



GENETIC DIVERSITY OF OPEN-POLLINATED AÇAÍ PALM (*EUTERPE OLERACEA* MART.) PROGENIES BASED ON MORPHOAGRONOMIC DESCRIPTORS IN THE TOCANTINS AMAZON

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ABSTRACT

Objective: To evaluate the genetic diversity and heritability of morphoagronomic descriptors in open-pollinated progenies of *Euterpe oleracea* Mart. cultivated in natural floodplain areas of the Tocantins Amazon, identifying traits with high selection potential for breeding and conservation.

Theoretical Framework: The study is grounded in quantitative genetics and morphoagronomic characterization, recognizing that *Euterpe oleracea*, an allogamous palm, exhibits high phenotypic plasticity and genetic segregation under open-pollinated conditions, essential for breeding programs in floodplain ecosystems.

Method: A randomized block design was applied to four floodplain populations, with 16 bunch and fruit descriptors measured per plant. Variance analysis, mean comparisons (Scott–Knott 5%), and genetic parameter estimates were performed using the software GENES and RStudio.

Results and Discussion: Significant genetic variability was detected for key traits such as total bunches, newly fertilized bunches, and bunch weight, with heritability values above 80%. These results confirm strong additive genetic control and high selection efficiency for reproductive and yield-related descriptors.

Research Implications: The findings provide robust evidence supporting the use of morphoagronomic traits as reliable predictors of genetic divergence, facilitating early selection and targeted breeding of superior genotypes for sustainable açai production in the Amazon floodplains.

Originality/Value: This study represents one of the first quantitative assessments of open-pollinated *Euterpe oleracea* progenies in the Tocantins Amazon, offering a methodological and genetic baseline for germplasm management, local adaptation studies, and the genetic enhancement of Amazonian palm crops.

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DIVERSIDADE GENÉTICA DE PROGÊNIES DE AÇAÍ (*EUTERPE OLERACEA* MART.) DE POLINIZAÇÃO ABERTA COM BASE EM DESCRITORES MORFOAGRONÔMICOS NA AMAZÔNIA TOCANTINENSE

RESUMO

Objetivo: Avaliar a diversidade genética e a herdabilidade de descritores morfoagronômicos em progênies de polinização aberta de *Euterpe oleracea* Mart. cultivadas em áreas naturais de várzea da Amazônia Tocantinense, identificando características com alto potencial de seleção para melhoramento genético e conservação.

Referencial Teórico: O estudo baseia-se na genética quantitativa e na caracterização morfoagronômica, reconhecendo que *Euterpe oleracea*, uma palmeira alógama, apresenta alta plasticidade fenotípica e segregação genética em condições de polinização aberta, essenciais para programas de melhoramento em ecossistemas de várzea.

Método: Foi utilizado um delineamento em blocos casualizados em quatro populações de várzea, com a medição de 16 descritores de cachos e frutos por planta. Análises de variância, comparações de médias (Scott-Knott 5%) e estimativas de parâmetros genéticos foram realizadas utilizando os softwares GENES e RStudio.

Resultados e Discussão: Foi detectada variabilidade genética significativa para características-chave, como número total de cachos, cachos recém-fertilizados e peso do cacho, com valores de herdabilidade acima de 80%. Esses resultados confirmam um forte controle genético aditivo e alta eficiência de seleção para descritores reprodutivos e relacionados à produção.

Implicações da Pesquisa: Os resultados fornecem evidências robustas que apoiam o uso de características morfoagronômicas como preditores confiáveis de divergência genética, facilitando a seleção precoce e o melhoramento direcionado de genótipos superiores para a produção sustentável de açaí nas várzeas amazônicas.

Originalidade/Valor: Este estudo representa uma das primeiras avaliações quantitativas de progênies de *Euterpe oleracea* de polinização aberta na Amazônia Tocantinense, oferecendo uma base metodológica e genética para o manejo de germoplasma, estudos de adaptação local e o aprimoramento genético de culturas de palmeiras amazônicas.

Palavras-chave: *Euterpe Oleracea* Mart., Variabilidade Genética, Descritores Morfoagronômicos, Melhoramento Genético, Amazônia.

DIVERSIDAD GENÉTICA DE PROGENIES DE PALMA DE AÇAÍ (*EUTERPE OLERACEA* MART.) DE POLINIZACIÓN ABIERTA BASADA EN DESCRIPTORES MORFOAGRONÓMICOS EN LA AMAZONÍA DE TOCANTINS

RESUMEN

Objetivo: Evaluar la diversidad genética y la heredabilidad de descriptores morfoagronómicos en progenies de polinización abierta de *Euterpe oleracea* Mart. cultivadas en áreas naturales de llanura aluvial de la Amazonía de Tocantins, identificando características con alto potencial de selección para el mejoramiento genético y la conservación.

