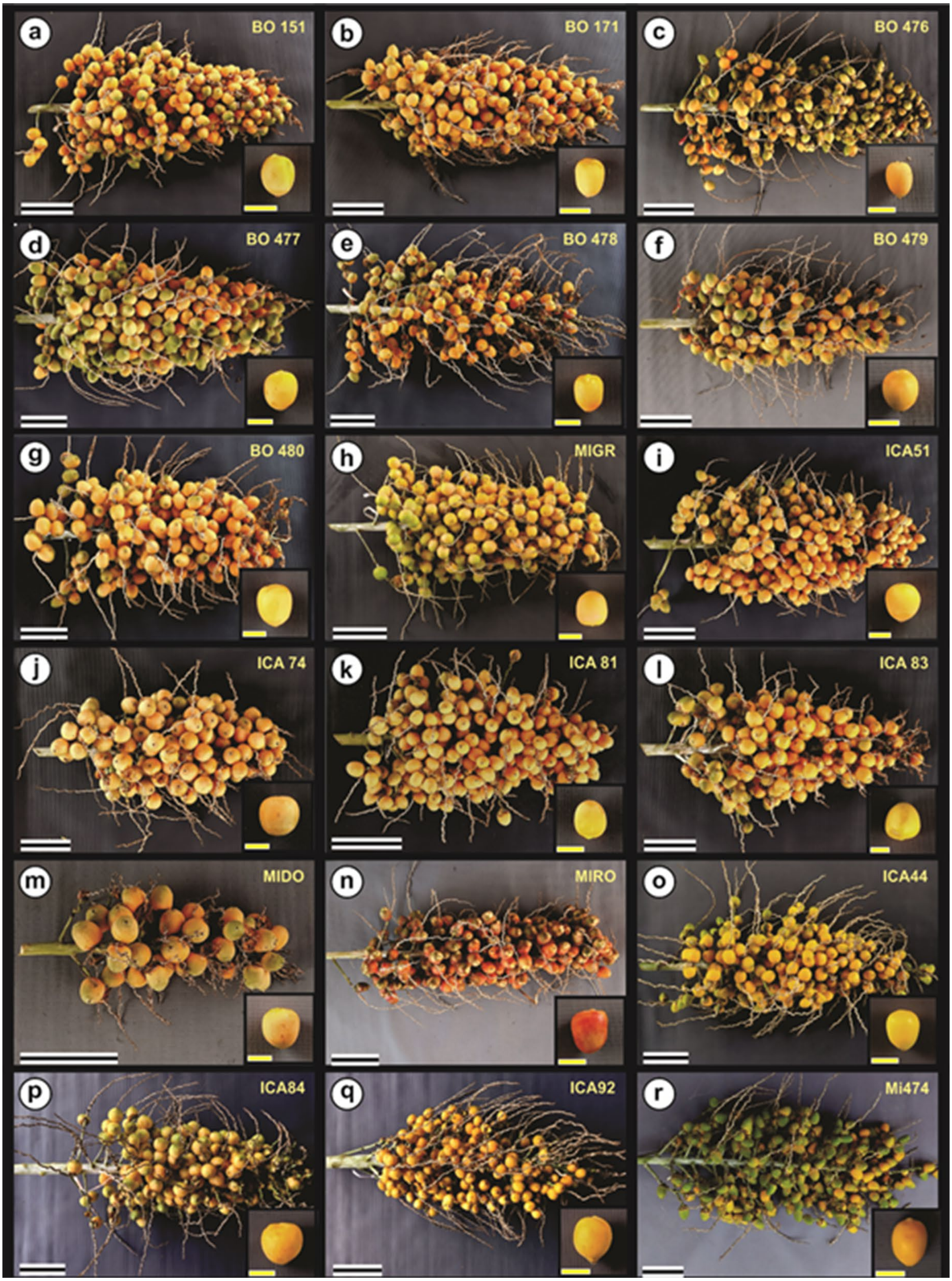
The phenotypic correlations (r_p) estimated between the 11 quantitative traits ranged from -0.47 to 0.99. Leaf length was significantly and positively correlated with all characters, except the fruit length to width ratio. The significance ranged from 0.01 to 0.05 for the T test (Table 4). The highest r_p value was observed between WFR and WBU ($r_p = 0.99$), followed by associations between FRN and WBU and FRN and WFR with values of 0.96 each. Another relevant association above 0.90 was between LEL and LEW. The ratio between fruit length and width was negatively correlated with fruit thickness, with a value of $r_p = -0.47$. Other significant and high associations were observed, among which we highlight: WBU and NBU; WFR and NBU and FRN and NBU, with values of 0.77, 0.77 and 0.70, respectively.

The first and second canonical variables (CV) accounted for 71.85% of the total variation, allowing the 11 quantitative characters used in the characterization of the 18 progenies to be reduced to a two-dimensional plane (Fig. 2). The first (CV1) accounted for 50,36% of the total variation and was correlated mainly with fruit flavor (0.64), leaf length (-0.46) and leaf width (-0.41). The characters of fruit length and width ratio (0.76), leaf length and width (-0.53) were mainly correlated with CV2, which explained 21.49% of the variation found. In addition, the analysis allowed identifying such characters as the most important for the characterization of genetic divergence in the studied population.

