

Estimates of genetic parameters based on reproductive and fruit biometric traits of babassu (*Attalea speciosa* Mart.) populations in Maranhão State, Brazil

Estimativas de parâmetros genéticos baseados em características reprodutivas e biométricas de frutos de populações de babaçu (*Attalea speciosa* Mart.) no estado do Maranhão, Brasil

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ABSTRACT

Babassu palm (*Attalea speciosa*) is a native species from the Cerrado-Amazon transition zone with socio-economic importance for agro-extractivist communities in Northeastern Brazil that rely on products derived from its fruits. Babassu productivity is declining due to unsustainable practices and habitat loss. Hence, this research aimed to estimate genetic parameters related to fruit traits of babassu and indicate superior populations for coconut mesocarp production. Babassu trees and fruits were sampled from natural populations in five cities of Maranhão State - Brazil, totaling 150 individuals and 1,500 fruits. The number of bunches and fruits per plant, plant and stipe height, and various fruit and seed morphological traits were measured and used for estimating genetic parameters by the REML/BLUP method with Selegen Software. Fruit width, fruit weight, and mesocarp weight showed high broad-sense heritability and accuracy, suggesting a strong genetic influence and making them excellent candidates for genetic improvement. The high coefficients of relative variation are suitable for selecting promising babassu genotypes. Babassu fruits sampled on Coroatá and Buritirana had the best characteristics for fruit and mesocarp production. We found significant genotypic correlations between various fruit traits (size and weight) that can simplify the selection of high-yield genotypes. Our results are the first report on genetic parameters of important babassu fruit traits, providing valuable data for future breeding programs aiming to increase productivity.

Index terms: Fruit biometric traits; plant breeding; plant genetic resources.

RESUMO

A palmeira babaçu (*A. speciosa*), nativa da zona de transição Cerrado-Amazônia, é de vital importância para comunidades agroextrativistas do Nordeste brasileiro, que utilizam subprodutos de seus frutos. Contudo, sua produtividade está em declínio devido a práticas de manejo insustentáveis e perda de habitat. Assim, esta pesquisa teve o objetivo de estimar parâmetros genéticos relacionados a características de interesse de frutos do babaçu, bem como indicar populações superiores para produção de mesocarpo de coco, acessando populações naturais do Estado do Maranhão, Brasil. Foram amostradas árvores em três localidades de cinco cidades do Maranhão, totalizando 150 indivíduos e 1500 frutos. Foram mensurados o número de cachos e frutos por planta, altura da planta e do estipe, e características morfológicas dos frutos e sementes. Os parâmetros genéticos foram estimados pela metodologia REML/BLUP, pelo Software Selegen. Os caracteres largura do fruto, peso do fruto e peso do mesocarpo apresentaram elevada herdabilidade e acurácia, sugerindo forte influência genética e, que esses caracteres têm potencial para o melhoramento genético da espécie. Os elevados coeficientes de variação relativa observados indicam variação genética suficiente para seleção de genótipos promissores. Frutos amostrados em Coroatá e Buritirana apresentaram melhor desempenho para características para produção. Foram encontradas correlações genotípicas significativas entre vários caracteres de tamanho e peso dos frutos, o que pode simplificar a seleção de genótipos para aumento da produtividade. Este é o primeiro estudo reportando parâmetros genéticos para caracteres de frutos em babaçu, fornecendo informações para seleção de genótipos superiores para programas de melhoramento da espécie.

Termos para indexação: Características biométricas de frutos; melhoramento de plantas; recursos genéticos vegetais.

Agricultural Sciences

Ciênc. Agrotec., 49:e017124, 2025
<http://dx.doi.org/10.1590/1413-7054202549017124>

Editor: Renato Paiva

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Received in August 7, 2024 and approved in December 18, 2024

Introduction

The Cerrado biome, primarily located in Brazil, covers over 2 million km² and is a global biodiversity hotspot (Colli, Vieira, & Dianese, 2020). It hosts more than 12,000 plant species, many are rare and endemic, and has been threatened by agricultural expansion and habitat loss (Mittermeier et al., 2004; Mendonça et al., 2008). Ballesteros-Mejia, Lima and Collevatti (2020) evidenced the highest plant genetic diversity and richness of Cerrado in the northern and central regions.

