From biochemistry to breeding: biochemical and genetic variability of *Acrocomia aculeata* seeds for selection strategies

Da bioquímica ao melhoramento: variabilidade bioquímica e genética de sementes de *Acrocomia aculeata* para estratégias de seleção

De la bioquímica al mejoramiento: variabilidad bioquímica y genética de semillas de *Acrocomia aculeata* para estrategias de selección

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ABSTRACT
Acrocomia aculeata is a species widely found in the Brazilian Cerrado, with significant economic and environmental potential. It is used for biofuels, construction, human and animal nutrition, and recovery of degraded areas. Evaluating the genetic variability of natural populations is crucial for characterizing *A. aculeata* seeds through the selection and correlation of their chemical compounds, such as starch, carbohydrates, lipids, micronutrients (N, P, K, Ca, Mg, and S), and reserve proteins. Seeds were collected from 30 open-pollinated matrix trees in a degraded area of the former "Engenheiro Sergio Motta" Hydroelectric Power Plant construction site in Rosana, São Paulo, Brazil. Statistical analyses, based on a randomized block design with 30 progenies and four replications, examined 13 characteristics by mean, variance, and standard deviation. Genetic correlations, divergence by the Generalized Mahalanobis Distance (D^2), grouping by the Tocher Optimization Method, and the Mulamba & Mock index were estimated, revealing five distinct groups of individuals (84% in the first group, 7% in the second, and 3% in each of the three

subsequent groups). The Mulamba & Mock index indicated satisfactory results for selection aimed at increasing biochemical compounds, highlighting the genetic variability of the population and potential sources for future breeding and conservation programs.

Keywords: degraded área, macauba, biochemical traits, palm tree.

RESUMO

Acrocomia aculeata é uma espécie amplamente encontrada no Cerrado brasileiro, com significativo potencial econômico e ambiental. É utilizada para biocombustíveis, construção civil, nutrição humana e animal e recuperação de áreas degradadas. Avaliar a variabilidade genética de populações naturais é crucial para caracterizar sementes de A. aculeata por meio da seleção e correlação de seus compostos químicos, como amido, carboidratos, lipídios, micronutrientes (N, P, K, Ca, Mg e S) e proteínas de reserva. Sementes foram coletadas de 30 árvores matrizes de polinização aberta em uma área degradada do antigo canteiro de obras da Usina Hidrelétrica "Engenheiro Sergio Motta" em Rosana, São Paulo, Brasil. As análises estatísticas, baseadas em um delineamento em blocos casualizados com 30 progênies e quatro repetições, examinaram 13 características por média, variância e desvio padrão. Correlações genéticas, divergência pela Distância Generalizada de Mahalanobis (D^2), agrupamento pelo Método de Otimização de Tocher e o índice de Mulamba & Mock foram estimados, revelando cinco grupos distintos de indivíduos (84% no primeiro grupo, 7% no segundo e 3% em cada um dos três grupos subsequentes). O índice de Mulamba & Mock indicou resultados satisfatórios para a seleção visando o aumento de compostos bioquímicos, destacando a variabilidade genética da população e potenciais fontes para futuros programas de melhoramento e conservação.

Palavras-chave: área degradada, macauba, características bioquímicas, palmeira.

RESUMEN

Acrocomia aculeata es una especie ampliamente distribuida en el Cerrado brasileño, con un importante potencial económico y ambiental. Se utiliza para biocombustibles, construcción, nutrición humana y animal, y recuperación de áreas degradadas. La evaluación de la variabilidad genética de las poblaciones naturales es crucial para caracterizar las semillas de A. aculeata mediante la selección y correlación de sus compuestos químicos, como almidón, carbohidratos, lípidos, micronutrientes (N, P, K, Ca, Mg y S) y proteínas de reserva. Se recolectaron semillas de 30 árboles matriz de polinización abierta en un área degradada del sitio de construcción de la antigua Central Hidroeléctrica "Engenheiro Sergio Motta" en Rosana, São Paulo, Brasil. Los análisis estadísticos, basados en un diseño de bloques aleatorios con 30 progenies y cuatro réplicas, examinaron 13 características mediante media, varianza y desviación estándar. Se estimaron las correlaciones genéticas, la divergencia mediante la Distancia Generalizada de Mahalanobis (D^2), la agrupación mediante el Método de Optimización de Tocher y el índice de Mulamba y Mock, revelando cinco grupos distintos de individuos (84 % en el primer grupo, 7 % en el segundo y 3 % en cada uno de los tres grupos subsiguientes). El índice de Mulamba y Mock indicó resultados satisfactorios para la selección orientada al aumento de compuestos bioquímicos, destacando la variabilidad genética de la población y las posibles fuentes para futuros programas de mejoramiento y conservación.

Palabras clave: área degradada, macauba, rasgos bioquímicos, palmera.

1 INTRODUCTION

The palm tree *Acrocomia aculeata* (Jacq.) Lodd. ex Mart., commonly known as "macaúba" or "bocaiuva", has a widespread distribution throughout the Brazilian territory and stands as a prime example of a species whose potential remains largely untapped. In the Brazilian Savanna (Cerrado biome) the presence of this palm tree is notable and easily identifiable in almost all environments Spetially between the states of São Pualo, Minas Gerais and Mato Grosso do Sul. Additionally, due to its wide-ranging nature, macaúba can also be found in biomes such as the Pantanal, Atlantic Forest, and Amazon (Militão & Morais, 2023; Lorenzi, 2006).

Among its various uses, food stands out prominently. This includes consumption of the fruit fiber or the seed kernel (Sarmento & Villela, 2010). The construction industry also utilizes macaúba, with its trunk serving as raw material for houses or transmission poles, and the fruit fibers being used with cement (Vale, 2007). Additionally, the species plays a significant role in handicrafts, as its large leaves not only serve as building coverings but are also transformed into baskets and utensils by indigenous or riverside populations (Lorenzi, 2006). Another use is as an important source for biodiesel production, such some authors highlight the growing importance of biofuel production on an international scale, given the prospect of global petroleum reserves depletion (Amaral, 2007). Initiatives have been taken at an international level to obtain and use vegetable-based fuel oils, in which *Acrocomia aculeata* plays a fundamental role.

Hiane *et al.* (2006) noted that the kernels of *A. aculeata,* extracted from the seeds, have a high content of lipids, proteins, and fibers, as well as a high level of calcium, phosphorus, and manganese compared to other fruit kernels like cashew or coconut. Apart from its high economic interest due to its potential use in biodiesel production, the species can also be considered an environmental indicator of well-drained soils, as mentioned by Kurihara *et al*. (2005). Furthermore, its presence can indicate the fertility level of the substrates in which it grows (Motta *et al*., 2002).

Considering these insights regarding this important species of the Brazilian Savanna, the objective of this study was to characterize the genetic variability in seeds of a natural population of *A. aculeata* by analyzing the levels of starch, carbohydrates, lipids, and proteins (albumins, globulins, glutenins, and prolamins) as well as micronutrients (nitrogen, phosphorus, potassium, calcium, magnesium, and sulfur). The aim was also to identify the most suitable seed traits for potential selection and improvement within this population located in an environmental preservation area in the former construction site of the Hydroelectric Power Plant "Eng. Sergio Motta", at the municipality of Rosana – São Paulo.

2 MATERIAL AND METHODS

2.1 MATERIAL

Seeds from *A. aculeata* plants were collected from 30 random and freely pollinated trees in a population located within the environmental preservation areas at the former construction site of the Hydroelectric Power Plant "Eng. Sergio Motta", municipality of Rosana, São Paulo State, Brazil. The collected trees of this population were georeferenced.

2.2 METHODS

The biochemical characteristics of the seeds were obtained in mg per g^{-1}, referring to the contents of starch, carbohydrates, lipids, and proteins (albumin, globulin, glutenin, and prolamin) and in g per Kg^{-1} for macronutrients (N, P, K, Ca, Mg, and S). The biochemical characteristics were determined through analysis of variance in randomized blocks, with the 30 families (mother trees) in 4 repetitions for each tree. This procedure was used for starch, carbohydrates, lipids, macronutrients, and protein content analysis.