The graphical dispersion showed the presence of isolated progenies indicating those most divergent from the others. It showed the MIRO progeny, with high values for the ratio between the length and width of the fruit (FRL/FRW). The MIGR progeny differed from the others mainly due to the taste of the fruit, however, with lower values.

Leaf length (LEL) and leaf width (LEW) showed greater relative importance, with 44.10% and 31.99%, respectively, using Singh's method (1981) (Fig. 3). Among the qualitative characters, yellow (YFR), orange (OFR), ovoid (OVFR), oblate (OTFR), oblong (OGFR), roundish (RUFR), reddish orange (ROFR) and cream (CRFR) fruits were the ones that most contributed for the description between the progenies (Fig. 4).

The quantitative descriptors allowed the formation of the dendrogram with four different groups, considering Mojena's cut-off point of 20.04 (Fig. 5). The MIRO progeny were grouped separately (Fig. 5), showing a reddish–purplish color on their epicarp (Fig. 1). The graphic representation of the averages of the *B. capitata* progenies showed that this progeny has high values for the ratio between length and width


a
BO 151
b
BO 171
c
BO 476
d
BO 477
e
BO 478
f
BO 479
g
BO 480
h
MIGR
i
ICA51
j
ICA 74
k
ICA 81
l
ICA 83
m
MIDO
n
MIRO
o
ICA44
p
ICA84
q
ICA92
r
Mi474

◂**Fig. 1** Random individual bunches and fruits of the progenies from the ICA/UFMG germplasm collection: **a** BO151; **b** BO171; **c** BO476; **d** BO477; and **e** BO478; **f** BO479; **g** BO480; **h** MIGR; **i** ICA51; **j** ICA74; **k** ICA81; **l** ICA83; **m** MIDO; **n** MIRO; **o** ICA44; **p** ICA84; **q** ICA92 and **r** MI474. The scale bar for bunches is 10 cm and for fruits is 2 cm

of the fruit and low values for the production characteristics, number of bunches (NBU), mass of bunches (WBU) and fruits (WFR), number of fruits (FRN) and length of fruits (FRW).

The second group, constituted by the progenies MI474, BO151, BO171, BO480 and ICA84 stood out from the others by the highest values of total titratable acidity (TTA) and smaller values for leaf length (LEW). The third group, with BO476 and BO479, was identified with lower LEL/LEW estimates. Finally, the fourth group, consisting of the other genotypes, did not show a pattern in their averages that would make their characterization possible. In this group, the ICA81 progeny stands out, which presented the highest averages for five of the 11 quantitative descriptors, mainly regarding the number and mass of bunches and fruits. On the other hand, some progenies had very low productive behavior such as MIDO and MIGR.

The dendrogram for qualitative descriptors discriminated the progenies into two groups, considering Mojena's cut-off point of 90.21 (Fig. 6). The progeny (MIRO) constituted the first group, while the others were in the second. This progeny stood out from the other genotypes due to the highest notes of purple male flower (PPMF), reddish orange fruit (ROFR), red fruit (RFR), purple fruit (PPRF) and low leaf density (CPD3).

In the joint analysis, the association between quantitative and qualitative traits resulted in the formation of two groups, by considering Mojena's cut-off point of 0.44 (Fig. 7). The MIRO progeny remains isolated in a group with very divergent fruit color and size characteristics, in addition to lower fruit production.

Mean dissimilarity estimates ranged from 12.17 to 27.47 for quantitative data, from 52.08 to 161.95 for qualitative data, and from 0.2 to 0.84 in the joint analysis (Table 5). In quantitative descriptors, the MI474 progeny was the most divergent (the most distant) in relation to most genotypes (55.56%), followed by the MIRO and ICA81 progenies. In the qualitative and joint analysis, the MIRO progeny was the most divergent.

The joint dissimilarity matrix showed a high correlation with the qualitative matrix, while in the associations between the quantitative dendrogram and the other matrices, the correlation indicated was, respectively, moderate and low (Table 6). However, all correlations were significant by the Mantel test ($p \leq 0.05$).

Discussion

The results of the present study indicated that of the 23 quantitative traits applied, 11 were efficient to evaluate the genetic diversity among the 18 progenies of *B. capitata*. Among the characters, three are vegetative while the others are associated with the reproductive system of the species. The residual variation coefficients of the descriptors associated with the vegetative part were low, indicating a smaller influence of environmental effects in the determination of these characters. On the other hand, for some characteristics associated with the reproductive part, the residual variation coefficient values were high.

In general, in plant species, the variations observed in the characteristics associated with the reproductive process, production and productivity, are largely due to the components of environmental effects and a small portion is determined by the genetic component (Resende 2015). Although in the present study, genetic parameters such as heritability were not estimated, other studies with palm tree species confirm the results of this study (Fajardo et al. 2018; Bedjaoui and Benbouza 2020).

