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BÁRBARA LINS CALDAS DE MORAES

"O EFEITO DAS MUDANÇAS CLIMÁTICAS E ALTERAÇÕES DE PAISAGENS NATURAIS SOBRE A DISTRIBUIÇÃO E DIVERSIDADE GENÉTICA DE PRIMATAS NO NORDESTE"

RECIFE
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Tese apresentada ao Curso de Pós-Graduação em Biologia Animal, Área de Concentração Centro de Biociências, da Universidade Federal de Pernambuco, como requisito à obtenção do título de Doutora em Biologia Animal.

Área de concentração: Biologia Animal

Orientadora: Profª. Drª Bruna Martins Bezerra

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RESUMO

Brasil possui uma posição de destaque em termos de biodiversidade de primatas com cerca de 115 espécies, mas cerca de 60% destas encontram-se ameaçadas de extinção. A agricultura e pecuária são as principais ameaças, devido a perda e fragmentação dos hábitats. Desta forma, estudos que avaliem o efeito da paisagem sobre a distribuição e dinâmica populacional de espécies são necessários para o planejamento de ações mitigadoras desses impactos antrópicos. O presente estudo objetivou avaliar as consequências das mudanças climáticas sob a distribuição espacial de três espécies de primatas do nordeste do Brasil e o efeito da paisagem na diversidade genética de populações de *Sapajus libidinosus* no estado de Pernambuco. No capítulo um dessa tese de doutorado foi avaliada a viabilidade a longo prazo de habitats adequados para a conservação de *Sapajus libidinosus* e de mais dois primatas brasileiros ameaçados (*Alouatta belzebul* e *Sapajus flavius*). Para tanto, foi realizada a identificação de áreas de distribuições atuais e futuras dessas espécies, a quantificação da presença de áreas protegidas e prioritárias, as estimativas da extensão da cobertura florestal remanescente e de hábitats futuros disponíveis para a manutenção e conservação das espécies frente a diferentes cenários de mudanças climáticas. Constatou-se que o estabelecimento de populações de primatas e sua capacidade de sobreviver nessas áreas a longo prazo estão sob risco. Nas condições atuais, 88% das áreas adequadas para as três espécies estão fora de áreas protegidas. Além disso projeções futuras, considerando um cenário severo de mudança climática, indicaram que *A. belzebul*, *S. flavius* e *S. libidinosus* podem perder até 93,64%, 97,66% e 54% de hábitats adequados, respectivamente. No capítulo dois, foi testado a transferibilidade de 14 marcadores microssatélites para uso em análises populacionais de *S. libidinosus*. Descobrimos que seis dos marcadores microssatélites testados (tetra-nucleotídeo) amplificaram em nossa espécie-alvo, *S. libidinosus*. Todos os *loci* foram polimórficos. O número de alelos variou de 4 a 7 e a heterozigosidade esperada variou de 0,588 a 0,869. Os marcadores microssatélites transferidos para *S. libidinosus* e caracterizados em nosso estudo serão uma ferramenta valiosa para avaliar a variabilidade genética de populações selvagens e em cativeiro. No terceiro capítulo, através de análise molecular e de paisagem foram avaliados diversidade genética, estrutura populacional, fluxo gênico e o efeito da paisagem sobre a conectividade entre seis populações de *S. libidinosus* no bioma Caatinga do Estado de Pernambuco, Nordeste do Brasil. Encontramos que as populações apresentam de moderada a alta diversidade e diferenciação genética. Além disso, nossos resultados evidenciaram que as

distâncias genéticas entre as populações estão relacionadas tanto ao tamanho do fragmento quanto a conectividade entre eles. Análises considerando a resistência da paisagem à dispersão da espécie indicaram que as áreas urbanas assim como as áreas de adequabilidade climática impedem o fluxo gênico entre essas populações. O presente estudo resultou na produção de novos conhecimentos a respeito da espécie *S. libidinosus*, que serão importantes para a reavaliação do seu status de conservação. Reavaliação, esta, que se faz necessária em função das pressões antrópicas atuais e potenciais futuras em suas populações e hábitats.

Palavras chaves: Macaco-prego. Distribuição de espécies. Mudanças climáticas. Genética de paisagem. Impacto antrópico.

