

Article

Reproductive Ecology of *Lecythis Pisonis* in Brazilian Agroforestry Systems: Implications for Conservation and Genetic Diversity

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Abstract: Agroforestry systems are essential in sustainable land use in the face of the growing global food demand and climate change. The southern region of Bahia, Brazil, is one of the places in the world where the tree species is particularly in abundance, primarily in cocoa agroforestry systems, contributing to biodiversity conservation. Understanding their reproductive patterns is crucial for the survival and sustainability of these trees. This study dealt with *Lecythis pisonis* (Sapucaia) trees by applying microsatellite markers for mixed-mating mode and paternity analyses for pollen dispersal. In particular, it was found that *Lecythis pisonis* offspring are produced through outcrossing, as the case may be, while random crossings and no nearby tree fertilization are the remaining factors that play a crucial role in myriad genetic diversity inversions. This phenomenon was indicated by paternity in nine offspring, with full siblings being from the same parents. The average distance of pollen flow was 6 km, which is why the pollinator, the bee *Xylocopa frontalis*, has a flight range aligning with distance. These data show the influence of habitat fragmentation, the function of Cabruca, and the conservation strategy.

Keywords: reproduction system; tree conservation; tropical forest; agroforestry; mixed-mating system; conservation



Academic Editor: Eduardo Notivol

Received: 20 February 2025

Revised: 31 March 2025

Accepted: 10 April 2025

Published: 23 April 2025

Citation: Waqar, Z.; Rodrigues, A.B.; Florence, C.T.; Mariano Neto, E.; Gaiotto, F.A. Reproductive Ecology of *Lecythis Pisonis* in Brazilian Agroforestry Systems: Implications for Conservation and Genetic Diversity. *Forests* **2025**, *16*, 718. <https://doi.org/10.3390/f16050718>

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1. Introduction

Human intervention has caused more than three-quarters of Earth's degradation, affecting 3.2 billion people and resulting in a loss of 10% of the annual gross product in ecosystem services and biodiversity, according to the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) [1]. The United Nations Convention on Biological Diversity is working on a post-2020 global biodiversity framework agenda to tackle these challenges through sustainable land use [2,3].

Agroforestry systems have been recognized as a sustainable land-use strategy that combines production and biodiversity conservation, providing economic, environmental, and social benefits, particularly in human-dominated landscapes where protected areas alone are insufficient to preserve biodiversity [4,5]. Agroforestry in the tropics contributes significantly to global food security and climate change issues by preserving ecological

balance and increasing genetic diversity [6,7]. In Brazil, agroforestry covers around 13.9 million hectares [8], with the Atlantic Forest—one of the world’s biodiversity hotspots—being a major focus of conservation efforts due to its less than 11% forest cover [5,9]. The “cabruca” is a particularly important agroforestry system in Bahia, where cacao is grown under the shade of selectively thinned native trees. It contributes to carbon sequestration and minimizing expected climatic impacts by 2050 [10]. These systems are quite similar to primary forests because they preserve soil fertility, ecological processes, and species richness, including commercially significant native trees [11–16]. Furthermore, agroforestry promotes genetic diversity by enabling gene flow via pollen and seed dispersal, which is critical for conservation efforts and the long-term viability of tree populations [14,17,18].

Pollination and seed dispersal studies provide valuable information about the gene flow of the species, discussing possible limitations, distance, and vectors [19,20]. Studies on reproductive ecology also estimate other aspects of species, such as outcrossing, selfing, inbreeding, etc. [21]. Understanding pollen and seed dispersal processes is crucial for determining a species’ ability to persist in a degraded landscape [20,22]. Since pollen flow determines the gene exchange between distant trees, it directly influences the effective population size and the number of potential mating individuals [23]. Increased pollen flow reduces inbreeding risks, promotes genetic diversity, and ensures the long-term survival of populations. Identifying pollen distribution distances and patterns also helps with assessing pollinators’ involvement in preserving connectivity between fragmented populations, which is critical for developing conservation strategies [22]. All these topics are connected, and for conservation proposals, it is best that it should be supported by the reproductive ecology of the species [24]. The Atlantic Forest produces numerous edible fruit trees, and *Lecythis pisonis* Cambess, commonly known as Sapucaia, is one of them that has nutritional and economic value [25,26]. It is commonly grown in forest fragments and agroforests in Bahia and Espírito Santo [27].

