UNIVERSIDADE ESTADUAL PAULISTA "JÚLIO DE MESQUITA FILHO"
FACULDADE DE ENGENHARIA
CAMPUS DE ILHA SOLTEIRA

FRANCINE BEATRIZ DE SOUZA

Historic pollen and seed dispersal in fragmented populations of *Cariniana estrellensis* (Raddi) Kuntze and *Cariniana legalis* (Mart.) Kuntze

Ilha Solteira
2018

FRANCINE BEATRIZ DE SOUZA

Historic pollen and seed dispersal in fragmented populations of *Cariniana estrellensis* (Raddi) Kuntze and *Cariniana legalis* (Mart.) Kuntze

Tese apresentada à Faculdade de Engenharia do Campus de Ilha Solteira – UNESP como parte dos requisitos para obtenção do título de Doutor em Agronomia. Especialidade: Sistema de Produção.

Prof. Dr. Alexandre Magno Sebbenn
Orientador

Ilha Solteira
2018

FICHA CATALOGRÁFICA
Desenvolvido pelo Serviço Técnico de Biblioteca e Documentação

S729h

Souza, Francine Beatriz de.
Historic pollen and seed dispersal in fragmented populations of cariniana estrellensis (raddi) kuntze and cariniana legalis (mart.) kuntze / Francine Beatriz de Souza. -- Ilha Solteira: [s.n.], 2018
83 f. : il.

Tese (doutorado) - Universidade Estadual Paulista. Faculdade de Engenharia. Área de conhecimento: Sistemas de Produção, 2018

Orientador: Alexandre Magno Sebbenn
Inclui bibliografia

1. Effective population size. 2. Historical gene flow. 3. In situ genetic conservation. 4. Microsatellite loci. 5. Parentage analysis. 6. Tropical tree species.

Sandra Maria Clemente de Souza
DSTBO/STRAUD
Bibliotecária
CRB 8-4740

UNIVERSIDADE ESTADUAL PAULISTA

Câmpus de Ilha Solteira

CERTIFICADO DE APROVAÇÃO

TÍTULO DA TESE: Dispersão histórica de pólen e sementes em populações fragmentadas de Cariniana estrellensis (Raddi) Kuntze e Cariniana legalis (Martl) Kuntze

AUTORA: FRANCINE BEATRIZ DE SOUZA
ORIENTADOR: ALEXANDRE MAGNO SEBBENN

Aprovada como parte das exigências para obtenção do Título de Doutora em AGRONOMIA, especialidade: SISTEMAS DE PRODUÇÃO pela Comissão Examinadora:

Prof. Dr. ALEXANDRE MAGNO SEBBENN
Secretaria do Meio Ambiente do Estado de São Paulo / Instituto Florestal de São Paulo - IFSP

Prof. Dr. MARIO LUIZ TEIXEIRA DE MORAES
Departamento de Fitotecnia, Tecnologia de Alimentos e Sócio Economia / Faculdade de Engenharia de Ilha Solteira - SP

Prof. Dr. MARCO EUSTAQUIO DE SÁ
Departamento de Fitotecnia, Tecnologia de Alimentos e Sócio Economia / Faculdade de Engenharia de Ilha Solteira

Prof. Dr. CELSO LUIS MARINO
Departamento de Genética / Instituto de Biociências de Botucatu - UNESP

Prof. Dr. EDJAIR AUGUSTO DAL BEM
Engenharia Florestal / Faculdade de Ciências Sociais e Agrárias de Itapeva

Ilha Solteira, 09 de fevereiro de 2018

DEDICO

Aos meus Pais Edson Wanderley de Souza e Vânia Aparecida Rodrigues Souza, e

Ao meu Irmão Fábio Henrique de Souza,

que sempre me fizeram acreditar na realização dos meus sonhos e trabalharam muito para que eu pudesse realizá-los, pelo amor, apoio, confiança e motivação incondicional. Que sempre me impulsiona em direção às vitórias dos meus desafios.

AGRADECIMENTOS

À DEUS, por sempre me conceder sabedoria nas escolhas dos melhores caminhos, coragem para acreditar, força para não desistir e proteção para me amparar.

Ao Prof. Dr. Alexandre Magno Sebbenn pela orientação, dedicação, amizade, incentivo e ensinamentos fundamentais para a conclusão deste trabalho, uma pessoa ímpar, onde busco inspirações para me tornar melhor em tudo faço.

À toda minha família Souza's e Rodrigue's, por serem parte responsável da pessoa que sou hoje, pelo Amor, carinho, compreensão e pela ajuda sempre.

Ao Otávio André Brogin Perez, pelo Amor, companheirismo, por todo seu apoio, incentivo, ajuda e compreensão na realização deste projeto de vida. Desde os melhores momentos até os piores sempre ao meu lado, obrigada por existir em minha vida.

Ao Prof. Dr. Mário Luiz Teixeira de Moraes, pela ajuda, ensinamentos, orientações, incentivo e contribuições. Por me receber em seu laboratório de portas abertas e sempre estar à disposição, respondendo minhas dúvidas e me incentivando sempre, se tornando parte essencial deste trabalho.

À pesquisadora da EMBRAPA/Floresta Ananda Virginia de Aguiar pela amizade, ensinamentos, ajuda e conselhos.

Aos professores do curso de Pós Graduação que contribuíram para minha formação acadêmica e profissional.

À Selma Maria Bozzetti de Moraes, pelos ensinamentos de laboratório e amizade.

Aos colegas do Laboratório de Genética de Populações I e II, pela amizade e ajuda nos trabalhos realizados.

A todos meus amigos que me ajudaram e me incentivaram durante o Doutorado.

À Faculdade de Engenharia de Ilha Solteira FEIS/ UNESP por tornar possível o desenvolvimento desse trabalho.

Aos funcionários da Fazenda de Ensino, Pesquisa e Extensão da Faculdade de Engenharia de Ilha Solteira/UNESP, em especial ao José Cambuim.

À CAPES pelo apoio, incentivo e suporte financeiro, que foi de fundamental importância para o desenvolvimento deste trabalho.

À todos que contribuíram direta ou indiretamente em mais esta etapa da minha vida, meus sinceros agradecimentos.

“Que os vossos esforços desafiem as impossibilidades, lembrai-vos de que as grandes coisas do homem foram conquistadas do que parecia impossível.”
Charles Chaplin

RESUMO

Cariniana estrellensis e *Cariniana legalis* são uma das maiores árvores dos biomas florestais da Amazônia e Mata Atlântica, sendo atualmente vulneráveis à extinção devido ao intenso desmatamento desses biomas. Estratégias para conservação *in situ* e *ex situ* são urgentes e estudos de diversidade genética e fluxo de genes são chaves e para esses propósitos. Assim, investigamos a diversidade genética, a estrutura genética espacial (SGS) e o fluxo histórico de genes em populações fragmentadas de ambas as espécies, utilizando marcadores de microssatélites. Todas as árvores encontradas nas populações foram mapeadas, medidas para o diâmetro na altura do peito (DAP) e amostrado o cambio de casca. O índice de fixação (F), em alguns casos, foi significativamente maior em árvores com menor DAP, indicando que as árvores menores apresentam um maior parentesco do que as maiores. Foi detectada SGS significativa para populações de ambas as espécies (60-350 m), indicando um padrão de dispersão de genes de isolamento pela distância (IBD). Para ambas as espécies, foi observada alta imigração de semente (38,5-61,5%) e pólen (80,1-100%), mostrando que as populações não são isoladas geneticamente. Não foi detectada autofecundação, mas o cruzamento entre árvores relacionadas foi detectado nas espécies (8,9-12,5%), sugerindo uma seleção mais forte contra árvores de autofecundação do que se originou do cruzamento entre árvores relacionadas. A distância de dispersão de pólen e sementes em *C. estrellensis* atingiu longa distância (> 3 km) do que em *C. legalis* (máximo de 385 m). No entanto, o pólen e as sementes em *C. estrellensis* e o pólen em *C. legalis* foram dispersos em um padrão de IBD. Os resultados sugerem que as populações estudadas são adequadas para conservação *in situ* e *ex situ*.

Palavras-chave: Conservação genética *in situ*. Espécies arbóreas tropicais. Fluxo gênico histórico. Marcadores microssatélites. Análise de parentesco. Tamanho efetivo populacional.

ABSTRACT

Cariniana estrellensis and *Cariniana legalis*, two of the largest trees in the Amazon and Atlantic Forest biomes, are currently vulnerable to extinction due to the intense deforestation of these biomes. Strategies for *in* and *ex situ* conservation are urgent, and studies of genetic diversity and gene flow are key aspects needed to develop these strategeis. Thus, we investigate the genetic diversity, spatial genetic structure (SGS), and historical gene flow in fragmented populations of both species, using microsatellite markers. All trees found in the study populations were mapped, measured for diameter at breast height (DBH), and sampled for bark cambium. Our results show that in some cases, fixation index (F) was significantly higher in trees with lower DBH, indicating that smaller trees have higher levels of inbreeding than larger ones. Significant SGS was detected in populations of both species (60-350 m), indicating a gene dispersal pattern of isolation by distance (IBD). For both species, we found high seed (38.5-61.5%) and pollen (80.1-100%) immigration demonstrating that populations are not genetically isolated. No self-fertilization was detected, but we did find evidence of mating among related trees (8.9-12.5%), suggesting stronger selection against selfed individuals than those originated from mating among relatives. Pollen and seed dispersal distance for *C. estrellensis* reached longer distances (> 3 km) than for *C. legalis* (maximum of 385 m). However, pollen and seeds of *C. estrellensis* and pollen of *C. legalis* were dispersed in an IBD pattern. The results suggest that the studied populations are suitable for *in* and *ex situ* conservation.

Keywords: Effective population size. Historical gene flow. *In situ* genetic conservation. Microsatellite loci. Parentage analysis. Tropical tree species.

LISTA DE FIGURAS

LISTA DE TABELAS

SUMÁRIO

1 INTRODUCTION

Over the last several centuries, human intervention in forests has caused fragmentation which has led to the degradation of a variety of forest functions, such as productivity and plant pollination, while also reducing plant species richness (HADDAD et al., 2015). The intense exploitation of natural ecosystems for the extraction of forest resources, along with land conversion for agricultural and livestock production and urbanization, causes environmental imbalances that result in irreversible consequences, such as changes in the environment and the extinction of animal and plant species (KASHIMSHETTY; PELIKAN; ROGSTAD, 2015). The isolation of tree species populations in small fragments reduces the number of reproductive individuals and population density, affecting genetic processes such as genetic drift, gene flow, selection, and mating systems (YOUNG; BOYLE 2000), while also isolating reproductive populations and increasing spatial genetic structure within populations (CARVALHO et al., 2010).

Deforestation and a lack of forest conservation strategies leads to fragmentation, and without adequate intervention, can result in the disappearance of forests over time (KASHIMSHETTY; PELIKAN; ROGSTAD, 2015). Loss of alleles is inevitable in exploited forests, leading to changes in allele frequencies that can be detected in the mating systems of species due to the spatial distance between trees, affecting the outcrossing rate and paternity correlation. There is also an expected increase in the rate of self-fertilization and crosses between relatives resulting in changes to the effective size of populations.

Cariniana estrellensis (Raddi) Kuntze (Lecythidaceae), also known as jequitibá-branco, is one of the tallest tree species in Brazil (LISBOA et al., 2016). The species can reach between 35 to 45 m in height and 120 cm in diameter at breast height or DBH (LORENZI, 2002; CARVALHO, 2003). The species is considered a rare or low population density species within its region of occurrence (GUIDUGLI et al., 2011), and its wood can be used for a variety of purposes. Jequitibá Rosa, *Cariniana legalis* (Mart.) Kuntze (Lecythidaceae), in turn, can reach 60 m in height and 4 m in DBH (TAMBARUSSI et al., 2015). Because it has been widely exploited for use in the furniture industry (CARVALHO, 1994, TAMBARUSSI, et al., 2013), it is currently on the list of endangered species.

Information about gene flow through pollen and seeds is a key factor in understanding the evolutionary potential of tree species, providing support for conservation and management practices. Estimates of historical gene flow is an indirect method in which levels of gene flow

are estimated based on the distribution of genetic diversity among populations (HAMRICK; NASON, 1996). Pollen flow is considered to be one of the main aspects influencing the genetic structure of tree species. Broad gene flow through pollen generates high rates of genetic variation within populations and limited differentiation between populations, as it is the main mechanism that maintains the genetic cohesion of a species (DICK; ETCHELECU; AUSTERLITZ, 2003). Similarly, because seed flow accounts for more than half the size of the genetic neighborhood, understanding the extent of seed flow is of paramount importance in establishing the reproductive dimensions of tropical tree species populations (HAMILTON, 1999).

Genetic conservation combined with sustainable management of forests allows for the preservation of biodiversity, thus maintaining the genetic diversity of species and ensuring their suitability for reproduction. To achieve this ideal, it is essential to study the behavior of individuals in natural populations using methodologies based on parentage analysis through molecular markers, such as genetic diversity, pollination distance, spatial genetic structure, and other factors that may contribute to development (TAMBARUSSI et al., 2015). This information is crucial for the development of effective management and conservation programs.

1.1 OBJECTIVES

The aim of this study was to use microsatellite loci to investigate the genetic diversity, inbreeding, effective population size, intrapopulation spatial genetic structure (SGS), and historic pollen and seed dispersal distance in small, fragmented populations of *C. estrellensis* and *C. legalis*. We specifically addressed the following questions:

1) Is genetic diversity and inbreeding lower in trees with smaller diameter at breast height (DBH) than with larger DBH?

2) Is the effective population size sufficient for *in situ* conservation over the short and long term?

3) What is the rate of historic pollen and seed immigration and the distance and patterns within populations?

4) What is the historic effective neighborhood size within the populations?

2 LITERATURE REVIEW

2.1 FOREST FRAGMENTATION

The consequences of anthropogenic activities on forest areas are of concern to the scientific community, as well as to society in general. Forest fragmentation and the selective harvesting of trees alters the demography and size of reproductive tropical tree species populations and, consequently, their mating system and pollen and seed dispersal patterns (SEBBENN, 2006; DEGEN, SEBBENN, 2014). This may increase the rate of self-fertilization, correlated matings (YOUNG; BOYLE, 2000; DEGEN; SEBBENN, 2014), intrapopulation spatial genetic structure (SGS), and kinship within populations (CARVALHO et al., 2010). In addition, it leads to reproductive isolation of the remaining populations after fragmentation (FUCHS; LOBO; QUESADA, 2003; SEBBENN et al., 2011), resulting in mosaics of small fragments and isolated individuals across the landscape. This process reduces the efficiency of pollinators and dispersers especially for tropical forest tree species (RAMOS; LEMOS-FILHO; LOVATO, 2009). Several studies on tropical arboreal species in populations located in fragmented areas report a reduction in the rate of pollen migration (e.g., FUCHS; LOBO; QUESADA, 2003; BITTENCOURT; SEBBENN, 2007; COLLEVATTI et al., 2010; LLORENS et al., 2012; ROSAS et al., 2011; SEBBENN et al., 2011; MANOEL et al. 2012a; DEGEN; SEBBENN, 2014; TAMBARUSSI et al., 2015; SPOLADORE et al., 2017) and seed migration (eg, BITTENCOURT; SEBBENN, 2007; GAINO et al., 2010; SEBBENN et al., 2011). This can result in genetic drift, which increases relatedness and inbreeding within populations (COLLEVATTI et al., 2010; SEBBENN et al., 2011) and reduces the amount of fruit produced in comparison with non-fragmented environments (AIZEN; FEINSIGER, 1994). In the presence of appropriate pollinators, isolated plants tend to show an increase in pollen dispersal distance, but this increase is associated with the dominance of a few effective pollen donors, generating correlated mating and leading to an increase in kinship among the produced seeds (HANSON et al., 2008). A reduction in population size may also lead to random loss of rare alleles, and if isolation persists alleles may remain fixed within each fragment due to genetic drift (FUCHS; HAMRICK, 2011).

With forest fragmentation, there is an increase in the fixed genetic load within populations (WILLI; VAN BUSKIRK; FISHER, 2005) and small and isolated populations often show reduced fitness (SPIELMAN; BROOK; FRANKHAM, 2004; REED, 2005).

Genetic problems, coupled with a disruption of plant–pollinator interactions and demographic and environmental stochasticity, increase the risk of extinction for small, isolated populations (NEWMAN; PILSON, 1997; SACCHERI et al., 1998). For a given population, genetic issues can be severe as there is a tendency towards continuous accumulation of genetic load and inbreeding, leading to mutational fusion over time (LYNCH; GABRIEL, 1990). Plant populations in fragmented environments tend to exhibit an increase in rates of self-fertilization and correlated mating, which causes an increase in inbreeding and genetic divergence (HANSON et al., 2008). Inbreeding also reduces species heterozygosity and adaptability, thus increasing the likelihood of extinction (MATTHIES et al., 2004).

One strategy used to connect and increase the size of small populations has been the introduction of individuals from neighboring populations, which can neutralize genetic deterioration and make populations viable (ANDREWARTHA; BIRCH, 1954; HANSKI, 1999). Therefore, many populations may be viable as metapopulations, which consist of populations structured as interconnected demes, considering extinction and recolonization events (HANSKI, 1999). Studying the species *Silene latifolia* Poir, Richards, Emery, and McCauley (2003) considered several parameters, such as population size, within population genetic diversity (number of alleles and expected heterozygosity), and genetic differentiation among populations measured by Fst-statistics. They observed that some populations overcame inbreeding depression through gene flow across a group of small populations. In a study of the tree *Magnolia stellata*, which is threatened with extinction, Setsuko et al. (2007) used cpSSR and nSSR (nuclear DNA microsatellite markers) and found that gene flow via pollen and seeds was accompanied by a reduction in the differentiation between populations. They concluded that the maintenance of the entire population, preserving the metapopulation structure and gene flow among subpopulations, is important for the conservation of the species. Considering the current state of forest fragmentation in Brazil, this theme is highly relevant for several tree species, particularly large trees that occupy the upper canopy and are responsible for the formation of the forest structure. It is also relevant for species with low population density that produce economically valuable seeds consumed by animals and humans, such as *Araucaria angustifolia* Bert. O. Ktze, *Cariniana estrellensis* (Raddi) Kuntze, and *Cariniana legalis* Mart. O. Ktze, among many others.

2.2 GENE FLOW

Gene flow can be defined as the movement of genes within a population and from one population to another (SLATKIN, 1987). Gene flow is responsible for the spatial homogenization of genetic diversity within and between populations which counteracts the effects of natural selection, mutation, and genetic drift that lead to differentiation within and among populations (HAMRICK; MURAWSKI; NASON, 1993).

Estimates of pollen and seed flow are necessary to predict the effects of forest fragmentation on the genetic structure of arboreal species (AGUILAR et al., 2008). These estimates are also used to define the number of seed trees required for seed collection for *ex situ* conservation and reforestation for environmental restoration, as well as define the minimum distance required between fragmented populations (SEBBENN, 2006).

In general, studies of gene flow based on genetic markers can be classified as historial or realized (occurring either in the past or present), or effective, which occurs in the present (BURCZYK et al., 2004). The estimates of gene flow for trees can be obtained directly or indirectly. Historical gene flow can be investigated using: i) an indirect method based on the distribution of genetic diversity among populations (HAMRICK; NASSON, 1996); ii) an indirect method based on the model of equilibrium between gene immigration and genetic drift (VEKEMANS; HARDY, 2004); or iii) a direct method based on parentage analysis of established individuals (regenerants) in populations assessed through the sampling of seedlings or juveniles (MEAGUER; THOMPSON, 1987). Effective gene flow can be investigated using: i) an indirect method based on pollen dispersal models (AUSTERLITZ et al., 2001); and ii) a direct method based on parentage analysis of open-pollinated seeds (MEAGUER, 1986). Indirect methods use spatial genetic autocorrelation analysis and refer to the historical or realized gene flow (VEKEMANS; HARDY, 2004). Direct estimates of gene flow based on parentage analysis requires samples of regenerants (realized) and/or open-pollinated seeds from known mothers (effective) and all reproductive plants in the population, i.e., all possible parents of the regenerants and seeds. Parentage analysis is not based on the assumptions of dispersion models; thus, the observed patterns may represent the true patterns if the polymorphism of the loci used is sufficient to discriminate among parental candidates (paternity exclusion). Based on the dispersion of pollen obtained through paternity analysis, it is possible to determine the effective number of pollen donors that fertilize seeds from parent trees (SMOUSE; SORK, 2004; WANG et al., 2010; FUCHS; HAMRICK, 2011), which

enables estimates of the effective size of progeny arrays (GAINO et al., 2010; MORARES; SEBBENN, 2011). However, the difference between historical vs. realized pollen dispersal (i.e., fertilization vs. the establishment of seedlings and growth into juveniles) is substantial and many stochastic and deterministic processes may occur during this period (BURCZYK; DIFAZIO; ADAMS, 2004), including random mortality, predation, dispersal of seeds at a distance, and selection. The realized pollen and seed dispersal distances can be measured by sampling established seedlings and juvenile individuals (BURCZYK; LEWANDOWSKI; CHALUPKA, 2004).

Pollen dispersal distances vary according to the dispersal vector and is influenced by population density, reproductive neighborhood, mechanisms that impede self-fertilization, and abiotic factors (i.e., humidity, wind direction, etc.). For insect pollinated tree species, pollen dispersal has been detected at distances ranging from 5 to 10,800 m, with a mean of 489.4 m (Table 1). For bat pollinated trees, distances have been detected from 48 to 5,229 m, with a mean of 801.1 m (Table 2). For bee pollinated trees, distances range from 61 to 1,509 m, with a mean of 431.2 m (Table 3), while for bird pollinated trees, distances range from 8 to 963 m, with a mean of 173.2 m (Table 4). Finally, for wind pollinated trees the pollen dispersal distance ranges from 3 to 9,460 m, with a mean of 974 m (Table 5).

Similarly, for seed dispersal, the distance depends on several factors. Species for which seeds are dispersed by animals, the distance ranges from 3 to 6000 m with a mean of 917 m; for wind dispersion, the distance ranges from 8 to 140 m with a mean of 50.6 m. In some species, seed dispersal can occur by gravity, ranging from 9 to 175 m, with an average of 84 m (Table 6).

Table 1- Mean pollen dispersal distance for insect pollinated tree species.

Species	**Mean (m)**	**Reference**
Acacia saligna	381–997	Millar et al. (2012)
Acacia saligna subsp. *saligna*	37	Millar et al. (2008)
Acacia lindleyi	288–1,202	Millar et al. (2012)
Acrocomia aculeata	105	Araújo et al. (2017)
Aesculus turbinata	189–289	Isagi et al. (2007)
Astrocaryum aculeatum	81	Ramos et al. (2016)
Aucoumea klaineana	128	Born et al. (2008b)
Baillonella toxisperma	9,800 – 10,800	Ndiade-Bourobou et al. (2010)
Baillonella toxisperma	690	Duminil et al. (2016a)
Cabralea canjerana	65–206	Melo; Franceschinelli (2016)
Carapa guianensis	175–195	Martins et al. (2012)
Carapa guianensis	75–268	Cloutier et al. (2007)
Castanea crenata	3–243	Hasegawa; Suyama; Seiwa (2009)
Castanopsis sieboldii	35	Nakanishi et al. (2012)
Castanopsis sieboldii	44	Nakanishi et al. (2015)
Centaurea corymbosa	21	Hardy et al. (2004)
Dysoxylum malabaricum	600–6,525	Ismail et al. (2012)
Entandrophragma cylindrum	266–385	Lourmas et al. (2007)
Erythrophleum suaveolens	195–1,001	Duminil et al. (2016b)
E. aggregata and *E. rubida*	22–64	Field et al. (2011)
Eucalyptus caesia	39	Bezemer et al. (2016)
Eucalyptus camaldulensis	94	Gonzaga et al. (2016)
Eucalyptus globulus	69–149	Mimura et al. (2009)
Eucalyptus grandis	58	Jones et al. (2008)
Eucalyptus incrassata	870–1,134	Breed et al. (2015)
Eucalyptus wandoo	30–49	Byrne et al. (2008)
Eugenia dysenterica	80	Rodrigues et al. (2016)
Ficus cyrtophylla	1,095–1,115	Zhou; Chen (2010)
Ficus insipida	3,000	Heer et al. (2015)
Ficus pumila	989–1,712	Wang et al. (2009)
Gomortega keule	709	Lander; Boshier; Harris (2010)
Himatanthus drasticus	65	Baldauf et al. (2014)
Kandelia candel	15	Geng et al. (2008)
Magnolia obovata	131	Isagi et al. (2000)
Magnolia stellata	19–25	Setsuko et al. (2007)
Magnolia stellata	602	Setsuko; Nagamitsu; Tomaru (2013)
Malus sylvestris	60	Larsen; Kjær (2009)
Manilkara huberi	47	Azevedo et al. (2007)
Oenocarpus bataua	303	Ottewell et al. (2012)
Parashorea tomentella	177–416	Kettle et al. (2011b)

Table 1- Mean pollen dispersal distance for insect pollinated tree species. (continued)

Species	**Mean (m)**	**Reference**
Pithecellobium elegans	142	Chase et al. (1996)
Prosopis alba	5–24	Bessega et al. (2012)
Prosopis flexuosa	5–20	Bessega et al. (2017)
Prunus africana	18–2,350	Yineger et al. (2015)
Prunus avium	45–162	Konnert et al. (2011)
Prunus avium	42–134	Jolivet et al. (2012)
Prunus mahaleb	100	Garcia et al. (2005)
Prunus lannesiana var. *speciosa*	12–15	Shuri et al. (2012)
Sinojackia rehderiana	24	Yao et al. (2011)
Sinojackia xylocarpa and *S. rehderiana*	185	Zhang et al. (2010)
Shorea curtisii	65–81	Tani et al. (2012)
Shorea lumutensis	122–220	Lee et al. (2006)
Shorea maxwelliana	662–817	Masuda et al. (2013)
Shorea xanthophylla	56–119	Kettle et al. (2011b)
Sorbus domestica	1,200	Kamm et al. (2009)
Sorbus torminalis	59–148	Hoebee et al. (2007)
Sorbus torminalis	267–1,077	Oddou-Muratorio; Klein; Austerlitz (2005)
Sorbus torminalis	248	Oddou-Muratorio; Klein, (2008)
Sorbus torminalis	738	Klein; Desassis; Oddou-Muratorio (2008)
Swartzia glazioviana	60–516	Spoladore et al. (2017)
Theobroma cacao	28	Silva et al. (2011a)
Theobroma cacao	826–922	Schawe et al. (2013)
Vateria indica	139–158	Ismail et al. (2014)
Mean	489.4	

Table 2- Mean pollen dispersal distance for bat pollinated tree species.

