

Diversity and Genetic Structure of a Natural Population of *Mauritia flexuosa* L. f. in APA-Pandeiros, Using Microsatellite Markers

Bárbara Rayane Ramos Muniz Nassau¹, Márcia Regina da Costa¹, Elytânia Veiga Menezes²,
Demerson Arruda Sanglard³, Tiago Vieira Sousa⁴ & Marcio Antonio Silva Pimenta⁵

¹ Programa de Pós-Graduação em Produção Vegetal, Universidade Federal dos vales do Jequitinhonha e Mucuri, Diamantina, MG, Brazil

² Programa de Pós-Graduação em Biotecnologia, Universidade Estadual de Montes Claros, Montes Claros, MG, Brazil

³ Programa de Pós-Graduação em Produção Vegetal, Instituto de Ciências Agrárias, Universidade Federal de Minas Gerais, Montes Claros, MG, Brazil

⁴ Programa de Pós-Graduação em Proteção de Plantas, Instituto Federal Goiano (IFGoiano), Universidade Federal do Triângulo Mineiro, Iturama, MG, Brazil

⁵ Programa de Pós-Graduação em Biodiversidade e Uso dos Recursos Naturais, Universidade Estadual de Montes Claros, Montes Claros, MG, Brazil

Correspondence: Marcio Antonio Silva Pimenta, Programa de Pós-Graduação em Biodiversidade e Uso dos Recursos Naturais, Universidade Estadual de Montes Claros, Montes Claros, MG 39401-089, Brazil. Tel: 55-38-3229-8191. E-mail: marcio.pimenta@unimontes.br

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Abstract

Genetic diversity is essential to ensure that species maintain high adaptive evolutionary potential to resist environmental stochasticity. Thus, this research aimed to estimate the genetic diversity and structure of a natural population of *Mauritia flexuosa* and its stages, using five microsatellite primers. DNA was extracted from leaves collected from individuals of the three classes (G1-adult, G2-juvenile and G3-regenerant). Genetic diversity estimates indicated an average of 7.8 alleles/locus and lower observed heterozygosity (H_o) than expected heterozygosity (H_e) in the population (0.272-0.395 and 0.275-0.401, respectively). The Shannon Index (I) indicated moderate genotypic diversity and richness in the analyzed population, and exclusive alleles were found at the different stages. Also found were a lower population index ($F_{ST} = 0.019$) and a higher individual fixation index ($F_{IS} = 0.169$). Classes G1 and G2 exhibited greater genetic similarity to each other than to G3, which had more distant genetic characteristics. These results revealed lower genetic diversity among regenerating (G3) individuals and greater genetic diversity among adults (G1). Immediate strategies for *in situ* and *ex situ* genetic conservation of *M. flexuosa* are essential to preserve its genetic variability and assist future programs for the improvement.

Keywords: Buriti, SSR, genetic structure, fragmentation, conservation

1. Introduction

The Brazilian Cerrado is one of the largest biomes of the Americas and exhibits a great variety of ecosystems that maintain a high diversity of flora and fauna (Oliveira & Marquis, 2002), being considered a “hot spot” with extreme priority for conservation (Klink & Machado, 2005). *Mauritia flexuosa* L. (Arecaceae), commonly known as buriti, is widely distributed in the Cerrado biome and characterizes a typical ecosystem of central Brazil known as vereda. *Mauritia flexuosa* is a palm tree found in forest borders and has a wide distribution in South America (Brazil, Colombia, Venezuela, French Guiana, Ecuador, Peru and Bolivia). In the Cerrado, *M. flexuosa* is widely distributed in humid environments of rural areas, periurban environments, and ecological reserves, being pollinated by coleoptera from the families Nitidulidae, Curculionidae and Cucujidae (Knudsen et al., 2001; Matos, et al., 2014). Anthropogenic actions have affected buriti populations, through the reduction of individuals in their populations, mainly caused by deforestation, silting, fragmentation and drainage of veredas (Bahia et al., 2009; Matos et al., 2014).

Biological diversity is harmed by anthropic habitat fragmentation (Olifiers & Cerqueira, 2006). This can happen quickly and on a large scale, generating genetic, spatial and structural variation in populations and, consequently, the extinction of species (Jain et al., 2020; Doherty et al., 2021).

Genetic diversity refers to the variability of alleles for each gene, which promotes the expression of different characteristics in a population. Genetic diversity also ensures that species maintain high adaptive evolutionary potential to resist environmental stochasticity (Cerqueira et al., 2003). The ephemeral reduction of genetic diversity of populations is one of the greatest effects of fragmentation (Scriven et al., 2017; Gray et al., 2019; Ovaskainen et al., 2019).

Studies and concepts regarding diversity and genetic structure are relevant to the management of forest genetic resources and conservation programs (Brandão et al., 2015; Smith et al., 2018; Aguilar et al., 2019). In fact, they are important for evaluating the impacts of exploitation and fragmentation, as well as determining sampling strategies for natural populations (Rossi et al., 2014; Lompo et al., 2020; Mazal et al., 2021).

Microsatellite molecular markers (SSR-Simple Sequence Repeats) are highly polymorphic, codominant, and multi-allelic, and accelerate the acquisition of desirable genotypes. They can be linked to loci that determine characteristics of interest without being influenced by environmental variation. They also present a considerable level of transferability between different species and are the most used markers for determining genetic diversity, paternity, and gene flow and for population analysis in studies of ecology and conservation (Braga 2016; Araújo et al., 2017; Moraes et al., 2020).