The tropical forest ecosystem has high species richness, and most tropical trees are insect-pollinated, particularly bees [28]. Sapucaia are pollinated by the bee *Xylocopa frontalis* [26], and its seeds are mainly dispersed by the bat *Phyllostomus hastatus*, which eats the aril and discards the seeds [29]. There is great interest in gaining knowledge about the mating system of Sapucaia to understand its resilience for conservation purposes. Mating system studies, for example, can estimate the extent to which species cross to form progeny. These studies can estimate the extent of outcrossing, the number of pollen donors, and the rate of inbreeding. The mating system is one of the factors that affect the genetic diversity and structure of species [30]. Therefore, the present study was conducted to understand the reproduction pattern of the tropical tree *Lecythis pisonis* Cambess growing in an agroforest system to predict survival ability and to propose viable conservation efforts for the species.

2. Materials and Methods

2.1. Study Area and Sampling Design

This research was carried out on farms located in the rural areas of the municipalities of Ilhéus and Uruçuca in the state of Bahia, Brazil (Figure 1). The survey of the collection area involved mapping the existing “cabruças” on the properties in advance to include them in the study. This mapping was conducted with the help of property employees, with a monetary reward for each tree found (Figure 1).

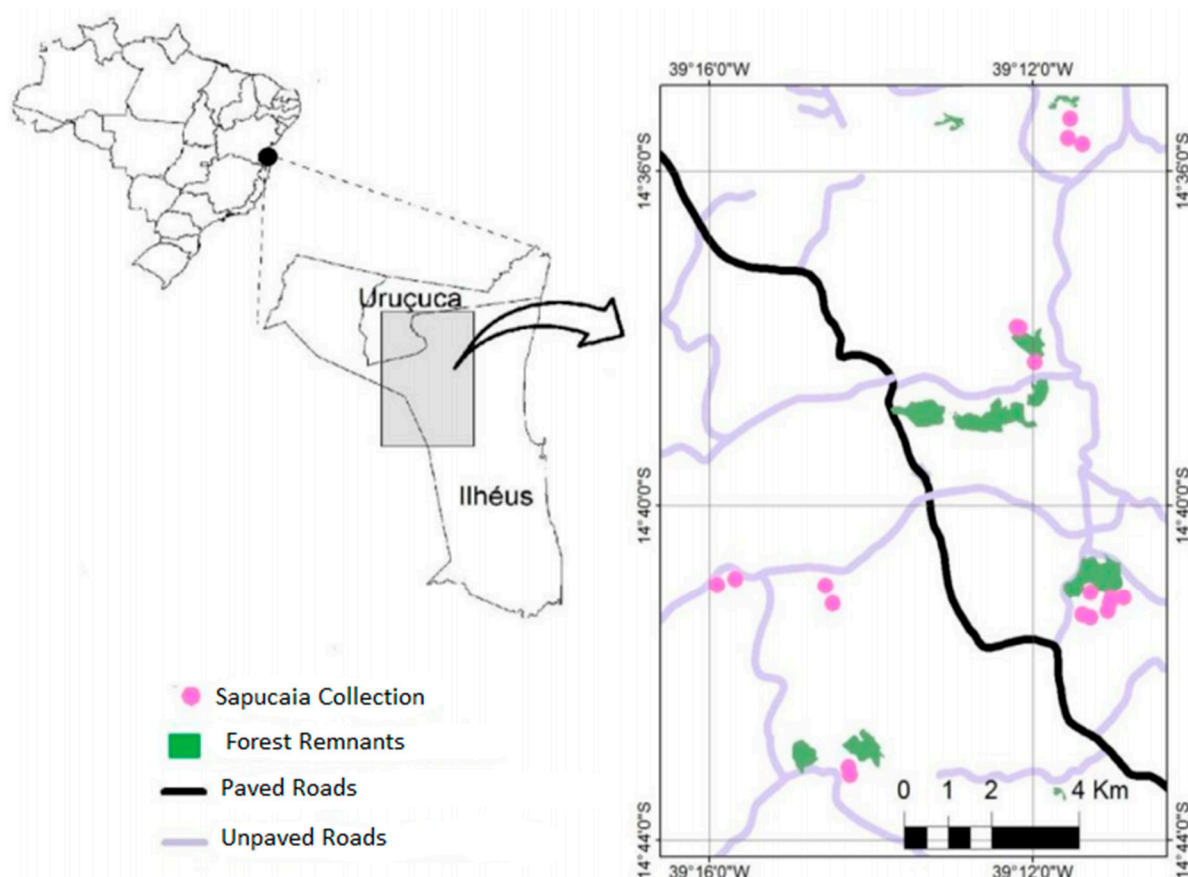


Figure 1. Map of the studied landscape with the location of sampled Sapucaia's matrices in Southern Bahia, Brazil.