Marco teórico: El estudio se fundamenta en la genética cuantitativa y la caracterización morfoagronómica, reconociendo que *Euterpe oleracea*, una palma alógama, exhibe alta plasticidad fenotípica y segregación genética en condiciones de polinización abierta, esenciales para los programas de mejoramiento genético en ecossistemas de llanura aluvial.

Método: Se aplicó un diseño de bloques aleatorizados a cuatro poblaciones de llanura aluvial, con 16 descriptores de racimos y frutos medidos por planta. Se realizaron análisis de varianza, comparaciones de medias (Scott-Knott 5%) y estimaciones de parámetros genéticos utilizando los programas GENES y RStudio.



Resultados y discusión: Se detectó variabilidad genética significativa para características clave como el número total de racimos, racimos recién fertilizados y peso del racimo, con valores de heredabilidad superiores al 80%. Estos resultados confirman un fuerte control genético aditivo y una alta eficiencia de selección para descriptores reproductivos y relacionados con el rendimiento.

Implicaciones de la investigación: Los hallazgos proporcionan evidencia sólida que respalda el uso de características morfoagronómicas como predictores confiables de divergencia genética, facilitando la selección temprana y el mejoramiento genético dirigido de genotipos superiores para la producción sostenible de açaí en las llanuras aluviales amazónicas.

Originalidad/Valor: Este estudio representa una de las primeras evaluaciones cuantitativas de progenies de *Euterpe oleracea* de polinización abierta en la Amazonía de Tocantins, ofreciendo una base metodológica y genética para la gestión del germoplasma, estudios de adaptación local y el mejoramiento genético de los cultivos de palmas amazónicas.

Palabras clave: *Euterpe Oleracea* Mart., Variabilidad Genética, Descriptores Morfoagronómicos, Mejoramiento Genético, Amazonía.

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1 INTRODUCTION

The açaí palm (*Euterpe oleracea* Mart.) is a species of outstanding socioeconomic relevance in the Amazon region, particularly for riverine communities and the agro-industrial chain of pulp and bioactive compounds (Sanchez-Capa *et al.*, 2023; Teixeira *et al.*, 2025). Driven by the increasing global demand for its fruit, not only as a nutritional product but also as a source of anthocyanins and other functional metabolite, the need for controlled domestication and well-structured breeding programs has become evident (Barbosa *et al.*, 2022; Da Silveira *et al.*, 2023; Carlini-Garcia *et al.*, 2025). Despite recent advances, significant knowledge gaps remain regarding the characterization of genetic diversity in open-pollinated progenies, the applicability of morphoagronomic descriptors specifically adapted to the soil, climate, and management conditions of the Tocantins Amazon, and the generation of robust datasets to support the establishment of active germplasm banks and early selection strategies Canal *et al.*, 2025; Teixeira *et al.*, 2025).

The assessment of genetic variability in perennial species such as açaí requires the adoption of well-defined morphoagronomic descriptor, covering plant, inflorescence, bunch, and fruit trait, that enable discrimination of genetic divergence, correlation with potential genetic gains, and guidance for strategic breeding decisions. For instance, the identification of redundant traits, have become standard procedures to quantify phenotypic variability in açaí germplasm (Dos Santos Galate *et al.*, 2019; Canal *et al.*, 2023).



Within the northern region of Brazil, and particularly in the Tocantins Amazon, an emerging frontier for açaí cultivation, the evaluation of open-pollinated progenies represents a strategic pathway to capture existing variability, accelerate the identification of promising genotypes, and simultaneously preserve intrapopulational genetic diversity (Lopes *et al.*, 2019; Neves Fonseca and Lima, 2024). Moreover, this approach supports sustainable and participatory breeding efforts by involving genetic material that is readily accessible to local producers and communities.

Even under traditional management systems and natural gene flow, the açaí palm exhibits sufficient variability to distinguish groups of progenies and identify elite genetic material for use in future breeding programs, thus contributing to increased productivity, fruit quality, and agronomic resilience (Pereira *et al.*, 2019; Perrut-Lima *et al.*, 2023). In this context, this study aims to evaluate the genetic diversity of open-pollinated *Euterpe oleracea* Mart. progenies, based on bunch and fruit descriptors, in the municipality of Cametá, in northeastern Pará.