The high and significant phenotypic correlations found highlight once again to the characters such as number and mass of fruits, mass of bunches, length and width of leaves. The association between two traits can be determined by genetic, environmental components or the association of both, and the greater the correlation, the greater the chance that the genes that control the number of fruits could be linked or close to the genes that control the mass of the fruits and bunches (Valadares et al. 2022). Some authors working with palm trees, also observed high correlations between leaf growth and fruit production traits (Silva and Scariot 2013; Souza 2016). The present result may be related to the greater

Table 3 Estimates of the mean square of the genotypes (Qmg), coefficient of residual variation (CV), minimum (Min), maximum (Max) and mean value of the quantitative traits of progenies (n = 18) of *B. capitata*

Descritors	Abbrev.	Qmg	CV (%)	Min	Max	Mean (± SE)
Emited leafs	EMLE	4.5^{ns}	7.43	15.00	24.00	20.72 ± 0.89
Stem circumference	SCIRC	57.73^{ns}	41.02	6.50	49.00	28.35 ± 6.71
Tree height	TRH	43.28^{ns}	25.38	1.00	37.67	20.91 ± 3.06
Leaf length	LEL	444.03**	6.67	149.19	208.16	177.98 ± 6.86
Leaf width	LEW	180.1*	6.08	112.53	158.87	133.85 ± 4.7
Leaf length/Leaf width	LEL/LEW	0.01*	2.92	1.21	1.44	1.33 ± 0.02
Leaf number	LEN	18.57^{ns}	8.96	29.67	47.00	36.21 ± 1.87
Bunch length	BUL	19.78^{ns}	8.63	42.97	62.58	50.58 ± 2.52
Number of bunches	NBU	30.26*	15.80	12.00	32.00	22.54 ± 2.06
Weight of bunches	WBU	205.72*	31.05	5.75	66.02	30.23 ± 5.42
Weight of fruits	WFR	172.81*	31.29	5.14	58.65	27.2 ± 4.91
Fruit number	FRN	2390787.37*	34.26	625.00	7241.00	2891.21 ± 571.94
Weight per fruit	WPFR	2.49^{ns}	12.97	7.71	13.83	9.57 ± 0.72
Fruit length	FRL	2.43^{ns}	4.52	24.75	30.39	26.83 ± 0.7
Fruit width	FRW	2.39*	3.65	22.45	27.66	24.77 ± 0.52
Fruit thickness	FRTH	1.71^{ns}	19.45	5.30	12.25	6.86 ± 0.77
Fruit length/fruit width	FRL/FRW	0.01*	3.47	0.97	1.19	1.09 ± 0.02
Total soluble solids	TSS	1.29^{ns}	9.69	8.15	13.44	11.12 ± 0.62
pH	pH	0.02^{ns}	2.76	3.62	4.30	3.97 ± 0.06
Total titratable acidity	TTA	0.18*	14.93	0.81	2.80	1.86 ± 0.16
Ratio TSS/TTA	TSS/TTA	2.56^{ns}	25.56	4.40	12.76	6.48 ± 0.96
Ripening time	RITI	264.67^{ns}	3.70	293.41	366.63	335.04 ± 7.15
Fruit taste	FRTT	0.16*	6.75	2.77	4.20	3.56 ± 0.14

ns Not significant, *EP* Standard error of the mean

*Significant at 5% by F-test

**Significant at 0.01 by F-test

Table 4 Pearson correlation (r_p) between quantitative traits evaluated in 18 half-sib progenies of *B. capitata*

Caracter	LEL	LEW	LEL.LEW	NBU	WBU	WFR	FRN	FRW	FRL.FRW	TTA	FRTT
LEL	1										
LEW	0.92**	1									
LEL.LEW	0.50**	0.13^{ns}	1								
NBU	0.51**	0.41**	0.40*	1							
WBU	0.49**	0.31^{ns}	0.55**	0.77**	1						
WFR	0.46**	0.28^{ns}	0.54**	0.77**	0.99**	1					
FRN	0.43**	0.24^{ns}	0.56**	0.70**	0.96**	0.96**	1				
FRW	0.39*	0.45**	-0.03^{ns}	0.20^{ns}	0.07^{ns}	0.09^{ns}	-0.13^{ns}	1			
FRL.FRW	-0.20^{ns}	-0.29^{ns}	0.16^{ns}	-0.20^{ns}	0.07^{ns}	0.06^{ns}	0.14^{ns}	−0.47*	1		
TTA	0.32*	0.26^{ns}	0.24^{ns}	-0.09^{ns}	0.04^{ns}	0.03^{ns}	0.06^{ns}	0.08^{ns}	-0.12^{ns}	1	
FRTT	0.15^{ns}	0.03^{ns}	0.32*	0.17^{ns}	0.36*	0.36*	0.32*	-0.05^{ns}	0.04^{ns}	-0.21^{ns}	1