In this context, the present research aimed to use microsatellite markers (SSRs) to estimate the diversity and genetic structure of a natural population of *Mauritia flexuosa* and its stages in the Água Doce vereda (palm swamp) located in the Área Proteção Ambiental do Rio Pandeiros (Pandeiros River Environmental Protection Area) in the municipality of Bonito de Minas, state of Minas Gerais, Brazil, to support management, conservation, and recovery programs for degraded areas.

2. Method

2.1 Study Area, Sampling and Classification of Sampled Stages

The study vereda (palm swamp) is located in the Área Proteção Ambiental (APA) do Rio Pandeiros (Pandeiros River Environmental Protection Area), which encompasses the municipalities of Januária, Bonito de Minas and Cônego Marinho, in northern Minas Gerais State. APA-Rio Pandeiros was created by Law 11,901 on 1 September 1995. It covers 393,060 ha and includes several plant phytophysiognomies, such as cerrado *sensu stricto*, dry forest (Seasonal Deciduous Forest), riparian forests, veredas (palm swamps) and flood plain areas (Nunes et al., 2009).

The climate of the region is humid tropical (Aw), according to Köppen's classification, with well-defined dry and rainy seasons (Antunes, 1994). For the period of 1990-2009, the average annual precipitation was 920 mm and the temperature was 26.8 °C, according to data from the Instituto Nacional de Meteorologia (INMET, 2010), collected at the Januária Climatological Station 70-120 km from the study area. Individuals were sampled from the natural *Mauritia flexuosa* L. f. population of the Água Doce vereda (15°13'18.7"S 44°55'21.2"W) located in APA-Rio Pandeiros and characterized as an open forest community, with the presence of pastures, livestock and subsistence agriculture.

The demarcated area of the population was censused, and 160 individuals were sampled (sampling area approximately 301,785 m²) in October 2018, covering the three classes/stages (adult, juvenile and regenerants). The 61 adult, 47 juvenile and 52 regenerating plants were individually identified and mapped using GPS (Global Positioning System) to ensure they were not measured more than once and to monitor them over time. The samples were placed in plastic bags with silica gel to dry and preserve leaf tissue. The collected material was subsequently taken to the Laboratório de Biotecnologia, Instituto de Ciências Agrárias (ICA) of Universidade Federal de Minas Gerais (UFMG) and stored in an ultrafreezer at -80 °C until DNA extraction.

Individuals were classified to stage depending on the characteristics they exhibited. The adult stage class (G1) includes individuals with reproductive signs, including older plants (61 individuals). The juvenile stage class (G2) includes individuals that did not show reproductive signs, covering young plants (47 individuals). The regenerating stage class (G3) includes individuals that are less than 2-m in height and/or with flexible stems, thus including the youngest plants (52 individuals).

2.2 Molecular Analysis

DNA was extracted according to the CTAB 2% protocol (J. J. Doyle & J. L. Doyle, 1987) as modified by Machado et al. (2002). The integrity of the extracted DNA was determined by 2% agarose gel electrophoresis. Quantification of DNA amplification reactions used an Infinite® 200 PRO absorbance multimodal microplate reader (TECAN, BR) and standardized dilutions according to the amount of DNA extracted for each sample.

Five microsatellite *primers* (Thermo Fisher Scientific), developed by Menezes et al. (2012) for *Mauritia flexuosa*, were used for genotyping all sampled individuals (Table 1). Polymerase chain reactions (PCRs) were performed in a Mastercycler® nexus thermocycler (Eppendorf, SE), with 10 µL volume, using 5 ng of genomic DNA, 1X buffer, 200 µM dNTPs, 1.5 mM MgCl₂, 0.5 µM of each *primer*, and 1 U Taq polymerase (Ludwig-Biotec). The PCR protocol consisted of initial denaturation (94 °C, 5 min) followed by 35 cycles of 1 min at 94 °C, 30 s at the primer-specific annealing temperature (Table 1), 1 min at 72 °C and a final extension for 7 min at 72 °C. The amplification products were separated by 2% agarose gel electrophoresis in Sodium Borate buffer (SB 1X), at a constant voltage (120 V) for three hours. The size of the amplified fragments was estimated by comparison with a 100 bp/DNA molecular marker (Ludwig-Biotec), with visualization by staining with 3 µL of type IV dye [0.125% (m/v) bromophenol blue and 10% (m/v) sucrose] and 5 µL of GelRed™. Images of electrophoretic products were then integrated into a L-PIX EX Photodocumentator (Loccus Biotechnology, BR). These procedures were carried out at the Laboratório de Biotecnologia of ICA-UFMG.

Table 1. Polymorphic microsatellite primer pairs, locus name, repeat motif (repetitions), primer sequence, size range (bp) and specific hybridization temperature (T_m) developed for *Mauritia flexuosa* by Menezes et al. (2012) and used in this work

Locus	Repeat motif (repetitions)	Sequence (5'-3')	Size (bp)	T _m (°C)
MF03	GA (19)	TCACCGATCTAAGTTGACCAAA	100-135	59 °C
		TCCTTTCTCTCTTTGACCCAC		
MF08	AG (23)	ACCGATCATGGTGGTAGAACTC	101-171	58 °C
		AATTCACCGATCAAACCCC		
MF09	AG (19)	ATACATCGCGCATATCTCACTG	113-215	58 °C
		ATTCCCACACTCCCTCACTAGA		
MF17	AG (7), AG (8)	AGGGCTTCTGGAAGTGTCTATAG	155-191	59 °C
		TCCTCTCTCTCTCCCTCTTG		
MF18	CT (16)	ATCATCGAAGTTTCATCCATCA	154-192	50 °C
		CAGAGGGAAATGAACACAGAGA		

2.3 Data Analysis

The observed band patterns of the electrophoresis profile of each SSR gel were transformed into a data matrix, which was used to estimate genetic diversity (Nei, 1978). Cluster analysis, assessment of genetic similarity, individual grouping, polymorphic information content (PIC), heterozygosity and the Shannon Index (I) were calculated using the GENES software package (Cruz, 2008). Analysis of Molecular Variance (AMOVA, Excoffier et al., 1992), calculated using a Euclidean distance matrix (EDM), was used to estimate the occurrence of inter- and intra-population variance.