ABSTRACT

Brazil has a prominent position in terms of primate biodiversity with about 115 species, but about 60% of these are threatened with extinction. Agriculture and livestock are the main threats, due to habitat loss and fragmentation. Thus, studies that evaluate the effect of the landscape on the distribution and population dynamics of species are necessary to plan mitigating actions for these anthropic impacts. The present study aimed to evaluate the consequences of climate change on the spatial distribution of three primate species in northeastern Brazil and the effect of the landscape on the genetic diversity of populations of *Sapajus libidinosus* in the state of Pernambuco. In chapter one, the long-term viability of suitable habitats for the conservation of *Sapajus libidinosus* and two more threatened Brazilian primates (*Alouatta belzebul* and *Sapajus flavius*) was evaluated. To this end, the identification of areas of current and future distributions of these species was carried out, the quantification of the presence of protected and priority areas, the estimates of the extent of the remaining forest cover and future habitats available for the maintenance and conservation of the species in the face of different climate change scenarios. It has been found that the establishment of primate populations and their ability to survive in these areas in the long term are at risk. Under current conditions, 88% of the areas suitable for the three species are outside protected areas. Furthermore, future projections, considering a severe climate change scenario, indicated that *A. belzebul*, *S. flavius* and *S. libidinosus* may lose up to 93.64%, 97.66% and 54% of suitable habitats, respectively. In chapter two, the transferability of 14 microsatellite markers for use in population analysis of *S. libidinosus* was tested. We found that six of the tested microsatellite markers (tetra-nucleotide) amplified in our target species, *S. libidinosus*. All loci were polymorphic. The number of alleles ranged from 4 to 7 and the expected heterozygosity ranged from 0.588 to 0.869. Microsatellite markers transferred to S. libidinosus and characterized in our study will be a valuable tool to assess the genetic variability of wild and captive populations. In the third chapter, through molecular and landscape analysis, genetic diversity, population structure, gene flow and the effect of the landscape on the connectivity between six populations of *S. libidinosus* in the Caatinga biome of the State of Pernambuco, Northeast Brazil were evaluated. We found that populations have moderate to high diversity and genetic differentiation. In addition, our results showed that genetic distances between populations are related to both the size of the fragment and the connectivity between them. Analyzes considering the resistance of the landscape to the dispersion of the species indicated that urban

areas, as well as areas of climatic suitability, prevent the gene flow between these populations. The present study resulted in the production of new knowledge about the species *S. libidinosus*, which will be important for the reassessment of its conservation status. This reassessment is necessary due to current and potential future human pressures on their populations and habitats.

Keywords: Capuchin monkey. Species distribution. Climate change. Landscape genetics. Anthropic impact.

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Referencial teórico

Red alert: habitat viability for primate conservation in northeast south america

Microsatellite markers for bearded capuchins (*Sapajus libidinosus*): transferability and characterization

Do landscape characteristics affect the genetic population structure of the capuchin monkey in semiarid?

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1. INTRODUÇÃO

A Ordem Primates apresenta uma grande distribuição e é uma das ordens de mamíferos mais diversas (Mittermeier et al., 2013; Estrada et al., 2017). Este grupo conta, atualmente, com 788 taxons existentes, pertencentes a 508 espécies de 80 gêneros e 16 famílias (ITIS, 2018). Os primatas podem ser encontrados em quatro regiões: neotrópicos, África continental, Ásia e Madagascar, mas dois terços de suas espécies estão concentradas em quatro países Brasil, Madagascar, Indonésia e República Democrática do Congo (Estrada et al., 2017). A Ordem é formada por duas subordens: Strepsirrhini (Strepsi = torcido; rhin = nariz) e Haplorrhini (Haplo = simples; rhin = nariz), esta última engloba os primatas neotropicais que se encontram classificados na Parviordem Platyrrhini (Groves, 2016). Aproximadamente 60% das espécies de primatas estão classificadas como ameaçadas de extinção (IUCN, 2019; Estrada et al., 2017). Os fatores que ameaçam as populações de primatas variam de acordo com a região que habitam. Para as neotropicais, atividades como agricultura e pecuária afetam 59% das espécies, enquanto que em áreas como Madagascar, África e Ásia a ameaça predominante é a caça e o aprisionamento de animais, podendo afetar de 54 a 90% das espécies (Estrada et al., 2017).