Fruits from each adult tree (matrices) were collected from 12 Sapucaia in “cabruças” along a continuous forest gradient (the amount of forest present within a radius of 1 km) around each tree. From the fruits, some seeds were placed to germinate in the RPPN (Reserva Particular do Patrimônio Natural) Nova Angélica, which is located around the Una Biological Reserve. After 60 days, leaf material from 24 seedlings per family was collected from each one of the 12 families. The collection took place between the months of September to October; these months align with the peak seed maturation period.

The 12 families sampled were identified as: F6, F60, F66, F68, F76, F87, F92, F93, F354, F361, F376, and F377. The 287 descendants collected, in turn, were named P (offspring or progeny), followed by a number, for example, P1, P2, P3...P287. In order to understand the reproductive system of the Sapucaia, we used paternity analysis using nuclear microsatellite markers, which are specific to Sapucaia [31]. These species-specific markers were used to determine the gene flow and distance pollen traveled. A paternity analysis was conducted to understand the mating pattern and to estimate how far pollen can travel; this helps to understand the long-term viability and survival of species. For the paternity analysis, material was collected randomly from 40 single adult individuals from cabruças farms from Ilhéus and Uruçuca, Bahia, Brazil [31]. The collection of these 40 individuals was a part of the initial mapping of cabruças.

2.2. DNA Extraction and Quantification

The leaf samples from the seedlings were placed in plastic bags and sent to the Molecular Markers laboratory, located at the Center of Biotechnology and Genetics (CBG) at UESC (the State University of Santa Cruz). The genomic DNA was extracted using the CTAB 2% protocol [32]. After extraction, quantification of the extracted DNA was carried

out through comparative analysis with a molecular standard of known concentration (λ phage DNA) in 1.0% agarose gel, stained with Gel GreenTM (Nucleic Acid Gel Stain) diluted to 0.2%, and verified in a transilluminator with a blue LED lamp (470 nm). Then, this DNA was diluted in Milli-Q water to the concentration of use (2.5 ng/ μ L).

2.3. Amplification of SSR Loci and Genotyping

To genotype sampled individuals, the DNA sequence of interest was amplified via PCR, and eight microsatellites (SSR) were used (Table 1) among the previously developed 16 primers [31]. We selected eight microsatellite loci (Lec31, Lec41, Lec50, Lec144, Lec166, Lec172, Lec195, and Lec272) based on their high polymorphism, Hardy–Weinberg equilibrium compliance, and reliable amplification without genotyping errors. The amplification reaction was carried out in a solution containing the following: 7.5 ng of genomic DNA; 1.3 μ L of 10xbuffer, 3.25 mM of each dNTP, 3.25 mg of bovine serum albumin (BSA), 20 mM of MgCl₂, 1U of Taq DNA polymerase Phoneutria, Belo Horizonte, Minas Gerais, Brazil, 3.0 μ M of reverse and forward primers labeled with an M13 fluorescence tail (CAC-GACGTTGTAAAACGA), 0.03 μ M of M13 oligonucleotide, complementary to the tail of the forward primer, labeled with fluorochromes (6-FAM, VIC, or NED, Applied Biosystems, Foster City, CA, USA) and Mili-Q water, to a final volume of 13.0 μ L.

Table 1. Description and genetic characterization of 8 nuclear microsatellite loci developed for *Lecythis pisonis*.

Primer	Repeat Motif	Primer Sequences (5′–3′)	Range (bp)	T _a (°C)	GenBank No.
Lec31	(GA) _n	F: AGCCTGACATGAGTTCAG AAG R: TGAGCACCATAAGTTACGTC	180–186	58	KM92086
Lec41	(GA) _n	F: TGAGTGAGCGAGTAAGGAATG R: CACGTTTTGTTTTGTTGAG	224–230	58	KM92089
Lec50	(GA) _n	F: TGACATTACAAAGAGTATGG R: TTGAAGATGTTGTTGTTGAG	149–151	58	KM92092
Lec144	(GA) _n	F: TTGAGTTGGTAAGTGGAATG R: AGGTTGTTTGAGTGGGAG	224–230	58	KM92098
Lec272	(GA) _n	F: CAGTTTTGTTGTTGTTGAG R: GACCTTTGTTTGAGAGT	142–146	60	KM92099
Lec166	(TCA) _n	F: AGGCTGACCTGAGATGG R: AGTTAGAGGTTGTTGAGAG	237–253	58	KM92090
Lec172	(GA) _n	F: TGAGTGTTGTTGTTGAG R: AGGTTGAGTTGTTGTTGA	195–205	58	KM92095
Lec195	(GA) _n	F: TGAGTTGTTGTTGTTGAG R: GACGTTTTGTTTTGTTGAG	149–159	58	KM92096