Species	**Mean (m)**	**Reference**
Caryoca brasiliensir	132	Collevattii et al. (2010)
Ceiba aesculifolia	166-316	Quesada et al. (2013)
Hymenaea courbaril	952	Carneiro et al. (2011)
Hymenaea courbaril	827	Lacerda; Kanashiro; Sebbenn (2008b)
Hymenaea stigonocarpa	860-5,229	Moraes; Sebbenn (2011)
Pachira quinata	48-438	Rymer et al. (2015)
Mean	801.1	

Table 3- Mean pollen dispersal distance for bee pollinated tree species.

Species	**Mean (m)**	**Reference**
Cariniana legalis	63–352	Tambarussi et al. (2015)
Copaifera langsdorffi	94	Sebbenn et al. (2011)
Copaifera langsdorffi	74	Tarazi et al. (2013a)
Copaifera langsdorffi	118	Carvalho et al. (2010)
Copaifera langsdorffi	63	Manoel et al. (2012a)
Dicorynia guianensis	142	Latouche-Hallé et al. (2004)
Dinizia excelsa	417–1,288	Dick (2001)
Dinizia excelsa	212–1,509	Dick; Etchelecu; Austerlitz (2003)
Dipterocarpus tempehes	192–222	Kenta et al. (2004)
Dipterys odorata	688–1,092	Vinson et al. (2015b)
Dipteryx panamensis	240–557	Hanson et al. (2008)
Eurycorymbus cavaleriei	85–164	Wang et al. (2010)
Eurycorymbus cavaleriei	1,118–1,308	Wang; Kang; Huang (2014)
Eurycorymbus cavaleriei	293	Wang et al. (2008)
Guaiacum santum	1,276	Fuchs; Hamrick (2011)
Guibourtia chodatiana	61–91	Ojeda-Camacho; Kjær; Philipp (2013)
Jacaranda copaia	401–538	Vinson et al. (2015b)
Miconia affinis	101–804	Jha; Dick (2010)
Myracrodruon urundeuva	138–252	Gaino et al. (2010)
Neabalanocarpus heimii	188–195	Konuma et al. (2000)
Simarouba amara	334	Hardesty; Hubbell; Bermingham (2006)
Swietenia humilis	347–841	Rosas et al. (2011)
Swietenia macrophylla	75–255	Sebbenn et al. (2012)
Tabebuia aurea	308–396	Braga; Collevatti (2011)
Mean	431.2	

Table 4- Mean pollen dispersal distance for bird pollinated tree species.

Species	**Mean (m)**	**Reference**
Banksia hookeriana	30	Krauss et al. (2009)
Banksia menziesii	84	Frick; Ritchie; Krauss (2014)
Banksia sphaerocarpa var. *caesia*	8–84	Llorens et al. (2012)
Symphonia globulifera	154–963	Carneiro et al. (2009)
Symphonia globulifera	27–53	Degen; Bandou; Caron (2004)
Mean	173.2	

Table 5- Mean pollen dispersal distance for wind pollinated tree species.

Species	Mean (m)	Reference
Abies pinsapo	1487–1857	Sánchez-Robles et al. (2014)
Allocasuarina verticillata	70–200	Broadhurst (2015)
Araucaria angustifolia	344–2069	Bittencourt; Sebbenn (2007)
Araucaria angustifolia	105–298	Medina-Macedo et al. (2015a)
Araucaria angustifolia	343	Sant'Anna et al. (2013)
Austrocedrus chilensis	1032	Colabella et al. (2014)
Bagassa guianensis	308–844	Silva et al. (2008)
Bagassa guianensis	2501–2637	Arruda et al. (2015)
Betula spp.	1000	Siljamo et al. (2008)
Cercidiphyllum japonicum	666	Sato et al. (2006)
Fagus crenata	37	Hanaoka et al. (2007)
Fagus crenata	42–79	Oddou-Muratorio et al. (2010)
Fagus sylvatica	28–438	Wang (2004)
Fagus sylvatica	35–63	Gauzere; Klein; Oddou-Muratorio (2013)
Fagus sylvatica	62–162	Millerón et al. (2012)
Fagus sylvatica	133	Konnert et al. (2011)
Fagus sylvatica	24–184	Piotti et al. (2012)
Fraxinus excelsior	168	Beatty et al. (2015)
Fraxinus excelsior	206–285	Thomasset et al. (2014)
Fraxinus excelsior	2900	Bacles; Ennos (2008)
Juglans ailantifolia	233–392	Kimura et al. (2012)
Juglans cinérea	88	Hoban et al. (2012)
Juglans mandshurica	140	Bai et al. (2007)
Larix decidua	18	Pluess (2011)
Larix olgensis	95	Wei et al. (2015)
Nothofagus nervosa	11–312	Marchelli; Smouse; Gallo (2012)
Olea europaea	256,8	Beghe et al. (2017)
Phoenix canariensis	377,2	Saro et al. (2014)
Picea abies	9	Shimono et al. (2011)
Picea glauca	654–619	O'Connell; Mosseler; Rajora (2007)
Pinus attenuata	5	Burczyk; Adams; Shimizu (1996)
Pinus cembra	69–1266	Chybicki; Dzialuk (2014)
Pinus densiflora	10	Iwaizumi et al. (2010)
Pinus densiflora	325	Lian; Miwa; Hogetsu (2001)
Pinus fexilis	141–189	Schuster; Mitton (2000)
Pinus parviflora var. *parviflora*	371–1886	Iwasaki et al. (2013)
Pinus pinaster	78–174	de-Lucas et al. (2008)
Pinus sylvestris	17–29	Robledo-Arnuncio; Alía; Gil (2004)
Pinus sylvestris	37	Torimaru et al. (2012)
Pinus sylvestris	629	Robledo-Arnuncio; Gil (2005)
Pistacia lentiscus	229–412	Albaladejo et al. (2012)
Populus nigra	8198	Rathmacher et al. (2010)
Populus nigra	7652–9460	Niggemann et al. (2012)
Populus nigra x P. canadensis	10–230	Pospísková; Sálková (2006)
Populus trichocarpa	1249–7600	Slavov et al. (2009)

Table 5- Mean pollen dispersal distance for wind pollinated tree species. (continued)

Species	**Mean (m)**	**Reference**
Quercus castanea	5730–9160	Oyama et al. (2017)
Quercus frainetto	33–53	Curtu; Gailing; Finkeldey (2009)
Quercus lobata	65	Sork et al. (2002)
Quercus lobata	114	Pluess et al. (2009)
Quercus lobata	235-644	Sork et al. (2015)
Quercus macrocarpa	42	Craft; Ashley (2010)
Quercus macrocarpa	70-77	Dow; Ashley (1996)
Quercus macrocarpa	76	Dow; Ahley (1998)
Quercus oleoides	8	Deacon; Cavender-Bares (2015)
Quercus petraea	21-61	Curtu; Gailing; Finkeldey (2009)
Quercus petraea	24-49	Streiff et al. (1999)
Quercus petraea	69	Lagache et al. (2012)
Quercus petraea	92	Valbuena-Carabaña et al. (2005)
Quercus pubescens	37	Curtu et al. (2009)
Quercus pyrenaica	270	Valbuena-Carabaña et al. (2005)
Quercus robur	21–38	Streiff et al. (1999)
Quercus robur	13–48	Vranckx et al. (2014a)
Quercus robur	92	Curtu; Gailing; Finkeldey (2009)
Quercus robur	151	Lagache et al. (2012)
Quercus robur	8500	Moracho et al. (2016)
Quercus robur+Q.petraea	297–463	Chybicki; Burczyk (2010)
Quercus rubra, Q. velutina, Q. falcata	178.2	Moran; Clark (2011)
Quercus salicina	67	Nakanishi et al. (2004)
Quercus salicina	69	Nakanishi et al. (2009)
Quercus semiserrata	47–570	Pakkad; Ueno; Yoshimaru (2008)
Quercus sp	16–5371	Gerber et al. (2014)
Quercus velutina	24	Fernández-Manjarrés; Idol; Sork (2006)
Ulmus glabra	17–104	Nielsen; Kjær (2010)
Ulmus minor and *U. pumila*	2860–2930	Bertolasi et al. (2015)
Mean	794	

Table 6- Mean dispersal distance for animal, wind, and gravity seed dispersal vectors for tree species.

Species	**Mean (m)**	**Reference**
Animal		
Attalea phalerata	3	Choo; Juenger; Simpson (2012)
Baillonella toxisperma	4,000–6,000	Ndiade-Bourobou et al. (2010)
Fagus crenata	12	Oddou-Muratorio et al. (2010)
Fagus sylvatica	10	Oddou-Muratorio et al. (2010)
Ficus cyrtophylla	510–647	Zhou; Chen (2010)
Ficus pumila	< 989	Wang et al. (2009)
Prunus africana	80–2,159	Yineger et al. (2015)
Prunus avium	27–73	Konnert et al. (2011)
Prunus mahaleb	145	Garcia et al. (2007)
Sorbus torminalis	135	Oddou-Muratorio; Klein (2008)
Mean	917	
Wind		
Abies alba	34–42	Leonarduzzi et al. (2016)
Aucoumea klaineana	118	Born et al. (2008)
Banksia hookeriana	8	Krauss et al. (2009)
Cariniana estrellensis	120	Guidugli et al. (2016)
Fraxinus excelsior	14	Beatty et al. (2015)
Jacaranda copaia	40–59	Jones; Hubbell (2006)
Juglans cinerea	26	Hoban et al. (2012)
Myracrodruon urundeuva	124	Gaino et al. (2010)
Pinus taeda	50–140	Williams et al. (2006)
Quercus petraea	42	Valbuena-Carabaña et al. (2005)
Quercus pyrenaica	14	Valbuena-Carabaña et al. (2005)
Quercus robur	5–15	Vranckx et al. (2014a)
Quercus robur+Q.petraea (mixed)	9–16	Chybicki et al. (2010)
Quercus rubra, Q. velutina, Q. falcata	128	Moran; Clark (2011)
Quercus salicina	17	Nakanishi et al. (2009)
Mean	50.6	
Gravity		
Aesculus turbinata	25	Isagi et al. (2007)
Araucaria angustifolia	92	Bittencourt; Sebbenn (2007)
Araucaria angustifolia	131	Sant'Anna et al. (2013)
Carapa guianensis	114–175	Martins et al. (2012)
Castanopsis sieboldii	18	Nakanishi et al. (2015)
Copaifera langsdorffii	61	Sebbenn et al. (2011)
Copaifera langsdorffii	135	Tarazi et al. (2013b)
Sinojackia rehderiana	9	Yao et al. (2011)
Mean	84	

2.3 SPATIAL GENETIC STRUCTURE

Several evolutionary and ecological processes, such as seed dispersal, inter- and intraspecific competition, and environmental heterogeneity may affect the spatial distribution patterns of individuals within a population (LOVELESS; HAMRICK, 1984). Spatial aggregation of alleles in continuous populations is defined as spatial genetic structure or SGS (DERING; CHYBICKI; RACZKA, 2015). Restricted gene flow often results in intrapopulation SGS, which is as the non-random spatial distribution of genotypes within a population (VEKEMANS; HARDY, 2004). In addition, SGS may be the result of limited pollen and seed dispersal distance, local genetic drift, inbreeding, and selection, which may favor one or more genotypes (EPPERSON, 1992). As trees present long reproductive cycles, variations in intraspecific life histories of plants may arise due to phenotypic plasticity and shaped by environmental variation (KITTELSON; MARON, 2001), creating genetically different subpopulations as a result of spatial heterogeneity (JONES et al., 2005).

The identification of SGS within natural populations is important because it offers an understanding of the extent of gene dispersal within populations (ROUSSET, 2000; VEKEMANS; HARDY, 2004); therefore, it indirectly quantifies the dispersal distance of the species (ODDOU-MURATORIO et al., 2010) and provides insights into local reproduction and evolution (SMOUSE; PEAKALL, 1999). The knowledge and understanding of genetic diversity and micro-scale SGS are also important for the management of forest genetic resources, to evaluate the impacts of exploitation and fragmentation, and to establish sampling strategies in natural populations (SEBBENN, 2006). Forest fragmentation may increase SGS by disrupting gene flow and increasing local drift due to reduced population densities (YOUNG; MERRIAM, 1994). In contrast, changes in the landscape that improve the dispersal capacity of the species may reduce stochastic variables (YOUNG; MERRIAM, 1994). In the context of biological conservation, habitat fragmentation and disturbance may alter the SGS due to disruptions in the ecological processes that affect recruitment, such as competition with invasive plant species (EWERS; DIDHAM, 2006) and plant breeding (AGUILAR et al., 2006).

Since seeds and pollen are the two main agents of gene flow, the assessment of seed and pollen dispersal distances are essential to understanding SGS (HEUERTZ et al., 2003). Meanwhile, family structure is dependent on the dispersal of seeds and pollen. If the pollen is dispersed further than seeds, the SGS will be more influenced by maternal alleles and seed

dispersal than by pollen dispersal. However, if seeds are dispersed more widely than pollen, SGS will be more influenced by paternal alleles and pollen dispersal distances. If neither seeds nor pollen are widely dispersed, SGS will be influenced by both maternal and paternal alleles and determined by both seed and pollen dispersal distance (SEBBENN et al., 2011). For many temperate tree species that are wind pollinated, seed dispersal may have a much greater impact than pollen flow on SGS as seeds are not expected to travel as far as pollen (HEUERTZ et al., 2003; SATO et al., 2006). In the tropics, more than 90% of tree species depend on frugivorous animals to disperse their seeds (HOWE; SMALLWOOD, 1982).

Results obtained from analyses of SGS and contemporary gene flow have been used to identify gene flow patterns and support strategies for *in situ* and *ex situ* tree species conservation (RATHMACHER et al., 2010; GAINO et al., 2010; SANT'ANNA et al., 2013).

2.4 MICROSATELLITE MOLECULAR MARKERS (SSR)

The *in situ* and *ex situ* conservation of tree species depends directly on the knowledge obtained through ecological and genetic studies of populations, which are currently based on analyses of nuclear microsatellite markers. Microsatellite markers, also known as Simple Sequence Repeats (SSR), are an effective tool widely used in genetic studies of plant populations for a number of reasons: they are abundant and uniformly distributed throughout the genome; they have high polymorphism in terms of number of alleles within loci; they are reproducible and require small amounts of DNA; they have codominant inheritance, which allows the distinction between homozygous and heterozygous genotypes; and they present multi-allelism (BRONDANI et al., 2005).

Microsatellite markers are also useful for genetic mapping (GUPTA; VARSHNEY, 2000; BRONDANI et al., 2005), quantifying the genetic diversity and structure, inbreeding, kinship, intrapopulational spatial genetic structure, mating system, pollen and seed dispersal patterns (BRONDANI et al., 2005; ASHLEY, 2010; COLLEVATTI et al., 2010; MORAES; SEBBENN, 2011; MANOEL et al., 2012b; ELLSTRAND, 2014; TAMBARUSSI et al., 2015), assessing the origins of commercialized timber (DEGEN et al., 2007), and determining effective population size (SEBBENN, 2006; MORAES; SEBBENN, 2011). These markers are also valuable for phylogenetic studies between species (DEMESURE; COMPS; PETIT, 1996; COLLEVATTI et al., 2009, 2012) to determine the genetic proximity of individuals of different species, subspecies, and varieties of the same genus. This type of analysis is possible

because the DNA sequences flanking the microsatellite loci are generally conserved within the same species or between species of related genera (OLIVEIRA et al., 2006).

2.5 STUDIED SPECIES

2.5.1 *Cariniana estrellensis*

Cariniana estrellensis (Raddi) Kuntze (Lecythidaceae), or jequitibá-branco is an emerging Neotropical tree that prefers moist and deep soils (CARVALHO, 2003). The species occurs in Brazil from southern Bahia to Rio Grande do Sul and Acre, in the riparian forests of Central Brazil (CASTRO, 2011), Bolivia, Paraguay, and Peru (LEITE, 2007). In Brazil, *C. estrellensis* is one of the longest-living species and one of the few remaining large trees of this genus, reaching up to 45 m in height and 120 cm in diameter at breast height (DBH) (LORENZI, 2002; CARVALHO, 2003). The species is threatened with extinction due to intense exploitation of the biomes in which they occur (LISBOA et al., 2016). Populations may present low density, depending on the region of occurrence (LORENZI, 2002; CARVALHO, 2003). The species is hermaphroditic and pollination is carried out by small insects, mainly bees of the genus *Melipona* and *Trigona*. Fruits can contain up to 17 seeds, and the seeds are unilaterally winged, pyriform shaped, and dispersed by anemochory (LEITE, 2007), but this dispersion can be facilitated by monkeys (*Alouatta caraya*) that consume the seeds during the dry seasons (MORI, 1999; CARVALHO, 2003). The wood is considered to be hard and resistant, from light to moderately heavy, and offers good dimensional stability after manufacture (RECORD; HESS, 1972; CHUDNOFF, 1984). The species is also used in landscaping and has medicinal properties.

2.5.2 *Carianiana legalis*

Cariniana legalis (Mart.) Kuntze, commonly known as jequitibá-rosa is a Neotropical, late successional tree of the Lecythidaceae family that is one of the largest trees found in the Atlantic Forest (REITZ, 1981; CARVALHO, 2003; LORENZI, 2002). Trees of this species can reach 60 m in height and 4 m in DBH. The species is native to Brazil and found naturally in the south (Paraná State), southeast (Espírito Santo, Rio de Janeiro, São Paulo and Minas Gerais), northeast (Alagoas, Bahia, Paraíba and Pernambuco), and in Mato Grosso State (REITZ, 1981; CARVALHO, 2003). Endemic to the Atlantic Forest, *C. legalis* occurs at a

low population density (CARVALHO, 2003), generally less than one tree per hectare (SEBBENN et al., 2000; LEAL et al., 2014; TAMBARUSSI et al., 2015). The species is monoecious with hermaphrodite flowers and pollinated by bees of the genus *Melipona* and *Trigona* (PRANCE; MORI, 1979). Reproduction occurs mainly by outcrossing (SEBBENN et al., 2000; LEAL et al., 2014; TAMBARUSSI et al., 2015, 2016). Fruiting begins in trees at approximately 20 years of age and each fruit can contain more than ten seeds that are dispersed by gravity and anemochory (CARVALHO, 2003). Its wood is light and used in construction, as well as in the manufacture of furniture and shoes (CARVALHO, 2003). It is also used in the pulp industry to produce good quality paper (LORENZI, 2002).

The natural habitat of *C. legalis* has been degraded extensively in the last few decades, and the species has been heavily exploited for its wood. There are few remaining natural populations, which has led to the species being classified as endangered. Thus, it is necessary to develop *in situ* and *ex situ* conservation strategies of the remaining populations (SEBBENN et al., 2000), which requires an understanding of the species' genetic diversity, inbreeding, spatial genetic structure, mating system, and gene flow (SEBBENN et al., 2000; TAMBARUSSI et al., 2015).

3 MATERIAL AND METHODS

3.1 STUDY SITES AND SAMPLING

Samples were collected from two *Cariniana estrellensis* populations located in Ibicatu, São Paulo State, and Bataguassu, Mato Grosso do Sul State, and two populations of *C. legalis* in Ibicatu and Mogi-Guaçu, São Paulo State, Brazil.

3.1.1 Ibicatu

The Ibicatu State Forest (22°46' S, 47°43' W, altitude 448 to 576 m asl) is a 72 ha, spatially isolated forest fragment located near Piracicaba, São Paulo State, Brazil. The forest fragment is a remnant of a semi-deciduous forest that is currently bounded by agriculture, including sugarcane, eucalyptus, and pasture for livestock (Figure 1). In the past, the stand was subjected to several episodes of selective logging (about 30 years ago). Ibicatu is isolated from other populations or individuas of the species by at least 4 km. The climate is characterized as humid and mesothermal (Cwa, Köeppen 1948) with the mean monthly temperature varying between 14.3° C and 24.7° C., a mean annual temperature of 23.9° C, mean minimum of 16.1° C, and a mean maximum of 25° C. Mean annual precipitation is approximately 1,320 mm, with a dry season from May to August, and 86% of the precipitation occurring during the rainy season (September to April). The soils are yellow regosol and red podzolic "intergrades".

All *C. estrellensis* and *C. legalis* trees in the site were sampled (bark cambium), mapped (GPS III-Garmin, USA), measured for diameter at breast height (DBH), estimated for age based on the annual mean DBH increment, and genotyped. From this study area, we sampled all 26 *C. estrellensis* adult trees (0.36 trees/ha) and 65 *C. legalis* adult trees (0.93 trees/ha). The DBH of *C. estrellensis* ranged from 13 to 248 cm (mean 68.5 cm) and the estimated age ranged from 21 to 400 years, with a mean 110 years. The DBH of *C. legalis* ranged from 25 to 325 cm (mean 121 cm) and the estimated age ranged from 24 to 570 years, with a mean 160 years (Table 7, Figures 2 and 3).

Table 7- Sample size (*n*), population density (trees/ha), mean, standard deviation (SD), minimum and maximum (Min/Max) DBH, and estimated age of trees that were assigned parents, assigned as putative parents by parentage analysis, and total sample of *C. estrellensis* and *C. legalis* in the Ibicatu (IB) (72 ha), Bataguassu (BA) (448.2 ha), and Mogi-Guaçu (MG) (7.2 ha) forest fragments. The mean annual DBH increment for *C. estrellensis* is 0.61 cm/year and for *C. legalis* is 0.79 cm/year (CARVALHO, 2003).

	Sample	*n*	Trees/ha	Mean (SD) DBH (cm)	Min/Max (cm)	Mean age (years) (SD)	Min/Max (years)
Cariniana estrellensis							
Ibicatu	Assigned trees	16	-	45.1 (17.3)	13/76	73 (28)	21/121
Ibicatu	Assigned parents	11	-	96.6 (58.1)	41/248	156 (94)	66/400
Ibicatu	Total	26	0.36	68.5 (47.1)	13/248	110.3 (76)	21/400
Bataguassu	Assigned trees	123	-	56.8 (10.9)	37.6/95.5	91 (19)	36/157
Bataguassu	Assigned parents	93	-	76.9 (17.6)	48.7/147.1	126 (34)	80/241
Bataguassu[1]	Total	284	0.63	65.6 (17.9)	21/147	108 (29)	36/241
Cariniana legalis							
Ibicatu	Assigned trees	24	-	86.6 (37.6)	19/146	110 (48)	24/185
Ibicatu	Assigned parents	20	-	153.8 (52.8)	97/306	195 (67)	123/387
Ibicatu[2]	Total	65	0.93	121 (68.9)	25/325	160 (88)	24/570
Mogi-Guaçu	Assigned trees	10	-	46.6 (16.0)	21/68	59 (20.1)	27/86
Mogi-Guaçu	Assigned parents	6	-	96 (19.9)	65/110	122 (25)	82/141
Mogi-Guaçu[2]	Total	26	3.6	68 (26.3)	21/144	83 (33)	27/144

[1]Kubota (2017); [2]Tambarussi et al. (2015); $P < 0.05$.
Source: Prepared by author.

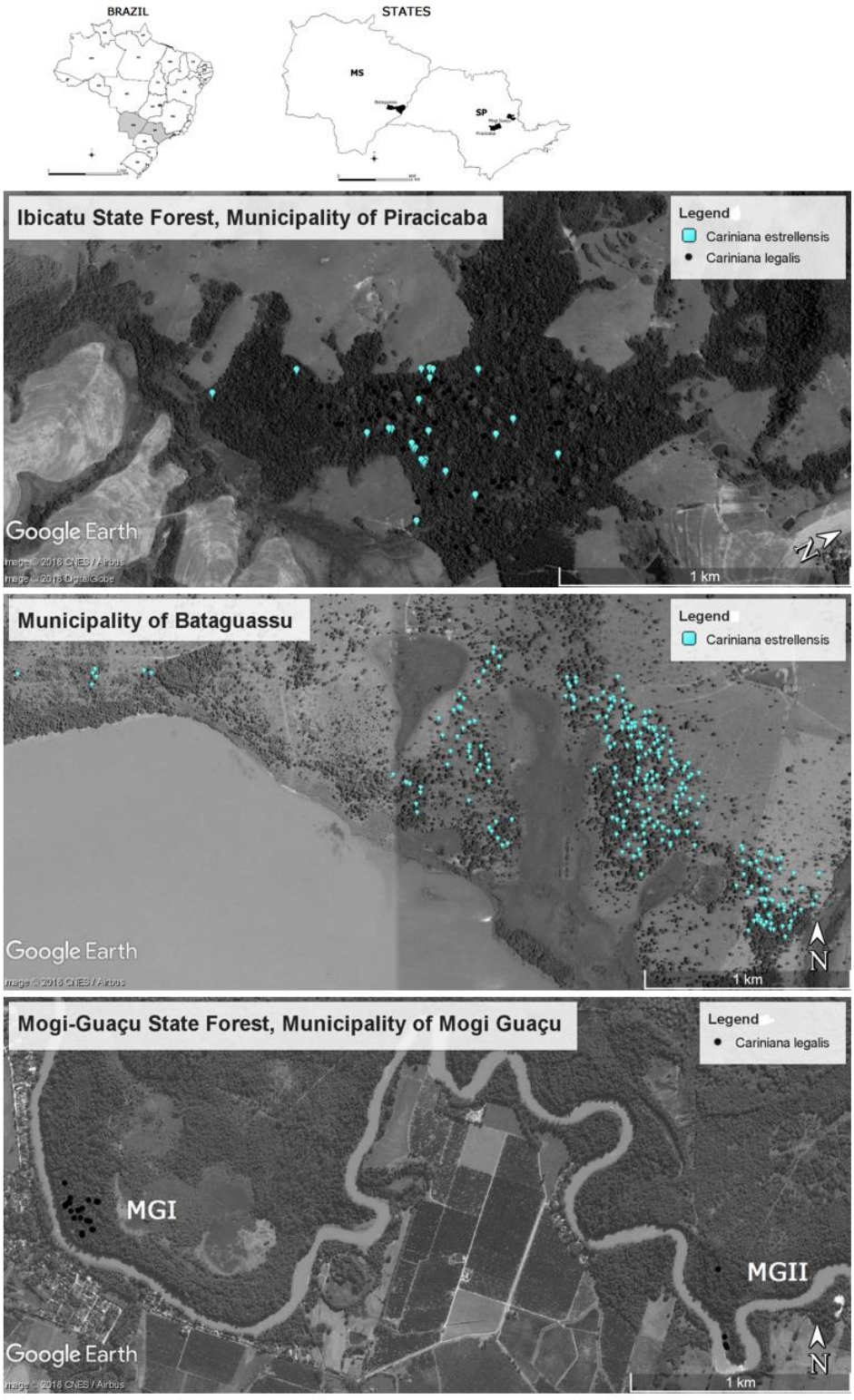
3.1.2 Bataguassu

The Bataguassu site covers 448.2 ha, consists of forest fragments and isolated trees (21° 38’00” S, 52° 14’02” W, 273.3 m asl), and is located in the city of Bataguassu, Mato Grosso do Sul State, Brazil, near the Pardo River (Figure 1). The region is characterized as a transition zone between the Savanna and Atlantic Forest biomes (IBGE, 2016) and is isolated, surrounded by monoculture crops (sugarcane and Eucalyptus) and pasture. The predominant soil in the region is dark red Oxisols of medium texture and low natural fertility. The climate is tropical humid with rainy summers and dry winters, an average temperature of 23.1°C, and annual rainfall ranging from 1,200 to 1,500 mm (INSTITUTO BRASILEIRO DE GEOGRAFIA E ESTATÍSTICA- IBGE, 2016). All 284 *C. estrellensis* trees (0.63 trees/ha) found in the landscape were georeferenced (GPS-Garmin), measured for DBH, sampled (foliar or cambial tissue), estimated for age based on the annual mean DBH increment, and genotyped (Table 7, Figure 2). The DBH of *C. estrellensis* ranged from 21 to 147 cm (mean 65.6 cm) and the estimated age ranged from 36 to 241 years (mean of 108 years).