Babassu is a common name for several palm tree species of the *Orbignya* and *Attalea* genera. The species *Attalea speciosa* (Mart. ex Spreng.) is native to the transition zone between the Cerrado and the Amazon open forests (Fakhouri, Da Silva, & Velasco, 2021). This palm can reach up to 30 m in height and 8 m

in length and starts producing fruits around 8 to 10 years (Santos et al., 2022). Babassu fruits consist of four main parts: the epicarp in the outer layer, the mesocarp, the rigid endocarp, and the almonds (3 to 4 per fruit) (Fakhouri, Da Silva, & Velasco, 2021).

Besides the classical utilization in charcoal production, handicrafts, almonds-oil extraction, and mesocarp flour, the scientific literature has evidenced enormous medicinal potential of active compounds of babassu nuts and mesocarp (Silva et al., 2018; Sales et al., 2020; Barroqueiro et al., 2024; Pinheiro, Corrêa, & Araujo 2024), as well as a biofuel production from nuts residuals (Protásio et al., 2014). However, the babassu production chain has a vulnerable socioeconomic background, since many families from Maranhão, Piauí, Tocantins, and Pará states depend on coconut extraction for their subsistence, living in poverty and social exclusion (Lemos, 2014). Women (known as ‘coconut crackers’) play a key role in these communities and family subsistence (Porro, Veiga, & Mota, 2011).

Babassu annual production has gradually reduced in the last years, and the State of Maranhão is responsible for 89% of Brazilian production (Instituto Brasileiro de Geografia e Estatística

- IBGE, 2024). The species is facing habitat and genetic losses, caused by cattle grazing advances, rudimentary agricultural practices, and unsustainable land management (Santos et al., 2015; Lemos, 2020; Santos et al., 2022). All these factors highlight the importance of accessing babassu natural genetic variability, not only to reinforce conservation and breeding programs, but also to support agro-extractivist communities obtaining palm trees with better productive traits. Therefore, this research aimed to estimate genetic parameters related to interesting fruit traits of babassu (*A. speciosa*), as well as indicate superior populations of babassu for coconut mesocarp production, by accessing natural populations of the Maranhão State.

Material and Methods

Sampling area and plant material

The study was conducted in five municipalities of Maranhão State, Brazil (São Luís, Cantanhede, Coroatá, Viana, and Buritirana) (Figure 1).