T_a = annealing temperature.

The thermocycling conditions for each polymerase chain reaction consisted of an initial denaturation step at 94 °C for 1 min, followed by 30 cycles consisting of a denaturation step at 94 °C for 1 min, an annealing step at a specific temperature for each primer pair [31] for 45 s, and an extension step at 72 °C for 1 min, followed by 8 cycles of M13 fluorescence annealing corresponding to 94 °C for 1 min, 53 °C for 1 min, and 72 °C for 1 min, plus a final extension step at 72 °C for 10 min.

The amplification reactions were subjected to capillary electrophoresis in the ABI 3500 automatic DNA analyzer (Applied Biosystems) in a multiload system. The Gene Mapper program version 4.1 (Applied Biosystems) was used for alleles genotyping.

2.4. Analysis of the Reproductive System

For the parameters that were estimated, we used the mixed-mating model proposed by Ritland and Jain [33] with the help of the MLTR 3.2 program [34]. This model is based on a few assumptions: (1) each mating event is due to random mating or self-fertilization; (2) the probability of crossing is independent of the maternal genotype; (3) the pollen pool is homogeneous across all maternal trees; (4) there is no selection between fertilization and analysis time for the progeny genotype; (5) alleles at different loci segregate independently [33].

The estimated parameters were as follows: matrix fixation index (maternal trees) (F_m), multilocus outcrossing rate (T_m), unilocus outcrossing rate (T_s), crossing rate between related individuals ($T_m - T_s$), paternity correlation (R_{pm}), and the correlation of the crossing rate between loci (R_t).

A 95% confidence interval was calculated using 10,000 resamples using the bootstrap method between families. For these calculations, the algorithm used was expectation maximization (EM), which has a better convergence to meet the maximum of the parameter, and the standard deviation is reduced in relation to the Newton–Raphson (NR) algorithm [35].

2.5. Paternity Analysis

To understand the individuals who donated the pollen grains to the germinated seedlings, a paternity analysis was carried out, and, for this purpose, the 12 sampled matrices were used to investigate the reproduction system of the 40 adult individuals used to characterize the loci-developed SSR [31]. Paternity analysis was carried out with the help of the CERVUS 3.0.7 program [36].

Firstly, the allele frequency analysis was estimated before the paternity analysis simulation. Utilizing the estimated allele frequencies, Cervus simulated potential parentage scenarios. This simulation accounts for factors such as the number of candidate fathers, the proportion of sampled parents, and the genotyping error rate. The purpose of these simulations is to establish critical values for the Logarithm of the Odds (LOD) scores, which are used to assess confidence in paternity assignments. For our analysis, we selected the LOD score as the criterion for paternity assignment. The LOD score represents the natural logarithm of the overall likelihood ratio, comparing the probability that a candidate is a true father versus not being the father. In paternity analysis, the LOD score is obtained by taking the logarithm natural (log in base 10) of the global likelihood ratio. For the positive score of LOD, paternity was assigned with 95% confidence, which means that the candidate's father is the alleged father. A LOD score of zero means that the candidate parent has the same probability of being the father as of not being the father. A score of negative LOD indicates that a candidate parent does not match the offspring in one or more loci, and therefore, the candidate father is probably not the real father [36]. Based on the simulations, Cervus assigns paternity to the candidate father with the highest LOD score, provided it exceeds the critical threshold established for a specified confidence level (e.g., 95%). This threshold ensures that the likelihood of a correct paternity assignment meets the desired confidence criteria.

2.6. Pollen Flow Distance Analysis

We estimated the dispersal distance of pollen using the geographic coordinates of each set of individuals assigned as progenitor–Progeny based on the paternity test. The coordinates were obtained in fieldwork using the GPS program TracMaKer 13.9.