Starch determination was conducted following the standard procedure described by Wang & Chong (2006), with absorbance readings taken at 505 nm using a fixed curve spectrophotometer. Carbohydrate extraction was performed according to the standard protocol, weighing 0.5 grams of seeds. Carbohydrate content was determined using the phenol-sulfuric acid method, based on the procedure by Dubois *et al.* (1956), with a glucose standard curve, and the absorbance readings were taken at 490 nm on a spectrophotometer.

Lipid extraction was carried out using the Soxhlet method, adapted from the analytical standards of the Adolfo Lutz Institute (Pregnolato and Pregnolato, 1985). The initial sample preparation for this analysis involved first removing the seed husks, leaving only the endosperm, followed by drying to reduce moisture content (Nadarajapillai and Wijewantha, 1967). The samples were then weighed, labeled, and processed following Soxhlet's extraction methods. No further analysis was performed on the oil's structure or composition.

The nutritional status evaluation (macronutrient content: N, P, K, Ca, Mg, and S) of *Acrocomia aculeata* seeds from selected trees was conducted following the methodology proposed by Malavolta (1989). Sulfuric digestion was used for nitrogen analysis, and nitric-perchloric digestion for phosphorus, potassium, calcium, magnesium, and sulfur analysis. Analytical determinations were obtained via the semimicro-Kjeldahl method (Bremmer, 1960) for nitrogen, metavanadate colorimetry for phosphorus, barium sulfate turbidimetry for sulfur, flame photometry for potassium, and EDTA complexometry for calcium and magnesium.

Storage proteins such as albumins (ALB), globulins (GLO), prolamins (PRO), and glutelins (GLU) were extracted based on their solubility, following the method described by Sturgis *et al.* (1952) and modified by Garcia-Agustin & Primo-Millo (1989). Aliquots of each extract were used for protein determinations according to the Lowry *et al.* (1951) method, based on their solubility: albumins (water), globulins (NaCl), glutelins (NaOH), and prolamins (ethyl alcohol), with adaptations, using bovine serum albumin as a standard. Absorbance readings were taken at 660 nm on a spectrophotometer.

The estimates of variance components and genetic parameters were obtained using the REML/BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction) procedure, employing the genetic-statistical software SELEGEN-REML/BLUP developed by Resende (2007b), following the procedure proposed by Resende (2002 and 2007a): $\boldsymbol{y} = \boldsymbol{Xr} + \boldsymbol{Zg} + \boldsymbol{\varepsilon}$ where: $\boldsymbol{y}$ is the data vector; $\boldsymbol{r}$ is the vector of repetition effects (assumed as fixed) added to the overall mean; $\boldsymbol{g}$ is the vector of genotypic effects (assumed as random), and $\boldsymbol{\varepsilon}$ is the vector of errors (random). The uppercase letters represent the incidence matrices for these effects (Model 96).

The Index Based on Rank Sum (or Ranks), proposed by Mulamba and Mock (1978) and described by Cruz and Regazzi (2001) and Cruz (2001), was used: $I = r_1 + r_2 + \ldots + r_n$; where: I: value of the index for a particular individual or family; r_j: ranking of an individual in relation to the j-th variable; n: number of variables considered in the index. The estimates of this index were based on the SELEGEN - REML/BLUP program (Resende, 2007b).

Genetic divergence among progenies was estimated using the Generalized Mahalanobis Distance (D^2). In quantitative data analysis, this methodology is most suitable as it considers the matrices of residual variances and covariances among the measured characters. The Generalized Mahalanobis Distance is described by the expression (Cruz & Regazzi, 2001): $D^2 = \delta$ where: D^2 = Mahalanobis distance between genotypes i and i'; $\delta = [d_1, d_2, \ldots, d_v]$, where $d_j = Y_{ij} - Y_{i'j}$; Ψ = residual variance and covariance matrix; Y_{ij} = mean of the i-th genotype for the j-th variable.

After obtaining the distance matrix (D^2) as per Resende (2007), cluster analysis was performed using the Tocher Optimization Method, described by Cruz & Regazzi (2001), where the criterion is that the mean intra-cluster D^2 values should be lower than the inter-cluster D^2 values. Tocher clustering was obtained using the REML/BLUP method, employing the genetic-statistical software Selegen (Resende, 2007).

3 RESULTS

3.1 BIOCHEMICAL COMPOUNDS ANALYSIS

In the analyzed population of *A. aculeata*, starch content obtained an overall mean of 0.27 mg/g-1 (Table 1). The Likelihood Ratio Test (LRT) analyzed for this trait was 146.8, showing significance at a 95% probability level and indicating genetic variability expression among the trees. The residual coefficient of variation (CVr(%)) was 11.39%, indicating a good level of data reliability, with accuracy (râa) reaching a high percentage of 98.33%, and the average genotype heritability (h_m^2) was 0,96 or 96%. The likelihood ratio test (LRT) is a widely used statistical method for comparing nested models in the analysis of quantitative genetic data. The application of the LRT in quantitative genetics allows for rigorous evaluation of hypotheses concerning genetic variability and the influence of specific loci on phenotypic traits (Berton, 2013). Lewis (2001) demonstrates that the LRT provides a robust approach for detecting genetic associations, surpassing traditional methods in terms of statistical power and precision in genetic parameter estimates.

The carbohydrate levels analyzed for *A. aculeata* seeds showed an overall mean (m) of 10.24 mg g^{-1} (Table 1). The LRT index analyzed for carbohydrates (210.24) showed significance at a 95% probability, indicating genetic variability expression among the mother trees collected in the experiment. The residual variation coefficient ($CVe_{(\%)}$) was 8.09%, indicating a good level of reliability to the data, providing that this characteristic can be an indicator for a potential breeding program anchored to accuracy data ($r_{\hat{a}a}$) obtained (98.51%) and mean genotype heritability ($\hat{h}_m^2$) of 99.25%.

Considering lipids, the contents analyzed for *A. aculeata* seeds showed an overall mean (m) value of 20.23 mg g^{-1} (Table 1). The relative variation coefficient ($CVr_{(\%)}$) was 26.5%, accuracy ($r_{\hat{a}a}$) was 98.57%, and the mean genotype heritability ($\hat{h}_m^2$) was 99.28%, indicating this characteristic as a starting point for a future breeding program.

The protein content in *A. aculeata* seeds varied from 41.82 mg g^{-1} for Globulin to 6.69 mg g^{-1} for Glutenin (Table 1), with these being the highest and lowest values found. Albumin and prolamin had average values of 16.40 mg g^{-1} and 21.81 mg g^{-1} respectively. The average genotype heritability remained high between 0.98 and 0.99 or 98% and 99% for all compounds that make up the proteins present in the seed, as well as accuracy, demonstrating that the values are part of a broad genetic inheritance, supporting possible breeding projects for the species based on these compounds. The coefficients of variation remained at good levels and demonstrated genetic variability and good viability of the samples and experiments.

Table 1: Estimates of genetic parameters for starch, carbohydrates, lipids, and proteins (albumin, globulin, glutenin, and prolamin) content in seeds of progenies from a natural population of *A. aculeata,* originating from the Pontal do Paranapanema region, municipality of Rosana – São Paulo. Source: Prepared by the authors (2025).

	Starch	Carbohydrates	Lipids	Proteins			
				Albumin	Globulin	Glutenin	Prolamin
σ_g^2	0,0074	11,37	22,95	10,86	119,65	2,93	26,46
σ_e^2	0,0010	0,69	0,03	0,62	7,95	0,08	1,78
σ_f^2	0,0084	12,06	22,98	11,48	127,60	3,01	28,24
h_g^2	0.87±0.24	0,94±0,25	0,99±0,36	0,94±0,25	0,93±0,25	0,97±0,25	0,93±0,39
h_m^2	0,96	0,99	0,99	0,98	0,98	0,99	0,98
$r_{âa}$	0,98	0,99	0,99	0,99	0,99	0,99	0,99
$CVg_{(\%)}$	30,82	32,93	23,68	20,10	26,15	25,57	23,57
$CVe_{(\%)}$	11,39	8,09	0,89	4,79	6,74	4,27	6,12
$CVr_{(\%)}$	2,70	4,06	26,50	4,19	3,87	5,98	3,85
m (mg g^{-1})	0,27	10,24	20,23	16,40	41,82	6,69	21,81
LRT (χ^2)	146,8*	210,24*	170,06*	215,21*	202,67*	274,02*	76,43*

* significant at 95% probability with 1 degree of freedom; σ_g^2: genotypic variance; σ_e^2: residual variance; σ_f^2: individual phenotypic variance; h_g^2: broad-sense heritability, i.e., of total genotypic effects; h_m^2: heritability of mean genotype, assuming no plot loss; $r_{âa}$: selection accuracy of genotypes, assuming no plot loss; *CVg*: genotypic coefficient of variation; *CVe*: residual coefficient of variation; *CVr*: relative coefficient of variation; *m*: overall mean in mg g^{-1}; χ^2: deviance chi-square; LRT: Likelihood Ratio Test.