3.1.3 Mogi-Guaçu

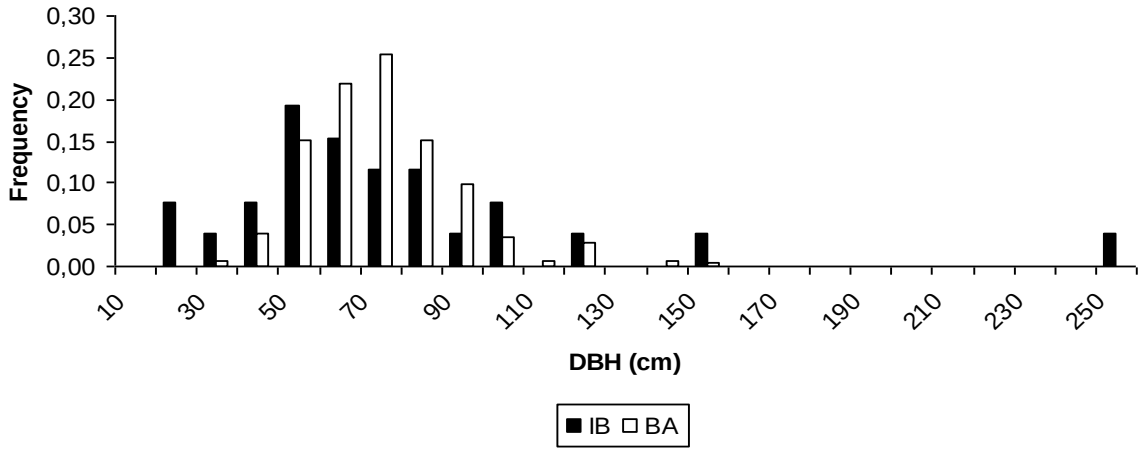
The Mata da Figueira (MGI) is a small, 7.2 ha, riparian forest fragment in the semi-deciduous plateau and part of the Mogi-Guaçu Ecological Station (22°16'S 47°11' W, mean altitude of 600 m asl). Located approximately 2.9 km from MGI is a cluster of four reproductively mature *C. legalis* trees, demonimated MGII (Figure 1). MGI and MGII are isolated from other populations by at least 4 km and are located approximately 75 km from Ibicatu. The climate is the same as that described for Ibicatu. All *C. legalis* trees in MGI and MGII were sampled (bark cambium), mapped (GPS III-Garmin, USA), measured for DBH, estimated for age based on annual mean DBH increment, and genotyped (Table 7, Figure 3). MGI contains 22 *C. legalis* trees and MGII contains 4 trees, for a total of 26 trees (3.6 trees/ha), with DBH ranging from 21 to 144 cm (mean 68 cm), and estimated age ranging from 27 to 144 years, with a mean of 83 years.

Figure 1- Spatial distribution of *Cariniana estrellensis* and *Cariniana legalis* trees sampled in the Ibicatu State Forest, Sao Paulo State, Brazil.



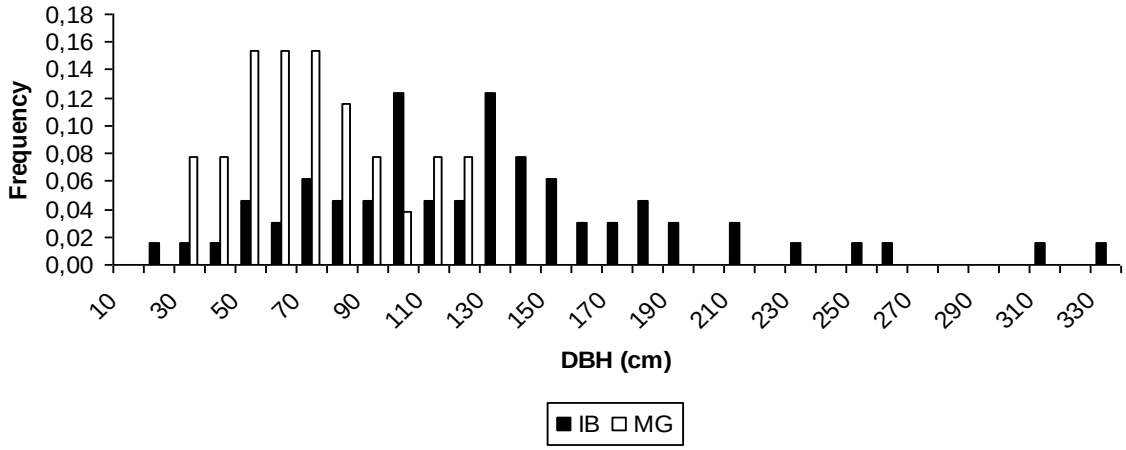
Source: Google Earth, (2018).

Figure 2- DBH frequency distribution for *Cariniana estrellensis* trees sampled in Ibicatu (IB) and Bataguassu (BA).



Source: Prepared by author.

Figure 3- DBH frequency distribution for *Cariniana legalis* trees sampled in Ibicatu (IB) and Mogi-Guaçu (MG).



Source: Prepared by author.

3.2 DNA EXTRACTION AND MICROSATELLITE AMPLIFICATION

The DNA extraction of *C. estrellensis* and *C. legalis* was carried out using the method described by Doyle and Doyle (1990). *Carianiana estrellensis* was genotyped for nine microsatellite loci (SSR) and *C. legalis* was genotyped for seven SSR loci (Table 8). Details on amplification and genotyping of the selected loci for *C. estrellensis* are given in Guidugli et al. (2009) and Tambarussi et al. (2013a). For *C. legalis*, details are described in Tambarussi et al. (2013a). All loci used for both species present Mendelian inheritance, an absence of genetic linkage, and genotypic linkage equilibrium (TAMBARUSSI et al., 2013b; KUBOTA et al., 2017).

Table 8- Microsatellite loci used for *Cariniana estrellensis* and *Cariniana legalis.*

	Primers	Reference
Cariniana estrellensis		
Ibicatu	Ce07, Ce18	Guidugli et al., 2009
Ibicatu	Cle01, Cle04, Cle05, Cle08, Cle09, Cle10, Cle12	Tambarussi et al., 2013a
Bataguassu	Ce01, Ce02, Ce04, Ce09, Ce10, Ce11, Ce13, Ce14, Ce18	Kubota et al., 2017
Cariniana legalis		
Ibicatu	Cle01, Cle04, Cle05, Cle08, Cle09, Cle10, Cle12	Tambarussi et al., 2013a
Mogi-Guaçu	Cle01, Cle04, Cle05, Cle08, Cle09, Cle10, Cle12	Tambarussi et al., 2013a

3.3 DATA ANALYSIS

3.3.1 Genetic diversity and inbreeding

Genetic diversity was quantified at the population level. In order to determine if there are differences based on tree age, the population was divided into two groups, 50% of trees with low DBH and the other 50% with high DBH. Genetic diversity indices estimated were: total number of alleles per locus (k), allelic richness (R), and observed (H_o) and expected (H_e) heterozygosity according to Hardy-Weinberg equilibrium. Inbreeding was quantified using the fixation index (F) and the statistical significance of F values were tested using

Monte Carlo permutation of alleles between individuals. All estimates were carried out using the FSTAT software (GOUDET, 1995). In order to test the indices for differences between samples, we used an unpaired t-test. The genetic differentiation (G_{st}) between the species was also estimated using the standardized genetic differentiation (G'_{st}) for microsatellite loci (HEDRICK, 2005) and the seven common loci between species (Cle01, Cle04, Cle05, Cle08, Cle09, Cle10 and Cle12). All of these estimates were carried out using the FSTAT software (GOUDET, 1995).

3.3.2 Estimates of group coancestry and variance effective size

Group coancestry (Θ) for the total sample of trees in each population was estimated as:

$$\Theta = \frac{\sum_{i=}^{n} 0.5(1+F_i) + \sum_{i=1}^{n}\sum_{j\neq i}^{n}\theta_{ij}}{n^2},$$

where n is the sample size, F_i is the inbreeding coefficient of the *i*-th individual, and θ_{ij} is the pairwise coancestry coefficient between the *i*-th and *j*-th individuals (LINDGREN et al., 1997). The θ_{ij} value was estimated using the Nason coancestry estimator (LOISELLE et al., 1995). The F_i and θ_{ij} indices were estimated using the Spagedi 1.3 software (HARDY; VEKEMANS, 2002). As the Θ index was derived from the inbreeding coefficient (ranging from 0 to 1) and true pairwise coancestry coefficient (ranging from 0 to 1), and we estimated F_i and θ_{ij} using coefficients of correlation (ranging from -1 to 1), all values lower than zero were assumed as zero. Furthermore, estimates of inbreeding and coancestry from gene markers may be biased due to the occurrence of null alleles, allele dropout, and genotyping errors (MORAES et al., 2013). F_i values lower than 0.125, the minimum inbreeding expected for mating between two half-sib individuals, were also assumed as zero, and values greater than 0.25, the minimum inbreeding expected for mating between two full-sib individuals, were assumed as 0.25. θ_{ij} values lower than 0.125, the minimum coancestry coefficient expected between two half-sib individuals, were also assumed as zero, and θ_{ij} values higher

than 0.25, the minimum coancestry coefficient expected between two full-sibs, were assumed as 0.25. The variance effective population size was calculated following Cockerham (1969) as $N_e = 0.5/\Theta$ and the relationship between N_e and the sample size (n) was calculated as N_e/n. The loss of observed heterozygosity per generation based on N_e and due to genetic drift was estimated using a model that assumes one locus with two alleles in random mating populations with discrete generations (not overlapping), $H_{o(t)}/H_{o(0)} = [1-(1/2N_e)]^t$, and the decrease in the heterozygosity in generation t as $H_{o(t)} = H_{o(0)}[1-(1/2N_e)]^t$ (FRANKEL; SOULE, 1981), where $H_{o(0)}$ and $H_{o(t)}$ are actual heterozygosity and heterozygosity in generation t, respectively.

3.3.3 Analysis of intrapopulation spatial genetic structure

The intrapopulation spatial genetic structure (SGS) was estimated based on the mean coancestry coefficient (θ_{ij}) between pairwise trees within distance classes, using the Nason coancestry estimator (LOISELLE et al., 1995) and Spagedi 1.3 software (HARDY; VEKEMANS, 2002). The statistical significance of θ_{ij} values was calculated by comparing the limits of the confidence interval at 95% probability of θ_{ij} for each distance class, calculated by Monte Carlo permutations of individuals between distance classes. Due to the differences in number of sampled trees and population density between populations, four distance classes were used for *C. estrellensis* (0–75, 75–150, 150–250, and 250–983 m) and for *C. legalis* (0–50, 50–100, 100–200, and 200–600 m). To compare SGS between species and populations, the *Sp* statistic (VEKEMANS; HARDY, 2004) was calculated as $Sp = -b_k/(1-\theta_l)$, where θ_l is the coancestry coefficient calculated between all pairs of individuals in the first distance class and b_k is the slope of regression of the coancestry coefficient on the logarithm of spatial distance between trees. To test for significance of SGS, the spatial position of each individual was permuted 1000 times to obtain the frequency distribution of b_k under the null hypothesis that θ_{ij} and $\ln(d_{xy})$ are uncorrelated.

3.3.4 Estimating historical gene dispersal

Historical gene dispersal (σ_g) for each population was estimated assuming that the SGS follows the isolation by distance pattern at equilibrium (HARDY et al., 2006). The effective neighborhood population size (Nb) was estimated as $Nb = (1-\theta_1)/b_k$ (VEKEMANS; HARDY, 2004), where b_k is the regression slope within a distance class of $\sigma_g < d_{ij} < 20\sigma_g$. Due to the fact that this estimate of Nb is dependent on the effective density (D_e) (HARDY et al., 2006), D_e was estimated as $D_e = D/2$ and $D_e = D/10$, where D is the actual population density (VEKEMANS; HARDY, 2004). The lower and upper bounds for the 95% confidence interval (95% CI) of Nb were estimated by jackknifing data over each locus (HARDY et al., 2006). The 95% CI of σ_g was estimated following Hardy et al. (2006). All analyses were carried out using the Spagedi 1.3 software (HARDY; VEKEMANS, 2002).

3.3.5 Parentage analysis

Combined non-exclusion probability of the first parent (P_1), combined non-exclusion probability of identity (Q_i), and realized pollen and seed dispersal in both species and all populations were carried out by parentage analysis (maternity and paternity), using the software CERVUS 3.0 (MARSHALL et al., 1998; KALINOWSKI; TAPER; MARSHALL, 2007). Cryptic gene flow (C_{gf}) was estimated as described in Dow and Ashley (1996). Parentage (maternity and paternity) analyses were based on the single exclusion method.

In order to identify parents for all sampled trees, all sampled individuals within populations were used as candidate parents. However, to accept a candidate parent as the true parent, we adopted the following approach: i) self-assignments were excluded; ii) positive assignment for descendants was accepted if there was a maximum of two mismatches between the descendant and the assigned putative parent or among the trio: descendant, first, and second assigned parent; iii) as *C. estrellensis* starts fruiting at 10 years of age, which corresponds to a DBH > 7 cm and *C. legalis* starts fruiting at approximately 20 years of age and a DBH > 20 cm (CARVALHO, 2003), putative *C. estrellensis* parents with less than 10

years differences in relation to the descendant tree, and putative *C. legalis* parents with less than 20 years differences in relation to the descendant tree were discarded.

To confirm positive assignments, the θ_{xy} was estimated between descendant and assigned putative parents, as well as between assigned parents and trees assigned to the same putative parents, as described above. The expected θ_{xy} value for parent-sib pairs is 0.25, between half-sibs is 0.125, and full-sibs is 0.25. Realized pollen dispersal distance was estimated as the distance between two putative parents when two parents (probable mother and father) were assigned. In cases where at least one putative parent was assigned, realized seed dispersal distance was estimated assuming that the sole assigned parent is the mother. When two putative parents were assigned, realized seed dispersal distance was based on the mean distance between the offspring and first and second parent. The minimum, maximum, and median pollen and seed dispersal distances were also calculated using the Euclidean distance between two points. Self-fertilization (s) was accepted only in cases where there was no mismatching between tested descendant and the assigned putative parent. Following Tambarussi et al. (2017), to estimate the rate of mating among related trees (t_r), assigned parents with $\theta_{xy} \geq 0.1$ were assumed to be genetically related. Effective pollination neighbor area (A_{ep}) corresponds to the circular area in which 63% of pollen donors that fertilized a mother tree are expected to be located; this was calculated based on Levin (1998) and the effective pollination radius (r_{ep}) based on Austerlitz and Smouse (2001).

4 RESULTS

4.1 GENETIC DIVERSITY AND INBREEDING

For *C. estrellensis* in IB and BA, we found a total of 46 and 75 alleles, respectively, and for *C. legalis* in IB and MG, we found a total of 100 and 97 alleles, respectively (Table 9). The observed (H_o) and expected (H_e) heterozygosity were similar between *C. estrellensis* (IB: H_o = 0.71; H_e = 0.66; BA: H_o = 0.65; H_e = 0.69) and *C. legalis* (IB: H_o =0.81; H_e = 0.86; MG: H_o = 0.82; H_e = 0.89) populations. The results for fixation index (F) were significantly (P< 0.05) higher than zero for *C. estrellensis* of BA (F = 0.06) and *C. legalis* of IB (F = 0.06), indicating inbreeding. According to the unpaired t-test, comparing 50% of trees with <DBH and >DBH, the allelic richness (R), H_o, H_e and F were not significantly different (Table 10). However, F values of *C. estrellensis* in BA (0.06) and *C. legalis* in IB (0.09) were significantly higher than zero in trees with < DBH, suggesting the occurrence of inbreeding. Genetic differentiation (G'_{st}) between species (G'_{st} = 0.550 ± 0.058, mean ± standard error) indicates that genetic diversity is mainly distributed among rather than within species.

Table 9- Genetic diversity and inbreeding in sampled *Cariniana estrellensis* and *Cariniana legalis* trees.

Sample	n	k	R (SE)	H_o (SE)	H_e (SE)	F (SE)
Cariniana estrellensis	310	144				
Ibicatu	26	46	-	0.71 (0.06)	0.66 (0.03)	-0.07 (0.08)
50%< DBH	13	37	3.95 (0.30)	0.71 (0.07)	0.64 (0.03)	-0.11 (0.10)
50%> DBH	13	44	4.68 (0.24)	0.70 (0.06)	0.69 (0.02)	-0.01 (0.08)
Bataguassu[1]	284	75	-	0.65 (0.03)	0.69 (0.02)	0.06 (0.08)*
50%< DBH	142	74	4.98 (0.67)	0.64 (0.05)	0.68 (0.05)	0.06 (0.04)*
50%> DBH	142	65	5.01 (0.63)	0.66 (0.06)	0.69 (0.05)	0.05 (0.05)
Cariniana legalis	91	130				
Ibicatu[2]	65	100	-	0.81 (0.02)	0.86 (0.01)	0.06 (0.02)*
50%< DBH	32	86	7.80 (0.47)	0.75 (0.04)	0.83 (0.03)	0.09 (0.07)*
50%> DBH	33	89	8.62 (0.53)	0.87 (0.03)	0.88 (0.02)	0.01 (0.05)
Mogi-Guaçu[2]	26	97	-	0.82 (0.07)	0.89 (0.01)	0.08 (0.07)
50%< DBH	12	79	9.85 (0.68)	0.82 (0.08)	0.92 (0.01)	0.10 (0.08)
50%> DBH	14	85	9.58 (0.68)	0.85 (0.06)	0.89 (0.02)	0.04 (0.06)

n is the sample size; k is the total number of alleles across all loci; R is the allelic richness for 10 genotypes in *C. estrellensis* and nine in *C. legalis*; H_o is the observed heterozygosity; H_e is the expected heterozygosity; F is the fixation index; SE is the standard error; [1]Kubota (2017); [2]Tambarussi et al. (2015); *P< 0.05.
Source: Prepared by author.

Table 10- Probability (P) of unpaired t-test between pairwise samples with 50% of trees with lower DBH vs 50% with higher DBH in *Cariniana estrellensis* and *Cariniana legalis*.

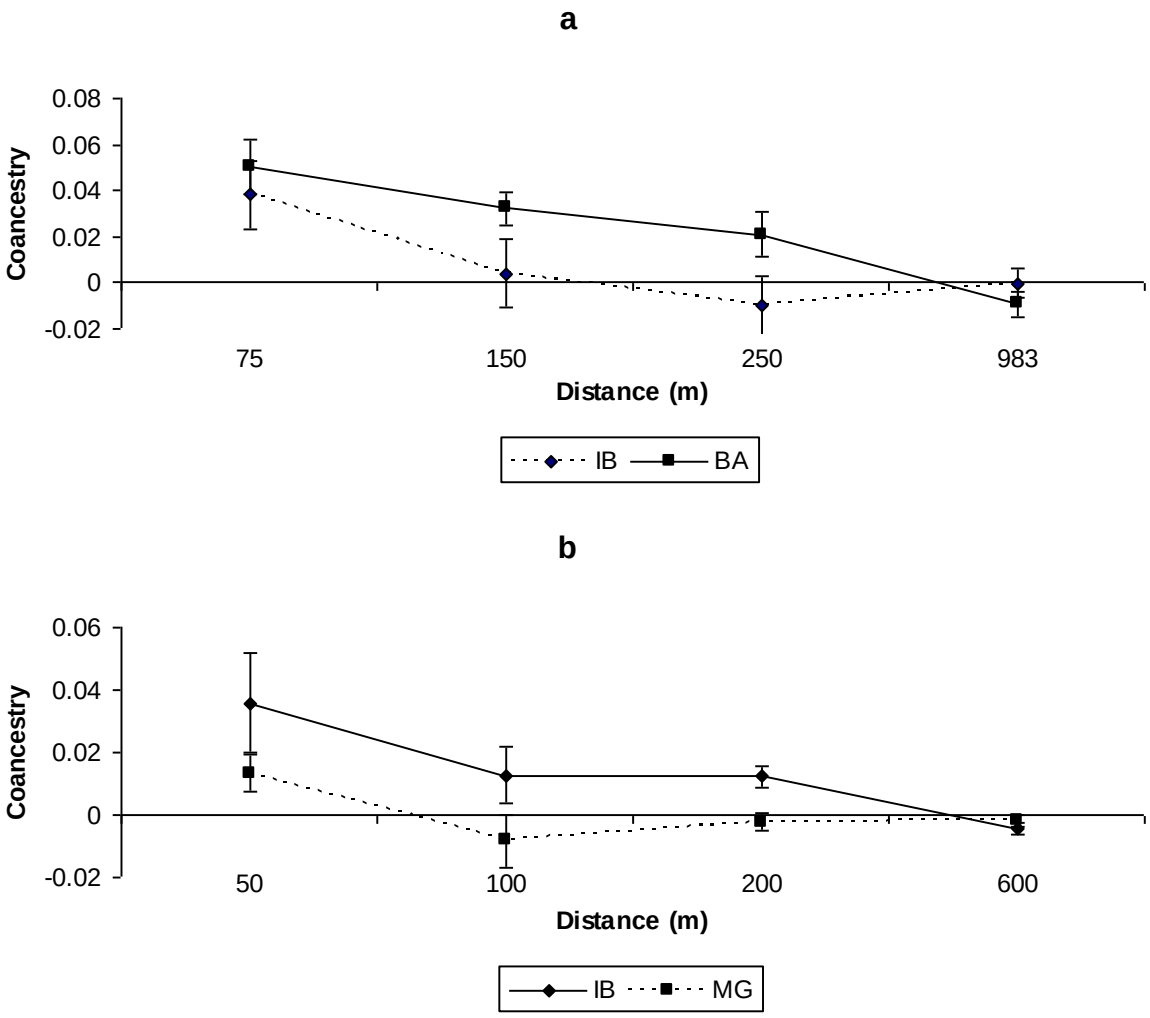
		R	H_e	H_o	F
Cariniana estrellensis					
Ibicatu	<50 *vs* ≥ 50%	0.079	0.189	0.913	0.473
Batagussu	<50 *vs* ≥ 50%	0.974	0.902	0.852	0.923
Cariniana legalis					
Ibicatu	<50 *vs* ≥ 50%	0.266	0.124	0.030	0.240
Mogi-Guaçu	<50 *vs* ≥ 50%	0.785	0.250	0.740	0.542

R is the allelic richness for nine genotypes; H_o is the observed heterozygosity; H_e is the expected heterozygosity; F is the fixation index.

4.2 INTRAPOPULATION SPATIAL GENETIC STRUCTURE

Significant spatial genetic structure (SGS) was detected for *C. estrellensis* up to approximately 115 m in IB and 350 m in BA (Figure 4). For *C. legalis*, SGS was significant up to approximately 250 m in IB and 60 m in MG (Figure 4). Beyond these distances, the mean pairwise coancestry coefficient decreased to non-significant or significantly lower than zero, indicating a typical pattern of isolation by distance. The intensity of SGS measured by the S_p-statistic was significant, but not significantly different between populations of each species (Table 11). Based on restricted b_k, the historical gene dispersal distance (σ_g) produced a maximum of 8.5 m and a Nb of 46 for *C. estrellensis* in IB and in BA the maximum was 140 m with a Nb of 78. For *C. legalis* in IB, we found a maximum σ_g of 54 m and a Nb of 152 and in MG, the maximum σ_g was 28 m and Nb was 155, assuming $D_e = D/10$.

Figure 4- Correlogram of coancestry coefficient (θ_{ij}) in four distance classes between *Cariniana estrellensis* trees located in Ibicatu and Bataguassu (a) and *Cariniana legalis*, located in Ibicatu and Mogi-Guaçu (b).



Source: Prepared by author.

Table 11- Estimates of spatial genetic structure indices for trees of both species in the studied populations.

	Cariniana estrellensis		*Cariniana legalis*	
	Ibicatu	Bataguassu	Ibicatu	Mogi-Guaçu
Trees/ha	0.36	0.063	0.93	3.6
First distance class (m)	0–75	0–25	0–100	0–63
Coancestry: θ_1	0.038*	0.127*	0.019*	0.004*
Regression slope: b_k	–0.019 ± 0.010*	–0.028 ± 0.018*	–0.015 ± 0.008*	–0.019 ± 0.010*
Distance where b_k was estimated (m)	0–200	0–600	0–200	0–150
Sp -statistic: ± SE	0.020 ± 0.011*	0.033 ± 0.022*	0.015 ± 0.007*	0.019 ± 0.006*
D_e	0.36	0.00063	0.0093	0.036
Nb ± SE	21 ± 22	48 ± 86	54 (41–70)	149 ± 150
σ ± SE (m) ($D_e = D/2$)	2.2 ± 0.9	78 ± 52	21 (19–24)	19.8 ± 8.8
D_e	0.05	0.000315	0.000451	0.015
Nb ± SE	46 (42–51)	78 ± NC	152 (62)	155 (109–201)
σ ± SE (m) ($D_e = D/10$)	8.5 (8.1–9.0)	140 ± NC	54 (10)	28 (24–33)

θ_1 is the mean pairwise coancestry coefficient in first distance class; b_k is the regression slope of θ_1 on log of spatial distance; Sp is the intensity of spatial genetic structure; ± 2SE is the standard error. *P< 0.05.