3. Results

3.1. Reproductive System

The multilocus and single locus outcrossing rates indicate the proportion of mating occurring between individuals in the populations. The multilocus outcrossing rate (T_m) is the rate of outcrossing estimated using multiple genetic loci, which was equal to 1.000. On the other hand, the single locus outcrossing rate (T_s), based on the average of estimations at a single genetic locus, was 0.960. Our results reveal that *Sapucaia* reproduces exclusively through crossbreeding, making it an obligate allogamous species. However, the positive difference ($T_m - T_s$) suggests some biparental inbreeding, indicating that outcrossing is occurring between related individuals. Corroborating this, we found the rate of the fixation index ($F_m = 0.431$), which led us to point out that some adult mating individuals are probably related. The multilocus paternity correlation (R_{pm}), which concerns the probability of two individuals chosen at random within progenies having the same pollen donor, indicated that part of the descendants share the same father. The correlation of the crossing rate between loci (R_t), which measures the proportion of inbreeding generated by crossing between related individuals and by self-fertilization, was null (Table 2).

Table 2. Estimates of the reproduction system of *Lecythis pisonis* from 10 SSR loci.

Parameters	Estimated	Standard Deviation
F_m	0.431	0.103
T_m	1.000	0.000
T_s	0.960	0.011
$T_m - T_s$	0.040	0.010
R_t	0.000	0.003
R_{pm}	0.306	0.064

F_m = matrix fixation index, T_m = multilocus outcrossing rate, T_s = unilocus outcrossing rate, $T_m - T_s$ = mating rate between related individuals, R_{pm} = multilocus paternity correlation, R_t = correlation of crossover rate between loci with a 95% confidence interval using 10,000 bootstrap resamples between families.

3.2. Paternity Analysis

Among the 287 descendants, 9 (3%) had their paternity alleged. Among the 40 total adults sampled, 29% (nine trees) were pollen donors of the descendants. Trees F60 and F354 were pollen donors for four of the nine seedlings that had parents alleged, each of these individuals having two offspring (Table 3).

Table 3. Seedlings that had paternity assigned, with the geographic coordinates of the maternal and paternal trees and the estimated LOD values for paternity at a 95% confidence level.

Progeny	Mother Plant	Father Plant	LOD	Distance of Pollen Flow (km)
P11	F6	F60	1.86×10^{14}	1.16
P20	F6	F60	4.94×10^{14}	1.16
P28	F60	F69	7.41×10^{13}	0.25
P31	F60	F66	2.18×10^{14}	0.29
P101	F76	F376	1.06×10^{14}	10.81
P104	F76	F354	1.08×10^{14}	7.83
P144	F87	F354	2.46×10^{14}	0.25
P147	F92	F48	1.01×10^{14}	15.12
P264	F376	F361	5.22×10^{14}	15.26

The offspring P11 and P20 have a family structure of full siblings since they had the same mother plant (F6) and the same father plant (F60). Individuals P28 and P31 had a

half-sibling family structure, as they only had the same mother plant (F60) with different parents. The half-sibling family structure was also observed in descendants P101 and P104, who shared the same tree maternal (F76), as well as in the P144 descendant, who shared the same paternal tree (F354) with P104 (Table 3).

3.3. Pollen Flow Distance

The pollen grain from the paternal tree F354 traveled the shortest distance to carry out pollination. The greatest distance traveled by pollen found in this research was 15.26 km and produced offspring P264 (Table 3).

The average distance traveled by the pollen of *L. pisonis* was approximately 5 km and 792 meters. In Figure 2, it is possible to observe the geographic location of the maternal and paternal trees and, thus, verify the spatial distance between such trees and consequently note the distances that the pollen grains traveled in the sampled area.