After analyzing the micronutrient contents (Table 2), the average levels of Nitrogen (N), Phosphorus (P), Potassium (K), Calcium (Ca), Magnesium (Mg), and Sulfur (S) were obtained. Nitrogen was the most abundant nutrient in the seed, with an average value of 23.6 g kg^{-1}, contrasting with calcium, which was determined at only 1.53 g kg^{-1}. For phosphorus, the value was 6.64 g kg^{-1}, potassium 3.33 g kg^{-1}, magnesium 1.80 g kg^{-1}, and sulfur 1.69 g kg^{-1}.

Table 2. Estimates of genetic parameters for micronutrient contents: nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), and sulfur (S) in seeds of a natural population of *Acrocomia aculeata*, derived from a natural population in Pontal do Paranapanema, in the municipality of Rosana - São Paulo. Source: Prepared by the authors (2025).

Estimates	Nitrogen (N)	Phosphorus (P)	Potassium (K)	Calcium (Ca)	Magnesium (Mg)	Sulfur (S)
σ_g^2	6,75	0,88	0,6051	0,1662	0,0708	0,0555
σ_e^2	3,21	0,05	0,0127	0,1365	0,0217	0,0067
σ_f^2	9,96	0,93	0,6178	0,3028	0,0926	0,0623
$\hat{h}_g^2$	0,67 ±0,21	0,94 ±0,25	0,97 ±0,25	0,54 ±0,19	0,76 ±0,22	0,89 ±0,24
$\hat{h}_m^2$	0,89	0,98	0,99	0,82	0,92	0,97
$r_{âa}$	0,94	0,99	0,99	0,91	0,96	0,98
$CVg_{(\%)}$	11,00	14,13	23,31	26,61	14,77	13,90
$CVe_{(\%)}$	7,58	3,32	3,38	24,12	8,18	4,84
$CVr_{(\%)}$	1,45	4,24	6,89	1,10	1,80	2,86
m (g kg^{-1})	23,60	6,64	3,33	1,53	1,80	1,69
LRT (χ^2)	64,58*	209,9*	287,69*	39,63*	88,26*	150,22*

* significant at 95% probability with 1 degree of freedom. σ_g^2: genotypic variance; σ_e^2: residual variance; σ_f^2: individual phenotypic variance; $\hat{h}_g^2$: broad-sense heritability, i.e., of total genotypic effects; $\hat{h}_m^2$: heritability of mean genotype, assuming no plot loss; $r_{âa}$: selection accuracy of genotypes, assuming no plot loss; *CVg*: genotypic coefficient of variation; *CVe*: residual coefficient of variation; *CVr*: relative coefficient of variation; *m*: overall mean; χ^2: deviance chi-square; LRT: Likelihood Ratio Test.

The relative coefficient of variation (*CVr*) was 1.10% for calcium, being the lowest among the other nutrients, and 6.89% for potassium, which had the highest value and proved to be a consistent variable for a breeding program. The genotypic coefficient of variation (*CVg*) ranged from 11% to 26.61% for the analyzed nutrients, with nitrogen having the lowest variation at 11% and calcium the highest at 26.61%. These values demonstrate the genetic richness of the species and the great genotypic variation that can occur in its populations.

The average genotype heritability ($\hat{h}_m^2$) showed satisfactory values close to expected for the genetic richness found in the species. Potassium once again had the highest value among all compounds, with a value of 0.99 indicating that its expressiveness is essentially guaranteed by genotypic variations. Calcium, on the other hand, had a value of 0.82, which although lower also indicates strong genotypic expression.

The genetic patterns determined for accuracy ($r_{\hat{a}a}$) pointed to significant values estimated between 0.91 to 0.99, attributed to calcium and potassium respectively. The other macronutrients had similar values, with 0.94 for nitrogen, 0.99 for phosphorus, 0.96 for magnesium, and 0.98 for sulfur. These values indicate a promising potential for the species in the context of plant breeding for commercial or environmental purposes since it indicates that the mentioned compounds can still be optimized if managed accordingly. Potassium once again proved to be the nutrient with the highest genetic variability for breeding purposes.

3.2 GENETIC VARIABILITY CORRELATIONS

The Mulamba & Mock index (Table 3), designed for selection aiming to increase the content of all biochemical compounds, revealed satisfactory values, indicating they are sources for a future Breeding or conservation program. The Mulamba & Mock index is a non-parametric statistical tool developed to enhance genotype selection in genetic improvement programs. Its essence lies in the sum of ranks attributed to various traits of interest, allowing the simultaneous selection of multiple desirable characteristics. This methodology is particularly useful in contexts where the correlation between traits is complex, and selection based on a single criterion may be insufficient or misleading (Teixeira *et al*., 2012; Dalbosco *et al*., 2018).

Table 3: Mulamba-Mock Index for genotype selection based on biochemical traits in seeds of a natural population of *Acrocomia aculeata*, from a natural population in Pontal do Paranapanema, Rosana - São Paulo. Source: Prepared by the authors (2025).

Order	Progeny	Average Rank	Gain	Gain (%)
1	11	93.846	93.846	65,16
2	16	97.692	95.769	61,85
3	14	110.769	100.769	53,82
4	18	124.615	106.731	45,23
5	13	126.923	110.769	39,93
6	26	126.923	113.462	36,61
7	28	129.231	115.714	33,95
8	23	130.000	117.500	31,91
9	8	133.846	119.316	29,91
10	25	135.385	120.923	28,18
11	5	139.231	122.587	26,44
12	9	140.000	124.038	24,96
13	24	144.615	125.621	23,39
14	4	146.154	127.088	21,96
15	3	153.077	128.821	20,32
16	30	155.385	130.481	18,79
17	19	156.154	131.991	17,43
18	6	161.538	133.632	15,99
19	20	161.538	135.101	14,73
20	29	166.923	136.692	13,39
21	10	173.846	138.462	11,94
22	21	173.846	140.070	10,66
23	15	182.308	141.906	92,27
24	12	190.000	143.910	77,06
25	27	190.000	145.754	63,44
26	22	190.769	147.485	50,95
27	1	196.923	149.316	38,07
28	7	203.846	151.264	24,70
29	17	206.154	153.156	12,04
30	2	208.462	155.000	0,00

Regarding Mahalanobis distances (D^2) (Table 4), the maximum observed was $D^2 = 31.75$ between progenies 14 and 3. The minimum distance, on the other hand, was $D^2 = 0.29$, observed between progenies 15 and 14, and 28 and 23, respectively. More divergent progenies with higher productive performance and/or greater genotypic value can be selected for controlled crosses, potentially aiding in obtaining more promising progenies in terms of productivity (Santos *et al.*, 2021). This analysis is a multivariate statistical technique that allows solving the problem of, given a set of "n" sample units (individuals, treatments, genotypes, etc.), which are measured according to p variables (characteristics), obtaining a scheme that allows grouping the units into a number of

groups such that there is homogeneity within and heterogeneity between the groups (Regazzi, 2006; Pereira *et al*., 2011).

Table 4: Mahalanobis Distances (D^2) of biochemical traits in seeds of a natural population of *Acrocomia aculeata,* originating from a natural population in Pontal do Paranapanema, Rosana municipality, São Paulo. Source: Prepared by the authors (2025).