4.3 EFFECTIVE POPULATION SIZE

The group coancestry coefficient (Θ) was low among all pairwise *C. estrellensis* (0.03473–0.00236) and *C. legalis* (0.00747–0.01375) trees suggesting that in random mating, the expected inbreeding from mating among related trees is very low (< 5%, Table 12). The variance effective population size (N_e) shows that the 26 and 284 *C. estrellensis* trees of IB and BA correspond to 10 and 119 unrelated and non-inbred individuals or a N_e/n of 0.37 and 0.42, respectively. For *C. legalis*, the estimated N_e suggests that of the 65 and 26 trees of IB and MG, 33 and 15 are unrelated and non-inbred individuals or a N_e/n of 0.5 and 0.57, respectively. The estimated loss of heterozygosity after 50 generations ($H_{o(t=50)}$), based on actual N_e, indicates that the observed heterozygosity for *C. estrellensis* in IB and BA is expected to be only 7.7% ($H_{o(t)}$ = 0.055) and 81.0% ($H_{o(50)}$ = 0.527), respectively, of the actual ($H_{o(0)}$: IB= 0.71; BA= 0.65). For *C. legalis* in IB and MG, the observed heterozygosity

is expected to be 46.6% ($H_{o(t)}$ = 0.378) and 18.4% ($H_{o(50)}$ = 0.151), respectively, of the actual ($H_{o(0)}$: IB= 0.81; MG= 0.82).

Table 12- Group coancestry (Θ), variance effective size (N_e) and expected decrease in heterozygosity after 50 generations ($H_{o(t=50)}$) by genetic drift for samples of *Cariniana estrellensis* and *Cariniana legalis*; n is the sample size; H_o is the actual observed heterozygosity; $H_{o(\text{exp})}$ is the expected values for H_o after 50 generations due to genetic drift.

Sample	n	Θ	N_e	N_e / n	$H_{o(t=50)}$	H_o	$H_{o(\text{exp})}$
Cariniana estrellensis							
Ibicatu	26	0.03473	9.5	0.37	0.077	0.71	0.06
Bataguassu[1]	284	0.00236	118.5	0.42	0.810	0.65	0.53
Cariniana legalis							
Ibicatu[2]	65	0.00747	32.5	0.50	0.466	0.81	0.38
Mogi-Guaçu[2]	26	0.01375	14.8	0.57	0.184	0.82	0.15

[1]Kubota (2017); [2]Tambarussi et al. (2015); *P< 0.05. SE is the standard error.
Source: Prepared by author.

4.4 PARENTAGE ANALYSIS

For all trees sampled, the combined non-exclusion probability of the first parent (P_1) was higher in *C. estrellensis* (IB= 0.045008; BA= 0.025563) than in *C. legalis* (IB= 0.002699; MG= 0.000383). This resulted in a cryptic gene flow (C_{gf}) higher in *C. estrellensis* (IB= 0.698; BA= 0.999) than *C. legalis* (IB= 0.161; MG= 0.010) populations, indicating a high probability that pollen and seed flow in *C. estrellensis* may be biased (Table 13). However, the combined non-exclusion probability of identity (Q_i) was lower for both *C. estrellensis* populations (IB= 0.00000002; BA= 0.0000054) than for *C. legalis* (IB= 0.00044367; MG= 0.00030133), indicating that all adults present different genotypes, which is favourable for the assignment of parents in parentage analysis.

Table 13- Combined non-exclusion probability of the first parent (P_1), cryptic gene flow (C_{gf}), and the combined non-exclusion probability of identity (Q_i) for samples of *Cariniana estrellensis* and *Cariniana legalis*.

	P_1	n	C_{gf}	Q_i
Cariniana estrellensis				
Ibicatu	0.045008	26	0.698	0.00000002
Batagassu	0.025563	284	0.999	0.00000540
Cariniana legalis				
Ibicatu	0.002699	65	0.161	0.00044367
Mogi-Guaçu	0.000383	26	0.010	0.00030133

At least one putative parent was found for 16 and 123 *C. estrellensis* trees of IB and BA, respectively, and for 25 and 10 *C. legalis* trees of IB and MG, respectively. These results suggest a respective seed immigration rate of 38.5 and 56.7% for *C. estrellensis*, and for *C. legalis* of 61.5% for both populations (Table 14). Two putative parents within the sample areas were detected for 5 and 28 *C. estrellensis* trees of IB and BA, respectively, and for 5 *C. legalis* tree of IB, suggesting a rate of pollen flow of 80.1 and 90.1% for *C. estrellensis*, and for *C. legalis* of 92.3 and 100%. No trees were themselves assigned as the parent tree, indicating an absence of realized self-fertilization. In general, mean coancestry coefficient between trees (θ_{xy}) and assigned putative parents was lower than expected for *C. estrellensis* in IB (0.18) and for *C. legalis* in IB (0.22) and MG (0.10). Assuming a minimum coancestry coefficient of 0.1 ($\theta_r \geq 0.1$) to determine parents as related individuals, we found two pairs in IB (θ_r = 0.17) and 11 pairs in BA (θ_r = 0.29) for *C. estrellensis*, and three pairs (θ_r = 0.20) in IB for *C. legalis* to be related parents (Table 14). Thus, the realized mating among related trees (t_r) for *C. estrellensis* in IB was 0.125 and in BA was 0.089 and in *C. legalis* in IB it was 0.120. The pairwise coancestry coefficient between assigned trees with at least one common parent ranged from –0.01 to 0.15. The mean fixation index (F) for assigned trees with at least one parent ranged from -0.14 to 0.13, assigned trees with two parents ranged from -0.01 to 0.09, and for assigned trees with related parents ranged from -0.12 to 0.14. The mean distance between related parents for *C. estrellensis* ranged from 615 to 398 m and for *C. legalis* the distance was 312 m.

4.5 POLLEN AND SEED DISPERSAL DISTANCE

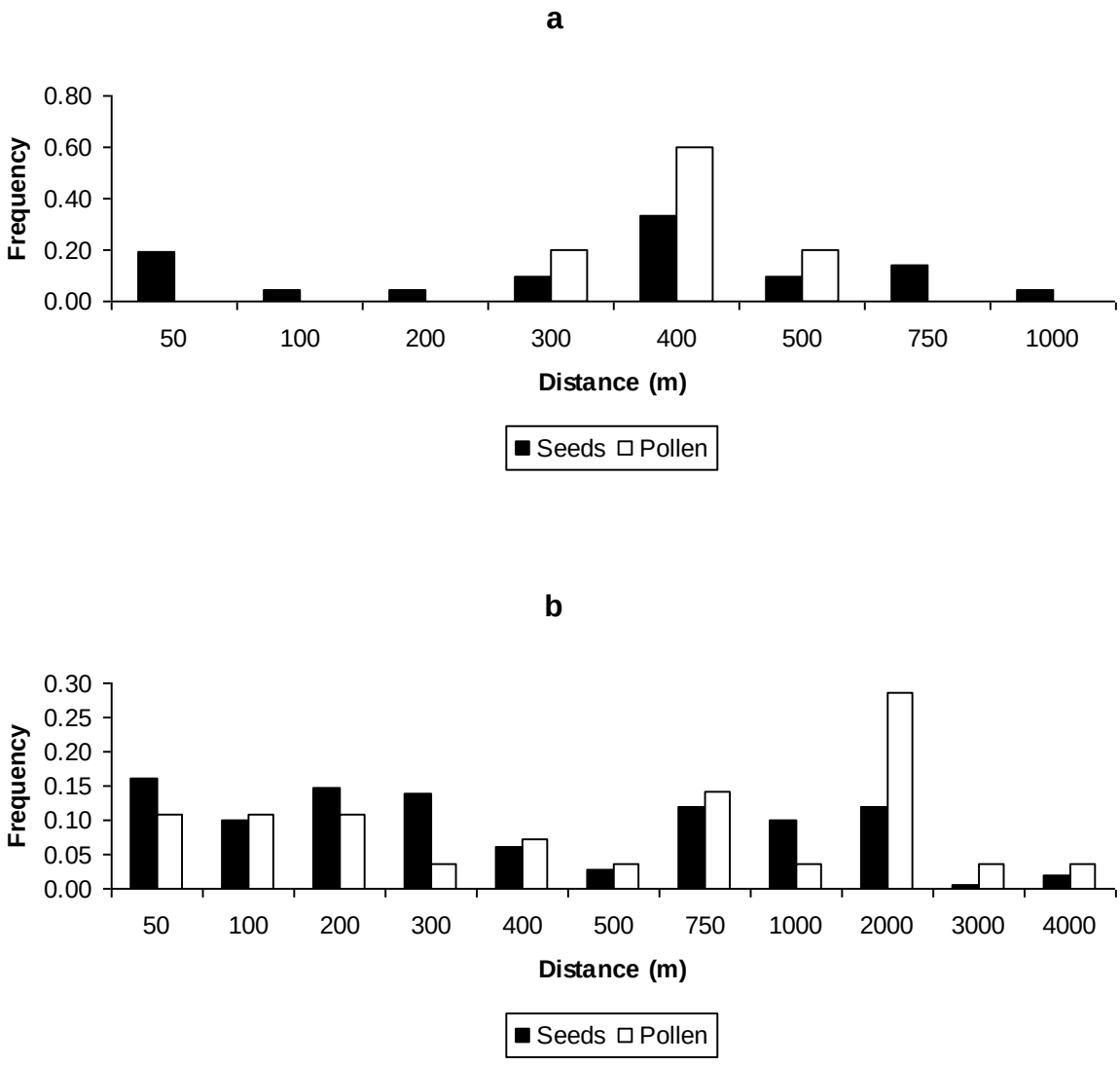
The pollen dispersal distance for *C. estrellensis* ranged from 10 to 3309 m, with a mean of 338 and 850 m in IB and BA, respectively. For *C. legalis*, the pollen dispersal distance ranged from 183 to 385 m, with a mean of 312 m in IB (Table 14, Figure 5). For *C. estrellensis*, the median pollen dispersal distance was lower (IB= 330 m, BA= 516 m) than the mean, indicating a pattern of isolation by distance. However, for *C. legalis* the median (322 m) was higher than the mean, indicating a random pollen dispersal pattern. The effective pollination area (A_{ep}) ranged from 3.9 to 476 ha for *C. estrellensis* and for *C. legalis* it was 3.2 ha, indicating an effective pollination radius (r_{ep}) ranging from 111 to 1,231 m for *C. estrellensis* and 101 m for *C. legalis* (Table 14). Seed dispersal distance for *C. estrellensis* ranged from 2 to 3483 m, with a mean of 308 m in IB, and in BA the minimum was 452 m and maximum was 615 m. For *C. legalis* seed dispersal distance ranged from 14 to 851 m, with a mean minimum and maximum of 338 and 393 m, respectively in IB, and in MG it was 72 m. The median seed dispersal distance was lower than the mean for the BA population of *C. estrellensis* and for both *C. legalis* populations, indicating a pattern of isolation by distance.

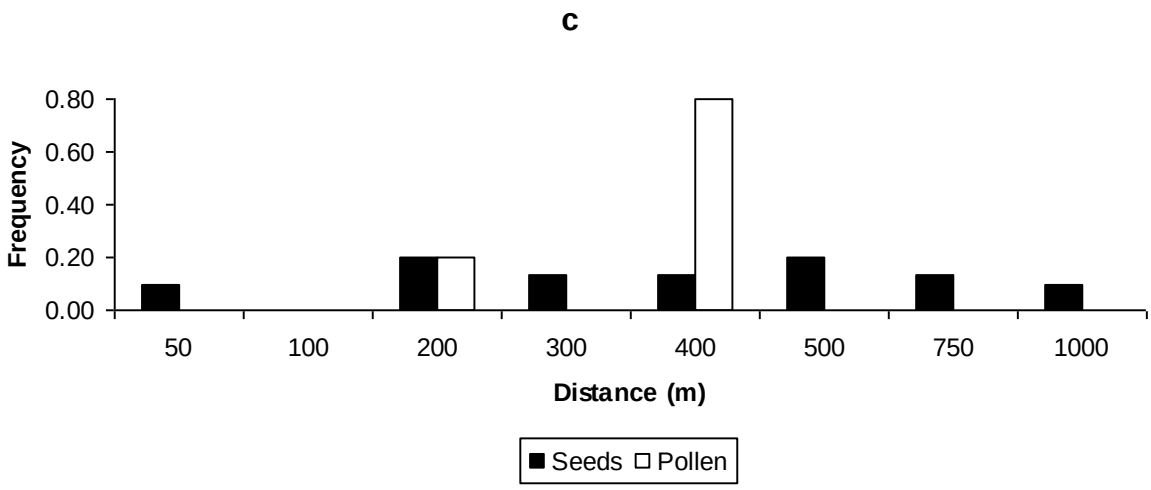
Table 14- Pollen and seed flow and dispersal distance, pairwise coancestry (θ_{xy}) and fixation index (F) for *Cariniana estrellensis* in Ibicatu (IB) and Bataguassu (BA) and *Cariniana legalis* in Ibicatu (IB) and Mogi-Guaçu (MG).

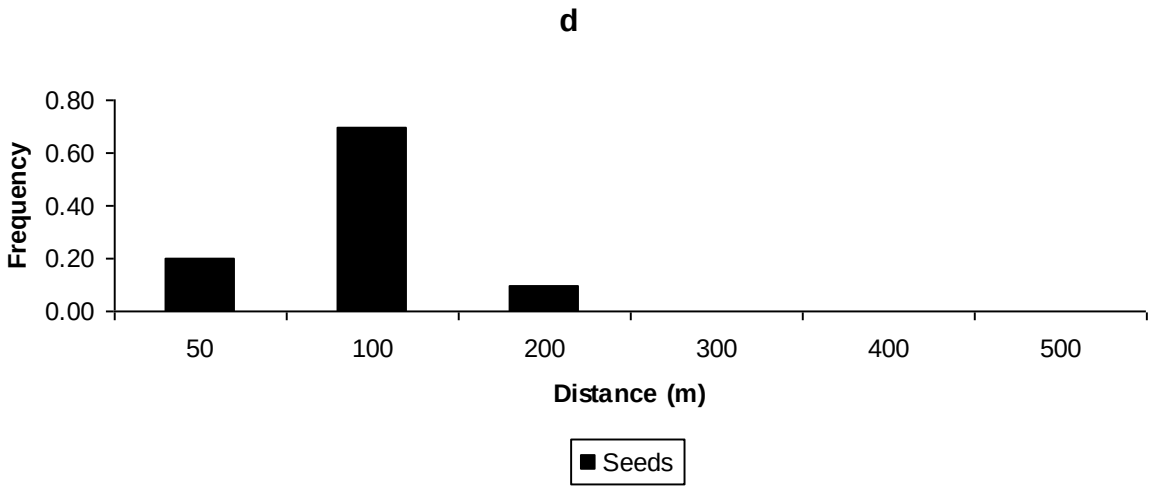
	Cariniana estrellensis				*Cariniana legalis*			
	IB		BA		IB		MG	
	Pollen	Seeds	Pollen	Seeds	Pollen	Seeds	Pollen	Seeds
Sample size: n	26	26	284	284	65	65	26	26
Number of unassigned trees (%)	21 (80.1)	10 (38.5)	256 (90.1)	161 (56.7)	60 (92.3)	40 (61.5)	26 (100)	16 (61.5)
Number of assigned trees	5	16	28	123	5	25	0	10
Mean distance (SD) m	338 (88)	308 (227)	850 (888)	452 (594)/615 (697)	312 (80)	338 (230)/393 (236)	-	72 (28)
Minimum/Maximum distance (m)	226/465	4/878	10/3309	2/3483	183/385	14/851	-	24/131
Median: Minimum/Maximum (m)	330	325	516	233/340	322	300/397	-	67
Effective pollination neighbor area: A_{ep} (ha)	3.9	-	476	-	3.2	-	-	-
Effective pollination radius: r_{ep} (m)	111	-	1231	-	101	-	-	-
Coancestry								
Assigned trees and parents (SD)	0.18 (0.04)	-	0.25 (0.00)	-	0.22 (0.01)	-		0.10 (0.04)
Between relative parents: $\theta_r \geq 0.1$ (SD)	0.17 (0.06)	-	0.29 (0.04)	-	0.20 (0.03)	-		-
Mating among relatives: t_r	0.125	-	0.089	-	0.120	-		-
One parent in common (SD)	0.15 (0.02)	-	0.02 (0.02)	-	0.08 (0.02)	-		0.01 (0.03)
Fixation index: F								
Assigned trees (SD)	-0.14 (0.05)	-	0.02 (0.02)	-	0.10 (0.2)	-		0.13 (0.04)
Assigned trees both parents (SD)	-0.01 (0.06)	-	0.07 (0.03)	-	0.09 (0.07)	-		
Inbreeds assigned for θ_r (SD)	-0.12 (0.06)	-	0.08 (0.03)	-	0.14 (0.07)	-		-

SD is the standard deviation.

Figure 5- Frequency distribution of seed and pollen dispersal distance in *Cariniana estrellensis* of Ibicatu (a) and Bataguassu (b) and *Cariniana legalis* of Ibicatu (c) and Mogi-Guaçu (d).







Source: Prepared by author.

5 DISCUSSION

5.1 GENETIC DIVERSITY

Genetic diversity is mainly distributed between species (G'_{st} = 0.550) rather than within species. Observed (H_o) and expected (H_e) heterozygosity were similar between populations of the species. The indices of heterozygosity, and particularly H_e are known to not be affected by sample size, due to the fact that they are dependent on gene frequencies. Thus, these indices are not the most effective in investigating processes that affect genetic diversity, such as forest fragmentation and logging (SEBBENN et al., 2008). However, for *C. legalis* in IB and *C. estrellensis* in BA, the fixation index (0.09 and 0.06, respectively) was significantly higher than zero in trees with low DBH, suggesting a reduction in levels of inbreeding as trees move from younger to older life stages, as well as mortality of inbred trees at early stages of growth due to inbreeding depression.

5.2 MATING SYSTEM AND INBREEDING

All assigned trees of both species were the result of outcrossing. This is consistent with previous analyses of open-pollinated *C. estrellensis* seeds (GUIDUGLI et al., 2016), suggesting selection against selfed individuals or self-incompatibility. In contrast, self-fertilization has been reported in studies on *C. legalis* based on open-pollinated seeds (4.3–17%, TAMBARUSSI et al., 2016) and juveniles established in provenance and progeny tests (1–9.9%, SEBBENN et al., 2001). This suggests stronger selection against selfed *C. legalis* individuals in natural populations than in experimental trials. However, realized mating among related individuals (t_r) was detected for both species (8.9–12.5%). In previous studies of *C. estrellensis*, no t_r was found based on open-pollinated seeds (GUIDUGLI et al., 2016), but for *C. legalis* mating among relatives has been detected in samples of open-pollinated seeds (4.4–26.6%, TAMBARUSSI et al., 2016) and in juveniles in experimental trials (5.9–9.1%, SEBBENN et al., 2001). These results further suggest selection against inbred individuals especially at early stages for *C. legalis*; however, in natural populations as well as in trials, inbred individuals may survive for a long time.

As no selfing was detected by parentage analysis, the inbreeding found in populations of both species can be attributed to mating between relatives. Both *C. estrellensis* and *C.*

legalis are subject to inbreeding depression. Kubota (2017) detected stronger inbreeding depression for survival in *C. estrellensis* at the seedling stage (8 months of age) for individuals produced from self-fertilization (2.6%) than from mating among relatives (0.2%). Tambarussi et al. (2017) also found greater inbreeding depression for survival in *C. legalis* seedlings produced from self-fertilization (3.9-36%) than from mating among relatives (0.2–30.4%). The stronger inbreeding depression for selfing than mating among related trees is supported by the absence of selfed trees in our study populations, with inbred individuals originated from mating among relatives surviving up to 91 years of age in *C. estrellensis* and 122 years of age in *C. legalis*.

Selfing results in inbreeding of at least 50% ($100\%(0.5(1+F_m))$, where F_m is the inbreeding in the mother) and mating among related individuals results in inbreeding equal to the coancestry between related parents ($F_r = \theta_r$); for example, if the parents are full-sibs ($\theta_{fs} = 0.25$), inbreeding of 25% is expected in their descendants. Thus, inbreeding originating from mating among related individuals is expected to result in lower homozygosis for identical by descent alleles than from selfing. As deleterious genes that produce inbreeding depression generally occur at low frequencies, mating among related individuals has low probability to be combined in the homozygosis stage and, consequently, some mating among related individuals do not result in inbreeding depression. Furthermore, the expression of inbreeding depression has been reported (KUBOTA, 2017) as stronger in early stages of tree development, which can explain the decreased levels of inbreeding among older trees. The fact that inbreeding in early stages was only detected for *C. legalis* in IB and for *C. estrellensis* in BA may be explained by the fact that the genetic load or the occurrence and frequency of deleterious alleles is variable between populations and individuals due to the life histories of mutation in the populations.

5.3 INTRAPOPULATION SPATIAL GENETIC STRUCTURE

Populations of both species presented spatial genetic structure (SGS), indicating that there is high probability that trees located within these distances are genetically related. A decrease in the mean pairwise coancestry coefficient with an increase in the distance between trees indicates a gene dispersal pattern of isolation by distance (IBD). This pattern is consistent with that expected for natural tree populations (HARDY et al., 2006; DEGEN; SEBBENN, 2014). SGS is mainly determined by seed and pollen dispersal (HARDY et al.,

2006; BORN et al., 2008). However, the absence of SGS beyond the detected distances does not mean that at these distances individuals are unrelated; some trees may be related but they are not grouped, and they can mate if pollen vectors visit such trees, as detected herein. The mean distance between assigned trees and related parents was greater than the SGS distance detected: for *C. estrellensis* it ranged from 398 to 615 m, and for *C. legalis* it was 312 m. Another factor that we must consider is that the study populations are located in an extensively fragmented forest landscape and deforestation in the area may have modified the original SGS due to logging.

The SGS intensity measured by the S_p-statistic was similar between populations and species (ranging from 0.015 to 0.033). This can be explained by the fact that both species have similar dispersal vectors: pollen by bees and seeds by wind. The S_p-statistic was lower than the estimates for other wind pollinated species using SSR markers, such as *Dicorynia guianensis* (0.100), and higher than the estimates for *Jacaranda copaia* (0.015) using RAPD (HARDY et al., 2006).

5.4 GENE FLOW

The results for both species suggest greater levels of pollen (80.1–100%) than seed immigration into the populations (38.5–61.5%). The coefficient of coancestry expected between parents and sibs is 0.25, or on average 25% of genes of parents and descendants are identical by descent. Mean pairwise coancestry coefficient between trees and assigned putative parents was lower than expected for both *C. estrellensis* (0.18–0.25) and *C. legalis* (0.10–0.22). The differences between the estimated and expected values (0.25) are due to difficulties in estimating kinship using genetic markers (CARVALHO et al., 2010). However, when several loci are used simultaneously, the mean value of loci tends to the expected value. Thus, we can consider that the estimates obtained herein reflect the expected relationship between parents and descendants. This may also explain the lower expected values for *C. legalis* which is likely an artefact of the sampling as the number of loci used (7 loci) was lower than for *C. estrellensis* (9 loci).

Nevertheless, the estimates of pairwise coancestry between parents and descendants were greater than zero, supporting the hypothesis that these individuals are indeed related, and the trees assigned to parents are likely correct. The majority of *C. estrellensis* and *C. legalis* trees that were not assigned a mother or father are remnants of the pre-fragmentation era (<

100 years) in the study populations. Thus, these results may be explained by the fact that parent trees were logged from the area around or within the forest fragments, died before sampling, or the trees originated from seed immigration from populations located outside of the sample areas. The results also demonstrate that the populations are not genetically isolated due to the occurrence of pollen and seed flow from outside the study populations. Pollen and seed flow introduces new alleles into a population, enabling increases in genetic diversity and effective population size.

5.5 POLLEN DISPERSAL DISTANCE

Both species are mainly pollinated by bees, which have the potential for long distance pollen dispersal (GHAZOUL, 2005). Realized pollen dispersal for *C. estrellensis* reached longer distance (3309 m) than for *C. legalis* (IB= 385 m). Mean realized pollen dispersal distance for *C. estrellensis* was greater in BA (850 m) than in IB (338 m) and that detected for *C. legalis* in IB (312 m). The same pattern was observed for the effective pollination area (A_{ep}) and effective pollination radius (r_{ep}) for the populations of the species (Table 14). However, it is important to note that these results are likely underestimates due to pollen immigration or mortality of pollen parents. In both populations of *C. estrellensis*, pollen was dispersed in a pattern of isolation by distance (IBD), with a higher frequency of pollination occurring between trees in closer proximity than more distant trees. However, in IB for *C. legalis* the pattern was random. This random pattern may be due to the underestimation of pollen dispersal distance due to pollen immigration, death or logging of the pollen parents.

The distances and realized patterns of pollen dispersal for both species can be attributed to many factors, such as sample design and types of individuals sampled, pollen dispersal vectors, flowering phenology, self-incompatible systems, inbreeding depression, among others. Studies carried out in small areas will result in lower mean and maximum dispersal distances than in larger areas. This can explain the longer pollen dispersal distance detected for *C. estrellensis* in BA, where the study area was larger (448.2 ha) than in IB (72 ha) for both species. Furthermore, as the sampling in this study did not include seeds, the results for both species represent the realized pollen dispersal and not the effective pollen dispersal, which occurs at fertilization. Based on samples of open-pollinated seeds of *C. estrellensis* from BA, effective pollen dispersal reached up to 3519 m, with a mean of 597 m, and also followed an IBD pattern (KUBOTA, 2017). Similarly, Guidugli et al. (2016) studied

a population of *C. estrellensis* in an eight ha forest fragment and detected a mean pollen dispersal of 146.9 m. Based on samples of open-pollinated seeds of *C. legalis*, pollen reached up to 922 m in IB, with a mean of 352 m and also followed an IBD pattern (TAMBARUSSI et al., 2015). We can see that the effective and realized maximum, mean, and pattern of pollen dispersal do not differ widely. The minimal differences can be due to many factors that can occur between fertilization and the current life cycle of the sampled trees, such as inbreeding depression, random mortality, disease, predation, and logging, which can change the effective pattern of pollen dispersal in relation to that detected here, the realized pollen dispersal pattern.