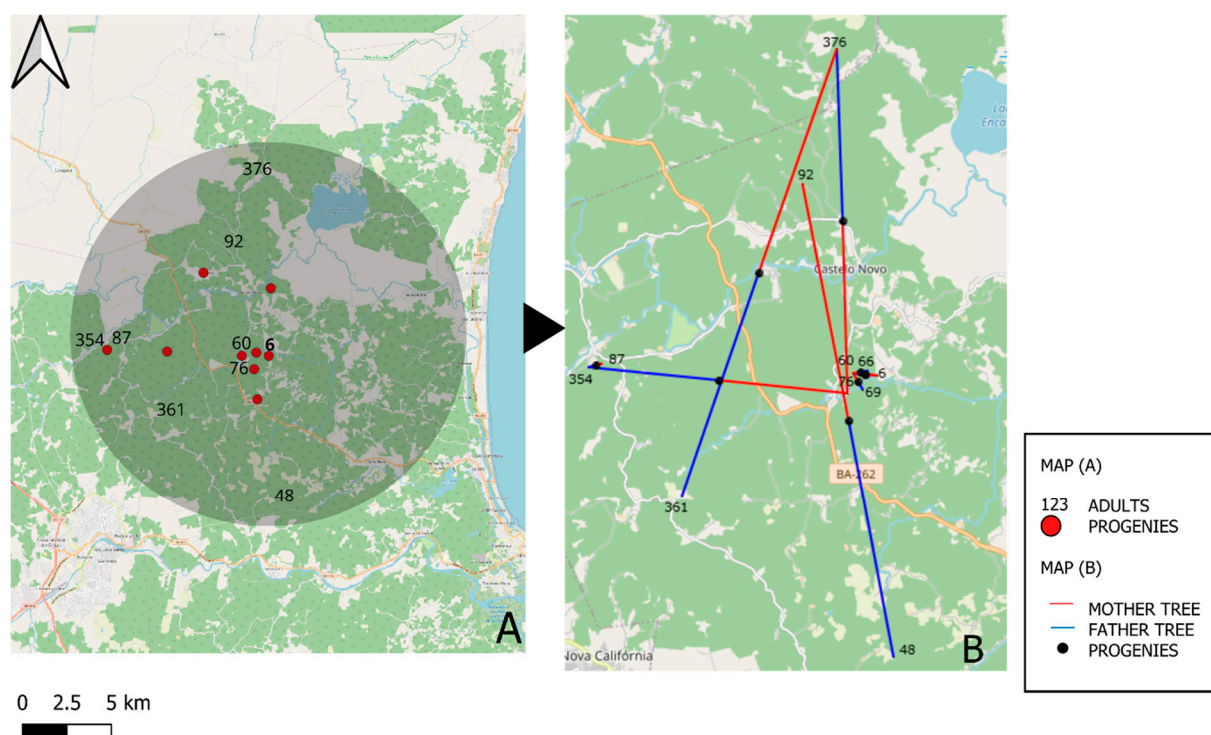


Figure 2. The map represents adult trees and their progenies. (A) The red pointer represents the location of the 9 descendants of maternal and parental trees that were sampled (B) The lines represent the pollen flow of the maternal tree (represented by red), parental trees (represented by blue), and their probable progeny (represented by green) in rural areas in South Bahia, Brazil.

4. Discussion

Our results provide insights into the reproductive behavior of Sapucaia, emphasizing its dependence on outcrossing and the absence of inbreeding within the sampled families. A mixed-model mating system was used to determine that Sapucaia exclusively relies on crossbreeding, suggesting that pollinators play an important role in the reproduction of this species. The paternity analysis identifies the descendants of the trees and estimates the gene flow that occurred, and the distance the pollen grain traveled was approximately 6 km, indicating the pollinator traveled over long distances. These findings highlight the diversity in family structures among the studied individuals, with two in a full-sibling relationship and four in various half-sibling relationships. We also found that pollen traveled to great distances, indicating active pollinators in the area. This study highlights some important reproductive aspects of *L. pisonis* that are necessary for its conservation in the agroforestry

system. Also, these findings suggest the need to maintain and enhance habitat connectivity to ensure diverse mating opportunities and facilitate gene flow to preserve the genetic health of *L. pisonis*.

Reproduction System, Paternity, and Pollen Flow Distance

The observed fixation index (F_m) within the matrix revealed significant kinship among maternal trees, implying a shared ancestry; it is likely that inbreeding occurred and pollens originated from the same source. This historical pattern of pollen dissemination elucidates the relatedness observed in the matrices. The implementation of “cabruca” involves thinning the Atlantic Forest, resulting in the removal of numerous trees and subsequently diminishing the available pollination options [37]. Understanding this context provides insight into the observed genetic relationships among the trees. Similar results were obtained in *Cariniana legalis* Mart Kuntze, where inbreeding occurs due to the size of fragments [38].