2 JUSTIFICATION

This study aimed to evaluate the genetic diversity and selection potential of open-pollinated progenies of *Euterpe oleracea* Mart. cultivated under floodplain conditions in the Tocantins Amazon. Despite the species' high socioeconomic and ecological importance, limited knowledge about its morphoagronomic variability and heritability constrains advances in breeding and conservation programs. Estimating genetic parameters and heritability for key reproductive and yield traits enables the identification of descriptors with strong genetic control and selection potential. The findings provide a solid foundation for developing superior genotypes adapted to local hydrological and edaphic conditions, strengthening the sustainable management and genetic conservation of this strategic species for Amazonian bioeconomic development.

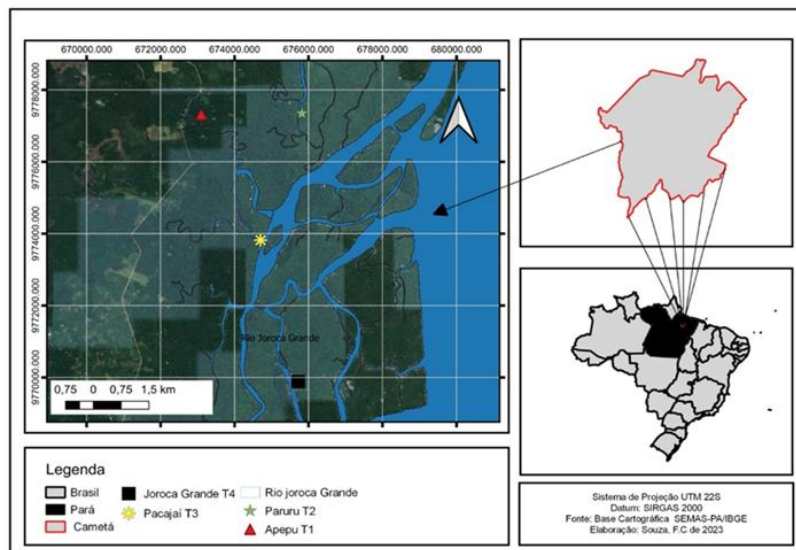
3 METHODOLOGY

The study was conducted in the floodplain areas of Apepú, Parurú, Pacajaí, and Joroca Grande (Figure 1), located in the Fourth District of the municipality of Cametá, Pará, during the production period from October to December 2023 and 2024.



Figure 1

Location of the experimental areas under açai cultivation, municipality of Cametá, Pará.



The predominant soils in the marginal floodplains of the Tocantins River and in the tidal-flooded islands of Cametá are classified as Eutrophic Haplic Gleysols, according to Ferreira et al., 2025. These soils present naturally favorable chemical fertility for the development and productivity of native palm species. The four populations studied were identified based on recommendations from fresh fruit buyers and extractivist producers, who indicated that fruits from these areas have higher pulp yield, better juice flavor, large bunches, and small fruits, resulting in higher market value and purchase price.

A randomized block design was adopted, with four treatments corresponding to the floodplain populations identified as: T1AAPEU= Apepú, T2APARU= Parurú, T3APAJA= Pacajaí, and T4AJOCG= Joroca Grande. Each area included 25 replicates, totaling 100 progenies, with 16 production traits evaluated per plant. The statistical method employed aimed to analyze the significance of the characteristic data for each population, considering randomness due to open pollination and environmental influence. Progenies were randomly selected in collaboration with local producers, considering bunch and fruit production at different developmental stages and sizes, based on the morphoagronomic descriptors proposed by Oliveira et al. (2006).

The evaluated bunch traits included the total number of bunches (TB, units), empty bunches (EB, units), newly fertilized bunches (NFB, units), bunches with green fruits (BGF, units), and bunches with ripe fruits (BRF, units), all obtained by direct visual counting on each plant. Additional yield components comprised total bunch weight (TBW, kg), empty bunch



weight (EBW, kg), and fruit weight per bunch (FWB, kg), all expressed in kilograms and measured using a portable digital hook scale (*Commerce Brasil*®).

Bunch morphology was characterized by the longitudinal diameter with fruits (LDBF, cm) and the transverse diameter with fruits (TDBF, cm), both measured in centimeters using a 150 cm flexible measuring tape. The number of fruits per rachis was also quantified according to their position within the bunch: at the base (FRB, units), middle (FRM, units), and apex (FRA, units). One representative bunch per plant was selected for this assessment, and all fruits were counted individually to capture spatial variation within the inflorescence. For fruit evaluation, one ripe bunch was harvested from each plant, and a random subsample of ten fruits per matrix was used for biometric determinations. The fresh fruit weight (FFW, g) was measured in grams using a *GALLIZZI*® digital precision balance. The longitudinal diameter of ripe fruits (LDRF, mm) and the transverse diameter of ripe fruits (TDRF, mm) were measured in millimeters using a *NOVE54*® digital caliper.