Genetic structure was estimated using the statistical coefficient F (Wright, 1951) to determine whether stages (G1-adult, G2-juvenile and G3-regenerant) differed. The coefficients F (total fixation index), *f* (fixation index) and Ø (differentiation between adults, juveniles and regenerants) were estimated from the variance of allele frequencies of individuals. A dendrogram was obtained using Nei's genetic dissimilarity and the UPGMA method (unweighted pair group method with arithmetic mean). All these analyses were performed with GENES software (Cruz, 2008), with 1000 randomizations and Bonferroni correction (Goudet, 2002).

3. Results

The five microsatellite markers evaluated for the studied *Mauritia flexuosa* population indicated 7.8 alleles/locus and an average locus ratio of 0.996. The effective number of alleles (N_e) analyzed in the population ranged from 4.8 for regenerant individuals (G3) to 6.6 (G1) for adults (Table 2). Observed heterozygosity (H_o) was lower than the expected heterozygosity (H_e) at all developmental stages, resulting in high and significant fixation rates (*f*) for adults, juveniles and regenerants.

Table 2. Average (Nm), total (Nt), rare (Na) and effective (Ne) number of alleles per polymorphic loci by stage (G1, G2 and G3) for the natural population of *Mauritia flexuosa* in APA-Pandeiros

Class	Nm	Nt	Na	Ne
G1-Adult	6.6	33	11.0	6.6
G2-Juvenile	6.2	31	8.2	6.2
G3-Regenerant	4.8	24	7.4	4.8

Note. Ne = total number of alleles of polymorphic loci/number of polymorphic loci.

The effectiveness of the markers was also evaluated using the average value corresponding to the effective number of alleles per polymorphic locus (Ne). This value ranged from 7 (SSR-MF03) to 9 (SSR-MF18), while He ranged from 0.144 (SSR-MF03) to 0.586 (SSR-MF18) and Ho from 0.944 (SSR-MF09) to 0.025 (SSR-MF17) (Table 3).

Table 3. Five polymorphic SSR markers available for *Mauritia flexuosa* used to study the genetic diversity of the studied natural population of the species in APA-Pandeiros

SSR markers	N	Ne	Ho	He	PIC
MF03	160	7	0.056	0.144	0.141
MF08	159	7	0.057	0.154	0.148
MF09	160	8	0.944	0.549	0.446
MF17	159	8	0.025	0.319	0.307
MF18	159	9	0.182	0.586	0.559

Note. N = population size; Ne = effective number of alleles; Ho = observed heterozygosity; He = expected heterozygosity; PIC = polymorphic information content.

Values of I were greater than 1.0 for stages G1 and G2, and lower than 1 (0.830) for G3 (regenerant) (Table 4). The results demonstrated low genetic diversity only for G3 (regenerant) (Figure 1), possibly due to environmental fragmentation and degradation in the area contributing to reduced genetic diversity among stages. PIC values were positive and significantly different from zero for all stages; class G3 had the lowest genetic variability (Ho = 0.272, PIC = 0.266) and class G1 the greatest (Ho = 0.395, PIC = 0.360) (Table 4). Classes G1 and G2 exhibited several rare alleles (Table 2).

Table 4. Estimated genetic diversity among stages (G1, G2 and G3) of the studied natural population of *Mauritia flexuosa* in APA-Pandeiros

Class	I	He	Ho	PIC
G1-Adult	1.183	0.401	0.395	0.360
G2-Juvenile	1.004	0.354	0.350	0.320
G3-Regenerant	0.830	0.275	0.272	0.266

Note. Classes = studied stages; I = Shannon Index; He = expected heterozygosity; Ho = observed heterozygosity; PIC = polymorphic information content.

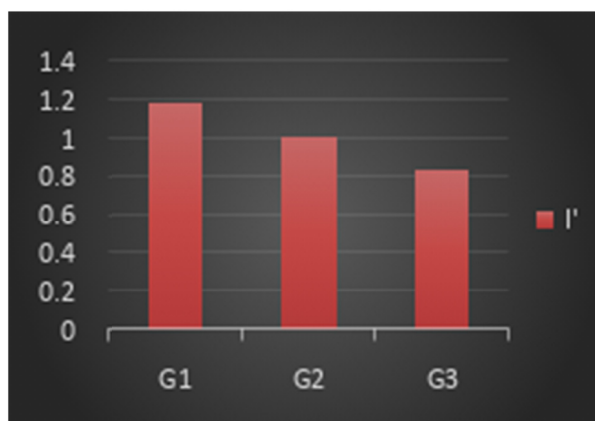


Figure 1. Comparison of the Shannon Index (genetic diversity) among the three studied stages (G1, G2 and G3) of *Mauritia flexuosa*

Inter and intrapopulation allele frequencies were estimated for the studied *M. flexuosa* population using the statistical coefficient F (Wright 1951). The fixation index for the population (FIT) was 0.186 ($p < 0.0001$), for stages (FST) 0.019 ($p < 0.0001$) and for individuals (FIS) 0.169 ($p < 0.0001$), indicating a high level of genetic differentiation among individuals and a low level among stages.