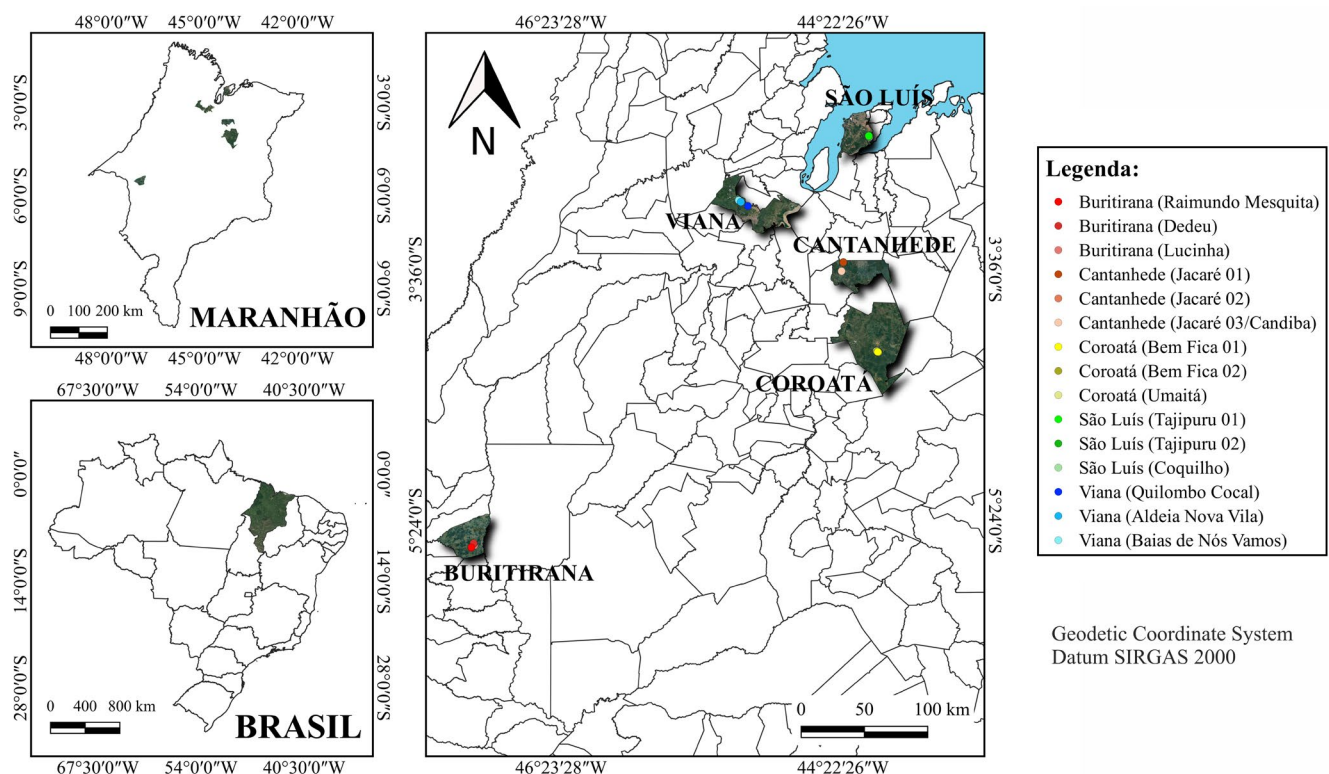


Figure 1: Location of the five municipalities where *Attalea speciosa* populations were sampled in Maranhão State, Brazil. Red dots: Buritirana, located on the Western Mesoregion of the state (sampled areas were three private properties: Raimundo Mesquita, Dedeu, and Lucinha). Orange dots: Cantanhede, located on the Northern Mesoregion of the state (sampled areas were Jacaré and Candiba communities). Yellow dots: Coroatá, located on the Eastern Mesoregion (sampled areas were Bem Fica Village and Umaitá Village). Green dots: São Luís, located on the North (sampled areas were Tajipurú and Coquilho). Blue dots: Viana, located on the North Region (samples areas were Quilombo Cocal, Nova Vila Village, and Baías de Nós Vamos).

In each municipality, three distinct areas of *A. speciosa* populations were analyzed, with a minimum distance of 500 m between areas. Ten individuals at the reproductive stage were randomly selected in each area, totaling 150 georeferenced individuals, and ten fruits per plant (a total of 1500 fruits) were sampled in October and November 2021, a transitional period from the dry to the rainy season. Fruits were packed in nylon bags and transported to the Associação das Mulheres Quebradeiras de Coco de Povoado Candiba (Cantanhede, Maranhão, Brazil) for extraction of the mesocarp and seeds. Mesocarp was weighed, packed in plastic bags after extraction, and stored at 10 °C at the Post-Harvest Laboratory (LAPOC), Maranhão State University (São Luís, MA, Brazil).

Morphometric descriptors of trees and fruits

The parameters analyzed in trees were the number of bunches per plant (NBP, unit), number of fruits per bunch (NFB, unit), stipe circumference at ground level (SCG, cm), stipe circumference at breast level (SCB, cm), and plant height (PH, m). A 20-m measuring tape was used to determine SCB. PH was determined using an Opti-Logic 1000LH rangefinder, which also allowed to measure the average distance between plants of 5 m.

For the morphological characterization of the fruits, a digital caliper (Zaas Precision®, Amatoools, Piracicaba-SP, Brazil) was used. Analyzed traits were: fruit length (FL, mm), fruit width (FW, mm), average fruit weight (AFW, g), nut length (NL, mm), average nut weight (ANW, g), and average mesocarp weight (AMW, g).

Estimation of genetic parameters and covariance components

Statistical analyses were performed using the software SELEGEN-REML/BLUP (Statistical System and Computerized Genetic Selection by Mixed Linear Models) version 2016, model 83 (Resende et al., 2016). The analysis of deviance (ANADEV) or likelihood ratio test (LRT) were carried out using the model with and without the effect, according to Resende (2007). Results were compared with the chi-square (χ^2) value (at 10, 5, and 1% significance level), considering one degree of freedom.

The genetic parameters were estimated using the mixed model Restricted Maximum Likelihood procedure and Best Linear Unbiased Prediction (REML/BLUP) methodology, following the model below (Equation 1):

$$y = Xu + Zg + e_2 \quad (1)$$

where: y is the observed data vector, u is the fixed effects vector (overall mean), g is the random effect vector of total genotypic effects, and e corresponds to the vector of errors/residuals (random). X and Z represent the incidence matrices for vectors u and g , effects, respectively.