Data were organized in a Microsoft Excel 2020® spreadsheet and subsequently subjected to analysis of variance in a randomized block design without missing plots. Mean values were compared using the Scott-Knott test at a 5% probability level. Genetic parameters were estimated using the method proposed by Farias et al. (2005), through the GENES computational software (Cruz, 2013).

4 RESULTS AND DISCUSSIONS

Analysis of variance revealed significant differences among the evaluated progenies of *E. oleracea* for most of the morphoagronomic traits (Table 1). These results indicate the existence of substantial genetic variability among open-pollinated açaí palm progenies, particularly in traits associated with bunch and fruit production. This variability is expected in open-pollinated populations, where cross-fertilization promotes broad genetic segregation and the maintenance of heterozygosity within populations.



Table 1

*Analysis of variance in randomized blocks for bunch and fruit traits of four açai palm (*E. oleracea*) populations from natural floodplain areas. Cametá, Pará, Brazil, 2024.*

Trait		MS	Maximum	Minimum	Mean	CV (%)
Bunch	TB	32.5**	5.24	2.60	3.72	36.0
	EB	2.03 ^{ns}	1.04	0.40	0.64	160.5
	NFB	3.07**	0.84	0.08	0.40	131.1
	BGF	22.3**	2.52	0.32	1.50	69.2
	BRF	0.60*	1.40	1.04	1.18	34.9
	TBW	5.61**	2.90	1.90	2.20	40.8
	EBW	0.55**	0.87	0.52	0.67	30.2
	FWB	3.14**	2.03	1.24	1.53	50.4
	LDBF	1316.0**	90.6	73.9	80.2	16.9
	TDBF	5334.9**	1468	115.7	137.5	14.7
	FRB	393.2**	15.1	7.12	10.7	58.0
	FRM	335.7**	19.7	11.8	14.9	49.9
	FRA	511.4**	19.9	9.80	13.6	55.2
Fruit	FFW	0.51**	2.03	1.7	1.89	17.1
	LD RF	1.40**	15.2	14.8	14.9	3.76
	TD RF	1.54 ^{ns}	13.4	12.9	13.2	9.28

Note: MS: Mean Square; CV(%): Coefficient of variation; ** and *: Significant at 1% and 5% probability levels, respectively, according to the F-test; ns: Not significant according to the F-test. TB: total bunches; EB: empty bunches; NFB: newly fertilized bunches; BGF: bunches with green fruits; BRF: bunches with ripe fruits; TBW: total bunch weight; EBW: empty bunch weight; FWB: fruit weight per bunch; LDBF: longitudinal diameter of bunch with fruits; TDBF: transverse diameter of bunch with fruits; FRB: fruits per rachis (base); FRM: fruits per rachis (middle); FRA: fruits per rachis (apex); FFW: fresh fruit weight; LD RF: longitudinal diameter of ripe fruit; TD RF: transverse diameter of ripe fruit. CV (%): coefficient of variation; Mean: overall mean of the trait.

Significant variation ($p < 0.01$) was observed among the evaluated progenies for total bunches (TB), newly fertilized bunches (NFB), bunches with green fruits (BGF), and total bunch weight (TBW). The coefficients of variation (CV%) ranged from moderate to high (20–70%), reflecting both environmental effects and genetic differentiation among open-pollinated progenies. As *Euterpe oleracea* is predominantly allogamous, its strong cross-fertilization promotes extensive genetic segregation and maintains high heterozygosity within natural populations (Bezerra et al., 2020; Díaz-Hernández et al., 2024).

The highest mean square values for BGF (22.31) and TB (32.53) confirm that these traits effectively discriminate genotypes based on yield potential. In contrast, empty bunches (EB) showed no significant differences ($p > 0.05$), indicating uniformity likely driven by environmental rather than genetic factors. The high variability in BGF and TB is consistent with the reproductive biology of *E. oleracea*, where cross-pollination enhances genetic recombination and generates marked differences in fruiting intensity (Qin, 2024; Canal et al., 2025). Similar findings were



reported for *E. precatoria* by Perrut-Lima et al. (2023) and Chaves et al. (2021), confirming that open-pollinated progenies express high variability in production-related traits.