ns Not significant

*Significant at 5% by T-test

**Significant at 0.01 by T-test

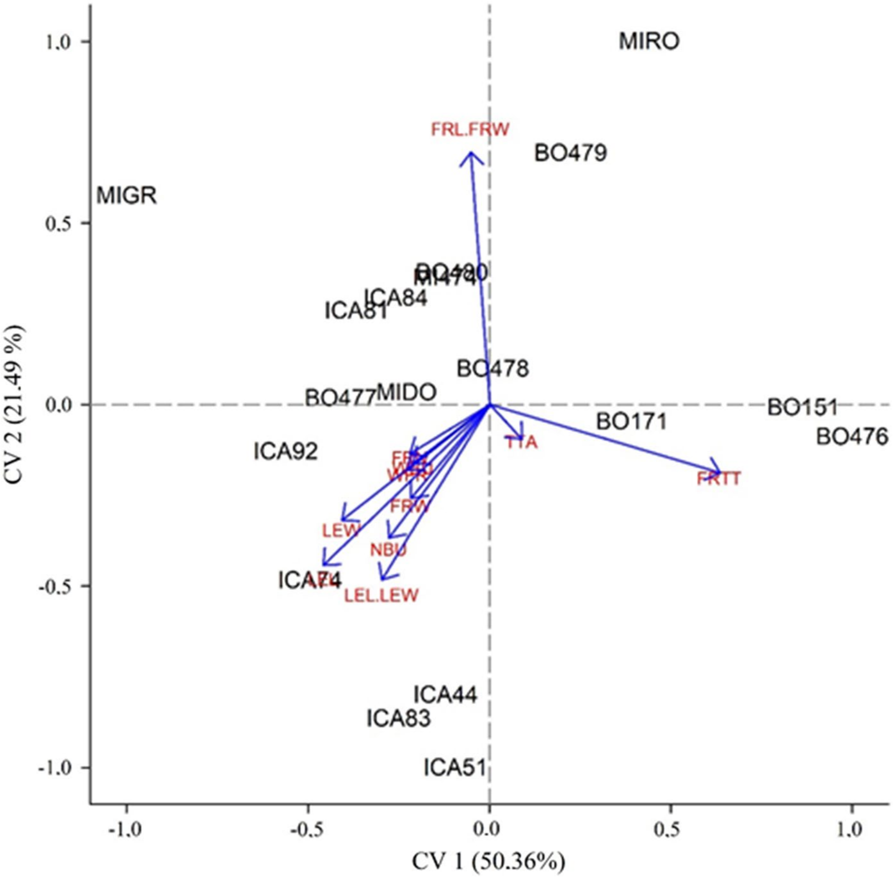


Fig. 2 Graphic dispersion of the canonical variables for the progenies (n = 18) of *B. capitata*. Fruit length to width ratio (FRL/FRW), fruit width (FRW), fruit flavor (FRTT), total titratable acidity (TTA), leaf length to width ratio (LEL/LEW), leaf length (LEL), leaf width (LEW), fruit number (FRN), fruit weight (WFR), bunch weight (WBU) and number of bunch (NBU)

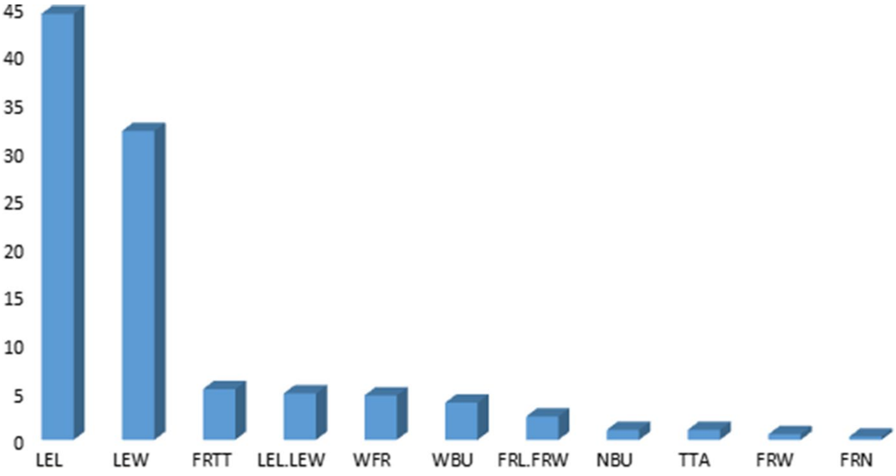


Fig. 3 Relative contribution of the evaluated quantitative characteristics (%), according to Singh's methodology (1981), in 18 progenies of *B. capitata*. Leaf length (LEL), leaf width (LEW), fruit flavor (FRTT), leaf length to width ratio (LEL/LEW), fruit weight (WFR), bunch weight (WBU), fruit length to width ratio (FRL/FRW), bunch number (NBU), total titratable acidity (TTA), fruit width (FRW) and fruit number (FRN)

production of photoassimilates by plants with larger leaves (Cunningham 1997), which indicates that more vigorous *B. capitata* plants produce more fruits. The existence of this relationship may favor a possible early selection of individuals in breeding programs for the species, since the evaluation of production traits only begins after sexual maturity, which can take several years, between 4 and 5 years for *B. capitata* (Dias et al. 2022).