Os primatas neotropicais, conhecidos também como primatas do novo mundo, compreendem as espécies que vivem nas florestas tropicais das Américas do Sul e Central (Groves, 2016). Diferentemente das espécies da África e Ásia, as espécies neotropicais são de pequeno a médio porte (125g a 15 kg), arborícolas e possuem uma locomoção predominantemente quadrúpede, com algumas espécies apresentando uma cauda preênsil (Mittermeier et al., 2013). Nesta região somam-se 171 espécies de primatas, das quais 115 ocorrem no Brasil (IUCN, 2019, Estrada et al., 2017). A classificação mais atual divide os primatas neotropicais em três famílias (Atelidae, Cebidae e Pitheciidae) formadas por 17 gêneros (Groves, 2016). A espécie Sapajus libidinosus está classificada na Família Cebidae, Subfamília: Cebinae, juntamente com os gêneros Cebus, Sapajus e Saimiri (Groves, 2016).

Sapajus (Kerr, 1792) e Cebus (Erxleben, 1777 by Hershkovitz, 1949, 1955), até 2011, eram classificados como um único gênero, o Cebus (Hershkovitz, 1949; Groves, 2001; Silva Jr, 2001; Oliveira e Langguth, 2006; Mendes Pontes et al., 2006), mas estudos considerando aspectos moleculares, biogeográficos, morfológicos, ecológicos e comportamentais apontaram que estes gêneros foram , separados durante o Mioceno, a cerca de 6,2 milhões de anos (Lynch- Alfaro et al., 2012a; Lynch-Alfaro et al., 2012b). O gênero Sapajus é conhecido, também, como macaco-prego de tufo ou robusto e o gênero Cebus como macaco-prego sem tufo ou grácil

(Lynch-Alfaro et al., 2012a). Esta diferenciação entre robusto e grácil se dá principalmente devido a características morfológicas, o gênero Sapajus, ao contrário de Cebus, apresenta um esqueleto mais robusto com estruturas cranianas e dentárias especializadas para a exploração de alimentos duros (Lynch-Alfaro et al., 2012a). O número de espécies de macacos-prego ainda é controverso e estudos filogenéticos veem sendo realizados para avaliar a sua diversidade (Ruiz-Garcia et al., 2016; Lima et al., 2017; 2018; Martins et al., 2018). A IUCN (2019) reconhece oito espécies e duas subespécies pertencentes ao gênero Sapajus e 19 espécies e quatro subespécies ao gênero Cebus.

Dos 21 primatas encontrados no nordeste do Brasil, metade encontram-se ameaçado de extinção (IUCN, 2019). Desde 2010, o Instituto Brasileiro de Biodiversidade Chico Mendes (ICMBio), vem produzindo uma série de planos de ação de conservação para espécies de primatas ameaçadas de extinção (ICMBio, 2020). Dentre estes planos foi criado o de conservação para os primatas do nordeste brasileiro (ICMBio-CPB 2018) em que foram incluídas seis espécies (bugio vermelho *Alouatta belzebul*, bugio da Caatinga *Alouatta ululata*, macaco titi loira *Callicebus barbarabrownae*, macaco Titi de Coimbra-Filho *Callicebus coimbrai*, macaco-prego-galego *Sapajus flavius* e capuchin amarelo-breasted *Sapajus xanthosternos*). As principais ameaças que afetam esses primatas são a destruição e a fragmentação de habitats, a caça e o comércio de animais de estimação (ICMBio-CPB 2018).

O presente estudo trata da análise de distribuição de três espécies de primatas do nordeste do Brasil e a influência de impactos antrópicos e mudanças climáticas sobre suas distribuições. Além disso, avalia geneticamente seis populações da espécie *Sapajus libidinosus* no semiário pernambucano e identifica variáveis que podem estar interferindo no fluxo gênico entre essas populações. A pesquisa foi realizada utilizando técnicas de modelagem de distribuição de espécies e genética de paisagem.

1.1 OBJETIVOS

1.1.1 Objetivo geral

- Avaliar as consequências das mudanças climáticas sob a distribuição espacial de três espécies de primatas do nordeste do Brasil e o efeito da paisagem na diversidade genética de populações de *Sapajus libidinosus* no estado de Pernambuco.