The lack of significant variation for EB likely results from low heritability or environmental uniformity. As noted by Mota Rios et al. (2021) and Teixeira et al. (2025), the occurrence of empty bunches is strongly influenced by nutrient availability, pollination efficiency, and microclimatic conditions, all of which minimize genetic expression. Consequently, EB behaves as an environmentally dependent trait, whereas TB and BGF are genetically controlled and reliable indicators of productive potential.

Bunch morphometry exhibited strong differentiation, with longitudinal (LDBF) and transverse diameters (TDBF) significant at the 1% level and presenting high mean squares (1316.04 and 5334.87, respectively). These descriptors, related to bunch structure and fruit set density, are valuable indicators of reproductive efficiency and productivity. The low CV values (9.60% for LDBF and 14.70% for TDBF) confirm high experimental precision and genetic stability. Similar results were obtained by Santos Galate et al. (2019) and Delgado et al. (2024), who emphasized bunch compactness and size as indirect indicators of yield potential in *E. oleracea*.

Significant variation in the number of fruits per rachis (FRB, FRM, FRA) further supports genetic divergence among progenies. The highest variability occurred at the apex (CV = 55.15%), attributed to asynchronous fruit maturation, a common feature in natural açaí populations (Freitas et al., 2021; Santos et al., 2025). This heterogeneity reflects unequal assimilate distribution along the rachis and can be exploited as a selection criterion for genotypes with uniform fruit set, an advantageous trait for mechanized harvesting and yield uniformity.

Fruit-related descriptors also showed significant differentiation. Fresh fruit weight (FFW) and longitudinal diameter of ripe fruits (LDRF) were both significant at the 1% level, confirming their discriminant power in evaluating progenies. The CV values (19.47% for FFW; 5.36% for LDRF) denote high precision, while the non-significant transverse diameter (TDRF) indicates limited phenotypic variation, likely due to stabilizing selection acting on fruit shape. These patterns align with Bannoud et al. (2024) and Chaves et al. (2021), who reported similar morphological stability in floodplain populations, reflecting selection toward uniformity under domestication pressure.

Overall, the results demonstrate that the evaluated populations of *E. oleracea* express substantial genetic variability and phenotypic plasticity in morphoagronomic traits related to reproductive efficiency and yield. The strong significance of bunch and fruit descriptors reinforces their usefulness as selection criteria for identifying superior genotypes adapted to the hydrological and edaphic conditions of Amazonian floodplains (Silva et al., 2020; Perrut-Lima et al., 2023; Bronze et al., 2024).



Table 2

*Mean comparison for bunch and fruit traits by the Scott-Knott test at 5% probability level for four açai palm (*E. oleracea*) populations from natural floodplain areas. Cametá, Pará, Brazil, 2024.*

Trait		T1AAPEU	T2APARU	T3APAJA	T4AJOCG	Mean	CV
Bunch	TB	5.24±1.13a*	2.60±1.55c	3.16±1.60c	3.88±1.56b	3.72	39.3
	EB	0.48±0.82a	1.04±1.34a	0.64±1.15a	0.40±0.76a	0.64	158.9
	NFB	0.84±0.55a	0.08±0.28c	0.16±0.55c	0.52±0.65b	0.40	126.9
	BGF	2.52±1.08a	0.32±0.56d	1.24±1.36c	1.92±1.01b	1.50	66.7
	BRF	1.40±0.51a	1.16±0.47b	1.12±0.33b	1.04±0.22b	1.18	31.8
	TBW	2.06±0.81b	1.93±0.81b	1.90±0.75b	2.90±1.24a	2.20	40.8
	EBW	0.52±0.16b	0.61±0.21b	0.66±0.18b	0.87±0.26a	0.67	30.5
	FWB	1.54±0.72b	1.33±0.67b	1.24±0.63b	2.03±1.06a	1.54	50.2
	LDBF	73.9±11.2b	77.5±6.66b	78.7±8.37b	90.6±23.5a	80.2	15.5
	TDBF	115.7±21.1b	144.7±21.8a	146.8±22.9a	142.8±17.2a	137.5	15.1
	FRB	13.0±8.40a	7.12±4.37b	7.64±4.25b	15.1±7.46	10.7	57.0
	FRM	15.9±8.94a	11.8±5.94b	12.3±6.14b	19.7±7.63a	14.9	47.9
Fruit	FRA	13.7±8.72b	9.82±5.42b	10.9±6.00b	19.9±9.01a	13.6	53.6
	FFW	2.03±0.32a	1.95±0.45a	1.87±0.26a	1.70±0.19b	1.89	15.9
	LDRF	15.2±0.59a	15.1±0.57a	14.8±0.66b	14.8±0.52a	14.9	3.91
	TDRF	13.4±0.68a	13.4±0.54a	12.9±0.58a	13.1±2.23a	13.2	7.64