AMOVA, also based on the statistical coefficient F (Wright 1951), estimated greater genetic variation for stages (97.79%) than for individuals (2.20%) (Table 5). Evaluation of the genetic diversity of the analyzed stages using the matrix generated from Nei's (1978) genetic dissimilarity coefficients revealed the greatest genetic similarity between G1 and G2 and the lowest between G1 and G3.

Table 5. Analysis of Molecular Variance (AMOVA), based on SSR data, of 160 individuals from a natural population of *Mauritia flexuosa* in APA-Pandeiros and their stages

Source of Variation	DF	SS	MS	CV	V (%)	p
Individuals	2	1.931	0.965	0.009	2.201	< 0.0001
Stages	157	69.126	0.440	0.440	97.798	< 0.0001
Total	159	71.057	0.446	0.450	100.000	

Note. DF = degrees of freedom; SS = sum of squares; MS = mean square; CV = coefficient of variation; V = percentage of variation; p = probability of variation in components greater than those observed randomly. Probabilities were estimated from 1000 random permutations.

Results of the grouping of individuals of the studied *M. flexuosa* population using Nei's (1978) genetic dissimilarity coefficient and UPGMA are shown in the dendrogram of Figure 2.

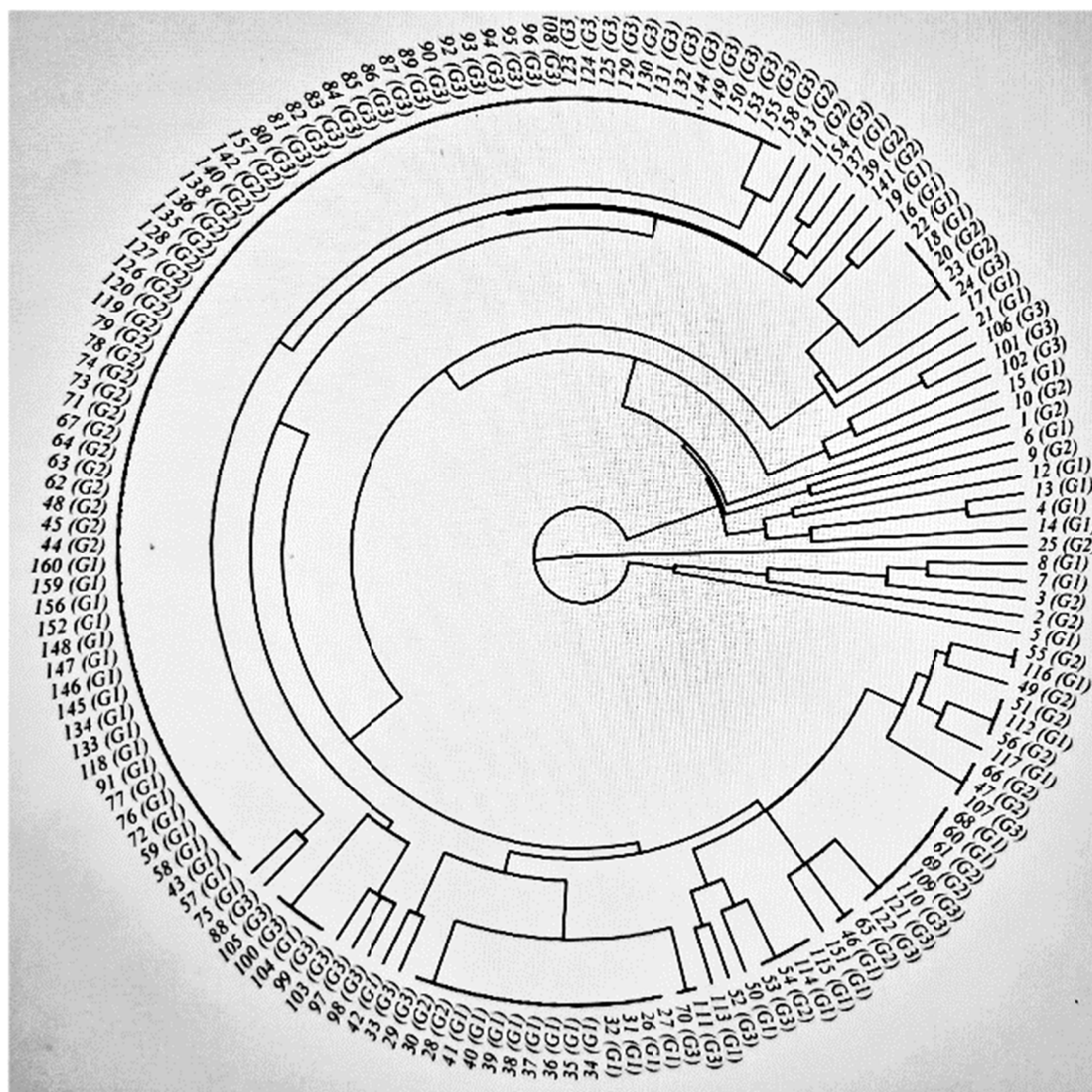


Figure 2. Dendrogram based on a matrix of Nei's genetic dissimilarity coefficients and UPGMA, showing the distribution of individuals of a natural population of *Mauritia flexuosa*

The fixation index (f) and total fixation index (F) were significant for SSR-MF03, SSR-MF08, SSR-MF17 and SSR-MF18, with SSR-MF17 and SSR-MF18 having the highest values (Table 6). However, the mean estimate of f and F (0.336) for stages was significant ($p = 0.001$) (Table 6). Values of Φ and G_{ST} (coefficient of genetic differentiation between stages) were significant for most markers ($p = 0.001$), the exception being SSR-MF09, indicating population differentiation. Average values for Φ and G_{ST} were 0.026 (Table 6) and 0.012, respectively. Genetic differentiation among the studied stages was significant, with less differentiation between G1 (adult) and G2 (juvenile) and greater differentiation between G2 and G3 (regenerant).