Progeny	Highest (%)	Progeny	Lowest (%)	Progeny
1	18,52	9	0,94	11
2	13,57	23	0,85	27
3	31,75	14	3,20	29
4	12,52	3	0,50	16
5	19,80	3	0,96	8
6	17,93	14	1,11	10
7	18,46	7	0,53	16
8	25,71	3	0,96	5
9	18,52	1	1,10	20
10	18,06	14	1,11	6
11	18,42	30	0,94	1
12	16,19	17	1,11	7
13	14,46	23	1,73	15
14	31,75	3	5,22	24
15	17,99	14	0,29	28
16	14,73	17	0,50	4
17	20,33	23	1,20	21
18	17,13	23	1,31	19
19	15,40	3	0,75	25
20	12,46	17	1,10	9
21	18,61	5	1,20	17
22	15,85	17	1,38	23
23	20,33	17	1,38	22
24	14,96	3	2,01	20
25	15,57	3	0,75	19
26	15,17	10	2,27	24
27	9,82	14	0,85	2
28	17,53	23	0,29	15
29	16,30	14	1,35	2
30	18,42	11	1,35	9
Maximum	31,75	**Progenies**	14 e 3	
Minimum	0,29	**Progenies**	15 e 14, 28 e 23	

The Tocher clustering for Mahalanobis Distances (D^2) (Table 5) showed convergence for biochemical traits, revealing five distinct groups of parent trees. The results show that the largest group indicated by the analysis was Group I, representing approximately 75% of the analyzed

individuals, thus, with 25 Progenies. Group II followed closely with 2 progenies, while Groups II, IV, and V each comprised only one progeny.

Table 5: Tocher clustering for Mahalanobis Distances (D^2) in seeds of a natural population of *Acrocomia aculeata*, originating from a natural population in Pontal do Paranapanema, in the municipality of Rosana – São Paulo. Source: Prepared by the authors (2025).

Groups	Progenies
I	1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 17, 18, 19, 20, 21, 23, 24, 25, 27, 28, 29
II	10, 26
III	16
IV	30
V	22

4 DISCUSSION

4.1 BIOCHEMICAL COMPOUNDS

The analysis of biochemical compounds is fundamental to understanding plant physiology, improving agricultural practices and its use in industry. These components are crucial for photosynthesis, respiration, nutrient translocation, and defense against environmental stresses. The balance between these macro and micronutrients is essential for plant health and productivity, highlighting the importance of detailed studies on plant biochemistry. The use of fruit pulp of *A. aculeata* is widely studied for industrial purposes, but the use of seeds is still scarce.

Starch is a fundamental energy reserve in higher plants, playing a vital role in the plant life cycle. Its synthesis occurs in chloroplasts during photosynthesis, primarily stored in starch granules found in storage organs such as seeds, tubers, and roots (Smith, 2012). The analysis of starch biosynthesis, mobilization, and degradation in plants has been the subject of intense research, revealing valuable data about the molecular mechanisms underlying these complex processes. Recent studies have emphasized the importance of fine-tuning these processes to optimize starch production in agricultural crops, aiming to increase productivity and food quality (Cho & Kang, 2020; Tetlow *et al*., 2004).

Understanding the factors that influence starch synthesis and degradation in plants is essential for developing biotechnological strategies aimed at improving desirable agronomic traits such as yield, resistance to abiotic stresses, and nutritional quality. Additionally, the analysis of mutants deficient in key enzymes involved in starch metabolism has provided valuable insights into the function of these proteins and their interactions within metabolic pathways. These studies have significant implications for both agriculture and plant basic biology, contributing to a deeper

understanding of the physiological and biochemical processes underlying plant development (Apriyanto *et al.*, 2022; Hostettler *et al*., 2011; Macneill *et al*., 2017; Pfister & Zeeman, 2016).

Also, native Brazilian palm trees, such as *Mauritella armata* (Buriti-Mirim), represent an important source of starch with potential food and industrial applications. Studies conducted by Morais *et al.* (2024) for this species yielded results of 2.66 g 100 g^{-1}, indicating values higher than those of *A. aculeata* for this compound. Santos *et al.* (2017), in their study of species such as Bacaba (*Oenocarpus bacaba* Mart.), Buriti (*Mauritia flexuosa* L.), Inajá (*Maximiliana maripa* (Aubl.) Drude), Pupunha (*Bactris gasipaes* Kunth), and Tucumã (*Astrocaryum vulgare* Mart.), other prominent palm trees evaluated for the quality of their fruits and oils, also inferred higher percentages of starch content compared to Macaúba, ranging from 2.15% (Buriti) to 214.89% (Pupunha) of this compound in fruits, indicating a vast potential for use not only in food but also in cosmetic and medicinal applications.

In addition to its direct applications, the starch from native palm trees possesses unique physicochemical and functional characteristics that can be explored in the development of new products. Guedes *et al*. (2021) highlight the importance of characterizing these properties to enhance their use in various sectors, as demonstrated in the analysis of *Eugenia pyriformis* (Uvaia), whose starch showed innovative properties for the food industry. The investigation of Albino Peach Palm (*Bactris gasipaes*) starch by Soares *et al.* (2023) demonstrated how the cooking and drying process influences its characteristics, paving the way for the creation of differentiated products with higher added value.

In native Brazilian palm trees, the analysis of carbohydrate levels reveals a complex range of compounds that play fundamental roles in plant physiology and the development of new products (Pires *et al.*, 2019). Palms such as *E. oleracea*, *O. bataua*, and *O. bacaba* also present an important source of carbohydrates, with levels above 40 g per 100 g^{-1} (Morais *et al.*, 2022). Furthermore, Morais *et al*. (2022) indicate that the palm tree closest in carbohydrate content to *A. aculeata* was Buriti (*M. flexuosa*), demonstrating the plant's potential for carbohydrate-based product production.

Lipids are a diverse group of hydrophobic or amphipathic organic compounds that play fundamental roles in living organisms, including higher plants. These compounds include fats, oils, waxes, phospholipids, sterols, among others. In higher plants, lipids not only serve as an energy reserve but also are essential components of cell membranes, providing fluidity and actively participating in cell signaling processes. The basic chemical structure of lipids involves fatty acid chains linked to a glycerol molecule, although the structural diversity is vast, reflecting the wide range of functions they perform in plant cells (Ahmed *et al*., 2022).

In higher plants, lipids are also crucial for adaptation and survival in diverse environments. They participate in the constitution of leaf cuticles, a protective layer that reduces water loss and provides protection against pathogens (Li-Beisson *et al.*, 2013). Additionally, specific lipids such as phospholipids and sphingolipids are involved in forming signaling platforms on membranes, essential for plant response to environmental stimuli and stresses (Fahy *et al.*, 2011). In addition to genetic variability, the high oil content presented by the progenies in macaúba is noteworthy, confirming the species' high capacity as an oilseed and a potential production source, as described by Fortes & Baugh (1999), who generated a large number of compounds such as hydrocarbons, aldehydes, and carboxylic acids through oil pyrolysis, highlighting its richness and methodology reproducibility for energy purposes.

Antoniassi *et al*. (2020) emphasize that, besides the potential for biodiesel, both the mesocarp and fruit kernel are edible, suggesting a comprehensive utilization of the plant. Oil content and fatty acid profile vary significantly among genotypes, highlighting the importance of genetic selection to optimize oil production. Studies like Alfaro-Solís *et al.* (2020) also reinforce the relevance of research on fruit morphology and oil composition to understand the species' genetic diversity and maximize its commercial use. In addition to biodiesel production, Macaúba has potential for degraded area restoration and promotes sustainable economic benefits. The diversification of Macaúba oil uses, ranging from the food industry to cosmetics, points to a growing demand supporting the development of sustainable productive chains based on this tropical species (da Silva-César, 2015).

Further studies on almond and macaw pulp oil composition confirm the richness in long-chain oils, with oleic acid predominating in pulp and lauric acid in seeds, justifying its use as an important source for the cosmetics industry and demonstrating the viability of exploiting the species commercially (Amaral *et al*., 2011; Machado, 2016). In other palm trees, Bacaba and Buritirana showed values close to *A. aculeata*, accounting for 21.02 and 21.01 g per 100 g^{-1}, respectively, surpassing species such as Juçara palm (*E. edulis*), Buriti (*M. flexuosa*), or Butiá (*B. odorata*) (Morais *et al*., 2022). These values demonstrate how *A. aculeata* is a promising species and an important lipid source to be commercially explored.