The limited multilocus outcrossing rate and the extremely high single locus outcrossing rate found in our results lead us to believe that the mother trees in the sampled area necessarily reproduce through crossings [39]. It is, therefore, an allogamous species, like most of the tropical trees [40,41], such as that also observed in other tropical trees, *Centrolebium tomentosum* Guill. ex Benth. (Fabaceae) [42] and *Euterpe precatoria* [43]. This result confirms the assumption made by [44] about Sapucaia in a study that lasted 6 years. In the study, the researchers reported that Sapucaia has the characteristics of an allogamous species. This was the only scientific research published in the past that investigated aspects related to the Sapucaia reproduction system. Therefore, the approach of this investigation is of great relevance for knowledge about the conservation of this tree species.

Mating among related trees was also detected (Table 2); however, we highlight that in this type of reproduction system, which is outcrossing, the presence of the pollinator has a fundamental influence on reproductive success. Several studies have shown that *L. pisonis* is a species dependent on the bee *Xylocopa frontalis* for fruit production [44–47].

The evolutionary process of the species appears to increase and maintain genetic variability among individuals, leading to the development of increasingly complex stamens. These characteristics lead to a reduction in the number of different species of pollinators that can penetrate the flower [44]. In general, the more specialized the stamen, the more specialized the pollinator that visits the flower [48]. This evolutionary process of trees favors specific pollens to fertilize them [49]. From this perspective, observations carried out on the Sapucaia crown in southern Bahia, Brazil, indicated that *Xylocopa frontalis* is the only bee that enters its flower [46]. Since geographically proximate individuals are more likely to interbreed and thus be genetically related, the observed value of the parameter ‘mating among relatives’ ($T_m - T_s$) indicates that, overall, mating occurs randomly within the population. This is positive for maintaining the genetic variability of individuals, families, and populations of the species under study, which is fundamental for the conservation of the species over generations.

Nevertheless, the value of 0.040 of the difference between multilocus and unilocus outcrossing rates ($T_m - T_s$) is low, indicating minimal mating between related individuals. These results suggest that the population engages in random mating. A possible explanation for why no crossing occurs between related individuals is the fact that the pollinating bee has a wide flight radius, a common pollinator in this type of species [38,42]. It reaches a daily average of 6.7 to 12 km [50,51], allowing it to visit the flowers of individuals distant from each other. This is beneficial for promoting genetic variability. The authors of [28] discussed that the *Xylocopa* bee makes frequent visits to several flowers with high foraging speed, leading to pollination success.

The result of the correlation of the outcrossing rate between loci (R_t) indicates that there are no crossings between relatives nor self-fertilization in the sampled families. This result corroborates the result obtained in the parameter T_m-T_s since it demonstrates the non-existence of crossings between relatives. Furthermore, as *Sapucaia* reproduces only through outcrossing, it was expected that there would be no self-fertilization. The non-occurrence of self-pollination contributes to the existence of greater genetic variability in the families studied. Beyond the anatomic and other biological aspects, the inexistence of self-pollination can also be favored by population density or size. The ecological aspects impacting reproduction biology were observed previously on *Cariniana legalis*, which is another tropical Atlantic Forest endemic tree, whose outcrossing rate can be affected by the population's size [38].

Self-compatibility is a self-recognition mechanism that results in the rejection of pollen by the female somatic tissues of the flower itself [52]. In fact, self-incompatibility is one of the mechanisms that promote allogamy, and according to [53], this is frequently found in tropical species. Around 50% of angiosperms develop self-incompatibility to favor outcrossing [54]. In the fruit tree *Bertholletia excelsa* (Bonpl.), similar phenomena are observed, where the tree is mostly reproduced by outcrossing due to its self-incompatible nature; inbreeding does not occur, even if the population size is small [55]. Another tropical tree, *Parkia multijuga* Benth, was observed to have similar phenomena of allogamy (outcrossing) as its primary reproductive strategy, which promotes genetic diversity and reduces inbreeding depression [56]. As it was not the focus of this research, it is not possible to state that *L. pisonis* is self-incompatible; however, our results provide genetic evidence that it is a possibility. There are other species of the same family (Lecythidaceae), such as *Bertholletia excelsa* [57], *Eschweilera ovata* [58], *Cariniana legalis* [59], *Cariniana estrellensis* [60], and *Schima wallichii* [28] that have a high rate of outcrossing and a mixed-mating system.