Table 6. Genetic structure of a natural population of *Mauritia flexuosa* based on analysis of variance of allele frequencies and allele sizes for five microsatellite loci

SSR markers	<i>f</i>	F	Ø
MF03	0.605	0.610	0.013
MF08	0.642	0.637	0.034
MF09	-0.721*	-0.722*	-0.009*
MF17	0.921	0.921	0.005
MF18	0.684	0.693	0.027

Note. *f* = fixation index, F = total fixation index, Ø = differentiation of stages.

**p* > 0.00 = not significant.

4. Discussion

Studies of the genetic diversity and structure of natural populations of *Mauritia flexuosa* are still rare, although current understanding is based on some work with molecular markers (Rossi et al., 2014; Menezes et al., 2012; Federman et al., 2012). Such work is highly relevant due to the severe pressures of environmental fragmentation and degradation, mainly due to the expansion of agribusiness and urban borders.

The SSR markers used in the present work were also used in other contexts, such as analyzing bioactive compounds (Oliveira, 2012). The average number of alleles per locus (7.8/locus) found here is higher than that mentioned in the literature (Federman et al., 2012; Federman et al., 2014), despite using only five SSR markers. The present study found moderate levels of genetic diversity associated with high PIC values, although Menezes et al. (2012) found lower values for both.

The determination of rare alleles, such as in the present study, is very useful to genetic conservation research of unique populations, as it can help adapt management (Table 2). Furthermore, a considerable sample should be obtained from the population, since population size can interfere with the results of analyses; that is, an excessively small sample can lead to unreliable results (Kalinowski, 2004; Marshall & Brown, 1975).

Values for observed heterozygosity (*H_o*) were lower than those for expected heterozygosity (*H_e*) for all studied markers and stages, except for the locus SSR-MF09, thus indicating a higher proportion of homozygous alleles per locus (Table 3). Some previous studies had similar results Federman et al. (2014) with *M. flexuosa*; Ramos et al. (2012) with *Astrocaryum aculeatum*; and Araújo et al. (2017) with *Acrocomia aculeata*, but there are also reports showing higher values for *H_o* than for *H_e* (Gomes et al., 2011) with *M. flexuosa*. The studied population of *M. flexuosa* revealed moderate genetic diversity and an excess of homozygotes (averages *H_o* < *H_e*) presumably resulting from intense inbreeding.

According to Botstein (1980), PIC is used to evaluate genetic polymorphism, with low PIC values indicating low genetic variation per locus, and PIC values between 0.25 and 0.50 being merely informative. Stages G1 and G2 showed moderate genetic variability, as they exhibited more polymorphic information (higher PIC values) (Table 4). This index showed that the analyses of the stages of *M. flexuosa* with the five SSR markers were very efficient in evaluating genetic diversity, revealing moderate variability within the analyzed stages, mainly within G1 (adult) but lower for G3 (regenerant). Some previous studies reported similar PIC values, such as Loiola et al. (2016) when studying genetic relationships in *Cocos nucifera* L.

Observed heterozygosity (*H_o*) was also lower than expected heterozygosity (*H_e*) for all stages of development (Table 4), further demonstrating that factors such as environmental fragmentation and degradation (present in the study area) contribute to reducing genetic diversity throughout development.

According to Holcomb et al. (1977), the Shannon Index (*I*) determines the diversity within a population to display genotypic richness through the certainty value of the genetic similarity estimate between individuals in the population. This index values rare species, as it is affected by them. Therefore, *I* values between 1.0 and 1.5 indicate moderate genetic diversity (Table 4) and values above 1.5 indicate high diversity (Shannon & Weaver, 1963). Therefore, the significant values of *I* found for the stages G1 and G2, but not G3 (*I* = 0.830), also indicate moderate diversity or genotypic richness of the analyzed population (Figure 1). Other studies using ISSR markers for *M. flexuosa*, and other species, described lower *I* values (Rossi et al., 2014; Silva et al., 2016). This result is probably due to SSR markers being more specific and contributing to a more thorough and discriminative analysis of the genetic structure of populations.

The allele fixation index (F) indicated lower genetic variability and higher homozygosity for the stages. Evolutionary factors such as effective size, mutation and selection, influence genetic diversity by changing allele frequencies through random crossing. The statistical coefficient F (Wright, 1951) revealed a high level of genetic differentiation among individuals and a low level among stages ($F_{IT} = 0.186$; $F_{ST} = 0.019$; $F_{IS} = 0.169$). Such results are associated with high F (fixation index) values and high homozygosity for each studied stage, suggesting a deviation from Hardy-Weinberg equilibrium, possibly due to parental crossing or self-fertilization.

The inbreeding coefficient (F) obtained for the studied population suggests a predisposition to inbreeding through crossing between parental individuals, since self-fertilization is disregarded due to the species being allogamous (Storti, 1993). Thus, such a scenario may be correlated with geographic isolation, which is reflected in low rates of gene flow, due to environmental degradation and fragmentation of natural populations, which impairs the dispersion and germination of pollen and seeds (Resende et al., 2011).

Therefore, the genetic diversity results of the present study also suggest maintaining accessions with lower F values in germplasm banks (Loiola et al., 2016). Furthermore, the total fixation index was low ($F_{ST} = 0.019$), which is common for *M. flexuosa*, as reported in other studies (Menezes et al., 2012; Federman et al., 2014). It is believed that excessive exploitation, primarily the expansion of agriculture and urban borders, in the study area directly affects the gene flow of *M. flexuosa*, as these factors intensify spatial fragmentation.