Proteins play important roles in all organisms, such as molecule transport, catalyzing chemical reactions, and structural functions (Ribeiro, 2014). In plants, these compounds are extremely important for their survival due to their ability to adapt and resist stress situations, an example being heat shock proteins (HSP) that contribute to temperature regulation through signaling, translation, and other mechanisms seeking a balance so that the individual's organism is not harmed due to these situations (Wang & Perry, 2013; Usman *et al*., 2014).

Albumin plays a vital role in nutrient storage and seed germination, significantly contributing to the initial growth of plants. Prolamins, on the other hand, are reserve proteins that provide essential amino acids during germination, ensuring the healthy development of seedlings (Shewry & Halford, 2002). Globulins, in turn, play a crucial role in nutrient transport and protection against environmental stresses, assisting plants in adapting to different conditions. On the other hand, glutenins, gluten-associated proteins, are fundamental in bread structure formation and other baking products, providing them with desirable elasticity and texture (Gupta & MacRitchie, 1994).

Regarding protein content in *A. aculeata*, Silva *et al*. (2008b) stated in their research that macauba cake is a protein-rich cake and is therefore highly valued as an ingredient in animal feed. It is a concentrate rich in Omega 3 and Omega 6, recommended for bird feed, standing out for increasing egg production and size. Silva *et al.* (2008b) thus conclude that almond cake stands out for its high protein value and can be recommended for feeding. The shell and pulp cakes were found to be poor in proteins but very rich in fibers, suitable for soil fertilization as well as fuel in boilers and foundries. Thus, the selection and use of genotypes with high seed content of these proteins can be an alternative to the food supply chain in industry.

Nutrients such as nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), and sulfur (S) are essential for the growth and development of plants. They participate in various biological functions, including biomolecule synthesis, osmotic regulation, and enzymatic activation. The efficiency in absorbing and utilizing these nutrients is crucial for photosynthetic capacity and, consequently, for the productivity and sustainability of agricultural systems (Marschner, 2012). Identifying and comparing these variations are crucial to optimize cultivation practices, improve nutrient absorption and utilization efficiency, and consequently maximize fruit and oil productivity and quality. Silva e*t al.* (2008a), in their analysis of various cerrado fruits, reported a low energy density in most fruits, except for those with a considerable amount of macronutrients, including *A. aculeata*. They also inferred that the macaúba tree had the highest calcium concentration among the analyzed cerrado fruits and that these fruits could contribute significantly to the recommended dietary intake, serving as alternative nutrient sources.

The analysis of nutrients highlighted the nutritional potential of the *A. aculeata* population studied, demonstrating its importance for a future breeding program aimed at enhancing its richness even further. It also revealed other potential uses of the species beyond its environmental function, such as serving as a nutrient source for both humans and large-scale production animals, thereby extending its socio-economic functions beyond those described in this study.

Investigating the nutritional profile of macaúba also contributes to the sustainable development of the species, providing robust data for the efficient use of natural resources and

minimizing environmental impact. Therefore, research focused on analyzing macronutrients and other compounds in *A. aculeata* is of great value for agronomy, bioenergy, and environmental sustainability. The analyses presented in this study are in line with those mentioned by Silva et al. (2008b), confirming that *A. aculeata* can be an important nutrient source for various uses, including animal and human nutrition or even soil fertilization, revealing its diverse role in nature.

4.2 GENETIC VARIABILITY CORRELATIONS

The application of the Mulamba & Mock index extends across a variety of fields within biostatistics and genetic improvement, standing out for its ability to integrate multiple phenotypic and genetic aspects into a single selection measure. This enables a holistic approach in identifying genetically superior matrices, promoting balanced and sustainable genetic gains over generations. Several studies have demonstrated the effectiveness of this index in selecting high-yield and quality genotypes, reflecting its practical relevance in optimizing improvement programs (Sousa *et al*., 2021).

The incorporation of the Mulamba & Mock index in modern genetic improvement studies highlights the importance of statistics as a fundamental pillar in scientific decision-making. Through the analysis of complex genetic data and effective trait selection, this index contributes significantly to the advancement of agricultural genetics and the sustainable production of high-performance crops. Its application transcends statistical theory, directly impacting the efficiency and accuracy of genetic selection processes and providing a solid foundation for continuous innovation in molecular genetics (Terres *et al*., 2015; Piza *et al*., 2023).

The Mahalanobis Distance (D^2) is a statistical measure developed by P.C. Mahalanobis in 1936, which quantifies the distance between a point and a distribution of points considering the covariance between variables. This metric is essential in statistics and genetics for identifying multivariate outliers and conducting cluster analyses, facilitating the selection of genetically superior matrices when comparing genetic diversity between populations (McLachlan, 1999).

In genetic breeding programs, the Mahalanobis Distance is applied to estimate genetic similarity between individuals or populations, allowing the selection of genotypes with desirable characteristics while maintaining genetic diversity. This approach contributes to the efficiency of selection programs by identifying individuals that excel in multiple desired traits, promoting genetic gains, and reducing the probability of inbreeding (Baltar *et al.*, 2014). In addition, the application of this analysis extends to detecting multivariate outliers in genetic data, essential for ensuring the validity of statistical analyses and avoiding erroneous conclusions. This ability to identify anomalous observations based on the correlation structure between variables makes D^2 a valuable

tool in scientific research, especially in the context of genetic and epidemiological association studies (2020).

The Mahalanobis Distance, along with the Tocher clustering method, is one of the most precise methodologies for clustering individuals, parents, or progenies into groups based on classification criteria (Santos *et al*., 2016; Santos *et al*., 2021). This is a robust methodology employed in biostatistics and genetics to classify entities into homogeneous groups based on their multivariate characteristics. This technique, using D^2, takes into account the correlation between variables, offering a more precise perspective on genetic diversity assessment and the identification of grouping patterns among genetic matrices. Silva *et al*. (2013) highlight the effectiveness of the Tocher method in obtaining a matrix similar to cophenetic, facilitating the interpretation of clusters and comparison between different clustering methods. In the selection of genetically superior matrices, this clustering method allows the identification of groups of individuals with similar genetic characteristics, optimizing breeding programs by directing strategic crossings. This is particularly relevant in conserving genetic resources, where maintaining genetic variability is crucial. The methodology facilitates the selection of genotypes that contribute to genetic diversity within the groups, promoting the efficient selection of desirable traits without compromising overall genetic diversity (Silva *et al*. 2013; Puiatti *et al.* 2014).

Puiatti *et al.* (2014) emphasize that this occurrence is due to the method using a global grouping criterion, which tends to form groups with only one genotype each in the case of genotypes with greater dissimilarity. Santos *et al.* (2021) found a similar result when studying two areas with 30 progenies each of *Cordia trichotoma,* representing about 86% of the individuals in Group 1. According to the authors, these results may indicate divergences among individuals from the same progeny, as well as characteristics of the soil or the planting system in which these individuals are inserted.

Furthermore, using Tocher clustering in biostatistics studies enhances the ability to analyze complex data, contributing to a deeper understanding of the genetic mechanisms underlying phenotypic traits. This approach enriches scientific research by providing an effective method for analyzing multivariate data, offering valuable insights for genetic selection and species improvement. Thus, Tocher clustering associated with Mahalanobis Distances establishes itself as an essential tool for researchers and breeders aiming to maximize genetic potential and population diversity (Santos *et al.* 2016; Santos *et al.* 2021; Santos *et al.* 2022).

5 CONCLUSIONS

The population of *Acrocomia aculeata* exhibits genetic variability in its seeds for all analyzed biochemical compounds, including starch, carbohydrates, lipids, and proteins (albumins, globulins, glutelins, and prolamins). It also showed variability for macronutrients (nitrogen, phosphorus, potassium, calcium, magnesium, and sulfur), indicating that the population present in Pontal do Paranapanema could support its use in a breeding program, both for economic and environmental purposes. This broadens the scope of knowledge and develops technologies for the utilization and promotion of the species in degraded areas.