Ghazoul (2005) notes that fragmented populations can be sustained if pollinators are able to travel long distances. The results of this study for *C. estrellensis* and *C. legalis*, which are mainly pollinated by bees, confirm this expectation. Our results suggest that, currently, there are favorable conditions for maintaining the genetic diversity of the studied populations, thus indicating their utility as sites for *in situ* conservation of these vulnerable species.

5.6 SEED DISPERSAL DISTANCE

Seed dispersal in *C. estrellensis* also reached long distances in the BA population (3483 m). The explanation for this result is the same as that discussed for pollen; the ability to measure gene dispersal depends on the sample design and as the sample area of BA was larger than the other studied populations of both species, we were able to detect longer seed dispersal distances. This also explains why mean seed dispersal distance for *C. estrellensis* was longer in BA (452–615 m) than in IB (308 m) and for *C. legalis* it was greater in IB (338–393 m) than MG (72 m). However, the seed dispersal pattern was isolation by distance.

The maximum seed dispersal was greater than pollen dispersal in all populations of *C. estrellensis* and in IB for *C. legalis*. This can be explained by the fact that for both species, seeds are dispersed by wind and pollen dispersed mainly by bees, both of which are vectors with the potential for long distance dispersal. Furthermore, aggregation of regenerants near to the parent trees can result in high mortality rates among juveniles due to predation, thus leading to lower levels of aggregation at advanced life stages (JANZEN, 1970), which may result in longer average seed dispersal distances.

For both species, the historical gene dispersal distance (σ_g), based on the model of equilibrium between immigration and genetic drift, resulted in lower gene dispersal distance

than that estimated from parentage analysis (*C. estrellensis*: 8.5–78 m; *C. legalis*: 20–54 m). The differences between the methods can be explained by the fact that parentage analysis is a direct method to determine gene dispersal, while the historical gene dispersal distance, measured by σ_g, is an indirect method that is heavily dependant on the distance at which the regression analysis is carried out. Furthermore, the model of equilibrium between immigration and genetic drift produced an effective population neighbour size (Nb) in *C. estrellensis* (BA= 78, IB= 46) and *C. legalis* (IB= 152, MG= 155) that is generally higher than the census number of the population. This indicates an overestimation, which is likely because our data does not fit the assumption of the model of equilibrium between immigration and genetic drift. Thus, the parentage analysis results are more robust to explain the gene dispersal in the species' populations.

5.7 FINAL CONSIDERATIONS

Cariniana estrellensis and *C. legalis* are Neotropical trees that are vulnerable to extinction and the results reported herein on pollen and seed flow and dispersal will inform strategies aimed at their *in situ* and *ex situ* conservation. First, for *in situ* conservation, the results show that the studied populations of both species are not reproductively isolated due to pollen flow from outside the study areas. However, it is important to maintain connectivity of the studied populations with other reproductive populations that were not included in this study to ensure continuation of gene flow. Thus, other forest fragments and trees of the species surrounding the forest fragments must be preserved.

The variance effective population size (N_e) was lower than census size (N) in all populations. This is related to the occurrence of SGS and inbreeding. Lower N_e than N has also been reported for other trees of the Atlantic Forest (BITTENCOURT; SEBBENN; 2007; GAINO et al., 2010; MORAES; SEBBENN, 2011; TAMBARUSSI et al., 2015; SPOLADORE et al., 2017). Furthermore, with the exception of the *C. estrellensis* population in BA (N_e = 119), the other populations (*C. estrellensis*: IB= 10; *C. legalis*: IB= 33, MG= 15) showed a N_e that is lower than that suggested (N_e = 70) for short term genetic conservation to avoid the effects of genetic drift, such as the occurrence of inbreeding (CABALLERO el al., 2016). If the N_e is low, the genetic drift in the populations will quickly decrease heterozygosity, resulting in a decrease in population fitness (KALINOWSKI; WAPLES,

2002; CABALLERO el al., 2016). The loss of heterozygosity after 50 generations ($H_{o(t=50)}$) based on actual N_e was higher in populations with low N_e (7.7–46.6%) than with higher N_e (*C. estrellensis*: BA= 81.0%). However, as both species present overlapping generations, the loss in heterozygosity is expected to be greater than that observed using this model due to the occurrence of mating between related trees. To avoid inbreeding depression due to genetic drift in small populations, for *in situ* conservation the N_e must be increased to at least 70. The N_e can be increased for *C. estrellensis* in IB and *C. legalis* in IB and MG through the introduction of about 60, 40, and 55 non-inbred and unrelated individuals, respectively. The introduced individuals must originate from other populations of the species within the same region to avoid other possible genetic problems, including outbreeding depression (SEBBENN, 2006). For practical reasons, following the recommendation of Spoladore et al. (2017), we suggest the introduction at least 150 individuals to mitigates against the possibile mortality of the introduced trees due to random mortality, predation, disease, and other factors.

The results for SGS provide fundamental information to develop strategies for seed collection for *ex situ* conservation, environmental reforestation, and tree breeding, as SGS defines the distance at which related individuals are likely to occur. Based on the results discussed herein, the distance between trees identified for seed collection must be population specific: for *C. estrellensis* the distance in BA is at least 350 m apart and 115 m apart in IB; for *C. legalis* the distance is at least 250 m in IB and 60 m in MG. The use of seeds that are inbred or from genetically related families, due to related mothers, must be avoided for conservation purposes because it will decrease the effective size of the sampled progeny arrays.

6 CONCLUSIONS

1. Genetic diversity is mainly distributed between species than within species;
2. Populations of both species present spatial genetic structure and near neighbor trees are likely to be genetically related;
3. The extend of SGS is similar between populations of both species;
4. Younger *C. estrellensis* trees from Bataguassu population present greater inbreeding than larger trees and young *C. legalis* trees from Ibicatu population present less heterozygosity and greater inbreeding than large trees due to inbreeding depression;
5. In natural populations of both species, inbreeding depression is stronger for selfed trees than from those originated from mating among related individuals;
6. The spatial isolation of populations of both species did not result in reproductive isolation due to pollen and seed immigration from other populations;
7. Estimates of pollen and seed dispersal distance are dependent on the sample design, with a greater ability to estimate long distances in large rather than small sample areas;
8. The realized dispersal distance of pollen and seeds for both species reached long distances, but in general followed a pattern of isolation by distance.

REFERENCES

AGUILAR, R.; ASHWORTH, L.; GALETTO, L.; AIZEN, M. A. Plant reproductive susceptibility to habitat fragmentation: review and synthesis through a meta-analysis. **Ecology Letters**, Oxford, v. 9, n. 8, p. 968-980, 2006.

AGUILAR, R.; QUESADA, M.; ASHWORTH, L.; HERRERIAS-DIEGO, Y.; LOBO J. Genetic consequences of habitat fragmentation in plant populations: susceptible signals in plant traits and methodological approaches. **Molecular Ecology**, Oxford, v. 17, n. 24, p. 5177-5188, 2008.

AIZEN, M. A.; FEINSIGER, P. Forest fragmentation, pollination, and plant reproduction in a Chaco Dry Forest, Argentina. **Ecology**, Washington, v. 75, n. 2, p. 330-351, 1994.

ALBALADEJO, R. G.; GUZMÁN, B.; GONZÁLEZ-MARTÍNEZ, S. C.; APARICIO, A. Extensive pollen flow but few pollen donors and high reproductive variance in an extremely fragmented landscape. **Plos One**, San Francisco, v. 7, n. 11, p. 1–9, 2012.

ALDRICH, P.R.; HAMRICK, J.L. Reproductive dominance of pasture trees in a fragmented tropical forest mosaic. **Science**, Washington, v. 281, n. 5373, p. 103–105, 1998.

ANDRÉ, T.; LEMES, M. R.; GROGAN, J.; GRIBEL, R. Post-logging loss of genetic diversity in a mahogany (*Swietenia macrophylla* King, Meliaceae) population in Brazilian Amazonia. **Forest Ecology Management**, Amsterdam, v. 255, n. 2, p.340–345, 2008.

ANDREWARTHA, H.G.; BIRCH, L.C. **The Distribution and migrants. Abundance of Animals**. Chicago: University of Chicago Press, 1954. 782 p.

ARAÚJO, M. R. G.; JÚNIOR, A. F. D. M.; MENEZES, ELYTANIA VEIGA BRANDÃO, M. M.; COTA, L. G.; OLIVEIRA, D. A.; ROYO, V. A.; VIEIRA, F. A. Fine-scale spatial genetic structure and gene fl ow in *Acrocomia aculeata* (Arecaceae): Analysis in an overlapping generation. **Biochemical Systematics and Ecology**, Oxford, v. 71, n. 1, p. 147–154, 2017.

ARRUDA, C.C.B.; SILVA, M.B.; SEBBENN, A.M.; KANASHIRO, M.; LEMES, M.R.; GRIBEL, R. Mating system and genetic diversity of progenies before and after logging: a case study of *Bagassa guianensis* (Moraceae), a low-density dioecious tree of the Amazonian forest. **Tree Genetics and Genomes**, Berlin, v. 11, n. 3, p. 1–9, 2015.

ASHLEY, M. V. Plant parentage, pollination, and dispersal: How DNA microsatellites have altered the landscape. **Critical Reviews in Plant Science**, Philadelphia, v. 29, n. 1, p. 148-161, 2010.

AUSTERLITZ, F.; DICK, C.W.; DUTECH, C.; KLEIN, E.K.; ODDOU-MURATORIO, S.; SMOUSE, P.E. Using genetic markers to estimate the pollen dispersal curve. **Molecular Ecology**, Oxford, v. 13, n. 4, p.937-954, 2004.

AUSTERLITZ, F.; SMOUSE, P.E. Two-generation analysis of pollen flow across a landscape. II. Relation Between Φ_{FI}, Pollen Dispersal and Interfemale distance. **Genetics**, Austin, v. 157, n. 2, p. 851-857, 2001.

AZEVEDO, V.C.R.; KANASHIRO, M.; CIAMPI, A.Y.; GRATTAPALIA, D. Genetic structure and mating system of *Manilkara huberi* (Ducke) a. chev., a heavily logged amazonian timber species. **Journal of Heredity**, Oxford, v. 98, n. 7, p. 646–654, 2007.

BACLES, C. F. E.; ENNOS, R. A. Paternity analysis of pollen-mediated gene flow for *Fraxinus excelsior* L. in a chronically fragmented landscape. **Heredity**, London, v. 101, n. 4, p. 368–380, 2008.

BAI, W.-N.; ZENG, Y.-F.; ZHANG, D.-Y. Mating patterns and pollen dispersal in a heterodichogamous tree, *Juglans mandshurica* (Juglandaceae). **New Phytologist**, Chichester, v. 176, n. 3, p. 699–707, 2007.

BALDAUF, C.; CIAMPI-GUILLARDI, M.; AGUIRRA, T. J.; CORRÊA, C. E.; DOS SANTOS, F. A. M.; DE SOUZA, A. P.; SEBBENN, A. M. Genetic diversity, spatial genetic structure and realised seed and pollen dispersal of *Himatanthus drasticus* (Apocynaceae) in the Brazilian savanna. **Conservation Genetics**, Dordrecht, v. 15, n. 5, p. 1073–1083, 2014.

BARREIRA, S.; SEBBENN, A.M.; SCOLFORO, J.R.S.; KAGEYAMA, P. Y. Diversidade genética e sistema de reprodução em população nativa de *Eremanthus erythropappus* (DC.) MacLeish sob exploração. **Scientia Forestalis**, Piracicaba, v. 71, p. 119–130, 2006.

BEATTY, G. E.; BROWN, J. A.; CASSIDY, E. M.; FINLAY, C. M. V; MCKENDRICK, L.; MONTGOMERY, W. I.; REID, N.; TOSH, D. G.; PROVAN, J. Lack of genetic structure and evidence for long-distance dispersal in ash (*Fraxinus excelsior*) populations under threat from an emergent fungal pathogen: implications for restorative planting. **Tree Genetics & Genomes,** Berlin, v. 11, n. 3, p. 53, 2015.

BEGHE, D.; PIOTTI, A.; SATOVIC, Z.; DE LA ROSA, R.; BELAJ, A. Pollen-mediated gene flow and fine-scale spatial genetic structure in *Olea europaea* subsp. *europaea* var. sylvestris. **Annals of Botany**, Oxford, v. 119, n. 4, p. 671–679, 2017.

BERTOLASI, B.; LEONARDUZZI, C.; PIOTTI, A.; LEONARDI, S.; ZAGO, L.; GUI, L.; GORIAN, F.; VANETTI, I.; BINELLI, G. A last stand in the Po valley: genetic structure and gene flow patterns in *Ulmus minor* and *U. pumila*. **Annals of Botany**, Oxford, v. 115, n. 4, p. 683–692, 2015.

BESSEGA, C.; POMETTI, C.; CAMPOS, C.; SAIDMAN, B. O.; VILARDI, J. C. Implications of mating system and pollen dispersal indices for management and conservation of the semi-arid species *Prosopis flexuosa* (Leguminosae). **Forest Ecology and Management**, Amsterdam, v. 400, p. 218–227, 2017.

BESSEGA, C.; POMETTI, C.L.; EWENS, M.; SAIDMAN, B.O.; VILARDI, J. C. Strategies for conservation for disturbed *Prosopis alba* (Leguminosae, Mimosoidae) forests based on mating system and pollen dispersal parameters. **Tree Genetics and Genomes**, Berlin, v. 8, n. 2, p. 277–288, 2012.

BEZEMER, N.; KRAUSS, S. L.; PHILLIPS, R. D.; ROBERTS, D. G.; HOPPER, S. D.

Paternity analysis reveals wide pollen dispersal and high multiple paternity in a small isolated population of the bird-pollinated *Eucalyptus caesia* (Myrtaceae). **Heredity**, London, v. 117, n. 6, p. 1–12, 2016.

BITTENCOURT, J. M.; SEBBENN, A. M. Patterns of pollen and seed dispersal in a small fragmented population of a wind pollinated *Araucaria angustifolia* in southern Brazil. **Heredity**, London, v. 99, n. 6, p. 580-591, 2007.

BITTENCOURT, J. V. M.; SEBBENN, A. M. Pollen movement within a continuous forest of wind-pollinated *Araucaria angustifolia*, inferred from paternity and TwoGener analysis. **Conservation Genetics**, Dordrecht, v. 9, n. 4, p. 855–868, 2008.

BOHRER, C. B. A.; DANTAS, H. G. R.; CRONENBERGER, F. M.; VICENS, R. S.; ANDRADE, S. F. Mapeamento da vegetação e do uso do solo no centro de diversidade vegetal de Cabo Frio, Rio de Janeiro, Brasil. **Rodriguésia,** Rio de Janeiro, v. 60, n.1, p. 1–23, 2009.

BORN, C.; HARDY, O. J.; CHEVALLIER, M. H.; OSSARI, S.; ATTÉKÉ, C.; WICKINGS, E. J.; HOSSAERT-MCKEY, M. Small-scale spatial genetic structure in the Central African rainforest tree species *Aucoumea klaineana*: a stepwise approach to infer the impact of limited gene dispersal, population history and habitat fragmentation. **Molecular Ecology**, Oxford, v. 17, n. 8, p. 2041–2050, 2008a.

BORN, C.; KJELLBERG, F.; CHEVALLIER, M. H.; VIGNES, H.; DIKANGADISSI, J.; WICKINGS, E. J.; HOHOSSAERT-MCKEY, M. Colonization processes and the maintenance of genetic diversity: insights from a pioneer rainforest tree, *Aucoumea klaineana*. **Proceedings of the Royal Society**, London, v. 275, n. 1647, p. 2171–2179, 2008b.

BRAGA, A. C.; COLLEVATTI, R. G. Temporal variation in pollen dispersal and breeding structure in a bee-pollinated Neotropical tree. **Heredity**, London, v. 106, n. 6, p. 911–919, 2011.

BRANDÃO, M. M.; VIEIRA, F. A.; CARVALHO, D. Fine-scale genetic structure of *Myrcia splendens* (Myrtaceae). **Revista Arvore**, Viçosa, v. 35, n. 5, p. 957–964, 2011.

BREED, M. F.; OTTEWELL, K. M.; GARDNER, M. G.; MARKLUND, M. H. K.; STEAD, M. G.; HARRIS, J. B. C.; LOWE, A. J. Mating system and early viability resistance to habitat fragmentation in a bird-pollinated eucalypt. **Heredity**, London, v. 115, n. 2, p. 100–107, 2015.

BREED, M.F.; MARKLUND, M. H. K.; OTTEWELL, K. M.; GARDNER, M. G.; HARRIS, J. B. C.; LOWE, A. J. Pollen diversity matters: revealing the neglected effect of pollen diversity on fitness in fragmented landscapes. **Molecular Ecology**, Oxford, v. 21, n. 24, p. 5955-5968, 2012.

BROADHURST, L. Pollen Dispersal in Fragmented Populations of the Dioecious Wind-Pollinated Tree, *Allocasuarina verticillata* (Drooping Sheoak, Drooping She-Oak; Allocasuarinaceae). **Plos one**, San Francisco, v. 10, n. 3, p. 1–17, 2015.

BRONDANI, R.P.V.; ZUCCHI, M. I.; BRONDANI, C.; RANGEL, P. H. N.; BORBA, T. C.D. O.; RANGEL, P. N.; MAGALHÃES, M. R.; VENCOVSKY, R. Genetic structure of wild rice *Oryza glumaepatula* populations in three Brazilian biomes using microsatellite markers. **Genetica**, Switzerland, v. 125, n. 2-3, p. 115–123, 2005.

BROSI, B. J. The effects of forest fragmentation on euglossine bee communities (Hymenoptera: Apidae: Euglossini). **Biological Conservation**, Boston, v. 142, n. 2, p. 414–423, 2009.

BURCZYK, J. L. A. W.; ADAMS, W. T.; SHIMIZU, J. Y. Mating patterns and pollen dispersal in a natural knobcone pine (*Pinus attenuata* Lemmon.) stand. **Heredity**, London, v. 77, n. 3, p. 251–260, 1996.

BURCZYK, J.; ADAMS, W.T.; MORAN, G.F.; GRIFFIN, A.R.; Complex patterns of mating revealed in a *Eucalyptus regnans* seed orchard using allozyme markers and the neighbourhood model. **Molecular Ecology**, Oxford, v. 11, n. 11, p. 2379-2391, 2002.

BURCZYK, J.; DIFAZIO, S. P.; ADAMS, W. T. Gene flow in forest trees: how far do genes really travel. **Forest Genetic**, Zvolen, v. 11, n. 3, p. 179-192, 2004.

BURCZYK, J.; LEWANDOWSKI, A.; CHALUPKA, W. Local pollen dispersal and distant gene flow in Norway spruce (*Picea abies* [L.] Karst.). **Forest Ecology and Management**, Amsterdam, v. 197, n. 1-3, p.39-48, 2004.

BYRNE, M.; ELLIOTT, C. P.; YATES, C. J.; COATES, D. J. Maintenance of high pollen dispersal in Eucalyptus wandoo, a dominant tree of the fragmented agricultural region in Western Australia. **Conservation Genetics**, Dordrecht, v. 9, n. 1, p. 97–105, 2008.

CABALLERO, A.; BRAVO, I.; WANG, J. Inbreeding load and purging: implications for the short-term survival and the conservation management of small populations. **Heredity**, London, v. 118, n. 2, p. 177–185, 2016.

CARNEIRO, F. D. S.; SEBBENN, A. M.; KANASHIRO, M.; DEGEN, B. Low inter-anual variation of mating systems anda gene flow of *Symphonia globulifera* in the Brazilian Amazon. **Biotropica**, Washington, v. 39, n. 5, p. 628–636, 2007.

CARNEIRO, F. S.; DEGEN, B.; KANASHIRO, M.; LACERDA, A. E. B.; SEBBENN, A. M. High levels of pollen dispersal detected through paternity analysis from a continuous *Symphonia globulifera* population in the Brazilian Amazon. **Forest Ecology and Management**, Amsterdan, v. 258, n. 7, p. 1260–1266, 2009.

CARNEIRO, F. S.; LACERDA, A. E. B.; LEMES, M. R.; GRIBEL, R.; KANASHIRO, M.; WADT, L. H. O.; SEBBENN, A. M. Effects of selective logging on the mating system and pollen dispersal of *Hymenaea courbaril* L. (Leguminosae) in the Eastern Brazilian Amazon as revealed by microsatellite analysis. **Forest Ecology and Management**, Amsterdam, v. 262, n. 9, p. 1758–1765, 2011.

CARVALHO, A. C. M.; FREITAS, M. L. M.; MORAES, S. M. B.; MORAES, M. L. T.; STRANGHETTI, V.; ALZATE-MARIN, A. L.; SEBBENN, A. M. Diversidade genética, endogamia e fluxo gênico em pequena população fragmentada de *Copaifera langsdorffii*. **Revista Brasileira de Botânica**, São Paulo, v. 33, n. 4, p. 599-606, 2010.

CARVALHO, P. E. R. **Espécies arbóreas brasileiras**. 2. ed. Brasília: Embrapa Informação Tecnológica, 2003. 1039 p.

CARVALHO, P.E.R. **Espécies florestais brasileiras:** recomendações silviculturais, potencialidades e uso da madeira. Colombo: Embrapa-CNPF, 1994. 638 p.

CARVALHO, P. E. R. **Jequitibá-branco**. Colombo: Embrapa Florestas, 2003b. 13 p. (Circular Técnica, 73).

CASCANTE, A.; QUESADA, M.; LOBO, J. J.; FUCHS, E. A. Effects of dry tropical forest fragmentation on the reproductive success and genetic structure of the tree Samanea saman. **Conservation Biology**, Boston, v. 16, n. 1, p. 137-147, 2002.

CASTRO, W. H. **Propagação vegetativa do jequitibá-rosa (*Cariniana estrellensis* (Raddi) Kuntze) e do pau-jacaré (*Piptadenia gonoacantha* (Mart.) Macbr.) por estaquia.** 2011. 72 f. Dissertação (Mestrado em Ciência Florestal) – Universidade Federal de Viçosa, Viçosa, MG, 2011.

CHASE, M.; MOLLER, R.C.; KESSELI, R.; BAWA, K.S. Distant gene flow in tropical trees. **Nature**, London, v .383, n. 6599, p. 398–399, 1996.

CHOO, J.; JUENGER, T. E.; SIMPSON, B. B. Consequences of frugivore-mediated seed dispersal for the spatial and genetic structures of a neotropical palm. **Molecular Ecology**, Oxford, v. 21, n. 4, p. 1019–1031, 2012.

CHUDNOFF, M. **Tropical timbers of the world**. Madison: Forest Products Laboratory, 1984. 26 p. (Agriculture Handbook, 607).

CHYBICKI, I. J.; BURCZYK, J. Simultaneous estimation of null alleles and inbreeding coefficients. **Journal of Heredity**, Oxford, v. 100, n. 1, p. 106–113, 2009.

CHYBICKI, I. J.; BURCZYK, J. Realized gene flow within mixed stands of *Quercus robur* L. and *Q. petraea* (Matt.) L. revealed at the stage of naturally established seedling. **Molecular Ecology**, Oxford, v. 19, n.10, p. 2137–2151, 2010.

CHYBICKI, I. J.; DZIALUK, A. Bayesian approach reveals confounding effects of population size and seasonality on outcrossing rates in a fragmented subalpine conifer. **Tree Genetics & Genomes**, Berlin, v. 10, n. 6, p. 1723–1737, 2014.

CLOUTIER, D.; KANASHIRO, M.; CIAMPI, A. Y.; SCHOEN, D. J. Impact of selective logging on inbreeding and gene dispersal in an Amazonian tree population of *Carapa guianensis* Aubl. **Molecular Ecology**, Oxford, v. 16, n. 4, p. 797–809, 2007.

COCKERHAM, C.C. Variance of gene frequencies. **Evolution**, Lancaster, v. 23, n. 1, p. 72-84, 1969.

COLABELLA, F.; GALLO, L. A.; MORENO, A. C.; MARCHELLI, P. Extensive pollen flow in a natural fragmented population of Patagonian cypress *Austrocedrus chilensis*. **Tree Genetics & Genomes,** Berlin, v. 10, n. 6, p. 1519–1529, 2014.

COLLEVATTI, R. G.; TELLES, M. P. C.; NABOUT, J. C.; CHAVES, L. J.; SOARES, T. N. Demographic history and the low genetic diversity in *Dipteryx alata* (Fabaceae) from Brazilian Neotropical savannas. **Heredity,** London, v. 111, n. 2, p. 97–105, 2013.

COLLEVATTI, R. G.; ESTOLANO, R.; GARCIA, S. F.; HAY, J. D. Short-distance pollen dispersal and high self-pollination in a bat-pollinated neotropical tree. **Tree Genetics & Genomes,** Berlin, v. 6, n. 4, p. 555-564, 2010.

COLLEVATTI, R. G.; LIMA-RIBEIRO, M. S.; SOUZA-NETO, A. C.; FRANCO, A. A.; TERRIBLE, L. V. Recovering the demographical history of a Brazilian Cerrado tree species *Caryocar brasiliense*: coupling ecological niche modeling and coalescent analyses. **Nature Conservancy**, Arlington, v. 10, n. 2, p. 169–176, 2012.

COLLEVATTI, R. G.; OLIVATTI, A. M.; TELLES, M. P. C.; CHAVES, L. J. Gene flow among *Hancornia speciosa* (Apocynaceae) varieties and hybrid fitness. **Tree Genetics and Genomes**, Berlin, v. 12, n. 4, p. 1–12, 2016.

COLLEVATTI, R.; GRATTAPAGLIA, D.; HAY, J.D. High resolution microsatellite based analysis of the mating system allows the detection of significant biparental inbreeding in *Caryocar brasiliense*, an endangered tropical tree species. **Heredity**, London, v. 86, n. 1, p. 60-67, 2001.

COLLEVATTI, R. G.; RABELO, S. G.; VIEIRA, R. F. Phylogeography and disjunct distribution in *Lychnophora ericoides* (Asteraceae), an endangered cerrado shrub species. **Annals of Botany**, Oxford, v. 104, n. 4, p. 655–664, 2009.

CÔRTES, M. C.; URIARTE, M.; LEMES, M. R.; KRESS, W. J.; SMOUSE, P. E. Low plant density enhances gene dispersal in the Amazonian understory herb *Heliconia acuminate*. **Molecular Ecology**, Oxford, v. 22, n. 22, p. 5716-5729, 2013.