1.1.2 Objetivos específicos

- Estimar a extensão atual e modelar a distribuição futura de Alouatta belzebul, Sapajus flavius e Sapajus libidinosus, enfatizando: i) as áreas de alta adequabilidade climática para sua ocorrência no Brasil, e ii) a representatividade dessas áreas dentro de unidades de Conservação, áreas prioritárias para a conservação da biodiversidade e áreas florestais;

- Testar a transferibilidade de marcadores genéticos do tipo microssatélite para caracterizar populações de Sapajus libidinosus;

- Analisar a influência das características de paisagem sobre a variabilidade genética das populações de Sapajus libidinosus no estado de Pernambuco.

2. REFERENCIAL TEÓRICO

2.1 MACACO-PREGO: UM PRIMATA NEOTROPICAL DO SEMIÁRIDO BRASILEIRO

A espécie *Sapajus libidinosus* apresenta uma distribuição geográfica que engloba estados do Nordeste do Brasil como Alagoas, Bahia, Ceará, Paraíba, Pernambuco, Piauí, Rio Grande do Norte e Maranhão e da região Centro-oeste como Goiás, Mato Grosso, Mato Grosso do Sul, Minas Gerais e Tocantins e em uma parte do Pará (Rylands e Kierulff, 2015) (Figura 1). Na região Nordeste suas áreas estão localizadas na região da Caatinga, enquanto no Centro-Oeste encontram-se no Cerrado (IBGE, 2012; Rylands e Kierulff, 2015). Essas áreas caracterizam-se por ambientes semi-áridos, com um clima seco e valores de precipitação anuais variando entre 250 - 1200 mm (Ratter et al., 1997; Prado, 2003) na Caatinga e 750 - 2000 mm, no Cerrado (Hunke et al., 2014).

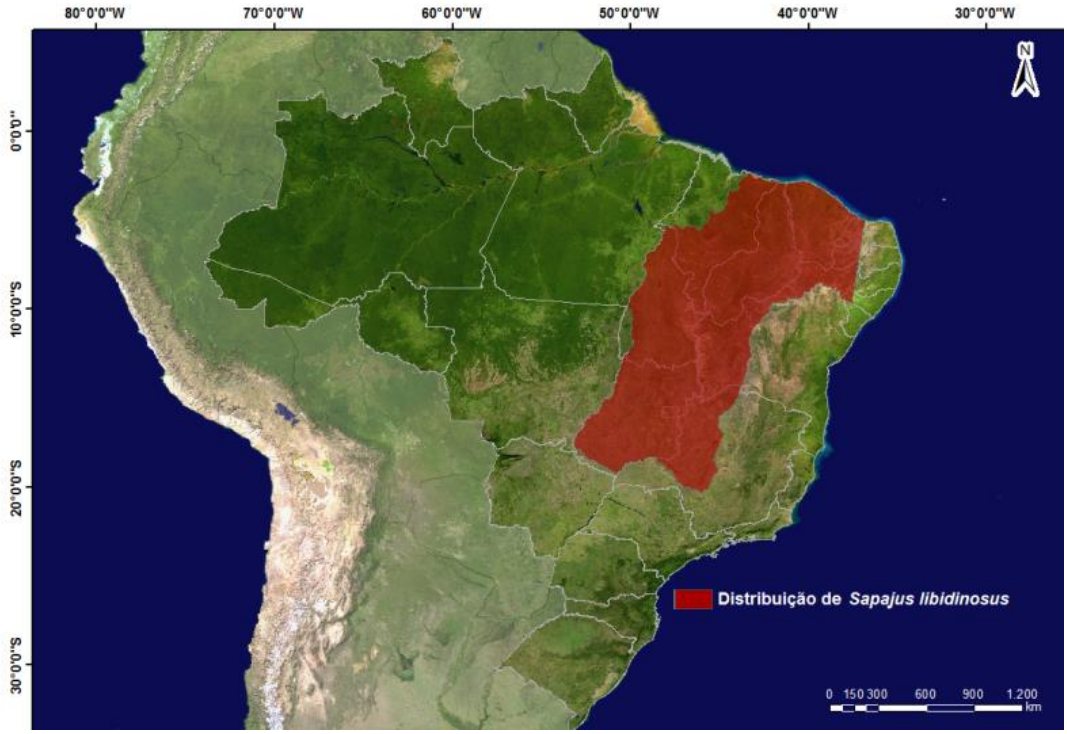

Figura 1. Distribuição geográfica da espécie *Sapajus libidinosus.* Fonte: ICMBio, 2019