From these analyses, it can be inferred that the *A. aculeata* population in Pontal do Paranapanema has significant genetic variability since most of the analyzed traits showed large variation among the mother trees. This allows for investment in genetic improvement programs and positions macaúba as an important species in the Brazilian flora, with various economic, environmental, and food-related uses.

In the environmental context, the genetic richness of the species is evident as the analyses indicate a strong genotypic relationship and association among its traits. These traits are responsible for the success of the plant in colonizing various environments, outcompeting other species for new areas. Moreover, through multivariate statistical analyses using gene correlation methods and Mahalanobis Distances, it can also be inferred that *A. aculeata* joins a select group of species with great genetic potential for genotype selection collectively. Thus, it can be the focus of major genetic improvement programs, enhancing its rich genetic variability and bringing various benefits to species production. This can have a significant role in various social and agricultural programs, for both large-scale production and small-scale family farming

Limitations and Future Perspectives

This study was developed during the author's undergraduate research period, which naturally imposed certain limitations related to time, laboratory scope, and financial resources. Although São Paulo State University (UNESP) offers robust infrastructure and academic support, the project faced restrictions regarding extensive field collections and advanced analytical procedures that would require larger-scale funding. These constraints limited the sampling range and the depth of some complementary analyses, such as molecular profiling or environmental replication across different sites.

Nevertheless, the results obtained here provide a solid foundation for future research. Expanding sampling to multiple populations across distinct biomes and integrating genomic, transcriptomic, and metabolomic analyses could deepen understanding of *Acrocomia aculeata*'s

adaptive and biochemical diversity. Further, the establishment of breeding and conservation programs supported by these data may enhance the sustainable use of this native species and strengthen its potential as a bioeconomic resource in the Brazilian Savanna.

Data Archiving Statement

All data supporting the results of this study are publicly available as supplementary material attached to the manuscript, and may be freely accessed for research and verification purposes.

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Contributions

M.A.M.A. contributed to fieldwork, laboratory analysis, statistical analysis and manuscript writing. B.C.R., A.C.S.F., A.C.B. contributed to manuscript writing. M.A.M.S. contributed to statistical analysis and manuscript writing. S.P. and P.F.A. contributed to laboratory analysis. C.L.M. contributed to manuscript review. M.L.T.M. and M.L.M.F contributed to project conception, supervision, direction, and manuscript review.

Consent to participate

The authors consent to participate in this study

Consent for publication

The authors consent to publish this study

Conflict of Interest

The authors declare no conflict of interest in this study.

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REFERENCES

Abdala L, Moraes MLT, Rechia CGV, Giorgini JF, Sá ME, Polizeli MLTM (2002) Biochemical traits useful for the determination of genetic variation in a natural population of Myracrodrum urundeuva. Pesqui Agropecu Bras 37 (7):909-916. https://doi.org/10.1590/S0100-204X2002000700003

Ahmed S, Shah P, Ahmed O (2022) Biochemistry, Lipids. In: StatPearls. Treasure Island (FL): StatPearls Publishing. https://doi.org/10.1053/BC004569

Alfaro-Solís JD, Montoya-Arroyo A, Jiménez VM, et al. (2020) Acrocomia aculeata fruits from three regions in Costa Rica: an assessment of biometric parameters, oil content and oil fatty acid composition to evaluate industrial potential. Agroforest Syst 94:1913-1927. https://doi.org/10.1007/s10457-020-00511-8

Amaral FP (2007) Estudo das características físico-químicas dos óleos da amêndoa e polpa da macaúba [Acrocomia aculeata (Jacq.) Lodd. ex Mart]. Dissertação, Faculdade de Ciências Agronómicas da Unesp - Campus de Botucatu. Botucatu, 66p. http://hdl.handle.net/11449/90468

Amaral FP, Broetto F, Batistella CB, Jorge SMA (2011) Extração e caracterização qualitativa do óleo da polpa e amendoas de frutos de macaúba [Acrocomia aculeata] (Jacq) [Lodd. ex Mart] coletada na região de Botucatu, SP. Rev Energ Agric 26 (1):12-20. https://doi.org/10.17224/EnergAgric.2011v26n1p12-20

Andrade MHC, Vieira AS, Aguiar HF, et al. (2006) Óleo do fruto da palmeira macaúba - parte i: uma aplicação potencial para indústrias de alimentos, fármacos e cosméticos. In: I TECNIQ Seminário sobre Tecnologia na Indústria Química, anais 3º seminario ALBIQUIM de tecnologia. Rio de Janeiro, 11p.

Anthonisen DG, Schirmer M, Silva SDAE, Freire EC (2006) Teor de óleo em sementes de mamona de variedades introduzidas na zona sul do Rio Grande do Sul. In: II Congresso Brasileiro de Mamona, Sergipe. Resumos. Sergipe, p.15-22.

Antoniassi R, Freitas SC, Silva TS, Santiago MCPA, Wilhelm AE, Junqueira NTV (2020) Impact of genotype on fatty acid profile, oil content and nutritional value of the sweet fruits of Acrocomia aculeata. Rev Bras Frutic 42 (6). https://doi.org/10.1590/0100-29452020796

Apriyanto A, Compart C, Fettke J (2022) A review of starch, a unique biopolymer – structure, metabolism and in planta modifications. Plant Sci 318. https://doi.org/10.1016/j.plantsci.2022.111223

Araujo AM (1996) Tamanho populacional e tamanho amostral: a minimização dos riscos. Rev Bras Genet 19 (4):1-5.

Baltar VT, Sousa CA, Westphal MF (2014) Mahalanobis' distance and propensity score to construct a controlled matched group in a Brazilian study of health promotion and social determinants. Rev Bras Epidemiol 17 (3):668-679. https://doi.org/10.1590/1809-4503201400030008

Bremmer JN (1960) Determination of nitrogen in soil by the Kjeldahl method. J Agric Sci 55:11-33. https://doi.org/10.1017/S0021859600021572

Canuto DSO (2005) Variação genética entre e dentro de populações Naturais de Dipteryx alata vog. Por caracteres fisiológicos e Bioquímicos de sementes. Tese de Doutorado, Faculdade de Engenharia de Ilha Solteira, Universidade Estadual Paulista, 88p.

Carpita NC, Gibeaut DM (1993) Structural models of primary cell walls in flowering plants: consistency of molecular structure with the physical properties of the walls during growth. Plant J 3 (1):1-30. https://doi.org/10.1111/j.1365-313X.1993.tb00007.x

Chuba CAM, Argandona EJS, Homem GR, Tommaselli MAG (2010) Modelo de viabilização da produção do consorcio: macaúba (Acrocomia acuelata) e cana-de-açúcar (Saccharum officinarum) XXX Encontro Nacional de Energia e Produção ENEGEP. São Carlos, SP, Brasil, 11p.

Ciconini G, Favaro SP, Roscoe R (2012) Caracterização de frutos e óleo de polpa de macaúba dos biomas Cerrado e Pantanal do estado de Mato Grosso do Sul, Brasil. Universidade Católica Dom Bosco, Campo Grande, 105p.

Cruz CD (2001) Programa Genes: aplicativo computacional em genética e estatística: versão Windows. Viçosa: Editora UFV, 648p.

Cruz CD, Regazzi AJ (2001) Modelos biométricos aplicados ao melhoramento genético. 2.ed.rev. Viçosa, Editora UFV, 390p.

Cho YG, Kang KK (2020) Functional analysis of starch metabolism in plants. Plants 9:1152. doi:10.3390/plants9091152

Dalbosco ED, Krause W, Neves LG, Araújo DV, Hiega KMR, Silva CG (2018) Parametric and non-parametric indexes applied in the selection of sour passion fruit progenies. Rev Bras Frutic 40(1) https://doi.org/10.1590/0100-29452018282

Dias LAS, Kageyama PY (1991) Variação genética em espécies arbóreas e consequências para o melhoramento florestal. Agrotrópica 3(3):119-127

Dubois M, Gilles KA, Hamilton JK, Rebers PA, Smith F (1956) Colorimetric method for determination of sugar and related substances. Anal Chem 28:350-356 https://pubs.acs.org/doi/pdf/10.1021/ac60111a017

Embrapa (2007) Agencia de informação Embrapa: Bioma cerrado. Disponível em: http://www.agencia.cnptia.embrapa.br/Agencia16/AG01/Abertura.html Brasil, Ministério da agricultura, Pecuaria e Abastecimento.