*Mean±Standard deviation and different letters in the same row indicate statistically distinct means according to the Scott–Knott grouping criterion. Based on the Scott–Knott test at the 5% probability level. **Note:** TB: total bunches; EB: empty bunches; NFB: newly fertilized bunches; BGF: bunches with green fruits; BRF: bunches with ripe fruits; TBW: total bunch weight; EBW: empty bunch weight; FWB: fruit weight per bunch; LDBF: longitudinal diameter of bunch with fruits; TDBF: transverse diameter of bunch with fruits; FRB: fruits per rachis (base); FRM: fruits per rachis (middle); FRA: fruits per rachis (apex); FFW: fresh fruit weight; LDRF: longitudinal diameter of ripe fruit; TDRF: transverse diameter of ripe fruit. CV (%): coefficient of variation; Mean: overall mean of the trait.

The total number of bunches (TB) ranged from 2.60 ± 0.55 (T2APARU) to 5.24 ± 1.13 (T1AAPEU), with a mean of 3.72 bunches plant⁻¹ (CV = 39.3%) (Table 2). The superior performance of T1AAPEU indicates greater reproductive activity and adaptation to local hydrological and edaphic conditions, consistent with Mota Rios et al. (2021), who associated higher bunch emission with more efficient assimilate partitioning toward reproductive structures.

The number of newly fertilized bunches (NFB) varied from 0.08 ± 0.25 (T3APAJA) to 0.84 ± 0.54 (T1AAPEU), while bunches with green fruits (BGF) ranged from 0.32 ± 0.56 (T2APARU) to 2.52 ± 1.08 (T1AAPEU). These results demonstrate that the Apeu population exhibits the most advanced reproductive stage and greater phenological synchrony. The wide variation (CV = 66–127%) reflects both genetic segregation and environmental modulation typical of open-pollinated systems in floodplain conditions.



Total bunch weight (TBW) ranged from 1.12 ± 0.30 kg (T3APAJA) to 2.94 ± 1.24 kg (T4AJOCG) (mean = 2.00 kg plant⁻¹; CV = 40.8%), and fruit weight per bunch (FWB) followed the same pattern (1.24 ± 1.05 kg to 2.90 ± 1.24 kg). The superior performance of T4AJOCG suggests genetic superiority for yield components, supported by greater fruit load and individual fruit mass.

The variation in NFB and BGF among populations results from the interaction of genetic heterogeneity, reproductive phenology, and environmental gradients characteristic of Amazonian floodplains (Nwosisi et al., 2019; Bacelar et al., 2024). In open-pollinated açaí progenies, extensive cross-fertilization and natural gene flow maintain high heterozygosity and phenotypic diversity (Neto et al., 2020; Canal et al., 2023). Populations such as T1AAPEU show greater floral synchrony and overlap, which enhance pollination efficiency and fruit set (Tandon et al., 2020). This genetic–environmental interplay generates significant $G \times E$ interactions, amplifying phenotypic variability.

The superior TBW and FWB observed in T4AJOCG indicate the presence of genotypes with high sink strength, capable of efficiently allocating photosynthates to developing fruits—a mechanism also described in other perennial palms with high reproductive output (Santos et al., 2021; Nogueira et al., 2023). These patterns confirm that morphoagronomic differentiation among açaí populations arises from the interaction between genetic potential and ecological adaptation.

Estimates of genetic and phenotypic parameters (Table 3) corroborate these findings, showing strong genetic control and high selection potential for most morphoagronomic descriptors, indicating that open-pollinated populations of *E. oleracea* retain substantial additive genetic variance suitable for breeding and conservation purposes.