The AMOVA (Table 5) showed greater variability among stages (97.79%) than among individuals (2.20%), which differs from some studies that found greater genetic diversity at the intrapopulation level (Rossi et al., 2014; Ellegren et al., 2016). In addition to inbreeding, it is likely that allelic flow for *M. flexuosa* is limited to short distances, which decreases interpopulation variation and increases intrapopulation variation.

According to Frankham et al. (2002), only differentiation values greater than 0.15 are indicative of significant differentiation between populations. Therefore, low genetic differentiation was verified for the studied stages ($\Phi = 0.026$; $G_{ST} = 0.012$; Table 6). This analysis indicated that regenerants (G3) are distanced from the other stages. The presence of rare alleles in this class may be due to pollen external to the studied area (Resende et al., 2011). The identification of rare alleles is very relevant to carrying out appropriate conservation initiatives aimed at preserving the genetic diversity of *M. flexuosa* (Kalinowski, 2004).

The dendrogram based on Nei's coefficient (Figure 2) indicated a correlation between genetic similarity and the presence of genetic structure at the shorter distance between G1 and G2, which is certainly due to seed dispersal occurring close to the parents. Certain studies have reported seed dispersal as the main cause of genetic structure (Lacerda et al., 2008; Araújo et al., 2017).

Therefore, the data obtained in the present study show that the analyses employed can be used in population genetic studies to obtain information that will help to design conservation, management and improvement strategies for *M. flexuosa*.

5. Conclusion

The results of this study indicate moderate genetic diversity with low F_{ST} and high F values for the *Mauritia flexuosa* population of APA-Pandeiros. They also reveal that the adult class (G1) has the highest genetic diversity and the regenerating class (G3) the lowest, as well as genetic structure between G1 and G2 over a short distance and the presence of exclusive alleles for the different stages.

References

- Aguilar, R., Cristóbal-Pérez, E. J., Balvino-Olvera, F. J., de Jesús Aguilar-Aguilar, M., Aguirre-Acosta, N., Ashworth, L., ... Quesada, M. (2019). Habitat fragmentation reduces plant progeny quality: A global synthesis. *Ecology letters*, 22(7), 1163-1173. <https://doi.org/10.1111/ele.13272>
- Antunes, F. Z. (1994). Caracterização climática. *Informe Agropecuário, Belo Horizonte/MG*, 17, 15-19.
- Araújo, M. R. G., de Melo Júnior, A. F., Menezes, E. V., Brandão, M. M., Cota, L. G., de Oliveira, D. A., ... Vieira, F. A. (2017). Fine-scale spatial genetic structure and gene flow in *Acrocomia aculeata* (Arecaceae): Analysis in an overlapping generation. *Biochemical Systematics and Ecology*, 71, 147-154. <https://doi.org/10.1016/j.bse.2017.02.005>
- Bahia, T. O., Luz, G. D., Veloso, M. D. M., Nunes, Y. R. F., Neves, W. V., Braga, L. L., & Lima, P. D. (2009). Veredas na APA do Rio Pandeiros: importância, impactos ambientais e perspectivas. *MG Biota*, 2(2), 4-13.
- Botstein, D., White, R. L., Skolnick, M. H., & Davis, R. W. (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphism. *American Journal of Human Genetics*, 32, 314-331.