Fahy E, Cotter D, Sud M, Subramaniam S (2011) Lipid classification, structures and tools. Biochim Biophys Acta 1811(11):637-647. https://doi.org/10.1016/j.bbalip.2011.06.009

Fortes ICP, Baugh PJ (1999) Study of Analytical On-line Pyrolysis of Oils from Macauba Fruit (Acrocomia sclerocarpa M) via GC/MS. J Braz Chem Soc 10(6):469-477. https://doi.org/10.1590/S0103-50531999000600009

Garcia-Agustin P, Primo-Millo E (1989) Ultrastructural and biochemical changes in cotyledon reserve tissues during germination of citrus seeds. J Exp Bot 40:383-390. https://doi.org/10.1093/jxb/40.3.383

Gonçalves JLM, Stape JL, Benedetti V, Fessel VAG, Gava JL (2000) Reflexo do cultivo mínimo e intenso do solo em sua fertilidade e na nutrição das árvores. In: Nutrição e fertilização florestal. Piracicaba: IPEF, pp 1-57

Guedes JS, Lima DC, Castanha N, Matta Junior MD, Augusto PDE (2021) Physicochemical and functional properties of a novel starch from uvaia (Eugenia pyriformis) seed, a native fruit from Brazil. J Food Process Preserv 45. https://doi.org/10.1111/jfpp.15845

Gupta RB, MacRitchie F (1994) Allelic variation at glutenin subunit and gliadin loci, Glu-1, Glu-3 and Gli-1, of common wheats. II. Biochemical basis of the allelic effects on dough properties. J Cereal Sci 19(1):19-29. https://doi.org/10.1006/jcrs.1994.1004

Hiane PA, Baldasso PA, Marangoni S, Macedo MLR (2006) Chemical and nutritional evaluation of kernels of bocaiuva. Cienc Tecnol Campinas 26(3):683-689. https://doi.org/10.1590/S0101-20612006000300031

Hostettler C, Kölling K, Santelia D, Streb S, Kötting O, Zeeman SC (2011) Analysis of Starch Metabolism in Chloroplasts. In: Jarvis R (ed) Chloroplast Research in Arabidopsis. Methods Mol Biol 775. https://doi.org/10.1007/978-1-61779-237-3_21

Kurihara DL, Encinas JI, Paula JE (2005) Levantamento da arborização do campus da Universidade de Brasília. Cerne 11(2). https://www.redalyc.org/articulo.oa?id=74411203

Leitão AC, Silva OA (2004) Variação sazonal de macronutrientes em uma espécie arbórea de cerrado, na Reserva Biológica e Estação Experimental de Mogi-Guaçu, estado de São Paulo, Brasil. Rodriguésia 55(84). https://doi.org/10.1590/2175-78602004558408

Lewis PO (2001) A Likelihood Approach to Estimating Phylogeny from Discrete Morphological Character Data. Syst Biol 50(6):913-925. https://doi.org/10.1080/106351501753462876

Li-Beisson Y, Shorrosh B, Beisson F, et al. (2013) Acyl-Lipid Metabolism. The Arabidopsis Book 11. https://doi.org/10.1199%2Ftab.0161

Liberal OHT, Coelho RC (1980) Manual do laboratório de análise de sementes. Niterói: Empresa de Pesquisa Agropecuária do Estado do Rio de Janeiro, 95p

Lima MM, Pedrozo EA, Junqueira NTV (2008) Análise diagnóstica da filière de biodiesel da macaúba, no Cerrado brasileiro. In: 9º Simpósio nacional sobre o cerrado, 2º simpósio internacional sobre savanas tropicais, Brasília, 2008

Lorenzi GMA (2006) Acrocomia aculeata (Jacq.) Lodd. ex Mart. - Arecaceae: bases para o extrativismo sustentável. Tese. Programa de Pós-graduação em Agronomia, Universidade Federal do Paraná, 172p.

Lorenzi H (2010) Flora Brasileira: Arecaceae (Palmeiras). Instituto Plantarum de Estudos da Flora LTDA, Nova Odessa – SP, Brasil. https://repositorio.inpa.gov.br/handle/1/35944

Lowry OH, Rosebrough NJ, Farr AL, Randall RJ (1951) Protein measurement with the folin phenol reagent. J Biol Chem 193:265-275.

Machado C (2016) Manejo e conservação genética, Acrocomia aculeata (Jacq.) Lodd. ex Mart. no Pontal do Paranapanema. Tese de Mestrado. Faculdade de Engenharia de Ilha Solteira, Universidade Estadual Paulista, 67p. http://hdl.handle.net/11449/137948

MacNeill GJ, Mehrpouyan S, Minow MAA, et al. (2017) Starch as a source, starch as a sink: the bifunctional role of starch in carbon allocation. J Exp Bot 68(16):4433-4453. https://doi.org/10.1093/jxb/erx291

Malavolta E, Vitti GC, Oliveira SA (1989) Avaliação do estado nutricional das plantas: princípios e aplicações. 2nd ed. Piracicaba: POTAFOS, 319p

Manfio CE, Motoike SY, Santos CEMD, et al. (2011) Repeatability in biometric characteristics of macaw palm fruit. Ciência Rural, Santa Maria 41(1):70-76. https://doi.org/10.1590/S0103-84782011000100012

Mantovani JE, Pereira A (1998) Estimativa da integridade da cobertura vegetal de Cerrado através de dados TM/Landsat. In: Simpósio Brasileiro de Sensoriamento Remoto.

Marschner P (2012) Marschner's Mineral Nutrition of Higher Plants. 3rd ed. London: Academic Press. 621p. ISBN: 0123849063, 9780123849069

McLachlan GJ (1999) Mahalanobis Distance. Resonance 26. https://www.ias.ac.in/article/fulltext/reso/004/06/0020-0026

Mendes JA (1996) Distribuição espacial, fenologia e compartimentação de três espécies de Qualea (Vochysiaceae) na Reserva Biológica de Mogi-Guaçu - SP. Tese de Doutorado, Instituto de Biociências, UNESP, Rio Claro, 201p.

Militão FT, Morais GA (2023) Mudanças Multitemporiais no uso do solo e o efeito na distribuição das Arecaceae e na nidificação de Amazona aestiva em propriedades rurais de Ivinhema – MS, Brasil: Multi-temporal Land Use Changes and their Effects on the Distribution of Arecaceae and Nesting of Amazona aestiva in Rural Properties of Ivinhema - MS, Brazil. Brazilian Journal of Animal and Environmental Research, 6(3), 2364–2380. https://doi.org/10.34188/bjaerv6n3-033

Mooz ED, Castelucci ACL, Spoto MHF (2012) Potencial tecnológico e alimentício de frutos de macaúba Acrocomia aculeata (jacq.) Lodd. Revista Brasileira de Pesquisa em Alimentos, Campo Mourão 3(2):86-89.

Morais RA, Teixeira GL, Ferreira SRS, Cifuentes A, Block JM (2022) Nutritional Composition and Bioactive Compounds of Native Brazilian Fruits of the Arecaceae Family and Its Potential Applications for Health Promotion. Nutrients 14:4009. https://doi.org/10.3390/nu14194009

Morais RA, Teixeira GL, Martins GAS, Ferreira SRS, Block JM (2024) Comprehensive evaluation of the chemical profile and antioxidant potential of buritirana (Mauritiella armata) an underexplored fruit from Brazilian Cerrado. Food Research International 179. https://doi.org/10.1016/j.foodres.2024.113945

Mota JC, Almeida MM, Alencar VC, Curi WF (2009) Impactos e benefícios ambientais, econômicos e sociais dos biocombustíveis: uma visão global. Engenharia Ambiental, Espírito Santo do Pinhal 6(3):220-242.