The estimates of the variance components by REML via the EM algorithm were given by the following mixed model equations (Equations 2, 3, and 4):

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}((1-h^2)/h^2) \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix} \quad (2)$$

$$\hat{\sigma}_e^2 = [y'y - \hat{b}'X'y - \hat{g}'Z'y] / [N - r(X)] \quad (3)$$

$$\hat{\sigma}_g^2 = [\hat{g}'A^{-1}\hat{g} + \hat{\sigma}_e^2 trC^{22}] / N_g \quad (4)$$

$$C^{22} \text{ is from the form } \begin{bmatrix} C^{11} & C^{12} \\ C^{21} & C^{22} \end{bmatrix} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}(\sigma_e^2 / \sigma_g^2) \end{bmatrix}^{-1}$$

Where: $r(X)$ is the rank or number of linearly independent columns of X , N_g is the number of random elements (individuals), A is the additive genetic relatedness matrix, tr is the matrix of dash operator, given by the sum of the diagonal elements of the matrix; N is the total number of data, and h^2 is the individual broad sense heritability, also calculated by $h^2 = \hat{\sigma}_g^2 / (\hat{\sigma}_g^2 + \hat{\sigma}_e^2)$.

Estimated parameters were the broad-sense heritability h_a^2 , selective accuracy (r_{aa}), coefficient of genetic variation ($CVg\%$), experimental variation ($CVexp\%$), and coefficient of relative variation ($CVr = CVg\% / CVexp\%$), where the magnitude of h_a^2 and r_{aa} were classified according to Resende et al. (1998) (Table 1).

Table 1: Classification of the magnitudes of heritability h_a^2 and selective accuracy (r_{aa}) used to estimate the genetic parameters of *A. speciosa*.

Classification	Individual heritability	Selective accuracy
Low	$0.01 < h_a^2 < 0.15$	$0.1 < r_{aa} < 0.40$
Moderate	$0.15 < h_a^2 < 0.5$	$0.4 < r_{aa} < 0.7$
High	$h_a^2 > 0.5$	$r_{aa} > 0.7$

Estimation of selection index

The predicted genotypic values were used to calculate the selection index, based on the sum of ranks to classify the genotypes in terms of each trait (Mulamba & Mock, 1978). Subsequently, the values of each trait for the accessions were summed, resulting in an overall value considered as the selection index (Cruz et al., 2014).

Results and Discussion

CVr contributes to the detection of genetic variability in a population. The CVr for FL, AFW, and AMW were higher than unity (1.47, 1.34, and 1.15, respectively), suggesting

higher genetic variation for the selection of promising babassu genotypes based on these traits (Table 2).

We found high values of broad-sense heritability (>0.5) and high selective accuracy (80%) for FW, AFW, and AMW, confirming their precision and confidence in the estimated genetic values (Table 2). FW, ANW, and AMW are important for productivity, and their elevated heritability and accuracy indicate a substantial genetic influence, making these traits excellent candidates for genetic improvement.

NBP, NFB, PH, FL, and NL presented moderate significant broad-sense heritabilities (among 0.15 and 0.5) and high accuracies ($>80\%$) (Table 2), indicating a good potential for selection. In a study with peach palm (*Bactris gasipaes*) heritability was reported as >0.2 for the total bunch weight (Farias-Neto et al., 2013).

Selective accuracy represents a correlation between actual and predicted genetic values, and the higher its value, the higher the confidence in the evaluation of individuals (Pivetta et al., 2020). Neves et al. (2023) studied populations of licuri palm (*Syagrus coronata*), also native to the Cerrado biome, and found similar CVr (obtained from the evaluations of three fruits per bunch) with an accuracy rate of 90%. In a study with 51 progenies of *Acrocomia aculeata* (coco-de-espinho) a similar CVr was found, with 90% accuracy (Manfio et al., 2011). In our data, accuracy was also high for all traits evaluated, reflecting the great reliability of the estimated genetic values.

SCB was the only trait that showed considered low, but significant, with a high accuracy. Some babassu stipes were

affected by fires in the period of data collection, which may have influenced the SCB results. In Maranhão State, the post-burned areas have a massive presence of babassu and other secondary species that are resistant to fire. Babassu palm trees face pressure from large cattle ranchers, but also from family farmers who often remove babassu trees to establish their cultivation gardens, using felling and fire as instruments to clear their cultivation areas (Freitas, 2000; Lemos, 2020).

The analysis of deviance evidenced a significant effect of genotype ($p<0.05$) in all evaluated traits (Table 3). The high genetic variation reveals the possibility of obtaining genetic gains through the selection criteria.