- Braga, R. T. (2016). Spatial patterns of population abundance: A review of predictions and theoretical models in ecology and biogeography. *Bioikos, Campinas*, 30(1), 19-31. <https://doi.org/10.1007/s10980-015-0303-4>
- Brandão, M. M., Vieira, F. A., Nazareno, A. G., & Carvalho, D. (2015). Genetic Diversity of Neotropical Tree *Myrcia Splendens* (Myrtaceae) in a Fragment-corridor System in the Atlantic Rain forest. *Flora, Jena*, 216, 35-41. <https://doi.org/10.1016/j.flora.2015.07.006>
- Cerqueira, R., Brant, A., Nascimento, M. T., & Pardini, R. (2003). Fragmentação: alguns conceitos. In D. M. Rambaldi, & D. A. S. Oliveira (Eds.), *Fragmentação de ecossistemas: Causas, efeitos sobre a biodiversidade e recomendações de políticas públicas* (pp. 23-40). Brasília: MMA/SBF.
- Cruz, C. D. (2008). Software Genes: Aplicação Computacional em Genética e Estatística-Programa Genes. *Aplicativo Computacional em Genética e Estatística*. UFV, Viçosa, MG, Brazil.
- Doherty, T. S., Hays, G. C., & Driscoll, D. A. (2021). Human disturbance causes wides pread disruption of animal movement. *Nature Ecology& Evolution*, 5, 513-519. <https://doi.org/10.1038/s41559-020-01380-1>
- Doyle, J. J., & Doyle, J. L. (1987). Isolation of plant DNA from fresh tissue. *Focus*, 12, 13-15.
- Ellegren, H., & Galtier, N. (2016). Determinants of genetic diversity. *Nature Reviews Genetics*, 17, 443-434. <https://doi.org/10.1038/nrg.2016.58>
- Excoffier, L., Smouse, P. E., & Quattro, J. W. (1992). Analysis of molecular variance inferred from metric distance among DNA haplotypes: applications to human mitochondrial DNA restriction data. *Genetics*, 131, 479-491. <https://doi.org/10.1093/genetics/131.2.479>
- Federman, S., Hyseni, C., Clement, W., & Caccone, A. (2012). Isolation of 13 novel highly polymorphic microsatellite loci for the Amazonian palm *Mauritia flexuosa* (Arecaceae). *Conservation Genetics Resources*, 4, 355-367. <https://doi.org/10.1007/s12686-011-9547-8>
- Federman, S., Hyseni, C., Clement, W., Oatham, M. P., & Caccone, A. (2014). Habitat fragmentation and the genetic structure of the Amazonian palm *Mauritia flexuosa* L. f. (Arecaceae) on the island of Trinidad. *Conservation Genetics*, 15, 355-362. <https://doi.org/10.1007/s10592-013-0543-2>
- Frankham, R., Ballou, J. D., & Briscoe, D. A. (2002). *Conservation Genetics* (p. 617). Cambridge University Press, Cambridge, UK.
- Gomes, L. R. P., Lopes, M. T. G., Bentes, J. L. S., Barros, W. S., Costa Neto, P. Q., & Contim, L. A. S. (2011). Genetic diversity in natural populations of Buriti (*Mauritia flexuosa* L. f.). *Crop Breeding and Applied Biotechnology*, 11, 216-223. <https://doi.org/10.1590/S1984-70332011000300003>
- Goudet, J. (2002). *FSTAT, a program to estimate and test gene diversities and fixation indices* (Version 2.9.3.2). Retrieved from <http://www.unil.ch/izea/softwares/fstat.html>
- Goudet, T. J., Raymond, D. M., De-Meeus, T., & Rousset, F. (1996). Testing Differentiation in Diploid Populations. *Genetics*, 144, 1933-1940. <https://doi.org/10.1093/genetics/144.4.1933>
- Gray, R. E. J., Slade, E. M., Chung, A. Y. C., & Lewis, O. T. (2019). Movement of moths through riparian reserves within oil palm plantations. *Frontiers in Forests and Global Change*, 2, 68. <https://doi.org/10.3389/ffgc.2019.00068>
- Holcomb, J., Tolbert, D. M., & Jain, K. (1977). A diversity analysis of genetic resources in rice. *Euphytica*, 26, 441-449. <https://doi.org/10.1007/BF00027006>
- INMET (Instituto Nacional de Meteorologia). (2010). *Precipitação e temperatura, 1931-2000*. Retrieved from <http://www.inmet.gov.br>
- Jain, A., Chan, S. K. M., Vlasanek, P., & Webb, E. L. (2020). Impacts of habitat on butterfly dispersal in tropical forests, parks and grassland patches embedded in an urban landscape. *Biotropica*, 52, 404-409. <https://doi.org/10.1111/btp.12760>
- Kalinowski, S. T. (2004). Counting alleles with rare faction: Private alleles and hierarchical sampling designs. *Conservation Genetics*, 5, 539-543. <https://doi.org/10.1023/B:COGE.0000041021.91777.1a>
- Klink, C. A., & Machado, R. B. (2005). Conservation of the Brazilian Cerrado. *Conservation Biology*, 19, 707-713. <https://doi.org/10.1111/j.1523-1739.2005.00702.x>
- Knudsen, J. T., Tollsten, L., & Ervik, F. (2001). Flower scent and pollination in selected neotropical palms. *Plant Biology*, 3, 642-653. <https://doi.org/10.1055/s-2001-19366>