The multilocus paternity correlation was high and different from zero ($R_{pm} = 0.306$). This result indicated that part of the descendants share the same father, and a possible explanation for this is the fact that some paternal trees are relatively close to the maternal trees. This justification is completely plausible when looking at the results, occurring, for example, between the individuals P11 and P20 who share the father F60, and individuals P104 and P144, in which for both, the father is the tree F354. Thus, although the pollinator can fly great distances, it is plausible to imagine that it prefers to visit the flower of the nearest tree. With this behavior, the *Xylocopa frontalis* bee obtains resources (nectar and pollen) and saves energy. The pollinator behavior is one of the key factors affecting the outcrossing rate, as it occurs in the *Anadenanthera* species [61]. In *B. excelsa* studies, due to limited seed dispersal, mating between related individuals occurs, and a level of co-ancestry among parents is observed [62].

On the other hand, it is important to highlight that a small number of progenies were observed sharing the same father since, for the majority, it was not possible to determine the paternal tree. In turn, the non-sharing of the same father by most of the descendants is another favorable factor for the genetic variability of the species since it can promote an increase in the number of loci in heterosis, which is interesting for both conservation and management, as well as improvement [63,64].

Reproduction between genetically similar individuals increases the probability of different loci reaching the homozygous state [63]. Furthermore, the smaller number of genotypes in highly self-pollinated populations can reduce efficiency and genetic diversity, and restrict the ability of their populations to respond adaptively to an environmental change [65,66]. Only 3% of the descendants were attributed to paternity. This result highlights two possibilities: (i) that this is due to the distance of the area covered, where

the sampling design did not include all possible individuals, and (ii) pollen immigration from the Atlantic Forest remnants occurred around the collected families.

To summarize, our findings highlight the importance of outcrossing and long-distance pollen flow in maintaining genetic diversity in *Lecythis pisonis*. These results have significant implications for the conservation of this species in agroforestry systems. According to [67], the trend over time indicates that an increasing number of forests will be converted for agricultural use, preferentially as agroforestry. From this perspective, a long-term plan for biodiversity conservation must recognize this fact and focus not only on preserving the patches of native vegetation that remain but also on managing a landscape that presents a possible migration system. To promote the positive impact of the agroforestry system, it is important that farmers actively participate in management practices to conserve species diversity. Therefore, there is an urgent need to promote ecologically sustainable agriculture.

Considering the importance and scope of cocoa farming in southern Bahia, many studies have been carried out, seeking to better understand the interactions between “cabruca” and fragments of the Atlantic Forest, as well as the fauna and flora that constitute them [10,68–76]. In this sense, knowledge about the reproductive system of a species that occurs widely in “cabruca” is, above all, extremely applicable in understanding the genetic diversity present in this agroforestry system. This information allows strategies to conserve and maintain the variability of this species in the region. Consequently, the species grown in “cabruca” can become viable models for conservation.

5. Conclusions and Conservation Implications

This study highlights the importance of understanding the reproductive patterns of *Lecythis Pisonis* in agroforestry systems for its conservation and sustainable management. The results underscore the role of pollen flow and outcrossing, facilitated by pollinators like *Xylocopa frontalis*, in maintaining genetic diversity. As forests are increasingly converted to agricultural land, agroforestry systems like “cabruca” present a feasible strategy for the preservation of biodiversity while supporting economic activities. Farmers’ active participation and the integration of landscape management practices that promote habitat connectivity and species diversity are required for effective conservation. This research provides critical insights for developing conservation strategies that ensure the long-term viability of *L. pisonis* and other species in agroforestry systems.

Author Contributions: The study conception and design were performed by A.B.R., C.T.F., E.M.N. and F.A.G. Data collection was performed by A.B.R. and C.T.F. Material preparation and analyses were performed by A.B.R. Data analysis and writing—original draft was conducted by Z.W. Review and editing were performed by F.A.G. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the Rufford Foundation Grant (37431-1), the National Council of Scientific and Technological Development (CNPq) (#160160/2020-0) and the University of Santa Cruz (#00220.1100.1923). CNPq also supports the productivity fellowship for Fernanda Amato Gaiotto (#312065/2021-3).

Data Availability Statement: The data used in this study are publicly available and can be directly accessed from <https://doi.org/10.5061/dryad.0cfxpnwcp>. (accessed on 22 February 2025).

Acknowledgments: We are grateful to the postgraduate program in ecology and biodiversity conservation at the State University of Santa Cruz—UESC for providing the opportunity that substantially contributed to the development of this manuscript. We acknowledge the Conservation Genetics Group from UESC (gaiotto2.wixsite.com) for its insights and support.

Conflicts of Interest: The authors declare no conflicts of interest.

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