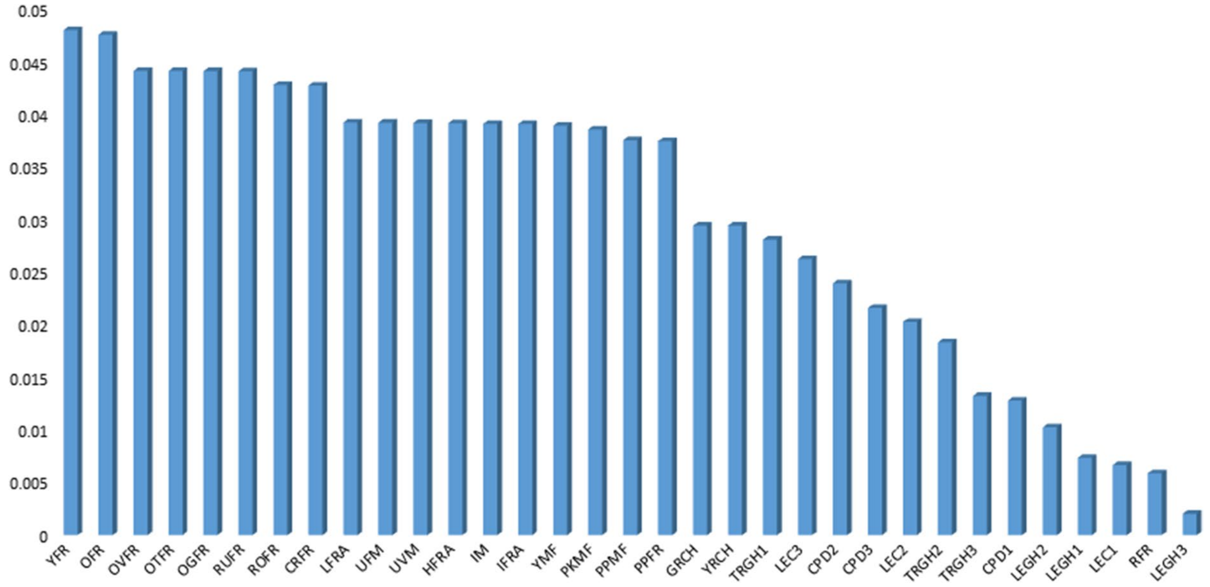


Fig. 4 Relative contribution of the evaluated qualitative characteristics (%), according to Singh's methodology (1981), in 18 progenies of *B. capitata*. Yellow fruit (YFR), orange fruit (OFR), ovoid fruits (OVFR), oblate fruits (OTFR), oblong fruits (OGFR), red fruit (RFR), reddish orange fruits (ROFR), fruits cream (CRFR), low frit adherence (LFRA), uniform ripeness (UFM), uneven ripeness (UVM), high fruit adherence (HFRA), medium ripeness (IM), intermediate fruit adherence (IFRA), yellow male flower (YMF), pink male flower (PKMF), purple male flower (PPMF), purple fruit (PPFR), green rachis (GRCH), yellow rachis (YRCH), tree growth habit-upright (TRGH1), leaf color-v dark green (LEC3), leaf density-intermediate (CPD2), leaf density-low (CPD3), leaf color light green (LEC2), intermediate tree growth habit (TRGH2), growth habit tree-prostrate (TRGH3), leaf density-high (CPD1), leaf growth habit intermediate (LEGH2), leaf growth habit-erect (LEGH1), leaf color grayish (LEC1), red fruits (RFR) and leaf growth habit-prostrate (LEGH3)

The characters with greater relative importance in the discrimination of the progenies were the same both in the canonical variables analysis and by the Singh method. In addition, the graphic dispersion data indicated the most divergent progenies. Determining the relative importance of a character is extremely important, besides reducing work, it informs the researcher precisely which are the main descriptors that need to be evaluated in a specific population (Iezzoni and Pritts 1991).

For *Cocos nucifera*, it was defined that, among the most important characters, some were similar to those of the present study (Sobral et al. 2019). This methodology has been successfully used in studies on genetic divergence in various plant species (Sobral et al. 2018; Brito et al. 2021). Similarly, in *Phoenix dactylifera* (date palm) cultivars, the traits leaf width, fruit width and epicarp color were the most efficient in separating genotypes (Elsafy et al. 2015). In this way, these characteristics should be prioritized in future stages of the breeding program for *B. capitata*, since it consists of an important contribution to identifying the dissimilarity of the families and the real possibility of obtaining gains by selection, representing the rational use labor, saving time and material resources. On the other hand, characteristics with little contribution to the calculation of genetic dissimilarity such as number of bunches, total titratable acidity, fruit width, number of fruits, plant growth habit, density and color of leaves can be disregarded in future evaluations (Machado et al. 2017). In the studied population most of these characters are correlated and are redundant.