CRAFT, K. J.; ASHLEY, M. V. Pollen-mediated gene flow in isolated and continuous stands of bur oak, *Quercus macrocarpa* (Fagaceae). **American Journal of Botany**, Baltimore, v. 97, n. 12, p. 1999–2006, 2010.

CURTU, A. L.; GAILING, O.; FINKELDEY, R. Patterns of Contemporary hybridization inferred from paternity analysis in a four-oak-species forest. **BMC Evolutionary Biology**, London, v. 9, n. 284, p. 1–9, 2009.

DARDENGO, J. F. E.; ROSSI, A. A. B.; SILVA, B. M.; SILVA, I. V.; SILVA, J. S.; SEBBENN, A. M. Diversity and spatial genetic structure of a natural population of *Theobroma speciosum* (Malvaceae) in the Brazilian Amazon. **Revista de Biologia Tropical**, San Jose, v. 64, n. 3, p. 1091–1099, 2016.

DEACON, N. J.; CAVENDER-BARES, J. Limited pollen dispersal contributes to population genetic structure but not local adaptation in *Quercus oleoides* Forests of Costa Rica. **Plos one**, San Francisco, v. 10, n. 9, p. 1–25, 2015.

DEGEN, B.; WARD, S. E.; LEMES, M. R.; NAVARRO, C.; CAVERS, S.; SEBBENN, A. M. Verifying the geographic origin of mahogany (*Swietenia macrophylla* King) with DNA-fingerprints. **Forensic Sci Int-Gen,** Amsterdam, v. 7, n. 1, p. 55–62, 2013.

DEGEN, B.; BANDOU, E.; CARON, H. Limited pollen dispersal and biparental inbreeding in *Symphonia globulifera* in French Guiana. **Heredity**, London, v. 93, n. 6, p. 585-591, 2004.

DEGEN, B.; SEBBENN, A. M. Genetics and tropical forests. In: KÖHL, M.; PANCEL L. **Tropical forestry handbook**. Berlin: Springer-Verlag Berlin Heidelberg, 2014. 30 p.

DE-LUCAS, A. I.; ROBLEDO-ARNUNCIO, J. J.; HIDALGO, E.; GONZÁLEZ-MARTÍNEZ, S. C. Mating system and pollen gene flow in Mediterranean maritime pine. **Heredity**, London, v. 100, n. 4, p. 390–399, 2008.

DEMESURE, B.; COMPS, B.; PETIT, R. J. Chloroplast DNA phylogeography of the common beech (*Fagus sylvatica* L.) in Europe. **Evolution**, Lancaster, v. 50, n. 6, p. 2515–2520, 1996.

DERING, M.; CHYBICKI, I. J.; RACZKA, G. Clonality as a driver of spatial genetic structure in populations of clonal tree species**. Journal of Plant Research**, Tokyo, v. 128, n. 5, p. 731–745, 2015.

DICK, C. W. Genetic rescue of remnant tropical trees by an alien pollinator. **The Royal Society**, London, v. 268, n. 1483, p. 2391–2396, 2001.

DICK, C. W.; ETCHELECU, G.; AUSTERLITZ, F. Pollen dispersal of tropical trees (*Dinizia excelsa*: Fabaceae) by native insects and African honeybees in pristine and fragmented Amazonian rainforest. **Molecular Ecology**, Oxford, v. 12, n. 3, p. 753–764, 2003.

DOW, B. D.; ASHLEY, M. V. High Levels of Gene Flow in Bur Oak Revealed by Paternity Analysis Using Microsatellites. **Journal of Heredity**, Oxford, v. 89, n. 1, p. 62–70, 1998.

DOW, B. D.; ASHLEY, M. V. Microsatellite analysis of seed dispersal and parentage of saplings in bur oak, *Quercus macrocarpa*. **Molecular Ecology**, Oxford, v. 5, n. 5, p. 615–627, 1996.

DOYLE, J. J.; DOYLE, J. L. Isolation of plant DNA from fresh tissue. **Focus**, Berlin, v. 12, n. 1, p. 13–15, 1990.

DUMINIL, J.; ABESSOLO, D. T. M.; BOUROBOU, D. N.; DOUCET, J.; LOO, J.; HARDY, O. J. High selfing rate, limited pollen dispersal and inbreeding depression in the emblematic African rain forest tree *Baillonella toxisperma* – Management implications. **Forest Ecology and Management**, Amsterdam, v. 379, p. 20–29, 2016a.

DUMINIL, J.; DAÏNOU, K.; KAVIRIRI, D. K.; GILLET, P.; LOO, J.; DOUCET, J.; HARDY, O. J. Relationships between population density, fine-scale genetic structure, mating system and pollen dispersal in a timber tree from African rainforests. **Heredity**, London, v. 116, n. 3, p. 295–303, 2016b.

DURIGAN, G.; NOGUEIRA, J.C.B. **Recomposição de matas ciliares**. São Paulo: Instituto Florestal, 1990, 14p. (IF Série Registros, 4).

EL MOUSADIK, A.; PETIT, R. J. High level of genetic differentiation for allelic richness among populations of the argan tree [Arginiaspinosa (L.) Skeels] endemic to Morroco. **Theoretical and Applied Genetics**, Berlin, v. 92, n. 7, p. 832-839, 1996.

ELLSTRAND, N. C.; ELAM, D. R. Population genetic consequences of small population size: implications for plant conservation. **Annual Review of Ecology and Systematics,** Palo Alto, v. 24, n. 1, p. 217–242, 1993.

ELLSTRAND, N.C. Is gene flow the most important evolutionary force in plants? American **Journal of Botany**, Columbus, v. 5, n. 5, p. 737-753, 2014.

EPPERSON, B. K. Spatial structure of genetic variation within populations of forest trees. In: Adams WT, Strauss SH, Copes DL, Griffin AR (eds) **Population genetics of forest trees**. Netherlands: Springer, 1992. p. 257–278.

EWERS, R. M.; DIDHAM, R. K. Confounding factors in the detection of species responses to habitat fragmentation. **Biological Reviews**, Oxford, v. 81, n. 1, p. 117-142, 2006.

FOOD AND AGRICULTURE ORGANIZATION- FAO. Panel of experts on forest gene resources. Roma**:** Food and Agriculture Organization of the United Nation, 2002. 101p.

FERES, J. M.; SEBBENN, A. M.; GUIDUGLI, M. C.; MESTRINER, M. A.; MORAES, M. L. T.; ALZATE-MARIN, A. L. Mating system parameters at hierarchical levels of fruits, individuals and populations in the Brazilian insect-pollinated tropical tree, *Tabebuia roseo-alba* (Bignoniaceae). **Conservation Genetics**, Dordrecht, v. 13, n. 2, p. 393-405, 2012.

FERNÁNDEZ-MANJARRÉS, J. F.; IDOL, J.; SORK, V. L. Mating patterns of black oak *Quercus velutina* (Fagaceae) in a missouri oak-hickory forest. **Journal of Heredity**, Oxford, v. 97, n. 5, p. 451–455, 2006.

FERREIRA, M. E.; GRATTAPAGLIA, D. **Introdução ao uso de marcadores moleculares em análises genéticas**. Brasília: EMBRAPA- CENARGEN, 1998. 220 p.

FIELD, D. L.; AYRE, D. J.; WHELAN, R. J.; YOUNG, A. G. The importance of pre-mating barriers and the local demographic context for contemporary mating patterns in hybrid zones of *Eucalyptus aggregata* and *Eucalyptus rubida*. **Molecular Ecology**, Oxford, v. 20, n. 11, p. 2367–2379, 2011.

FIGLIOLIA, M. B.; SILVA, A.; AGUIAR, I. B.; PERECIN, D. Conservação de sementes de *Cariniana estrellensis* kuntze em diferentes condições de acondicionamento e armazenamento. **Revista Árvore**, Viçosa, v. 24, n. 4, p. 121-134, 2000.

FRANKEL, O. H.; SOULE, M. S. **Conservation and evolution**. Cambridge: Cambridge University Press, 1981.

FRICK, K. M.; RITCHIE, A. L.; KRAUSS, S. L. Field of dreams: restitution of pollinator services in restored bird-pollinated plant populations. **Restoration Ecology**, Washington, v. 22, n. 6, p. 832–840, 2014.

FUCHS, E. J.; LOBO, J. A.; QUESADA, M. Effects of forest fragmentation and flowering phenology on the reproductive success and mating patterns of the tropical dry forest tree *Pachira quinata*. **Conservation Biology**, Boston, v. 17, n. 1, p. 149-157, 2003.

FUCHS, E. L.; HAMRICK, J. L. Mating system and pollen flow between remnant populations of the endangered tropical tree, *Guaiacum sanctum* (Zygophyllacea). **Conservation Genetics**, Dordrecht, v. 12, n. 1, p. 175-185, 2011.

GAINO, A. P. S. C.; SILVA, A. M.; MORAES, M. A.; ALVES, P. F.; MORAES, M. L. T.; FREITAS, M. L. M.; SEBBENN, A. M. Understanding the effects of isolation on seed and pollen flow, spatial genetic structure and effective population size of the dioecious tropical tree *Myracrodruon urundeuva*. **Conservation Genetics**, Dordrecht, v. 11, n. 5, p. 1631-1643, 2010.

GAOUE, O. G.; LEMES, M. R.; TICKTIN, T.; SINSIN, B.; EYOG-MATIG, O. Non-timber forest product harvest does not affect the genetic diversity of a tropical tree despite negative effects on population fitness. **Biotropica,** Washington, v. 46, n. 6, p. 756–762, 2014.

GARCIA, C.; ARROYO, J. M.; GODOY, J. A.; JORDANO, P. Mating patterns, pollen dispersal, and the ecological maternal neighbourhood in a *Prunus mahaleb* L. population. **Molecular Ecology**, Oxford, v. 14, n. 6, p. 1821–1830, 2005.

GARCIA, C.; JORDANO, P.; GODOY, J. A. Contemporary pollen and seed dispersal in a *Prunus mahaleb* population: Patterns in distance and direction. **Molecular Ecology**, Oxford, v. 16, n. 9, p. 1947–1955, 2007.

GAUZERE, J.; KLEIN, E. K.; ODDOU-MURATORIO, S. Ecological determinants of mating system within and between three *Fagus sylvatica* populations along an elevational gradient. **Molecular Ecology**, Oxford, v. 22, n. 19, p. 5001–5015, 2013.

GENG, Q.; LIAN, C.; GOTO, S.; TAO, J.; KIMURA, M.; ISLAM, M. S.; HOGETSU, T. Mating system, pollen and propagule dispersal, and spatial genetic structure in a high-density population of the mangrove tree *Kandelia candel*. **Molecular Ecology**, Oxford, v. 17, n. 21, p. 4724–4739, 2008.

GERBER, S.; CHADOEUF, J. L.; GUGERLI, F.; LASCOUX, M.; BUITEVELD, J.; COTTRELL, J.; DOUNAVI, A. FINESCHI, S.; FORREST, L. L.; FOGELQVIST, J.; GOICOECHEA, P. G.; JENSEN, J. S.; SALVINI, D.; VENDRAMIN, G. G.; KREMER, A. High rates of gene flow by pollen and seed in oak populations across Europe. **Plos One**, San Francisco, v. 9, n. 1, p. 1-16, 2014.

GHAZOUL, J. Pollen and seed dispersal among dispersed plants. **Biological Reviews**, Oxford, v. 80, n. 3, p. 413-443, 2005.

GILLET, E.; HATTEMER, H.H. Genetic analysis of isoenzyme phenotypes using single tree progenies. **Heredity**, London, v. 63, p. 135-141, 1989.

GONZAGA, J. M. S.; MANOEL, R. O.; SOUSA, A. C. B.; SOUZA, A. P.; MORAES, M. L. T.; FREITAS, M. L. M.; SEBBENN, A. M. Pollen contamination and nonrandom mating in a *Eucalyptus camaldulensis* Dehnh seedling seed orchard. **Silvae Genetica**, Frankfurt, v. 65, n. 1, p. 1–11, 2016.

GONZALES, E.; HAMRICK, J. L.; SMOUSE, P. E.; TRAPNELL, D. W.; PEAKALL, R. The impact of landscape disturbance on spatial genetic structure in the guanacaste tree, *Enterolobium cyclocarpum* (fabaceae). **Journal of Heredity**, Oxford, v. 101, n. 2, p. 133–143, 2010.

GOOGLE. **Google earth**. [S.l.: s.n., 200-]. Disponível em: <https://www.google.com.br/intl/pt-BR/earth>. Acesso em: 12 fev. 2018.

GOUDET, J. FSTAT. (Version 2.9.3.2.): a computer program to calculate F-statistics. **Heredity**, London, v. 86, n. 6, p. 485-486, 1995.

GOUDET, J. FSTAT. (Version 2.9.3.2.): a computer program to calculate F-statistics. **Journal of Heredity**, Oxford, v. 86, n. 6, p. 485-486, 2002.

GUIDUGLI, M. C. **Estudos genéticos da espécie florestal *Cariniana estrellensis* (Raddi) Kuntez: diversidade, sistema de cruzamento e fluxo gênico comtemporâneo**. 2011. 170 f. Tese (Doutorado)- Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto.

GUIDUGLI, M. C.; NAZARENO, A. G.; FERES, J. M.; CONTEL, E. P. B.; MESTRINER, M. A.; ALZATE-MARIN, A. L. Small but not isolated: a population genetic survey of the tropical tree *Cariniana estrellensis* (Lecythidaceae) in a highly fragmented habitat. **Heredity**, London, v. 116, n. 3, p. 339–347, 2016.

GUIDUGLI, M. C.; ACCORONI, K. A. G.; MESTRINERI, M. A.; CONTELI, E. P. B.; MARTINEZ, C. A.; ALZATE-MARIN, A. L. Genetic characterization of 12 heterologous microsatellite markers for the giant tropical tree *Cariniana legalis* (Lecythidaceae). **Genetics and Molecular Biology**, Ribeirão Preto, v. 1, n. 33, p. 131-134, 2010.

GUIDUGLI, M. C.; CAMPOS, T.; SOUZA, A. C. B.; FERES, J. M.; SEBBENN, A. M.; MESTRINER, M. A.; CONTEL, E. P. B.; ALZATE-MARIN, A. L. Development and characterization of 15 microsatellite loci for *Cariniana estrellensis* and transferability to *Cariniana legalis*, two endangered tropical tree species. **Conservation Genetics**, Dordrecht, v. 10, p. 1001-1004, 2009.

GUPTA, P. K.; VARSHNEY, R. K. The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. **Euphytica**, Netherlands, v. 113, n. 3, p. 163–185, 2000.

HADDAD, N. M.; BRUDVIG, L. A.; CLOBERT, J.; DAVIES, K. F.; GONZALEZ, A.; HOLT, R. D.; LOVEJOY, T. E.; SEXTON, J. O.; AUSTIN, M. P.; COLLINS, C. D.; COOK, W. M.; DAMSCHEN, E. I.; EWERS, R. M.; FOSTER, B. L.; JENKINS, C. N.; KING, A. J.; LAURANCE, W. F.; LEVEY, D. J.; MARGULES, C. R.; MELBOURNE, B. A.; NICHOLLS, A. O.; ORROCK, J. L.; SONG, D.X.; TOWNSHEND, J. R. Habitat fragmentation and its lasting impact on Earth's ecosystems. **Science Advances**, Washington, v. 1, n. 2, p. 1–9, 2015.

HAMILTON, M. B. Tropical tree gene flow and seed dispersal. **Nature**, London, v. 401, n. 9, p. 129-130, 1999.

HAMRICK, J. L.; MURAWSKI, D. A.; NASON, J. D. The influence of seed dispersal mechanisms on the genetic structure of tropical tree populations. **Plant Ecology**, Oxford, v. 107, n. 1, p. 281-297, 1993.

HAMRICK, J. L.; NASON, J. D. Consequences of dispersal in plants. In: RHODES, Jr. O. E.; CHESSER, R. K.; SMITH, M. H. **Population dynamics in ecological space and time**. Chicago: University of Chicago Press, 1992. p. 203–236.

HAMRICK, J. L. Response of forest trees to global environmental changes. **Forest Ecology and Management**, Amsterdam, v. 197, n. 1-3, p. 323-335, 2004.

HANAOKA, S.; YUZURIHARA, J.; ASUKA, Y.; TOMARU, N.; TSUMURA, Y.; KAKUBARI, Y.; MUKAI, Y. Pollen-mediated gene flow in a small, fragmented natural population of *Fagus crenata*. **Canadian Journal of Botany**, Ottawa, v. 85, n. 4, p. 404–413, 2007.

HANSKI, I. **Metapopulation ecology**. Oxford: Oxford University Press, 1999. 328 p.

HANSON, T. R.; BRUNSFELD, S. J.; FINEGAN, B.; WAITS, L. P. Pollen dispersal and genetic structure of the tropical tree *Dipteryx panamensis* in a fragmented Costa Rican landscape. **Molecular Ecology**, Oxford, v. 17, n. 8, p.2060-2073, 2008.

HARDESTY, B. D.; HUBBELL, S. P.; BERMINGHAM, E. Genetic evidence of frequent long-distance recruitment in a vertebrate-dispersed tree. **Ecology Letters**, Oxford, v. 9, n. 5, p. 516–525, 2006.

HARDY, O. J.; GONZÁLEZ-MARTÍNEZ, S. C.; FRÉVILLE, H.; BOQUIEN, G.; MIGNOT, A.; COLAS, B.; OLIVIERI, I. Fine-scale genetic structure and gene dispersal in *Centaurea corymbosa* (Asteraceae) I. Pattern of pollen dispersal. **Evolution Biology**, Landcaster, v. 17, n. 4, p. 795–806, 2004.

HARDY, O. J.; MAGGIA, L.; BANDOU, E.; BREYNE, P.; CARON, H.; CHEVALLIER, M. H.; DOLIGEZ, A.; DUTECH, C.; KREMER, A.; LATOUCHE-HALLÉ, C.; TROISPOUX, V.; VERON, V.; DEGEN, B. Fine-scale genetic structure and gene dispersal inferences in 10 neotropical tree species**. Molecular Ecology**, Oxford, v. 15, n. 2, p. 559–571, 2006.

HARDY, O. J.; VEKEMANS, X. SPAGEDI: a versatile computer program to analyze spatial genetic structure at the individual or population levels. **Molecular Ecology Notes**, Oxford, v. 2, n. 4, p. 618-620, 2002.

HARTL, D. L.; CLARK, A. G. **Princípios de genética de populações**. 4. ed. Porto Alegre: Artmed, 2010. 660 p.

HASEGAWA, Y.; SUYAMA, Y.; SEIWA, K. Pollen donor composition during the early phases of reproduction revealed by DNA genotyping of pollen grains and seeds of *Castanea crenata*. **New Phytologist**, Chichester, v. 182, n. 4, p. 994–1002, 2009.

HEDRICK, P. W. A standardized genetic differentiation measure. **Evolution,** Lancaster, v. 59, n. 8, p. 1633–1638, 2005.

HEDRICK, P. W. Mating systems and evolutionary genetics. In: WOHRMANN, K.; JAIN, S.K. (Ed.). **Population biology**: ecology and evolutionary viewpoints. New York: Springer-Verlag, 1990. p. 83-114.

HEER, K.; KALKO, E. K. V; ALBRECHT, L.; GARCÍA-VILLACORTA, R.; STAEPS, F. C.; HERRE, E. A.; DICK, C. W. Spatial scales of genetic structure in free- standing and strangler figs (Ficus, Moraceae) Inhabiting Neotropical Forests. **Plos One**, San Francisco, v. 10, n. 7, p. 1–18, 2015.

HEUERTZ, M.; VEKEMANS, X.; HAUSMAN, J. F.; PALADA, M.; HARDY, O. J. Estimating seed vs. pollen dispersal from spatial genetic structure in the common ash. **Molecular Ecology**, Oxford, v. 12, n. 9, p. 2483–2495, 2003.

HIRAO, A. S.; KAGEYAMA, P. Y.; OHARA, M.; ISAGI, Y.; KUDO, G. Seasonal changes in pollinator activity influence pollen dispersal and production of the alpine shrub *Rhododendron aureum* (Ericaceae). **Molecular Ecology**, Oxford, v. 15, n. 4, p. 1165-1173, 2006.

HOBAN, S. M.; SCHLARBAUM, S. E.; BROSI, S. L.; ROMERO-SEVERSON, J. A rare case of natural regeneration in butternut, a threatened forest tree, is parent and space limited. **Conservation Genetics**, Dordrecht, v. 13, n. 6, p. 1447–1457, 2012.

HOEBEE, S. E.; ARNOLD, U.; DUGGELIN, C.; GUGERLI, F.; BRODBECK, S.;

ROTACH, P.; HOLDEREGGER, R. Mating patterns and contemporary gene flow by pollen in a large continuous and a small isolated population of the scattered forest tree *Sorbus torminalis*. **Heredity**, London, v. 99, n. 1, p. 47–55, 2007.

HOWE, H. F.; SMALLWOOD, J. Ecology of seed dispersal. **Annual Review of Ecology and Systematics**, Palo Alto, v. 13, p. 201–228, 1982.

IBANES, B.; SEBBENN, A. M.; AZEVEDO, V. C. R.; MORENO, M. A.; GANDARA, F. B.; TAMARUSSI, E. V.; FERRAZ, E. M.; DAMASCENO-SILVA, K. J.; LIMA, P. S. C.; CARVALHAES, M. A. Genetic diversity and spatial genetic structure in populations of *Orbignya phalerata* Mart. under different exploration intensities in the Brazilian savanna. **Silvae Genetica**, Frankfurt, v. 64, n. 5–6, p. 201–211, 2015.

INSTITUTO BRASILEIRO DE GEOGRAFIA E ESTATÍSTICA- IBEGE. **Cidades Mato Grosso do Sul- Bataguassu**. [S.l: s.n., 200-]. Disponível em: <http://cidades.ibge.gov.br>. Acesso em: 13 mar. 2016.

ISAGI, Y.; KANAZASHI, T.; SUZUKI, W.; TANAKA, H.; ABE, T. Microsatellite analysis of the regeneration process of *Magnolia obovata* Thunb. **Heredity**, London, v. 84, n. 2, p. 143–151, 2000.

ISAGI, Y.; SAITO, D.; KAWAGUCHI, H.; TATENO, R.; WATANABE, S. Effective pollen dispersal is enhanced by the genetic structure of an *Aesculus turbinata* population. **Journal of Ecology**, London, v. 95, p. 983–990, 2007.

ISMAIL, S. A.; GHAZOUL, J.; RAVIKANTH, G.; KUSHALAPPA, C. G.; SHAANKER, R. U.; KETTLE, C. J. Fragmentation genetics of *Vateria indica*: implications for management of forest genetic resources of an endemic dipterocarp. **Conservation Genetics**, Dordrecht, v. 15, n. 3, p. 533–545, 2014.

ISMAIL, S. A.; GHAZOUL, J.; RAVIKANTH, G.; UMA SHAANKER, R.; KUSHALAPPA, C. G.; KETTLE, C. J. Does long-distance pollen dispersal preclude inbreeding in tropical trees? Fragmentation genetics of *Dysoxylum malabaricum* in an agro-forest landscape. **Molecular Ecology**, Oxford, v. 21, n. 22, p. 5484–5496, 2012.

IWAIZUMI, M. G.; TAKAHASHI, M.; WATANABE, A.; UBUKATA, M. Simultaneous evaluation of paternal and maternal immigrant gene flow and the implications for the overall genetic composition of *Pinus densiflora* dispersed seeds. **Journal of Heredity**, Oxford, v. 101, n. 2, p. 144–153, 2010.

IWASAKI, T.; SASE, T.; TAKEDA, S.; OHSAWA, T. A.; OZAKI, K.; TANI, N.; IKEDA, H.; SUZUKI, M.; ENDO, R.; TOHEI, K.; WATANO, Y. Extensive selfing in an endangered population of *Pinus parviflora* var. *parviflora* (Pinaceae) in the Boso Hills, Japan. **Tree Genetics and Genomes**, Berlin, v. 9, n. 3, p. 693–705, 2013.

JANZEN, D.H. Euglossine bees as long-distance pollinators of tropical plants. **Science,** Washington, v. 171, n. 3967, p. 203–205, 1971.

JHA, S.; DICK, C. W. Native bees mediate long-distance pollen dispersal in a shade coffee landscape mosaic. **Proceedings of the National Academy of Sciences**, Washington, v. 107, n. 31, p. 1–5, 2010.

JOLIVET, C.; DEGEN, B. Spatial genetic structure in wild cherry (*Prunus avium* L.): II. Effect of density and clonal propagation on spacial genetic structure based on simulation studies**. Tree Genetics & Genomes**, Berlin, v. 7, n. 3, p. 541-552, 2011.

JOLIVET, C.; HÖLTKEN, A. M.; LIESEBACH, H.; STEINER, W.; DEGEN, B. Mating patterns and pollen dispersal in four contrasting wild cherry populations (*Prunus avium* L.). **European Journal of Forest Research**, Kudan-Kita, v. 131, n. 4, p. 1055–1069, 2012.

JONES, F. A.; CHEN, J.; WENG, G-J.; HUBBELL, S. P. A genetic evaluation of seed dispersal in the neotropical tree *Jacaranda copaia* (Bignoniaceae). **American National**, Washington, v. 166, n. 5, p. 543–555, 2005.

JONES, F. A.; HUBBELL, S. P. Demographic spatial genetic structure of the Neotropical tree, *Jacaranda copaia*. **Molecular Ecology**, Oxford, v. 15, n. 11, p. 3205–3217, 2006.

JONES, M. E.; SHEPHERD, M.; HENRY, R.; DELVES, A. Pollen flow in *Eucalyptus grandis* determined by paternity analysis using microsatellite markers. **Tree Genetics & Genomes**, Berlin, v. 4, n. 1, p. 37–47, 2008.

JUMP, A. S.; RICO, L.; COLL, M.; PEÑUELAS, J. Wide variation in spatial genetic structure between natural populations of the European beech (*Fagus sylvatica*) and its implications for SGS comparability. **Heredity**, London, v. 108, n. 6, p. 633–639, 2012.

KALINOWSKI, S. T.; TAPER, M. L.; MARSHALL, T. C. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. **Molecular Ecology**, Oxford, v. 16, n. 5, p. 1099–1106, 2007.

KALINOWSKI, S. T.; WAPLES, R. S. Relationship of effective to census size in fluctuating populations. **Conservation Biology**, Boston, v. 16, n. 1, p. 129–136, 2002.