Os macacos-pregos são animais sociais, vivem em grupos multi-macho/multi-fêmea (Fragaszy et al., 2004) que podem variar de 3 a 40 indivíduos (Lynch e Rímoli, 2000; Mannu e Ottoni, 2009), com uma densidade estimada de 9,8 indivíduos/km^2 (Moura, 2007; Henriques e Cavalcante, 2004) (Figura 2). Apresentam um ciclo de vida longo, uma baixa taxa de natalidade

e um desenvolvimento lento, vivendo em torno de 55 anos em cativeiro (Fragaszy et al., 2004). Em vida livre, se registrou indivíduos vivendo pelo menos 35 anos (Robinson, 1986). Seus filhotes são totalmente dependentes das mães ou alo-cuidadores para alimentação, locomoção e defesa contra predadores (Verderane, 2010). Fragaszy et al. (2004) estudando os macacos-prego em cativeiro, observaram que os infantes passam cerca de 14 meses para se tornarem independentes dos pais. São primatas onívoros, alimentando-se de frutos, sementes, flores, invertebrados, ovos e pequenos vertebrados (Cazzadore, 2007; Ludwig et al., 2006). Possuem uma alta capacidade manipulativa, incluindo o uso de ferramentas para acessar alimentos duros, encapsulados ou enterrados (Mannu e Ottoni, 2009; Santos, 2010; Souto et al., 2011; Moraes et al., 2014). Utilizam principalmente o substrato arbóreo, podendo ter deslocamentos terrestres (Figura 3) em algumas ocasiões com locomoção vertical bípede (Visalberghi et al., 2005; Falótico et al., 2016).

Figura 2. Grupo de macacos-prego (*Sapajus libidinosus*) da Serra da Maravilha, localizada no município de Betânia, Pernambuco, Brasil.

Figura 3. Macho adulto da espécie *Sapajus libidinosus* em deslocamento terrestre.

Os grupos de macacos-prego apresentam uma hierarquia de dominância mantida pelos machos e as fêmeas são filopátricas, ou seja, os machos dispersam e as fêmeas permanecem no grupo (Verderane, 2010; Izar et al., 2012). Estas características sociais são consideradas imprescindíveis ara a manutenção da diversidade genética das populações. A hierarquia de dominância por machos pode reduzir drasticamente o tamanho efetivo do grupo social e aumentar a diferenciação genética entre grupos (Di Fiore, 2003). Um macho ou um pequeno conjunto de machos acaba sendo responsável pela maior parte da paternidade dentro de um grupo social durante algum período de tempo (Fragaszy et al., 2004). Enquanto que a filopatria das fêmeas pode ocasionar uma baixa diversidade de DNA mitoncondrial dentro dos grupos e maiores diferenças interpopulacionais (Di Fiore, 2003). Grupos que se tornam isolados, seja por barreiras naturais ou fragmentação de habitat, podem sofrer com diminuição de aptidões, aumento da consanguinidade e consequentemente do risco de extinção (Johansson et al., 2007). É importante que o sucesso de dispersão seja garantido e que haja fluxo gênico entre as populações locais para que a diversidade genética se mantenha tanto entre como dentro delas (Di Fiore, 2003).

A espécie *S. libidinosus* não está classificada como em perigo de extinção, mas os hábitats que ocupam sofrem fortes impactos de perda de vegetação (IUCN, 2019). Segundo a WWF (2015) a expansão de pastagens para criação de gado, o cultivo de soja, os desmatamentos para produção de carvão vegetal nativo e os incêndios florestais de causa antrópica têm sido os principais vetores de degradação do Cerrado. Estima-se que 44% de sua cobertura vegetação nativa foi perdida (Brasil, 2014b, MapBiomas, 2018). Esta mesma proporção, de perda de cobertura vegetal, foi estimada para o bioma Caatinga (Brasil, 2011). Além de impactos de perda de habitat, os macacos-prego são afetados pelo tráfico ilegal de animais (Rylands e Kierulff, 2015). São comumente encontrados em centros de triagem de animais silvestres no Brasil, e o tráfico pode estar relacionado a motivos culturais, sociais ou econômicos (Nascimento et al., 2013). O entendimento sobre a forma como esses animais e as suas populações interagem com a paisagem, muitas vezes co-habitada por humanos, é importante para nortear as decisões quanto a gestão das áreas e conservação da espécie.