Among the grouping analyzes carried out (quantitative, qualitative data and joint analysis), the use of 11 quantitative descriptors was the most informative and was able to discriminate the 18 progenies into four groups. Additionally, it is worth mentioning that in all generated dendrograms it is possible to verify that the MIRO progeny was grouped alone, whether considering quantitative or qualitative descriptors or a combination of both. Some characters were more

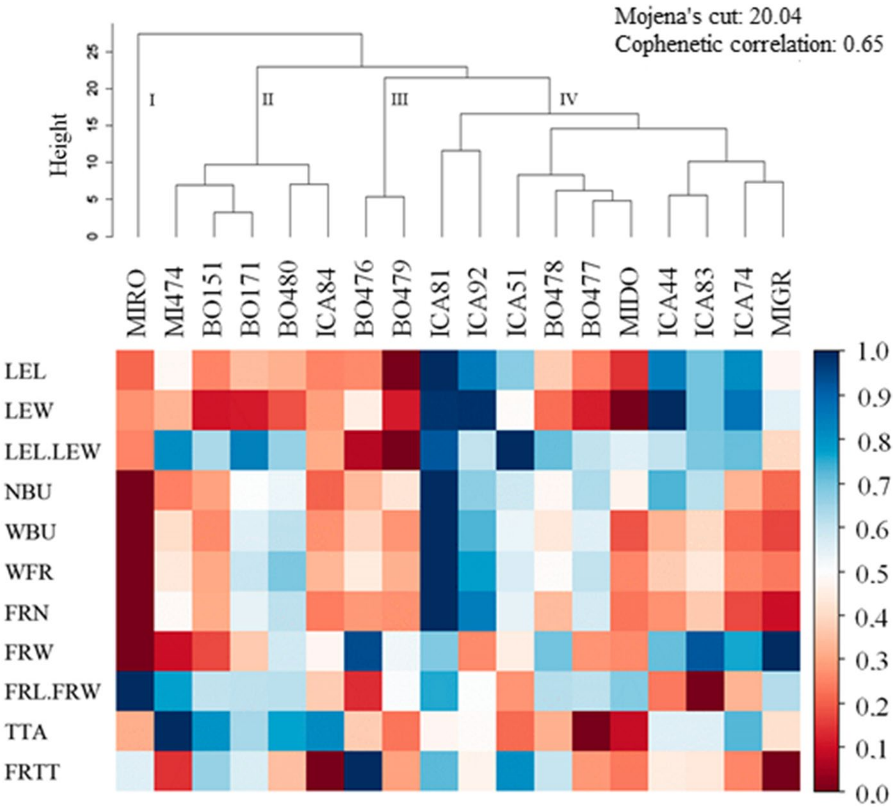


Fig. 5 Dendrogram obtained by the UPGMA method using dissimilarity matrices and graphical representation of phenotypic values between progenies (n = 18) of *B. capitata* for 11 quantitative traits

expressive in the characterization of diversity in *B. capitata* and also allowed the allocation of the MIRO progeny, alone in a group, both in the cluster analysis by UPGMA and in the analysis of canonical variables, as well as by the Singh method, which scored the color of the fruit and leaf size as characters of high relative importance. Therefore, MIRO can be considered the most divergent material, which may contribute to its classification as a morphotype or variety of *B. capitata*. Although this genotype has low productive performance, the reddish-purplish fruits highlight it both for its potential as a functional food, due to the bioactive compounds in its epicarp (Aguiar et al. 2014), and for its use in landscaping. The unusual coloration of the fruits in the MIRO progeny would be another attraction for the ornamental use of the species (Pivetta et al. 2010; Moraes et al. 2015).

Another worth mentioning progeny is ICA-81, which presented high and significant averages for the main quantitative characteristics identified in this study, among them: length and width of leaves, number and mass of bunches and number and mass of fruits. These descriptors were identified as the most relevant in all analyzes performed (ANOVA, phenotypic correlations, canonical variables, Singh's method and in the cluster analysis and graphical representation of phenotypic values between progenies). Considering the genetic divergence data and the average performance of the progenies, the combination of ICA-81 with other progenies such as MIRO and MI474 should be considered for the continuation of the species improvement program. The progenies from this site originated from plants established in an experimental orchard, unlike the others that originated from naturally occurring populations. The distribution of the species in the natural environment is aggregated in low lands (Carvalho et al. 2015). Therefore, although most of the genetic diversity in native areas is distributed within the population (Magalhães et al. 2015), denser planting may have contributed to greater crossbreeding among all individuals, generating more related progenies and constituting a more uniform group.