The highest positive values of genotypic correlations were found between the factors FW and AFW (0.99), and AFW and AMW (0.95). FW and AMW, FL and AMW, FL and AFW, and FL and FW had the same value of 0.91 (Table 4).

Genotypic correlations of *A. speciosa* traits indicate that fruit size directly influences FW and, consequently, AMW, facilitating the selection process of individuals with interesting agro-extractivist production characteristics. This fact only confirms what the extractivists already observed in the field, as they prefer larger fruits that generate higher yields for seeds and mesocarp. In a study with açai fruits (*Euterpe oleracea*) a positive genetic correlation was found between the total weight of the fruits and the number of bunches (Farias Neto et al., 2008). Marçal et al. (2015) also found a positive correlation between the weight of the juçara fruit and the longitudinal diameter of fruits (*Euterpe edulis*).

Table 2: Estimates of genetic parameters from morphological traits of *A. speciosa*. Legend of traits: number of bunches per plant (NBP), number of fruits per bunch (NFB), stipe circumference at breast level (SCB), plant height (PH), fruit length (FL), fruit width (FW), average fruit weight (AFW), nut length (NL), and average mesocarp weight (AMW).

Trait	Parameters						
	Vg	Ve	Vf	CVr	h_a^2	r_{aa} (%)	M
NBP (unit)	1.50	6.53	8.04	0.48	0.19	83.6	5.23
NFB (unit)	11054.36	14888.14	25942.5	0.86	0.43	87.5	379.18
SCG (cm)	0.01	0.13	0.14	0.28	0.11	79.0	1.15
SCB (cm)	0.01	0.10	0.11	0.18	0.10	78.9	1.15
PH (m)	2.42	6.83	9.26	0.60	0.26	85.0	9.83
FL (mm)	16.35	46.78	63.13	0.60	0.25	85.4	84.96
FW (mm)	45.20	20.78	65.99	1.47	0.68	89.0	55.60
AFW (g)	2123.90	1177.12	3301.03	1.34	0.64	88.4	88.35
NL (mm)	3.50	15.21	18.73	0.48	0.19	83.6	38.63
ANW (g)	2.84	34.96	37.80	0.52	0.07	75.3	10.58
AMW (g)	192.50	143.81	336.31	1.15	0.57	88.3	37.21

NBP: number of bunches per plant; NFB: number of fruits per bunch; SCG: stipe circumference at ground level; SCB: stipe circumference at breast level; PH: plant height; FL: fruit length; FW: fruit width; AFW: average fruit weight; NL: nut length; ANW: average nut weight; AMW: average mesocarp weight; Vg: genotypic variance between individuals; Ve: residual variance; Vf: individual phenotypic variance; CVr: coefficient of relative variation; h_a^2 : individual broad-sense heritability; r_{aa} : selective accuracy; and M: the overall mean of the experiment.

Table 3: Analysis of deviance (ANADEV) for the morphological variables evaluated in babassu palm trees (*A. speciosa*) native to the State of Maranhão.

Trait	Effect	Deviance	LRT (Likelihood Ratio Test)
NBP	Clones	459.06	17.15***
	Complete model	441.91	
NFB	Clones	1655.49	57.25***
	Complete model	1598.24	
SCG	Clones	-137.81	4.54**
	Complete model	-142.35	
SCB	Clones	-171.01	7.43***
	Complete model	-178.44	
PH	Clones	477.95	27.65***
	Complete model	450.30	
FL	Clones	763.95	27.2***
	Complete model	736.75	
FW	Clones	756.93	134.85***
	Complete model	622.08	
AFW	Clones	1341.27	117.67***
	Complete model	1223.6	
NL	Clones	585.06	16.45***
	Complete model	567.95	
ANW	Clones	693.03	4.51**
	Complete model	688.52	
AMW	Clones	1003.3	94.11***
	Complete model	909.19	

Tabulated chi-square: 2.71, 3.84, and 6.63 for 10, 5, and 1% significance levels, respectively. *, **, *** significance at 1, 5, and 10% probability by the chi-square test with 1 degree of freedom.

Table 4: Genetic correlation matrix for six fruit traits of babassu palm trees (*A. speciosa*) native to the State of Maranhão.