Table 3

*Estimates of genetic and phenotypic parameters for bunch and fruit traits in four açaí palm (*E. oleracea*) populations from natural floodplain areas. Cametá, Pará, Brazil, 2024.*

Trait		CVg (%)	CVg/CVe	σ^2_g	σ^2_e	h ² (%)
Bunch	TB	29.8	0.83	1.23	1.80	94.5
	EB	30.8	0.19	0.04	1.05	47.9
	NFB	83.5	0.64	0.11	0.27	91.0
	BGF	61.4	0.89	0.85	1.08	95.2
	BRF	11.1	0.32	0.02	0.17	71.8
	TBW	19.9	0.49	0.19	0.81	85.6
	EBW	21.4	0.71	0.02	0.04	92.6
	FWB	20.8	0.41	0.10	0.60	80.9
	LDBF	8.40	0.50	45.3	182.8	86.1
	TDBF	10.2	0.69	197.0	408.4	92.3
	FRB	35.1	0.60	14.2	38.8	90.1
	FRM	22.6	0.48	11.5	49.3	85.3
	FRA	31.4	0.57	18.2	56.3	89.0
Fruit	FFW	6.80	0.40	0.02	0.10	79.8
	LDRF	1.39	0.37	0.04	0.32	77.4
	TDRF	0.32	0.03	0.002	1.50	2.97

Note: TB: total bunches; EB: empty bunches; NFB: newly fertilized bunches; BGF: bunches with green fruits; BRF: bunches with ripe fruits; TBW: total bunch weight; EBW: empty bunch weight; FWB: fruit weight per bunch; LDBF: longitudinal diameter of bunch with fruits; TDBF: transverse diameter of bunch with fruits; FRB: fruits per rachis (base); FRM: fruits per rachis (middle); FRA: fruits per rachis (apex); FFW: fresh fruit weight; LDRF: longitudinal diameter of ripe fruit; TDRF: transverse diameter of ripe fruit. CVg (%): coefficient of genetic variation; CVg/CVe: ratio between genetic and environmental coefficients of variation, indicating the relative magnitude of genetic variance; σ^2_g : genotypic variance component; σ^2_e : environmental variance component; h² (%): broad-sense heritability, representing the proportion of phenotypic variance attributed to genetic factors.

The coefficients of genetic variation (CVg%) ranged from 10.2% (TDBF) to 83.5% (NFB), indicating wide genotypic variability for traits related to reproductive performance. The highest CVg values for NFB (83.5%), BGF (61.4%), and TB (29.8%) confirm strong heterogeneity and genetic segregation among open-pollinated progenies, as expected in an allogamous species. The CVg/CVe ratio exceeded one for TB (0.83), NFB (0.64), and BGF (0.89), evidencing that genetic variance predominates over environmental variance in phenotypic expression. This reinforces the high selection efficiency of these traits, since variables with CVg/CVe > 1 tend to respond consistently to selection pressure.

Heritability (h²) values were high for most bunch-related traits, particularly TB (94.5%), NFB (91.0%), and BGF (95.2%), confirming strong additive genetic control. These results indicate that phenotypic performance reliably reflects genotypic potential and that substantial genetic gains can be achieved through selection. Bunch morphometric traits such as LDBF



(86.1%) and TDBF (92.3%) also exhibited high heritability, confirming that bunch size and structure are genetically stable and minimally influenced by environmental variation. Similarly, the high heritability of FRB (90.0%), FRM (85.3%), and FRA (89.0%) supports the genetic control of fruit distribution along the bunch, highlighting these traits as robust indicators of reproductive efficiency.

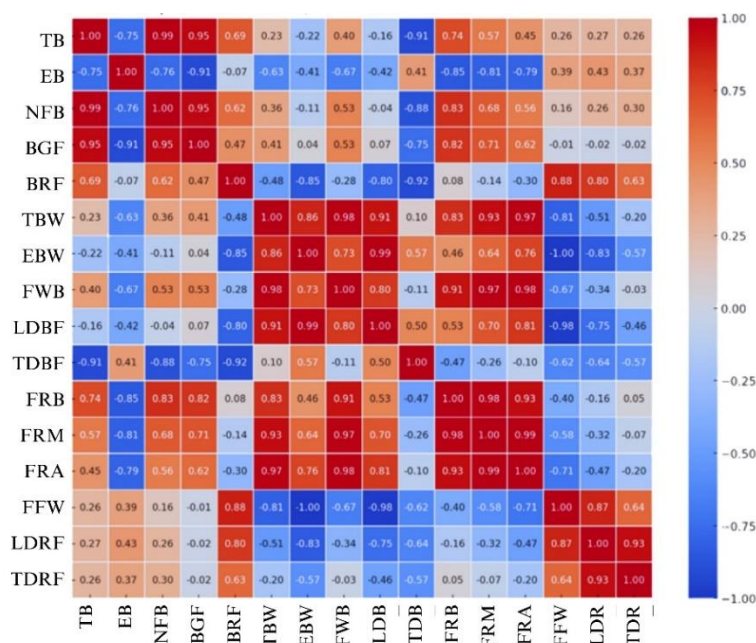
For fruit-related traits, the genetic coefficient of variation was lower—6.8% (FFW), 1.39% (LDRF), and 0.32% (TDRF), revealing a narrower genetic base compared with bunch characteristics. Nevertheless, heritability remained moderate to high (77.4% for FFW, 79.8% for LDRF), indicating that their phenotypic expression is still largely determined by genetic factors. The low heritability of TDRF (2.97%) and minimal CVg (0.32%) suggest stabilizing selection on fruit shape, typical of domesticated or semi-domesticated populations subjected to recurrent harvest and selection. Such patterns reflect selective pressure toward morphological uniformity, favored by market standards and cultivation practices. Overall, bunch-related traits exhibited greater heritability and genetic variability than fruit traits, making them more effective for genetic differentiation and early selection. Parameters such as number of bunches, bunch weight, and fruit distribution per rachis emerge as key descriptors for guiding breeding strategies focused on increasing yield and productivity in *Euterpe oleracea*.