KAMM, U.; ROTACH, P.; GUGERLI, F.; SIROKY, M.; EDWARDS, P.; HOLDEREGGER, R. Frequent long-distance gene flow in a rare temperate forest tree (*Sorbus domestica*) at the landscape scale. **Heredity**, London, v. 103, n. 6, p. 476-482, 2009.

KASHIMSHETTY, Y.; PELIKAN, S; ROGSTAD S. H. Variable gene dispersal conditions and spatial deforestation patterns can interact to affect tropical tree conservation outcomes. **Plos One,** San Francisco, v. 10, n. 5, p. 1-22, 2015.

KENTA, T.; ISAGI, Y.; NAKAGAWA, M.; YAMASHITA, M.; NAKASHIZUKA, T. Variation in pollen dispersal between years with different pollination conditions in a tropical emergent tree. **Molecular Ecology**, Oxford, v. 13, n. 11, p. 3575–3584, 2004.

KETTLE, C. J.; HOLLINGSWORTH, P. M.; BURSLEM, D. F. R. P.; MAYCOCK, C. R.; KHOO, E.; GHAZOUL, J. Determinants of fine-scale spatial genetic structure in three co-occurring rain forest canopy trees in Borneo: perspectives in plant ecology. **Evolution and Systematics**, Lancaster, v. 13, n. 1, p. 47–56, 2011a.

KETTLE, C. J.; MAYCOCK, C. R.; GHAZOUL, J.; HOLLINGSWORTH, P. M.; KHOO, E.; SUKRI, S. H.; BURSLEM, D. F. R. P. Ecological implications of a flower rize/number trade-off in tropical forest trees. **Plos One**, San Francisco, v. 6, n. 2, p. 1–11, 2011b.

KIMURA, M. K.; GOTO, S.; SUYAMA, Y.; MATSUI, M.; WOESTE, K.; SEIWA, K.

Morph-specific mating patterns in a low-density population of a heterodichogamous tree, *Juglans ailantifolia*. **Plant Ecology**, Oxford, v. 213, n. 9, p. 1477–1487, 2012.

KITTELSON, P. M.; MARON, J. L. Fine-scale genetically based differentiation of life-history traits in the perennial shrub *Lupinus arboreus*. **Evolution**, Lancaster, v. 55, n. 12, p. 2429–2438, 2001.

KLEIN, E. K.; DESASSIS, N.; ODDOU-MURATORIO, S. Pollen flow in the wildservice tree , *Sorbus torminalis* (L.) Crantz . IV . Whole interindividual variance of male fecundity estimated jointly with the dispersal kernel. **Molecular Ecology**, Oxford, v. 17, n. 14, p. 3323–3336, 2008.

KONNERT, M.; MAURER, W.; DEGEN, B.; KÄTZEL, R. Genetic monitoring in forests - early warning and controlling system for ecosystemic changes. **iForest - Biogeosciences and forestry**, Antalya, v. 4, p. 77–81, 2011.

KONUMA, A.; TSUMURA, Y.; LEE, C. T.; LEE, S. L.; OKUDA, T. Estimation of gene flow in the tropical-rainforest tree *Neobalanocarpus heimii* (Dipterocarpaceae), inferred from paternity analysis. **Molecular Ecology,** Oxford, v. 9, n. 11, p. 1843–1852, 2000.

KÖPPEN, W. **Climatologia:** con un estudio de los climas de la tierra. México: Fondo de Cultura Econômica, 1948. 478 p.

KRAMER, A. T.; ISON, J. L.; ASHLEY, M. V.; HOWE, H. F. The paradox of forest fragmentation genetics. **Conservation Biology**, Boston, v. 22, n. 4, p. 878-885, 2008.

KRAUSS, S. L.; HE, T.; BARRETT, L. G.; LAMONT, B. B.; ENRIGHT, N. J.; MILLER, B. P.; HANLEY, M. E. Contrasting impacts of pollen and seed dispersal on spatial genetic structure in the bird-pollinated *Banksia hookeriana*. **Heredity**, London, v. 102, n. 3, p. 274–285, 2009.

KUBOTA, T. Y. K. **Study of flow and contemporary pollen dispersal, mating system, spatial distribution of genotypes and inbreeding depression in fragmented population *Cariniana estrellensis* (Raddi) Kuntze, using microsatellite loci.** 2017. 69 f. Tese (Doutorado) – Faculdade de Engenharia, Universidade Estadual Paulista- UNESP, Ilha Solteira, 2017.

KUBOTA, T. Y. K.; SILVA, A. M.; CAMBUIM, J.; SILVA, A. A.; PUPIN, S.; SILVA, M. S.; MORAES, M. A.; MORAES, M. L. T.; SEBBENN, A. M. Mendelian inheritance, genetic linkage, and genotypic disequilibrium for nine microsatellite loci in *Cariniana estrellensis* (Raddi) Kuntze (Lecythidaceae). **Genetic Molecular Research**, Ribeirão Preto, v. 16, n. 2, p. 1-9, 2017.

LACERDA, A. E. B.; KANASHIRO, M.; SEBBENN, A. M. Effects of reduced impact logging on genetic diversity and spatial genetic structure of a *Hymenaea courbaril* population in the Brazilian Amazon Forest. **Forest Ecology and Management**, Amsterdam, v. 255, n. 3–4, p. 1034–1043, 2008b.

LACERDA, A. E. B.; KANASHIRO, M.; SEBBENN, A. M. 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**, Washington, v. 40, n. 4, p. 462–470, 2008a.

LAGACHE, L.; KLEIN, E. K.; GUICHOUX, E.; PETIT, R. J. Fine-scale environmental control of hybridization in oaks. **Molecular Ecology**, Oxford, v. 22, n. 2, p. 423-436, 2012.

LANDER, T. A.; BOSHIER, D. H.; HARRIS, S. A. Fragmented but not isolated: Contribution of single trees, small patches and long-distance pollen flow to genetic connectivity for *Gomortega keule*, an endangered Chilean tree. **Biological Conservation**, Boston, v. 143, n. 11, p. 2583–2590, 2010.

LARSEN, S. A.; KJAER, D. Pollen mediated gene flow in a native population of *Malus sylvestris* and its implications for contemporary gene conservation management. **Conservation Genetics**, Dordrecht, v. 10, n. 6, p. 1637-1646, 2009.

LATOUCHE-HALLÉ, C.; RAMBOER, A.; BANDOU, E.; CARON, H.; KREMER, A. Long-distance pollen flow and tolerance to selfing in a neotropical tree species. **Molecular Ecology**, Oxford, v. 13, n. 5, p. 1055–1064, 2004.

LEAL, J. B.; SANTOS, R.P.; GAIOTTO, F. A. Effect of selective logging on genetic diversity and gene flow in *Cariniana legalis* sampled from a cacao agroforestry system. **Genetic Molecular Research**, Ribeirão Preto, v. 13, n. 1, p. 626–635, 2014.

LEE, S. L.; NG, K. K. S.; SAW, L. G.; LEE, C. T.; MUHAMMAD, N.; TANI, N.; TSUMURA, Y.; KOSKELA, J. Linking the gaps between conservation research and conservation management of rare dipterocarps: A case study of *Shorea lumutensis*. **Biological Conservation**, Boston, v. 131, n. 1, p. 72–92, 2006.

LEITE, E. J. State-of-knowledge on *Cariniana estrellensis* (Raddi) Kuntze (Lecythidaceae) for genetic conservation in Brazil. **Research Journal Botanic,** New York, v. 2, n. 3, p. 138–160, 2007.

LEMES, M. R.; GRIBEL, R.; PROCTOR, J.; GRATTAPAGLIA, D. Population genetic structure of mahogany (*Swietenia macrophylla* King, Meliaceae) across the Brazilian Amazon, based on variation at microsatellite loci: implications for conservation. **Molecular Ecology**, Oxford, v. 12, n. 11, p. 2875-2883, 2003.

LEONARDUZZI, C.; PIOTTI, A.; SPANU, I.; VENDRAMIN, G. G. Effective gene flow in a historically fragmented area at the southern edge of silver fir (*Abies alba* Mill .) distribution. **Tree Genetics & Genomes**, Berlin, v. 12, n. 95, p. 1–14, 2016.

LEPSCH-CUNHA, N.; MORI, S. A. Reproductive phenology and mating potential in a low density tree population of *Couratari multiflora* (Lecythidaceae) in central Amazonia. **Journal of Tropical Ecology**, Cambridge, v. 15, n. 1, p. 97-121, 1999.

LEVIN, D. A.; KERSTER, H. W. Gene flow in seed plants. **Evolution Biology,** Lancaster, v. 7, p. 139–220, 1974.

LEVIN, D. A. The paternity pool plants. **The American Naturalist**, Chicago, v. 132, n. 3, p. 309-317, 1998.

LIAN, C.; MIWA, M.; HOGETSU, T. Outcrossing and paternity analysis of *Pinus densiflora* (Japanese red pine) by microsatellite polymorphism. **Heredity**, London, v. 87, n. 1, p. 88–98, 2001.

LISBOA, D. O.; SILVA, M. A.; MACHADO, A. R.; PINHO, D. B.; BORGES, L. S.; PEREIRA, O. L.; FURTADO, G. Q. First report of botryosphaeriaceous fungi causing canker on *Cedrela fissilis* and leaf spots on *Cariniana estrellensis* in forest nursery in Brazil. **Forest Pathology**, Berlin, v. 46, n. 4, p. 362–365, 2016.

LOBO, J. A.; QUESADA, M.; STONER, K.E. Effects of pollination by bats on the mating system of *Ceiba pentandra* (Bombacaceae) populations in two tropical life zones in Costa Rica. **American Journal of Botany**, Columbus, v. 92, n. 2, p. 370-376, 2005.

LOISELLE, B. A.; SORK, V. L.; NASON, J.; GRAHAM, C. Spatial genetic structure of a tropical understory shrub, *Psychotria officinalis* (Rubiaceae). **American Journal of Botany**, Columbus, v. 82, n. 11, p. 1420-1425, 1995.

LLORENS, T. M.; BYRNE, M.; YATES, C. J.; NISTELBERGER, H. M.; COATES, D. J. Evaluating the influence of different aspects of habitat fragmentation on mating patterns and pollen dispersal in the bird pollinated *Banksia sphaerocarpa* var. *caesia*. **Molecular Ecology**, Oxford, v. 21, n. 2, p. 314-328, 2012.

LÓPEZ-URIBE, M. M.; OI, C. A.; DEL LAMA, M. A. Nectar-foraging behavior of *Euglossine bees* (Hymenoptera: Apidae) in urban areas. **Apidologi**, v. 39, n. 4, p. 410–418, 2008.

LORENZI, H. **Árvores brasileiras**: manual de identificação e cultivo de plantas arbóreas nativas do Brasil. São Paulo. 4. ed. Nova Odessa: Instituto Plantarum, 2002. 352 p.

LOURMAS, M.; KJELLBERG, F.; DESSARD, H.; JOLY, H. I.; CHEVALLIER, M. Reduced density due to logging and its consequences on mating system and pollen flow in the African mahogany *Entandrophragma cylindricum*. **Heredity**, London, v. 99, n. 2, p. 151–160, 2007.

LOVELESS, M. D.; HAMRICK, J. L. Ecological determinants of genetic structure in plants populations. **Annual Review of Ecology and Systematics**, Palo Alto, v. 15, n. 1, p. 65–95, 1984.

LOWE, A.J.; CAVERS, S.; BOSHIER, D.; BREED, M.F.; HOLLINGSWORTH, P.M. The resilience of forest fragmentation genetics—no longer a paradox—we were just looking in the wrong place. **Heredity**, London, v. 115, n. 2, p. 97–99, 2015.

LYNCH, M.; GABRIEL, W. Mutation load and the survival of small population. **Evolution,** Lancaster, v. 44, n. 7, p. 1725-1737, 1990.

MANOEL, R. O.; ALVES, P. F.; DOURADO, C.; GAINO, A. P. S. C.; FREITAS, M. L. M.; MORAES, M. L. T.; SEBBENN, A. M. Contemporary pollen flow, mating patterns and effective population size inferred from paternity analysis in a small fragmented population of the Neotropical tree *Copaifera langsdorffii* Desf. (Leguminosae-Caesalpinioideae). **Conservation Genetics**, Dordrecht, v. 13, n. 3, p. 613-623, 2012a.

MANOEL, R. O.; CARDIN, L. T.; MOREIRA, J. P.; SILVA, E. C. B.; KUBOTA, T. Y. K.; FREITAS, M. L.M.; MORAES, M. L. T.; SEBBENN, A. M. Sistema de reprodução, parentesco e tamanho efetivo em sementes de polinização livre de populações fragmentadas de *Copaifera langsdorffii* Desf. por análise de locos microssatélites. **Scientia Forestalis**, Piracicaba, v. 40, n. 94, p. 145-155, 2012b.

MARCHELLI, P.; SMOUSE, P. E.; GALLO, L. A. Short-distance pollen dispersal for an outcrossed, wind-pollinated southern beech (*Nothofagus nervosa* (Phil.) Dim. et Mil.). **Tree Genetics and Genomes**, Berlin, v. 8, n. 5, p. 1123–1134, 2012.

MARSHALL, T. C.; SLATE, J.; KRUUK, L. E. B.; PEMBERTON J. M. Statistical confidence for likelihood-based paternity inference in natural populations. **Molecular Ecology**, Oxford, v. 7, n. 5, p. 639–655, 1998.

MARTINS, K.; RAPOSO, A.; KLIMAS, C. A.; VEASEY, E. A.; KAINER, K.; WADT, L. H. O. Pollen and seed flow patterns of *Carapa guianensis* Aublet . (Meliaceae) in two types of Amazonian forest. **Genetics and Molecular Biology**, Ribeirão Preto, v. 35, n. 4, p. 818–826, 2012.

MASUDA, S.; TANI, N.; UENO, S.; LEE, S. L.; MUHAMMAD, N.; KONDO, T.; NUMATA, S.; TSUMURA, Y. Non-density dependent pollen dispersal of *Shorea maxwelliana* (Dipterocarpaceae) revealed by a Bayesian mating model based on paternity analysis in two synchronized flowering seasons. **Plos One**, San Francisco, v. 8, n. 12, p. 1–12, 2013.

MATTHIES D.; BRAÜER I.; MAIBOM W.; TSCHARNTKE, T. Population size and the risk of local extinction: empirical evidence from rare plants. **Oikos**, Copenhagen, v. 105, n. 3, p. 481–488, 2004.

MEAGHER, T.R. Analysis of paternity within a natural population of *Chamaelirium luteum*. I. Identification of most-likely male parents. **American Naturalist**, Chicago, v. 128, n. 2, p. 199–215, 1986.

MEAGHER, T. R.; THOMPSON, E. Analysis of parentage for naturally established seedlings of *Chamaelirium luteum* (Liliaceae). **Ecology**, Washington, v. 68, n. 4, p. 803–812, 1987.

MEDINA-MACEDO, L.; DE LACERDA, A. E. B.; SEBBENN, A. M.; RIBEIRO, J. Z.; SOCCOL, C. R.; BITTENCOURT, J. V. M. Using genetic diversity and mating system parameters estimated from genetic markers to determine strategies for the conservation of *Araucaria angustifolia*(Bert.) O. Kuntze (Araucariaceae). **Conservation Genetics**, Dordrecht, v. 17, n. 2, p. 413–423, 2015b.

MEDINA-MACEDO, L.; SEBBENN, A. M.; LACERDA, A. E. B.; RIBEIRO, J. Z.; SOCCOL, C. R.; BITTENCOURT, J. V. M. High levels of genetic diversity through pollen flow of the coniferous *Araucaria angustifolia*: a landscape level study in Southern Brazil. **Tree Genetics & Genomes**, Berlin, v. 11, n. 814, p. 1–14, 2015a.

MELO JUNIOR, A. F.; CARVALHO, D.; POVOA, J. S. R.; BEARZOTI, E. Estrutura genética de populações naturais de pequizeiro (*Caryocar brasiliensi* Camb). **Scientia Forestalis**, Piracicaba, v. 1, n. 66, p. 56-65, 2004.

MELO, A. T. DE O.; FRANCESCHINELLI, E. V. Gene flow and fine-scale spatial genetic structure in *Cabralea canjerana* (Meliaceae), a common tree species from the Brazilian Atlantic forest. **Journal of Tropical Ecology**, Cambridge, v. 32, n. 2, p. 135–145, 2016.

MILLAR, M. A.; BYRNE, M.; NUBERG, I. K.; SEDGLEY, M. High Levels of Genetic Contamination in Remnant Populations of *Acacia saligna* from a Genetically Divergent Planted Stand. **Restoration Ecology**, Washington, v. 20, n. 2, p. 260–267, 2012.

MILLAR, M. A.; BYRNE, M.; NUBERG, I.; SEDGLEY, M. High outcrossing and random pollen dispersal in a planted stand of *Acacia saligna* subsp. *saligna* revealed by paternity analysis using microsatellites. **Tree Genetics and Genomes**, Berlin, v. 4, n. 3, p. 367–377, 2008.

MILLERÓN, M.; HEREDIA, U. L.; LORENZO, Z.; PEREA, R.; DOUNAVI, A.; ALONSO, J.; GIL, L.; NANOS, N. Effect of canopy closure on pollen dispersal in a wind-pollinated species (*Fagus sylvatica* L.). **Plant Ecology**, Oxford, v. 213, n. 11, p. 1715–1728, 2012.

MIMURA, M.; BARBOUR, R. C.; POTTS, B. M.; VAILLANCOURT, R. E.; WATANABE, K. N. Comparison of contemporary mating patterns in continuous and fragmented *Eucalyptus globulus* native forests. **Molecular Ecology**, Oxford, v. 18, n. 20, p. 4180–4192, 2009.

MORAES, M. L. T.; SEBBENN, A. M. Pollen dispersal between isolated trees in the Brazilian Savannah: A case study of the Neotropical tree *Hymenaea stigonocarpa*. **Biotropica**, Washington, v. 43, n. 2, p. 192-199, 2011.

MORAES, M. A.; MORAES, S. M. B.; SILVA, E. C. B.; KUBOTA, T. Y. K.; SILVA, A. M.; RESENDE, M.D.V.; MORAES, M. L. T. Variação genética em progênies de *Jacaranda cuspidifolia* Mart. utilizando o delineamento sistemático tipo leque. **Scientia Forestalis**, v. 41, n. 98, p. 175-184, 2013.

MORAES, M. A.; KUBOTA, T. Y. K.; SILVA, E. C. B.; SILVA, A. M.; CAMBUIM, J.; MORAES, M. L. T.; FURLANI JÚNIOR, E. SEBBENN, A. M. Short Communication Mendelian inheritance, linkage, and genotypic disequilibrium in microsatellite loci of *Hymenaea stigonocarpa* Mart. ex Hayne (Fabaceae-Caesalpinioideae). **Genetics and Molecular Research**, Ribeirão Preto, v. 15, n. 3, p. 1-8, 2016.

MORAN, E. V; CLARK, J. S. Estimating seed and pollen movement in a monoecious plant: a hierarchical Bayesian approach integrating genetic and ecological data. **Molecular Ecology**, Oxford, v. 20, n. 6, p. 1248–1262, 2011.

MOURA, T. M. ; SEBBENN, A. M.; CHAVES, L. J.; COELHO, A. S. G.; OLIVEIRA, G. C. X.; KAGEYAMA, P. Y. Diversidade e estrutura genética espacial em populações fragmentadas de *Solanum* spp . do Cerrado, por meio de locos microssatélites. **Scientia Forestalis**, Piracicaba, v. 37, n. 82, p. 143–150, 2009.

MURAWSKI, D. A.; HAMRICK. J. L. The effect of the density of flowering individuals on the mating systems of nine tropical tree species. **Journal of Heredity,** Oxford, v. 67 p. 167 – 174, 1991.

NAKANISHI, A.; TOMARU, N.; YOSHIMARU, H.; KAWAHARA, T.; MANABE, T.; YAMAMOTO, S. Patterns of Pollen Flow and Genetic Differentiation Among Pollen Pools in Quercus salicina in a Warm Temperate Old – growth Evergreen Broad-leaved Forest. **Silvae Genetica**, Frankfurt, v. 53, n. 5–6, p. 258–264, 2004.

NAKANISHI, A.; TOMARU, N.; YOSHIMARU, H.; MANABE, T.; YAMAMOTO, S. Effects of seed- and pollen-mediated gene dispersal on genetic structure among Quercus salicina saplings. **Heredity**, London, v. 102, n. 2, p. 182–189, 2009.

NAKANISHI, A.; YOSHIMARU, H.; TOMARU, N.; MIURA, M.; MANABE, T.; YAMAMOTO, S.-I. Patterns of pollen flow in a dense population of the insect-pollinated

canopy tree species *Castanopsis sieboldii*. **Journal of Heredity**, Oxford, v. 103, n. 4, p. 547–556, 2012.

NAKANISHI, A.; YOSHIMARU, H.; TOMARU, N.; MIURA, M.; MANABE, T.; YAMAMOTO, S.-I. Inbreeding depression at the sapling stage and its genetic consequences in a population of the outcrossing dominant tree species, *Castanopsis sieboldii*. **Tree Genetics & Genomes**, Berlin, v. 11, n. 62, p. 1–10, 2015.

NDIADE-BOUROBOU, D.; HARDY, O. J.; FAVREAU, B.; MOUSSAVOU, H.; NZENGUE, E.; MIGNOT, A.; BOUVET, J.-M. Long-distance seed and pollen dispersal inferred from spatial genetic structure in the very low–density rainforest tree , *Baillonella toxisperma* Pierre , in Central Africa. **Molecular Ecology**, Oxford, v. 119, n. 22, p. 4949–4962, 2010.

NEWMAN, D.; PILSON, D. Increased probability of extinction due to decreased genetic effective population size: experimental populations of *Clarkia pulchella*. **Evolution**, Lancaster, v. 51, n. 2, p. 354–362, 1997.

NIELSEN, L. R.; KJAER, E. D. Fine-scale gene flow and genetic structure in a relic *Ulmus laevis* population at its northern range. **Tree Genetics & Genomes**, Berlin, v. 6, n. 5, p. 643–649, 2010.

NIGGEMANN, M.; WIEGAND, T.; ROBLEDO-ARNUNCIO, J. J.; BIALOZYT, R. Marked point pattern analysis on genetic paternity data for uncertainty assessment of pollen dispersal kernels. **Journal of Ecology**, London, v. 100, p. 264–276, 2012.

NOREEN, A. M. E.; NIISSALO, M. A.; LUM, S. K. Y.; WEBB, E. L. Persistence of long-distance , insect-mediated pollen movement for a tropical canopy tree species in remnant forest patches in an urban landscape. **Heredity**, London, v. 117, n. 6, p. 472-480, 2016.

O'CONNELL, L. M.; MOSSELER, A.; RAJORA, O. P. Extensive long-distance pollen dispersal in a fragmented landscape maintains genetic diversity in white spruce. **Journal of Heredity**, Oxford, v. 98, n. 7, p. 640–645, 2007.

ODDOU-MURATORIO, S.; BONTEMPS, A.; KLEIN, E K; CHYBICKI I, V. G. G.; SUYAMA, Y. Comparison of direct and indirect genetic methods for estimating seed and pollen dispersal in *Fagus sylvatica* and *Fagus crenata*. **Forest Ecology and Management,** Amsterdam, v. 259, n. 11, p. 2151–2159, 2010.

ODDOU-MURATORIO, S.; KLEIN, E. K. Comparing direct vs . indirect estimates of gene flow within a population of a scattered tree species. **Molecular Ecology**, Oxford, v. 17, n. 11, p. 2743-2754, 2008.

ODDOU-MURATORIO, S.; KLEIN, E. K.; AUSTERLITZ, F. Pollen flow in the wildservice tree , *Sorbus torminalis* (L.) Crantz. II. Pollen dispersal and heterogeneity in mating success inferred from parent – offspring analysis. **Molecular Ecology**, Oxford, v. 14, n. 14, p. 4441–4452, 2005.

OJEDA-CAMACHO, M.; KJÆR, E. D.; PHILIPP, M. Population genetics of *Guibourtia chodatiana* (Hassl.); leonard, in a dry chiquitano forest of Bolivia. **Forest Ecology and Management**, Amsterdam, v. 289, p. 525–534, 2013.

OLIVEIRA, A. F; PÁDUA, J. G; ZUCCHI, M. I.; VENCOVSKY, R.; VIEIRA, M. L. C. Origin, evolution and genome distribution of microsatellites. **Genetics and Molecular Biology**, Ribeirão Preto, v. 29, n. 2, p. 294-307, 2006.

OTTEWELL, K.; GREY, E.; CASTILLO, F.; KARUBIAN, J. The pollen dispersal kernel and mating system of an insect-pollinated tropical palm, *Oenocarpus bataua*. **Heredity**, London, v. 109, n. 6, p. 332–339, 2012.

OYAMA, K.; HERRERA-ARROYO, M. L.; ROCHA-RAMÍREZ, V.; BENÍTEZ-MALVIDO, J.; RUIZ-SÁNCHEZ, E.; GONZÁLEZ-RODRÍGUEZ, A. Gene flow interruption in a recently human-modified landscape: The value of isolated trees for the maintenance of genetic diversity in a Mexican endemic red oak. **Forest Ecology and Management**, Amsterdam, v. 390, p. 27–35, 2017.

PAKKAD, G.; UENO, S.; YOSHIMARU, H. Gene flow pattern and mating system in a small population of *Quercus semiserrata*. **Forest Ecology and Management**, Amsterdam, v. 255, n. 11, p. 3819–3826, 2008.

PANDEY, M.; GAILING, O.; HATTEMER, H. H.; FINKELDEY, R. Fine-scale spatial genetic structure of sycamore maple (*Acer pseudoplatanus* L.). **European Journal of Forest Research**, Heidelberg, v. 131, n. 3, p. 739–746, 2012.

PIOTTI, A.; LEONARDI, S.; BUITEVELD, J.; GEBUREK, T.; GERBER, S.; KRAMER, K.; VETTORI, C.; VENDRAMIN, G. G. Comparison of pollen gene flow among four European beech (*Fagus sylvatica* L.) populations characterized by different management regimes**. Heredity**, London, v. 108, n. 3, p. 322–331, 2012.

PLUESS, A. R. Pursuing glacier retreat: genetic structure of a rapidly expanding *Larix decidua* population. **Molecular Ecology**, Oxford, v. 20, n. 3, p. 473–485, 2011.

PLUESS, A. R.; SORK, V. L.; DOLAN, B.; DAVIS, F. W.; GRIVET, D.; MERG, K.; PAPP, J.; SMOUSE, P. E. Short distance pollen movement in a wind-pollinated tree, *Quercus lobata* (Fagaceae). **Forest Ecology and Management**, Amsterdam, v. 258, n. 5, p. 735–744, 2009.