Trait	NBP	NFB	FL	FW	AFW	AMW
NBP	-	0.37*	-0.28	-0.48	-0.37	-0.08
NFB		-	-0.80	-0.82	-0.84	-0.77
FL			-	0.91*	0.91*	0.91*
FW				-	0.99*	0.91*
AFW					-	0.95*
AMW						-

NBP: number of bunches per plant; NFB: number of fruits per bunch; FL: fruit length; FW: fruit width; AFW: average fruit weight; AMW: average mesocarp weight. *Significant at 5% by the t-test.

The visual variability in fruit dimensions sampled from the different municipalities is shown in Figure 2. The average rank index for the best combinations of the studied traits is separated by the municipalities (Table 5). According to Mulamba and Mock (1978), the lowest values on the average rank indicate a more favorable position of the evaluated traits and the highest values represent an unfavorable combination. Fruits sampled in Coroatá and Buritirana ranked highest, demonstrating that these areas have plants with more favorable combinations of morphological traits (such as fruit weight, fruit size, etc) that are interesting for better production.

Fruits from Viana and Cantanhede had the lowest positions in the ranking, and these sampled areas are mostly located in natural reserves and/or protected areas (Figure 1). Studies with palm trees using the evaluation by the average rank index showed considerable genetic variability, favoring breeding programs (Farias Neto et al., 2013; Simiqueli et al., 2018).

The sampled areas were spatially distributed in different microregions of the State (Figure 1) and did not exhibit uniform vegetation cover. Our objective was to capture the greatest possible variability within the state. Some of the sampled areas were greatly transformed by human activity (cassava cultivation, extensive pastures, degraded areas, and secondary forests), but babassu trees also predominate. Gehring et al. (2011) found that babassu becomes dominant in areas affected by constant fires and degraded land, as it is quite tolerant to slash-and-burn practices in traditional agriculture.

Our results are innovative because we identified traits with high and significant heritabilities, important to establishing selection criteria for future babassu breeding programs. This study is the first report on the genetic control of productive traits of babassu and offers the opportunity to select individuals with superior fruit and mesocarp production based not only on their location but also on their morphological traits. However, further studies are necessary to accelerate the process of domestication of this palm.



Figure 2: Visual variability of *A. speciosa* fruits collected in different municipalities of the State of Maranhão. (A) Buritirana - medium to large sized fruits, with an oval-ellipsoid shape. (B) Cantanhede - smaller fruits, with a more elongated shape. (C) Coroatá - longer fruits, with a wider base. (D) São Luís - ellipsoid-shaped and uniform fruits. (E) Viana - medium size, rounded-ellipsoid shape. Scale bar: 1 cm.

Table 5: Classification based on the sum of ranks of babassu palm trees (*Attalea speciosa*) native to the State of Maranhão for different morphological variables.

	Genotype	NBP	NFB	FL	FW	AFW	AMW	Average rank
1st	Coroatá	1	3	2	2	2	1	1.83
2nd	Buritirana	5	5	1	1	1	2	2.5
3rd	São Luís	4	1	4	3	3	4	3.16
4th	Viana	2	4	3	4	4	3	3.33
5th	Cantanhede	3	2	5	5	5	5	4.16

NBP: number of bunches per plant; NFB: number of fruits per bunch; FL: fruit length; FW: fruit width; AFW: average fruit weight; AMW: average mesocarp weight (AMW).

Conclusions

The babassu populations analyzed exhibited genetic variability and the highest heritability and accuracy in fruit width, fruit weight, and mesocarp weight, indicating strong genetic control on these traits. We identified fruit weight and mesocarp weight as suitable traits for conducting genotypic correlation analyses. Populations of babassu from Coroatá and Buritirana municipalities produced fruits with superior characteristics. These data can assist efforts in selecting superior genotypes and developing technologies for the rational and sustainable exploitation of babassu palm fruits in the future.

Author Contribution

Conceptual idea: Pinheiro, E.M.; Araújo, J.R.G.; Corrêa, T.R.; Methodology design: Pinheiro, E.M.; Corrêa, T.R.; Data collection: Pinheiro, E.M.; Sousa, J.J.P.; Data analysis and interpretation: Araújo, J.R.G.; Corrêa, T.R.; Nobre, C.P.; Moraes, L.R.R.; Rivas, P.M.S. and Writing and editing: Pinheiro, E.M.; Moraes, L.R.R.; Rivas, P.M.S.; Nobre, C.P.

Acknowledgments

We acknowledge the infrastructure and technical support of the Post-Harvest Laboratory of Maranhão State University – LAPOC.

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