The Pearson correlation analysis among biometric variables (Figure 2) revealed consistent association patterns between morphological and productive traits. Strong positive correlations were found between mean blade length (MBL) and mean leaf length (MLL) ($r=0.89$), and between MLL and mean leaf width (MLW) ($r=0.86$). These results demonstrate that foliar development progresses proportionally in both linear and transverse dimensions, confirming leaf expansion as a reliable indicator of vegetative vigor and overall plant performance.



Figure 2

*Pearson correlation matrix among bunch and fruit traits of four açai palm (*E. oleracea*) populations from natural floodplain areas.*



Note: TB: total bunches; EB: empty bunches; NFB: newly fertilized bunches; BGF: bunches with green fruits; BRF: bunches with ripe fruits; TBW: total bunch weight; EBW: empty bunch weight; FWB: fruit weight per bunch; LDBF: longitudinal diameter of bunch with fruits; TDBF: transverse diameter of bunch with fruits; FRB: fruits per rachis (base); FRM: fruits per rachis (middle); FRA: fruits per rachis (apex); FFW: fresh fruit weight; LDRF: longitudinal diameter of ripe fruit; TDRF: transverse diameter of ripe fruit.

Plant height (PH) showed a moderate to strong positive correlation with mean leaf length (MLL; $r = 0.76$) and mean leaflet length (MLLf; $r = 0.69$), suggesting that taller plants tend to exhibit longer leaves and more developed leaflets (Figure 2). This pattern is consistent with the literature, which points to an intrinsic relationship between vegetative vigor and the expansion of photosynthetic organs, reflecting a greater capacity to intercept photosynthetically active radiation (Coelho et al., 20215; Baldocchi et al., 2020; Delgado et al., 2024).

Additionally, a moderate correlation was observed between stem diameter (SD) and mean leaflet width (MLW; $r = 0.57$) (Figure 2), indicating that greater structural robustness is associated with an increase in functional leaf area. This finding may reflect the role of stem diameter as an indicator of reserve accumulation and support for the emission of larger leaves, a relationship already described in studies with fruit species (Amaral et al., 2023; De Sousa et al., 2024; Rocha et al., 2025).

On the other hand, some variables showed weak or no correlation, suggesting relative independence in their variation. This result highlights that, while some vegetative traits are strongly associated, others respond more autonomously to the experimental and genetic



conditions evaluated. Overall, the results indicate that traits such as leaf length and width are highly correlated and may serve as surrogate indicators in growth analyses. Furthermore, the association between plant height, leaf length, and leaflet traits reinforces the importance of vegetative vigor as a determining component of morphological performance.

5 CONCLUSION

The evaluation of open-pollinated *Euterpe oleracea* progenies under floodplain conditions in the Tocantins Amazon revealed high genetic variability and heritability for key morphoagronomic traits related to reproductive efficiency and yield potential. Traits such as total number of bunches, newly fertilized bunches, and bunches with green fruits showed strong additive genetic control and wide phenotypic plasticity, typical of allogamous palms.

The consistently high heritability ($h^2 > 80\%$) and favorable genetic-to-environmental ratios confirm that bunch and fruit descriptors are stable and effective for early selection. In contrast, fruit shape traits exhibited lower variability, indicating stabilizing selection and partial domestication effects.

Overall, the results confirm that morphoagronomic descriptors are reliable indicators of genetic divergence, enabling the identification of superior genotypes adapted to Amazonian floodplain environments. The findings provide a solid foundation for breeding, conservation, and germplasm management strategies aimed at improving productivity and resilience in açaí cultivation.



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