The reproductive biology of *B. capitata* is an important factor that can lead to greater genetic diversity. The species presents monoecy and dichogamy

Fig. 6 Dendrogram obtained by the UPGMA method using dissimilarity matrices and graphical representation of the phenotypic values between the progenies (n = 18) of *B. capitata* and the qualitative characteristics

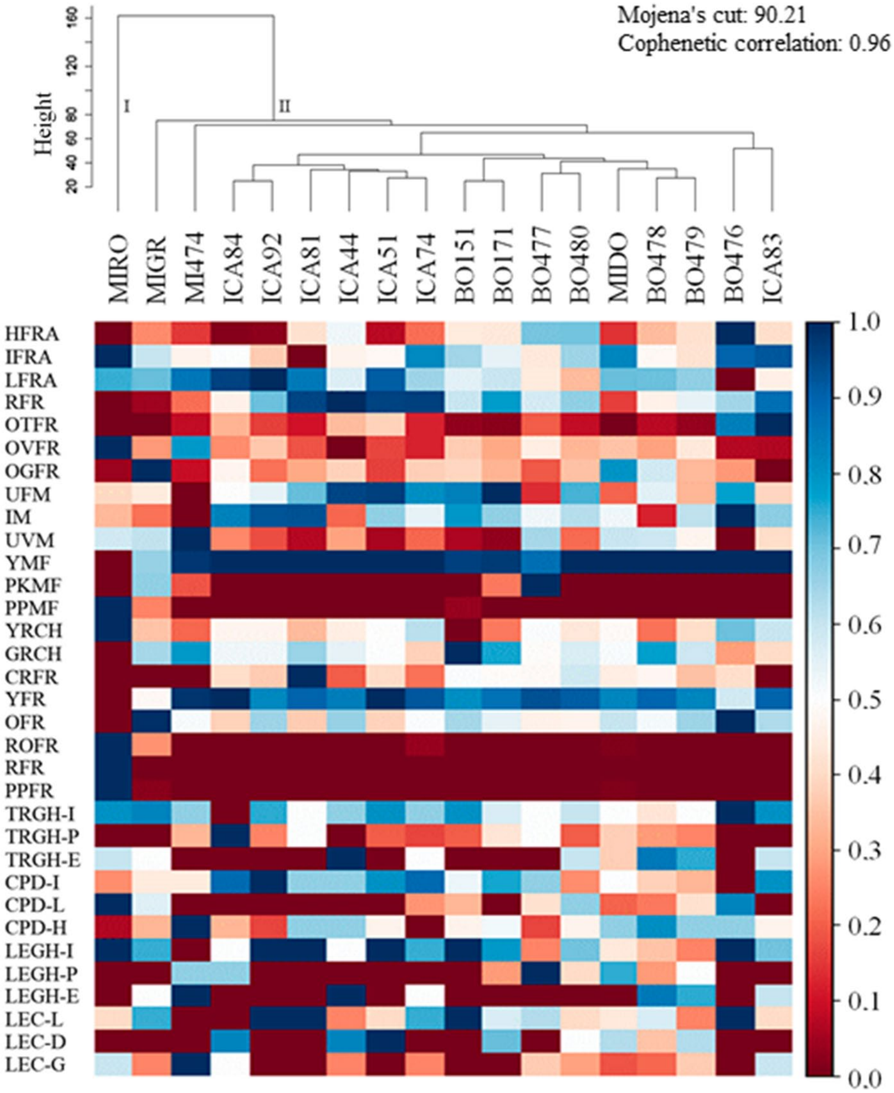


Fig. 7 Dendrogram obtained by the UPGMA method using dissimilarity matrices based on the set of quantitative and qualitative characteristics of *B. capitata*

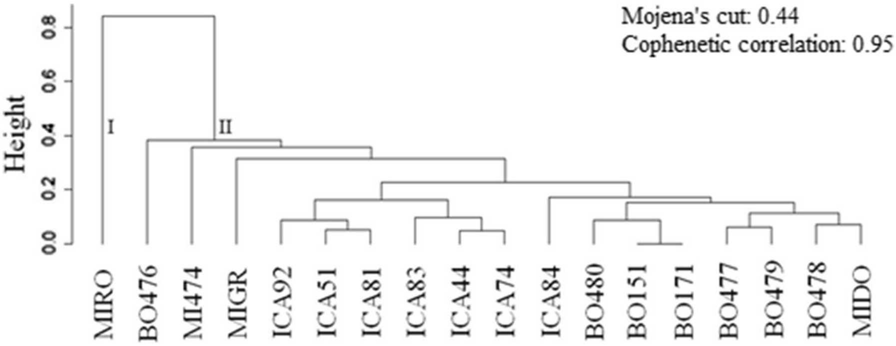


Table 5 Genotypic distances (dendrogram with isolated and combined observations of quantitative and qualitative characters) for progenies (n = 18) of *B. capitata*