- Lacerda, A. E. B., Kanashiro, M., & Sebbenn, A. M. (2008). Long-pollen movement and deviation of random mating in a low-density continuous population of a tropical tree *Hymenaea courbaril* in the Brazilian Amazon. *Biotropica*, 40(4), 462-470. <https://doi.org/10.1111/j.1744-7429.2008.00402.x>
- Loiola, C. M., Azevedo, A. O. N., Diniz, L. E. C., Aragão, W. M., Azevedo, C. D., Santos, P. H., ... Ramos, S. R. R. (2016). Genetic relationships among tall Coconut Palm (*Cocos nucifera* L.) accessions of the International Coconut Gene bank for Latin America and the Caribbean (ICG-LAC), evaluated using microsatellite markers (SSRs). *PLoS ONE*, 11, e0151309. <https://doi.org/10.1371/journal.pone.0151309>
- Lompo, D., Vinceti, B., Konrad, H., Duminil, J., & Geburek T. (2020). Data from: Fine-scale spatial genetic structure, mating, and gene dispersal patterns in *Parkia biglobosa* populations with different levels of habitat fragmentation. *American Journal of Botany*, 107(7), 1041-1053. <https://doi.org/10.1002/ajb2.1504>
- Machado, F. R. B., Vinson, C. C., Silva, V. P., & Ciampi, A. Y. (2022). *Extração de DNA Genômico de Câmbios de Espécies Madeiras Tropicais*. 53º Congresso Nacional de Botânica, Pernambuco, Brasil. Sociedade Brasileira de Botânica, Recife.
- Marshall, D. K., & Brown, A. H. D. (1975). Optimum sampling strategies in genetic conservation. In O. H. Frankel, & G. J. Hawkes (Eds.), *Crop genetic resources for today and tomorrow* (pp. 53-70). Cambridge University Press, Cambridge, UK.
- Matos, F. S., Nunes, Y. R. F., Silva, M. A. P., & Oliveira, I. S. (2014). Biometric Variations of Diaspores of Buriti (*Mauritia flexuosa* L.f.-Arecaceae) in 'Veredas' at Different Conservation Stages. *Ciência Florestal, Santa Maria*, 24(4), 833-842. <https://doi.org/10.5902/1980509816583>
- Mazal, L., Corenblit, D., Barsoum, N., Steiger, J., Skot, L., Fumanal, B., & Till-Bottraud, I. (2021). Fine-scale spatial genetic structure and intra-specific interactions of *Populus nigra* within a natural river corridor along the lower Allier River (France). *Flora*, 275, 151763. <https://doi.org/10.1016/j.flora.2021.151763>
- Menezes, E. V., Souto, W. F. S., Ciampi A. Y., Azevedo, V. C. R., Valério, H. M., & Pimenta, M. A. S. (2012). Development and characterization of DNA microsatellite primers for buriti (*Mauritia flexuosa* L.f.). *Genetics and Molecular Research*, 11(4), 4058-4062. <https://doi.org/10.4238/2012.September.17.6>
- Moraes, M. C., Mengarda, L. H. G., Canal, G. B., Pereira, P. M., Ferreira, A., & Ferreira, M. F. S. (2020). Genetic diversity in matrices and progenies of *Euterpe edulis* Mart. in managed area and in natural populations by microsatellites markers. *Scientia Florestalis*, 30(2), 583-594. <https://doi.org/10.5902/1980509837647>
- Nei, M. (1978). Estimativa de heterozigosidade média e distânciagenética de um pequenonúmero de indivíduos. *Genética*, 89, 583590.
- Nunes, Y. R. F., Azevedo, I. F. P., Neves, W. V., Veloso, M. D. D. M., Souza, R., & Fernandes, G. W. (2009). Pandeiros: O pantanal mineiro. *MG Biota, Belo Horizonte*, 2(2), 4-17.
- Olifiers, N., & Cerqueira, R. (2006). Fragmentação de habitat: Efeitos históricos e ecológicos. In C. F. Rocha, H. G. Bergallo, M. V. Sluys & M. A. S. Alves (Eds.), *Biologia da conservação: Essenciais* (pp. 261-279). RiMa, São Carlos.
- Oliveira, P. S., & Marquis, R. J. (2002). *The Cerrados of Brazil: Ecology and Natural History of a Neotropical Savanna*. Columbia University Press, New York. <https://doi.org/10.7312/oliv12042>
- Oliveira, V. B., Yamada, L. T., Fagg, C. W., & Brandão, M. G. L. (2012). Native foods from Brazilian biodiversity as a source of bioactive compounds. *Food Research International*, 48, 170-179. <https://doi.org/10.1016/j.foodres.2012.03.011>
- Ovaskainen, O., Ramos, D. L., Slade, E. M., Merckx, T., Tikhonov, G., Pennanen, J., ... Morales, J. M. (2019). Joint species movement modeling: How do traits influence movements? *Ecology*, 100(4), e02622. <https://doi.org/10.1002/ecy.2622>
- Ramos, S. L., Lopes, M. T., Batista, J. S., Formiga, K. M., Silva, P. P., Saulo-Machado, A. C., & Veasey, E. A. (2012). Microsatellite loci for tucumã of Amazonas (*Astrocaryum aculeatum*) and amplification in other Arecaceae. *American Journal of Botany*, 99(12), e508-10. <https://doi.org/10.3732/ajb.1100607>
- Resende, L., Ribeiro, R., & Lovato, M. (2011). Diversity and genetic connectivity among populations of a threatened tree (*Dalbergia nigra*) in a recently fragmented landscape of the Brazilian Atlantic Forest. *Dordrecht Genetica*, 139(9), 1159-68. <https://doi.org/10.1007/s10709-011-9618-5>

- Rossi, F. S., Rossi, A. A. B., Dardengo, J. D. F. E., Brauwiers, L. R., Silva, M. L. D., & Sebbenn, A. M. (2014). Diversidade genética em populações naturais de *Mauritia flexuosa* L. f. (Arecaceae) com uso de marcadores ISSR. *Scientia Florestalis*, 42, 631-693.
- Scriven, S. A., Beale, C. M., Benedick, S., & Hill, J. K. (2017). Barriers to dispersal of rain forest butterflies in tropical agricultural landscapes. *Biotropica*, 49, 206-216. <https://doi.org/10.1111/btp.12397>
- Shannon, C. E., & Weaver, W. (1963). *A Teoria Matemática da Comunicação*. University of Illinois Press, Urbana, IL, EUA.
- Silva, B. M., Rossi, A. A. B., Encinas, J. F., Arreguy, D. V., Araujo, A. C., Oliveira, L. O. V., & Clarindo, W. R. (2016). Genetic diversity estimated using inter-simple sequence repeat markers in commercial crops of cupuassu tree. *Ciência Rural*, 46(1), 108-113. <https://doi.org/10.1590/0103-8478cr20141634>
- Smith, J. R., Ghazoul, J., Burslem, D. F. R. P., Itoh, A., Khoo, E., Lee, S. L., ... Kettle, C. J. (2018). Are patterns of fine-scale spatial genetic structure consistent between sites within tropical tree species? *PLoS ONE*, 13(3), <https://doi.org/10.1371/journal.pone.0193501>
- Storti, E. F. (1993). Floral biology of *Mauritia flexuosa* Lin. Fil. In Manaus, AM, Brazil. *Acta Amazônica*, 23, 371-381. <https://doi.org/10.1590/1809-43921993234381>
- Wright, S. (1951). The genetical structure of populations. *Annals of Eugenics*, 15(4), 323-354. <https://doi.org/10.1111/j.1469-1809.1949.tb02451.x>

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Authors Contributions

Bárbara Rayane Ramos Muniz Nassau was responsible for data collection and paper writing; Márcia Regina da Costa was responsible for help in conceptualization and provided invaluable advice and mentorship throughout the manuscript's development; Elytânia Veiga Menezes helped in the interpretation of the data and manuscript writing review; Demerson Arruda Sanglard helped providing laboratory infrastructure to carry out the experiment; Tiago Vieira Sousa realized the statistical analysis of data; Marcio Antonio Silva Pimenta was responsible for conceptualization, design, methodology and writing review. All authors read and approved the final manuscript.

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