Motta PEF, Curi N, Oliveira-Filho AT, Gomes JBV (2002) Ocorrência da macaúba em minas gerais: relação com atributos climáticos, pedológicos e vegetacionais. Pesquisa Agropecuária Brasileira. Brasília 37(7):1023-1031. https://doi.org/10.1590/S0100-204X2002000700017

Mulamba NN, Mock JJ (1978) Improvement of yield potential of the Eto Blanco maize (Zea mays L.) population by breeding for plant traits. Egypt Journal of Genetics and Cytology, Alexandria 7:40-51. cabidigitallibrary.org/doi/full/10.5555/19791677302

Nadarajapillai N, Wijewantha RT (1967) Productivity potentials of rubber seed. Rubber Research Bulletin of Ceylon, Dartonfield 2:8-17.

Pires MB, Amante ER, Lopes AL, Rodrigues AMC, Silva LHM (2019) Peach palm flour (Bactris gasipae KUNTH): potential application in the food industry. Food Sci Technol 39(3):613-619. https://doi.org/10.1590/fst.34617

Piza MR, Luz SROT, Andrade VT, et al. (2023) Multiple Traits Selection Strategies: A Proposal for Coffee Plant Breeding. Agronomy 13:2033. https://doi.org/10.3390/agronomy13082033

Pfister B, Zeeman SC (2016) Formation of starch in plant cells. Cell Mol Life Sci 73:2781-2807. https://doi.org/10.1007/s00018-016-2250-x

Pregnolato W, Pregnolato NP (1985) Normas analíticas do Instituto Adolfo Lutz: métodos químicos e físicos para análise de alimentos. 3rd ed. São Paulo: Secretaria Estadual e Saúde. 533p.

Primack RB, Rodrigues E (2001) Biologia da conservação. Londrina: E. Rodrigues. 328p.

Queiroz FA (2009) Impactos de sojicultura de exportação sobre a biodiversidade do Cerrado. Sociedade & Natureza 21(1):193-209. https://doi.org/10.1590/S1982-45132009000200013

Quintana LG, Carvalho AM, Coser TR, Souza AM, Malaquias JV, Ferreira EA (2013) Liberação de nutrientes durante a decomposição de resíduos vegetais de macaúba em áreas com variações de lençol freático. 8° Congresso Internacional de Bioenergia, São Paulo. http://www.alice.cnptia.embrapa.br/alice/handle/doc/1001912

Resende MDV (2002) Genética biométrica e estatística no melhoramento de plantas perenes. Brasília: EMBRAPA Informação Tecnológica. 975p.

Resende MDV (2007a) Matemática e estatística na análise de experimentos e no melhoramento genético. Colombo: Embrapa Florestal. 561p.

Resende MDV (2007b) SELEGEN REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos. Colombo: Embrapa Florestas.

Ribeiro AJM (2014) Proteína. Revista de Ciência Elementar 2(3):1-5.

Rodwell VW, Bender DA, Botham KM, Kennelly PJ, Weil PA (2021) Bioquímica ilustrada de Harper. 31st ed. Porto Alegre: AMGH. ISBN: 6558040034, 9786558040033

Santos AP, Nunes ACP, Garuzzo MSPB, Corrêa RX, Marques FG (2022) Genetic variability and predicted gain in progeny tests of native Atlantic Forest timber species: Cariniana legalis, Cordia trichotoma, and Zeyheria tuberculosa. Ann For Res 65(1):85-96. https://doi.org/10.15287/afr.2022.2106

Santos MFG, Alves RE, Brito ES, Silva SM, Silveira MRS (2017) Quality characteristics of fruits and oils of palms native to the Brazilian Amazon. Rev Bras Frutic 39(Spe). https://doi.org/10.1590/0100-29452017305

Santos W, Araújo EG, Souza DCL, Silva JR, Recco CRSB, Moraes MLT, Aguar AV (2016) Divergência genética entre progênies de polinização aberta de Pinus caribaea var. hondurensis a partir de caracteres quantitativos. Pesq Flor Bras 36(86):127-133. https://doi.org/10.4336/2016.pfb.36.86.920

Santos W, Souza BM, Zulian DF, Alves GTR, Moraes MLT, Sousa VA, Aguiar AV (2021) Divergencia genética entre progenies de Cordia trichotoma en una plantación mixta con Dalbergia nigra. Madera y Bosques 27(2). https://doi.org/10.21829/myb.2021.2722188

Sarmento MB, Villela FA (2010) Sementes de espécies florestais nativas do sul do Brasil. Informativo Abrates, Londrina 20(1-2):39-44.

Shewry PR, Halford NG (2002) Cereal seed storage proteins: structures, properties and role in grain utilization. J Exp Bot 53(370):947-958. https://doi.org/10.1093/jexbot/53.370.947

Showalter AM (1993) Structure and function of plant cell wall proteins. The Plant Cell 5(1):9. https://doi.org/10.1105%2Ftpc.5.1.9

Silva AR, Dias CTS (2013) A cophenetic correlation coefficient for Tocher's method. Pesq Agropec Bras 48(6):589-596. https://doi.org/10.1590/S0100-204X2013000600003

Silva MR, Lacerda DBCL, Santos GG, Martins DMO (2008b) Caracterização química de frutos nativos do cerrado. Ciência Rural, Santa Maria 38(6):1790-1793. https://doi.org/10.1590/S0103-84782008000600051

Silva ND, Silva Júnior AG, Perez R, Ávila MBR (2008a) Avaliação da produção agrícola da macaúba. Bioenergia, Universidade Federal de Viçosa.

Smith AM (2017) Starch in the Arabidopsis plant. The Arabidopsis Book 15. https://doi.org/10.1002/star.201100163

Soares SD, Dos Santos OV, Da Conceição LRV, et al. (2023) Nutritional and technological properties of Albino Peach Palm (Bactris gasipaes) from the Amazon: influence of cooking and drying. Foods 12:4344. https://doi.org/10.3390/foods12234344

Sousa LA, Maciel GM, Juliatti FC, Beloti IF, Cardoso DBO, Siquieroli ACS (2021) Genetic parameters and selection of biofortified lettuce genotypes based on selection indices. Braz J Agric Environ Eng 25(11):772-778. https://doi.org/10.1590/1807-1929/agriambi.v25n11p772-778

Sturgis FE, Miears RJ, Walker RK (1952) Protein in rice as influenced by variety and fertilizer levels. Louisiana Exp Stn Tech Bull, Louisiana, pp.1-466. https://repository.lsu.edu/agexp/94

Teixeira DHL, Oliveira MSP, Gonçalves FMA, Nunes JAR (2012) Índices de seleção no aprimoramento simultâneo dos componentes da produção de frutos em açaizeiro. Pesq agropec bras, Brasília 47(2):237-243. https://doi.org/10.1590/S0100-204X2012000200012

Teles HDF, Pires LL, Garcia J, Rosa JQS, Farias JG, Naves RV (2011) Ambientes de ocorrência natural de macaúba. Pesq Agropec Trop, Goiânia 41(4):595-601. https://doi.org/10.5216/pat.v41i4.11851

Terres LR, Lenz E, Castro CM, Pereira AS (2015) Estimativas de ganhos genéticos por diferentes índices de seleção em três populações híbridas de batata. Hortic Bras 33:305-310. https://doi.org/10.1590/S0102-053620150000300005

Tetlow IJ, Morell MK, Emes MJ (2004) Recent developments in understanding the regulation of starch metabolism in higher plants. J Exp Bot 55(406):2131-2145. https://doi.org/10.1093/jxb/erh248

Usman MG, Rafii MY, Ismail MR, Malek MA, Latif MA, Oladosu Y (2014) Heat shock proteins: functions and response against heat stress in plants. Int J Sci Technol Res 3(11):107-114.

Vale AC (2007) Estudo Laboratorial da Viabilidade do Uso de Fibras de Coco em Misturas Asfálticas do Tipo SMA. Dissertação de Mestrado, Programa de Mestrado em Engenharia de Transportes, Universidade Federal do Ceará, Fortaleza, 125p. http://www.repositorio.ufc.br/handle/riufc/1445

Yamaguchi N, Winter CM, Wellmer F, Wagner D (2015) Identification of direct targets of plant transcription factors using the GR fusion technique. In: Alonso J, Stepanova A (eds) Plant Functional Genomics. Methods in Molecular Biology, vol 1284. Humana Press, New York, pp. 171-185. https://doi.org/10.1007/978-1-4939-2444-8_6