Progenies	Quantitatives			Qualitatives			Combined		
	DM	MP	MD	DM	MP	MD	DM	MP	MD
BO151	14.82	BO171	ICA81	62.96	BO171	MIRO	0.26	BO171	MIRO
BO171	14.9	BO151	ICA44	52.08	BO151	MIRO	0.21	BO151	MIRO
BO476	23.67	BO479	MI474	82.4	ICA83	MIRO	0.42	ICA83	MIRO
BO477	14.58	MIDO	MI474	57.36	BO479	MIRO	0.23	BO479	MIRO
BO478	12.77	BO171	MI474	53.6	BO479	MIRO	0.2	BO171	MIRO
BO479	21.17	BO476	MI474	48.61	BO478	MIRO	0.23	BO477	MIRO
BO480	20.32	ICA84	MIRO	52.77	BO171	MIRO	0.24	BO171	MIRO
ICA44	23.95	ICA83	MI474	56.66	ICA74	MIRO	0.29	ICA74	MIRO
ICA51	17.93	BO478	ICA84	57.57	ICA74	MIRO	0.25	ICA81	MIRO
ICA74	17.32	MIGR	BO479	54.73	ICA51	MIRO	0.24	ICA44	MIRO
ICA81	23.65	ICA51	ICA84	55.48	BO171	MIRO	0.28	ICA51	MIRO
ICA83	17.87	ICA44	MI474	65.05	ICA44	MIRO	0.29	ICA44	MIRO
ICA84	21.92	BO151	ICA81	54.43	ICA92	MIRO	0.26	BO171	MIRO
ICA92	19.45	ICA81	MIRO	54.35	ICA84	MIRO	0.25	ICA51	MIRO
MI474	26.07	BO151	BO476	76.75	BO479	MIRO	0.4	BO151	MIRO
MIDO	15.52	BO477	MI474	60.41	BO478	MIRO	0.25	BO478	MIRO
MIGR	16.47	ICA74	MIRO	78.56	MIDO	MIRO	0.35	MIDO	MIRO
MIRO	27.47	BO151	BO480	161.95	MIGR	ICA44	0.84	MIGR	ICA44

DM = Average distance, MP = Closest, MD = Farthest

Table 6 Correlation between dissimilarity matrices for progenies (n = 18) of *B. capitata*

Dendrogram	Correlation between dissimilarity matrices		
	Quantitative	Qualitative	Combined
Quantitative	1	0.35	0.57
Qualitative	< 0.01**	1	0.7
Combined	< 0.01**	< 0.01**	1

**Significant by Mantel test with 1000 simulations

of the protandry type, which contributes to greater cross-fertilization. Associated with this, propagation is carried out exclusively by seeds (Mercadante-Simões et al. 2006; Dias et al. 2022), which leads to the occurrence of high levels of segregating individuals. These reproductive mechanisms provide greater gene flow and were identified as possibly responsible for the high genetic diversity in *E. oleracea*, verified by means of a molecular marker (RAPD) (Oliveira et al. 2007a).

The high genetic diversity observed in *B. capitata* is promising for conservation and improvement programs for the species. However, deforestation rates in the Cerrado biome are high (Hofmann et al. 2021) and the demand for fruits continues to exceed the supply, which puts the survival of the species outside protected reserves at risk (CNCFlora 2012). Based on the results of the present study we suggest that the population of the ICA/UFMG germplasm collection can support programs of conservation and genetic improvement. The present work stands out for being the first study in which *B. capitata* is evaluated under cultivation, and, consequently, for exploring the existing potential in the germplasm, which is crucial for the development of strategies that could allow the conservation of the species and the development of improved cultivars for agronomic use.

It is important to emphasize that this is the first study to characterize the morphoagronomic diversity in *B. capitata*. However, other studies demonstrate, through molecular markers, that the genetic diversity within the genus *Butia* is high (Nunes et al. 2008; Buttow et al. 2010; Gaiero et al. 2011; Nazareno et al. 2011; Nazareno and dos Reis 2014; Magnabosco et al. 2020). In *B. capitata*, only one study characterized diversity at the molecular level (Magalhães et al. 2015), confirming the potential of the species for genetic improvement programs.

In addition to finding a high variability among the 18 evaluated progenies, the statistical tools applied in the present study efficiently indicated: (1) the most divergent progenies; and (2) the most relevant quantitative and qualitative descriptors that should be prioritized in future evaluations of germplasm or segregating populations in *B. capitata*.

Conclusions

This study shows the high phenotypic diversity among the progenies of the *B. capitata* germplasm collection, considering both the univariate and multivariate approaches. The integration of these techniques facilitates the selection and use of characters of interest and also confirms the potential of the species for improvement. Leaf length and width, fruit length and width ratio, fruit flavor and fruit color are the characteristics that most contribute to the discrimination of progenies, and may be prioritized in future research. The evaluation of individuals in the same area, using local control, reduces the influence of the environment and allows inferring that a large part and the phenotypic variation found in the progenies of *B. capitata* is due to genetic factors. The definition of characters of interest is important as a subsidy for improvement programs for this important neotropical palm tree and the methodology used here may be useful in studies with other species of Arecaceae.

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Author contributions PSNL, AMA and SN designed the experiments. PNSS and FHPA contributed to the phenotypic evaluation. PNSS and AMA contributed to the statistical analysis. PNSS wrote the manuscript, PSNL and LMR conceived and supervised the entire study. All authors contributed to the manuscript.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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