POSPÍŠKOVÁ, M.; ŠÁLKOVÁ, I. Population structure and parentage analysis of black poplar along the Morava River. **Canadian Journal of Forest Research**, Ottawa, v. 36, n. 5, p. 1067–1076, 2006.

PRANCE, G. T.; MORI, S. A. Lecythidaceae-part 1. **Flora Neotropical Monograph**, New York, v. 21, n. 2, p. 1-272, 1979.

QUESADA, M.; HERRERÍAS-DIEGO, Y.; LOBO, J. A.; SÁNCHEZ-MONTOYA, G.; ROSAS, F.; AGUILAR, R. Long-term effects of habitat fragmentation on mating patterns and gene flow of a tropical dry forest tree, *Ceiba aesculifolia* (Malvaceae: Bombacoideae). **American Journal of Botany**, Baltimore, v. 100, n. 6, p. 1095–1101, 2013.

RAJORA, O.M.; MOSSELER, A. Challenges and opportunities for conservation of forest genetic resources. **Euphytica**, Wageningen, v. 118, n. 2, p. 197-212, 2001.

RAMOS, A. C. S.; LEMOS-FILHO, J. P.; LOVATO, M. B. Phylogeographical structure of the Neotropical forest tree *Hymeneae courbaril* (Leguminosae: Caesalpinioideae) and its

relationship with the vicariant *Hymenaeae stigonocarpa* from Cerrado. **Journal of Heredity**, Oxford, v. 100, n. 2, p. 206-216, 2009.

RAMOS, S. L. F.; DEQUIGIOVANNI, G.; SEBBENN, A. M.; LOPES, M. T. G.; KAGEYAMA, P. Y.; DE MACÊDO, J. L. V.; KIRST, M.; VEASEY, E. A. Spatial genetic structure, genetic diversity and pollen dispersal in a harvested population of *Astrocaryum aculeatum* in the Brazilian Amazon. **BMC Genetics**, London, v. 17, n. 63, p. 1–10, 2016.

RATHMACHER, G.; NIGGEMANN, M.; KÖHNEN, M.; ZIEGENHAGEN, B.; BIALOZYT, R. Short-distance gene flow in *Populus nigra* L. accounts for small-scale spatial genetic structures: implications for in situ conservation measures. **Conservation Genetics**, Dordrecht, v. 11, n. 4, p. 1327–1338, 2010.

RECORD, S. J.; HESS, R. W. **Timbers of the new world:** use and abuse of america's natural resources. New York, Arno, 1972. 640 p.

REED, D. H. Relationship between population size and fitness. **Conservation Biology,** Oxford, v. 19, n. 2, p. 563–568, 2005.

REITZ, R. **Lecitidáceas**. Itajaí: Herbário Barbosa, 1981. 32 p.

RIBEIRO, M. C.; METZGER, J. P.; MARTENSEN, A. C.; PONZONI, F.; HIRATO, M. M. The Brazilian Atlantic Forest: how much is left, and how is the remaining forest distributed? implictions for conservation. **Biology Conservation**, Boston, v. 142, n. 6, p. 1141–1153, 2009.

RICHARDS, C. M.; EMERY, S. N.; McCAULEY, D. E. Genetic and demographic dynamics of small populations of *Silene latifolia.* **Heredity**, London, v. 90, n. 2, p. 181–186, 2003.

RITLAND, K. Correlated matings in the partial selfer Mimulus guttatus. **Evolution**, Lancaster, v. 43, n. 4, p. 848-859, 1989.

RITLAND, K. Extensions of models for the estimation of mating systems using n independent loci. **Heredity**, London, v. 88, n. 4, p. 221-228, 2002.

RITLAND, K.; JAIN, S. A model for the estimation of outcrossing rate and gene frequencies using independent loci. **Heredity**, London, v. 47, n. 1, p. 35-52, 1981.

RITCHIE, A. L.; NEVILL, P. G.; SINCLAIR, E. A.; KRAUSS, S. L. Does restored plant diversity play a role in the reproductive functionality of *Banksia* populations? **Restoration Ecology**, Washington, v. 25, n. 3, p. 414–423, 2017.

ROBLEDO-ARNUNCIO, J. J.; ALÍA, R.; GIL, L. Increased selfing and correlated paternity in a small population of a predominantly outcrossing conifer, *Pinus sylvestris*. **Molecular Ecology,** Oxford, v. 13, n. 9, p. 2567–2577, 2004.

ROBLEDO-ARNUNCIO, J. J.; GIL, L. Patterns of pollen dispersal in a small population of *Pinus sylvestris* L. revealed by total-exclusion paternity analysis. **Heredity**, London, v. 94, n. 1, p. 13–22, 2005.

RODRIGUES, E. B.; COLLEVATTI, R. G.; CHAVES, L. J.; MOREIRA, L. R.; TELLES, M. P. Mating system and pollen dispersal in *Eugenia dysenterica* (Myrtaceae) germplasm

collection: tools for conservation and domestication. **Genetica**, Switzerland, v. 144, n. 2, p. 139–146, 2016.

ROSAS, F.; QUESADA, M.; LOBO, J. A.; SORK, V. L. Effects of habitat fragmentation on pollen flow and genetic diversity of the endangered tropical tree *Swietenia humilis* (Meliaceae). **Biological Conservation**, Beijing, v. 144, n. 12, p. 3082-3088, 2011.

ROUSSET, F. Genetic differentiation between individuals. **Journal of Evolution and Biology,** v. 13, n. 1, p 58–62, 2000.

RYMER, P. D.; SANDIFORD, M.; HARRIS, S. A.; BILLINGHAM, M. R.; BOSHIER, D. H. Remnant *Pachira quinata* pasture trees have greater opportunities to self and suffer reduced reproductive success due to inbreeding depression. **Heredity**, London, v. 115, n. 2, p. 115–124, 2015.

SACCHERI, I.; KUUSSAARI, M.; KANKARE, M.; VIKMAN, P.; FORTELIUS, W.; HANSKI, I. Inbreeding and extinction in a butterfly metapopulation. **Nature**, London, v. 32, n. 2, p.491-494, 1998.

SAGNARD, F.; ODDOU-MURATORIO, S.; PICHOT, C.; VENDRAMIN, G. G.; FADY, B. Effects of seed dispersal, adult tree and seedling density on the spatial genetic structure of regeneration at fine temporal and spatial scales. **Tree Genetics and Genomes**, Berlin, v. 7, n. 1, p. 37–48, 2011.

SÁNCHEZ-ROBLES, J. M.; GARCÍA-CASTAÑO, J. L.; BALAO, F.; TERRAB, A.; NAVARRO-SAMPEDRO, L.; TREMETSBERGER, K.; TALAVERA, S. Effects of tree architecture on pollen dispersal and mating patterns in *Abies pinsapo* Boiss. (Pinaceae). **Molecular Ecology**, Oxford, v. 23, n. 24, p. 6165–6178, 2014.

SANT'ANNA, C. S.; SEBBENN, A. M.; KLABUNDE, G. H. F.; BITTENCOURT, R.; NODARI, R. O.; MANTOVANI, A.; REIS, M. S. Realized pollen and seed dispersal within a continuous population of the dioecious coniferous Brazilian pine [*Araucaria angustifolia* (Bertol.) Kuntze]. **Conservation Genetics**, Dordrecht, v. 13, n. 6, p. 601–613, 2013.

SARO, I.; ROBLEDO-ARNUNCIO, J.; GONZÁLEZ-PÉREZ, M.; SOSA, P. Patterns of pollen dispersal in a small population of the Canarian endemic palm (*Phoenix canariensis*). **Heredity**, London, v. 113, n. 3, p. 215–223, 2014.

SATO, T.; ISAGI, Y.; SAKIO, H.; OSUMI, K.; GOTO, S. Effect of gene flow on spatial genetic structure in the riparian canopy tree *Cercidiphyllum japonicum* revealed by microsatellite analysis. **Heredity**, London, v. 96, n. 1, p. 79–84, 2006.

SCHAWE, C. C.; DURKA, W.; TSCHARNTKE, T.; HENSEN, I.; KESSLER, M. Gene flow and genetic diversity in cultivated and wild cacao (*Theobroma cacao*) In Bolivia. **American Journal of Botany**, Baltimore, v. 100, n. 11, p. 2271–2279, 2013.

SCHUSTER, W. S. F.; MITTON, J. B. Paternity and gene dispersal in limber pine (*Pinus fexilis* James). **Heredity**, London, v. 84, n. 3, p. 348–361, 2000.

SEBBENN, A. M. Sistema de reprodução em espécies arbóreas tropicais e suas implicações para a seleção de árvores matrizes para reflorestamentos ambientais. In: HIGA, A. R.;

SILVA, L. D. (Ed.). **Pomares de sementes de espécies nativas**. Curitiba: FUDEP, 2006. p. 193-198.

SEBBENN, A. M.; CARVALHO, A. C. M.; FREITAS, M. L. M.; MORAES, S. M. B.; SILVA, J. M.; JOLIVET, C.; MORAES, M. L. T. Low levels of realized seed and pollen gene flow and strong spatial genetic structure in a small, isolated and fragmented population of the tropical tree *Copaifera langsdorffii* Desf. **Heredity**, London, v. 106, n. 1, p. 134-145, 2011.

SEBBENN, A. M.; KAGEYAMA, P. Y.; SIQUEIRA, A. C. M. F.; ZANATTO, A. C. S. Mating system in populations of *Cariniana legalis* Mart. O. Ktze: implications for genetic conservation and improvement. **Scientia Forestalis**, Piracicaba, v. 58, p. 25–40, 2000.

SEBBENN, A. M.; LICONA, J. C.; MOSTACEDO, B.; DEGEN, B. Gene flow in an overexploited population of *Swietenia macrophylla* King (Meliaceae) in the Bolivian Amazon. **Silvae Genetica**, Frankfurt, v. 61, n. 4–5, p. 212–220, 2012.

SEBBENN, A. M.; SEOANE, C. E. Estimativa de tamanho efetivo de endogamia por marcadores genéticos. **Revista Arvore**, Viçosa, v. 29, n. 1, p. 1-7, 2005.

SEBBENN, A.M.; KAGEYAMA, P.Y.; VENCOVSKY, R. Conservação genética *in situ* e número de matrizes para a coleta de sementes em população de *Genipa americana*. **Scientia Forestalis**, Piracicaba, v. 63, p. 13-22, 2003.

SEBBENN, A.M.; KAGEYAMA, P.Y.; VENCOVSKY, R. Variabilidade genética, sistema reprodutivo e estrutura genética espacial em *Genipa americana* L. através de marcadores isoenzimáticos. **Scientia Forestalis**, Piracicaba, v. 53, p. 15-30, 1998.

SETSUKO, S.; ISHIDA, K.; UENO, S.; TSUMURA, Y.; TOMARU, N. Population differentiation and gene flow in a metapopulation of a threatened tree, *Magnolia stellata* (Magnoliaceae). **American Journal of Botany**, Baltimore, v. 94, n. 1, p. 128–136, 2007.

SETSUKO, S.; NAGAMITSU, T.; TOMARU, N. Pollen flow and effects of population structure on selfing rates and female and male reproductive success in fragmented *Magnolia stellata* populations. **BMC Ecology**, London, v. 13, n. 10, p. 1-12, 2013.

SHIMONO, A.; WANG, X.; TORIMARU, T.; LINDGREN, D.; KARLSSON, B. Spatial variation in local pollen flow and mating success in a *Picea abies* clone archive and their implications for a novel “breeding without breeding” strategy. **Tree Genetics & Genomes**, Berlin, v. 7, n. 3, p. 499–509, 2011.

SHURI, K.; SAIKA, K.; JUNKO, K.; MICHIHARU, K.; NAGAMITSU, T.; IWATA, H.; TSUMURA, Y.; MUKAI, Y. Impact of negative frequency-dependent selection on mating pattern and genetic structure: a comparative analysis of the S -locus and nuclear SSR loci in *Prunus lannesiana* var . speciosa. **Heredity**, London, v. 109, n. 1, p. 188–198, 2012.

SILJAMO, P.; SOFIEV, M.; SEVEROVA, E.; RANTA, H.; KUKKONEN, J.; POLEVOVA, S. KUBIN, E.; MININ, A. Sources, impact and exchange of early-spring birch pollen in the Moscow region and Finland. **Aerobiologia**, v. 24, n. 4, p. 211–230, 2008.

SILVA, C. R. S.; ALBUQUERQUE, P. S. B.; ERVEDOSA, F. R.; MOTA, J. W. S.; FIGUEIRA, A.; SEBBENN, A. M. Understanding the genetic diversity, spatial genetic structure and mating system at the hierarchical levels of fruits and individuals of a continuous

Theobroma cacao population from the Brazilian Amazon. **Heredity**, London, v. 106, n. 6, p. 973–985, 2011a.

SILVA, M. B.; KANASHIRO, M.; CIAMPI, A. Y.; THOMPSON, I.; SEBBENN, A. M. Genetic effects of selective logging and pollen gene flow in a low-density population of the dioecious tropical tree *Bagassa guianensis* in the Brazilian Amazon. **Forest Ecology and Management**, Amsterdam, v. 255, n. 5–6, p. 1548–1558, 2008.

SILVA, P. H. M.; POGGIANI, F.; SEBBENN, A. M.; MORI, E. S. Can Eucalyptus invade native forest fragments close to commercial stands? **Forest Ecology and Management**, Amsterdam, v. 261, n. 11, p. 2075–2080, 2011b.

SLATKIN, M. Gene flow and the geographic structure of natural populations. **Science**, Washington, v. 236, n. 4803, p. 787, 1987.

SLAVOV, G.T.; LEONARDI, S.; BURCZYK, J.; ADAMS, T.; STRAUSS, S.H.; DIFAZIO, S. P. Extensive pollen flow in two ecologically contrasting populations of *Populus trichocarpa.* **Molecular Ecology**, Oxford, v. 18, n. 2, p. 357–373, 2009.

SMOUSE, P. E.; SORK, V. L. Measuring pollen flow in forest trees: an exposition of alternative approaches. **Forest Ecology Management**, Amsterdam, v. 197, n. 1-3, p. 21–38, 2004.

SMOUSE, P.E.; PEAKALL, R. Spatial autocorrelation analysis of individual multiallele and multilocus genetic structure. **Heredity**, London, v. 82, p. 561–573, 1999.

SORK, V. L.; DAVIS, F. W.; SMOUSE, P. E.; APSIT, V. J.; DYER, R. J.; FERNANDEZ-M, J. F. Pollen movement in declining populations of California Valley oak, *Quercus lobata*: where have all the fathers gone? **Molecular Ecology**, Oxford, v. 11, n. 9, p. 1657–1668, 2002.

SORK, V. L.; SMOUSE, P. E.; GRIVET, D.; SCOFIELD, D. G. Impact of asymmetric male and female gamete dispersal on allelic diversity and spatial genetic structure in valley. **Evolutionary Ecology**, Arizona, v. 29, n. 6, p. 927–945, 2015.

SPIELMAN, D.; BROOK, B. W.; FRANKHAM, R. Most species are not driven to extinction before genetic factors impact them. **Proceedings of the National Academy of Sciences,** Washington, v. 101, n. 15, p. 261-264, 2004.

SPOLADORE, J.; MONSANO, V. F.; LEMES, M. R.; FREITAS, L. C. D. ; SEBBENN, A. M. Genetic conservation of small populations of the endemic tree *Swartzia glazioviana* (Taub.) Glaz. (Leguminosae) in the Atlantic. **Conservation Genetics**, Dordrecht, v. 18, n. 5, p. 1105–1117, 2017.

STEFENON, V. M.; GAILING, O.; FINKELDEY, R. Genetic structure of *Araucaria angustifolia* (Araucariaceae) populations in Brazil: Implications for the in situ conservation of genetic resources. **Plant Biology**, Oxford, v. 9, n. 4, p. 516–525, 2007.

STREIFF, R.; DUCOUSSO, A.; LEXER, C.; STEINKELLNER, H.; GLOESSL, J.; KREMER, A. Pollen dispersal inferred from paternity analysis in a mixed oak stand of *Quercus robur* L. *and Q. petrae* Liebl**. Molecular Ecology**, Oxford, v. 8, n. 5, p. 831–841, 1999.

TAMBARUSSI, E. V.; BOSHIER, D.; VENCOVSKY, R.; FREITAS, M. L. M.; SEBBENN, A. M. Inbreeding depression from selfing and mating between relatives in the Neotropical tree *Cariniana legalis* Mart. Kuntze. **Conservation Genetics**, Dordrecht, v. 18, n. 1, p. 225–234, 2016.

TAMBARUSSI, E. V.; BOSHIER, D. H.; VENCOVSKY, R. FREITAS, M. L. M.; SEBBENN, A. M. Inbreeding depression from selfing and mating between relatives in the Neotropical tree *Cariniana legalis* Mart. Kuntze. **Conservation Genetics,** v. 18, n. 1, p. 225–234, 2017.

TAMBARUSSI, E.V.; SEBBENN, A.M.; MORENO, M.A.; FERRAZ, E.M.; KAGEYAMA, P. Y.; VENKOVSKY, R. Microsatellite markers for *Cariniana legalis* (Lecythidaceae) and their transferability to *Cariniana estrellensis*. **Applications in Plant Sciences**, v. 1, n. 6, p. 1-3, 2013a.

TAMBARUSSI, E. V.; VENCOVSKY, R.; FREITAS, M. L. M.; SEBBENN, A. M. Mendelian inheritance, genetic linkage, and genotypic disequilibrium at nine microsatellite loci of *Cariniana legalis* (Mart.) O. Kuntze. **Genetics and Molecular Research**, Ribeirão Preto, v. 12, n. 4, p. 5442-5457, 2013.

TAMBARUSSI, E.V.; BOSHIER, D.; VENCOVSKY, R.; FREITAS, M.L.M.; SEBBENN, A.M. Paternity analysis reveals significant isolation and near neighbor pollen dispersal in small *Cariniana legalis* Mart. Kuntze populations in the Brazilian Atlantic Forest. **Ecology and Evolution**, Oxford, v. 5, n. 23, p. 5588-5600, 2015.

TANI, N.; TSUMURA, Y.; FUKASAWA, K.; KADO, T.; TAGUCHI, Y.; LEE, S. L.; LEE, C. T.; MUHAMMAD, N.; NIIYAMA, K.; OTANI, T.; YAGIHASHI, T.; RIPIN, A.; KASSIM, A. R. Male fecundity and pollen dispersal in hill dipterocarps : significance of mass synchronized flowering and implications for conservation. **Journal of Ecology**, London, v. 100, n. 2, p. 405–415, 2012.

TARAZI, R.; SEBBENN, A.M.; KAGEYAMA, P.Y.; VENCOVSKY, R. Edge effects enhance selfing and seed harvesting efforts in the insect-pollinated Neotropical tree *Copaifera langsdorffii* (Fabaceae). **Heredity**, London, v. 110, n. 6, p. 578-585, 2013a.

TARAZI, R.; SEBBENN, A.M.; KAGEYAMA, P.Y.; VENCOVSKY, R. Long-distance dispersal in a fire- and livestock-protected savanna. **Ecology and Evolution**, Amsterdam, v. 3, n. 4, p. 1003-1015, 2013b.

THOMASSET, M.; HODKINSON, T. R.; RESTOUX, G.; FRASCARIA-LACOSTE, N.; DOUGLAS, G. C.; FERNÁNDEZ-MANJARRÉZ, J. F. Thank you for not flowering : conservation genetics and gene flow analysis of native and non-native populations of *Fraxinus* (Oleaceae) in Ireland. **Heredity**, London, v. 112, n. 6, p. 596–606, 2014.

TORIMARU, T.; WENNSTRÖM, U.; LINDGREN, D.; WANG, X. R. Effects of male fecundity, interindividual distance and anisotropic pollen dispersal on mating success in a Scots pine (*Pinus sylvestris*) seed orchard. **Heredity**, London, v. 108, n. 3, p. 312–321, 2012.

TSUDA, Y.; NAKAO, K.; IDE, Y.; TSUMURA, Y. The population demography of *Betula maximowicziana* , a cool-temperate tree species in Japan , in relation to the last glacial period: its admixture-like genetic structure is the result of simple population splitting not admixing. **Molecular Ecology**, Oxford, v. 24, n. 7, p. 1403–1418, 2015.

VALBUENA-CARABAÑA, M; GONZÁLEZ-MARTÍNEZ, S. C.; SORK, V. L.; COLLADA, C; SOTO, A; GOICOECHEA, P. G.; GIL, L. Gene flow and hybridisation in a mixed oak forest (*Quercus pyrenaica* Willd. and *Quercus petraea* (Matts.) Liebl.) in central Spain. **Heredity**, London, v. 95, n. 6, p. 457–465, 2005.

VEKEMANS, X., HARDY, O. J. New insights from fine-scale spatial genetic structure analyses in plant populations. **Molecular Ecology**, Oxford, v. 13, n. 4, p. 921–935, 2004.

VINSON, C. C.; DAL'SASSO, T. C. S.; SUDRÉ, C. P.; MANGARAVITE, E.; OLIVEIRA, L. O. Population genetics of the naturally rare tree *Dimorphandra wilsonii* (Caesalpinioideae) of the Brazilian Cerrado. **Tree Genetics & Genomes**, Berlin, v. 11, n. 46, p. 1–10, 2015a.

VINSON, C. C.; KANASHIRO, M.; HARRIS, S. A.; BOSHIER, D. H. Impacts of selective logging on inbreeding and gene flow in two Amazonian timber species with contrasting ecological and reproductive characteristics. **Molecular Ecology**, Oxford, v. 24, n. 1, p. 38–53, 2015b.

VRANCKX, G.; JACQUEMYN, H.; MERGEAY, J.; COX, K.; KINT, V.; MUYS, B.; HONNAY, O. Transmission of genetic variation from the adult generation to naturally established seedling cohorts in small forest stands of pedunculate oak (*Quercus robur* L.). **Forest Ecology and Management**, Amsterdam, v. 312, p. 19–27, 2014a.

VRANCKX, G.; MERGEAY, J.; COX, K.; MUYS, B.; JACQUEMYN, H.; HONNAY, O. Tree density and population size affect pollen flow and mating patterns in small fragmented forest stands of pedunculate oak (*Quercus robur* L.). **Forest Ecology and Management**, Amsterdam, v. 328, p. 254–261, 2014b.

WANG, J.; KANG, M.; GAO, P.; HUANG, H. Contemporary pollen flow and mating patterns of a subtropical canopy tree *Eurycorymbus cavaleriei* in a fragmented agricultural landscape. **Forest Ecology and Management**, Amsterdam, v. 260, n. 12, p. 2180-2188, 2010.

WANG, J.; KANG, M.; HUANG, H. Long-distance pollen dispersal ensures genetic connectivity of the low-density tree species, *Eurycorymbus cavaleriei*, in a fragmented karst forest landscape. **Conservation Genetics**, Dordrecht, v. 15, n. 5, p. 1163–1172, 2014.

WANG, J.; YE, Q.; KANG, M.; HUANG, H. Novel polymorphic microsatellite loci and patterns of pollen-mediated gene flow in an *ex situ* population of *Eurycorymbus cavaleriei* (Sapindaceae) as revealed by categorical paternity analysis. **Conservation Genetics**, Dordrecht, v. 9, n. 3, p. 559-567, 2008.

WANG, K. S. Gene flow in European beech (*Fagus sylvatica* L .). **Genetica**, Switzerland, v. 122, n. 2, p. 105–113, 2004.

WANG, R.; AI, B.; GAO, B.Q.; YU, S.; LI, Y. Y.; CHEN, X. Y. Spatial genetic structure and restricted gene flow in a functionally dioecious fig, *Ficus pumila* L . var . *pumila* (Moraceae). **Population Ecology**, v. 51, n. 2, p. 307–315, 2009.

WEI, Z.; QU, Z.; HOU, C.; LIU, Y.; ZHANG, L.; YANG, C.; WEI, H. Genetic diversity and paternal analysis of open-pollinated progenies of *Larix olgensis* seed orchard. **Journal of Nature and Science**, Los Angeles, v. 1, n. 1, p. 1–6, 2015.

WILLI, Y.; Van BUSKIRK, J.; FISHER, M. A threefold genetic allele effect: population size effects load in the self compatibility, inbreeding depression and drift load in the self-incompatible *Ranunculus reptans*. **Genetics**, Austin, v. 169, n. 4, p. 2255– 265, 2005.

WILLIAMS, C. G.; LADEAU, S. L.; OREN, R.; KATUL, G. G. Modeling seed dispersal distances: implications for transgenic pinus taeda. **Ecological Applications**, Washington, v. 16, n. 1, p. 117–124, 2006.

WRIGHT, S. Systems of mating. **Genetics**, Austin, v. 6, n. 4, p. 11-178, 1921.

YAO, X.; ZHANG, J.; YE, Q.; HUANG, H. Fine-scale spatial genetic structure and gene flow in a small, fragmented population of *Sinojackia rehderiana* (Styracaceae), an endangered tree species endemic to China. **Plant Biology**, Oxford, v. 13, n. 2, p. 401–410, 2011.

YINEGER, H.; SCHMIDT, D. J.; TEKETAY, D.; ZALUCKI, J.; HUGHES, J. M. Gene dispersal inference across forest patches in an endangered medicinal tree: comparison of model-based approaches. **Biological Journal of the Linnean Society**, Oxford, v. 114, n. 4, p. 887–904, 2015.

YOUNG, A.; BOYLE, T. Forest Fragmentation. In: YOUNG, A.; BOSHIER, D.; BOYLE, T. (Ed.). **Forest conservation genetics:** principles and practice.) Collingwood: CSIRO Publishing, 2000. p. 123-132.

YOUNG, A. G., MERRIAM, H. G. Effects of forest fragmentation on the spatial genetic structure of *Acer saccharum* Marsh (Sugar Maple) populations. **Heredity**, London, v. 72, n. 2, p. 201–208, 1994.

ZHANG, J.; YE, Q.; YAO, X.; HUANG, H. Microsatellite diversity and mating system of *Sinojackia xylocarpa* (Styracaceae), a species extinct in the wild. **Biochemical Systematics and Ecology**, Oxford, v. 38, n. 2, p. 154–159, 2010.

ZHOU, H. P.; CHEN, J. Spatial genetic structure in an understorey dioecious fig species: The roles of seed rain, seed and pollen-mediated gene flow, and local selection. **Journal of Ecology**, Cambridge, v. 98, n. 5, p. 1168–1177, 2010.