2.2 MODELAGEM DE DISTRIBUIÇÃO DE ESPÉCIES COMO FERRAMENTA PARA CONSERVAÇÃO DA BIODIVERSIDADE

Métodos aplicados à modelagem de distribuição de espécies utilizam dados de localização e de variáveis ambientais para explicar e prever faixas de ocorrência de espécies e nichos ambientais (Pearce e Ferrier, 2000; Phillips, 2008; Hao et al., 2018). O desenvolvimento e o aprimoramento de banco de dados climáticos globais, como o WordClim (Hijmans et al., 2005) e mais recentemente o WordClim2 (Fick e Hijmans, 2017), de dados de biodiversidade como Global Biodiversity Information Facility (GBIF, www.gbif.org), Species link (http://splink.cria.org.br/), Portal da biodiversidade (https://portaldabiodiversidade.icmbio.gov.br), além de dados de sensoriamento remoto, abriu um leque de oportunidades para gerar previsões para diferentes cenários ambientais tanto relacionados à mudanças climáticas como a de características da paisagem (Koshkina et al., 2017; Booth, 2018). Os bancos de dados sobre biodiversidade só foram possíveis devido a digitalização dos acervos das coleções científicas de museus e universidades. Os métodos de modelagens podem ser aplicados a uma gama de estudos de conservação como mudanças climáticas passadas e futuras, hipóteses biogeográficas, manejo de espécies ameaçadas, planejamento de áreas de proteção ambiental, previsão das faixas prováveis de espécies invasoras (Elith e Leathwick 2009; Bateman et al., 2013; Breiner et al. 2015; Guillera-Arroita et al., 2015), entre outros.

A escolha do método a ser utilizado em um estudo de modelagem de distribuição leva em consideração alguns parâmetros como a seleção de modelos, o ajuste das funções e interações, a força de associação, vícios e erros de predição (Hao et al., 2018). A formulação de um bom modelo vai depender da escolha de um algoritmo adequado e de uma abordagem estatística ideal para o tipo de análise que se deseja realizar (Hallgren et al., 2019). Os algoritmos são aplicados para classificar a probabilidade de presença (e ausência) em função das variáveis ambientais (Pearson, 2010). Abordagens usadas para a aplicação de modelagem de espécies vão desde métodos estatísticos como Modelos Lineares Generalizados (GLMs, McCullagh, 1984), Modelos Aditivos Generalizados (GAM, Guisan et al., 2002), Regressão Adaptativa Multivariada por Splines (MARS, Friedman, 1991), Árvores de regressão (BRT, Breiman, 2001) e Análise discriminante com mistura (MDA, Hastie et al., 1994) a técnicas de aprendizagem de máquinas como o modelo de máxima entropia (MaxEnt, Phillips et al., 2006) e Redes Neurais Artificiais (NNA, Lek e Guégan, 1999). Uma das diferenças importantes na

forma de operar esses algoritmos são os tipos e fontes de dados empregados em cada um deles (Pearson, 2010).

Algoritmos como GLM, GAM, BRT, MARS, NNA requerem dados de presença e ausência, mas dados de ausência observada de espécies nem sempre estão disponíveis, dificultando o emprego desses métodos em análises de modelagem (Guisan e Zimmermann, 2000; Hao et al., 2018). Desta forma, é preciso empregar outros métodos que requerem apenas dados de presença como o BIOCLIM e o DOMAIN, em que as predições são realizadas sem qualquer referência à outras amostras da área de estudo (Guisan e Zimmermann, 2000; Hallgren et al., 2019). Outro método que não exige dados de ausência é o de máxima entropia (MaxEnt), neste caso a análise é realizada relacionando o ambiente onde estão localizados os dados de ocorrência com o ambiente do restante da área de estudo, ou seja o "background" (plano de fundo) (Phillips et al., 2006; 2008). O uso de múltiplos métodos também vem ganhando espaço nas análises de distribuição de espécies como o BIOMOD e o Open Modeller, em ambos os casos são utilizados diversos modelos individuais (até 10 métodos no caso do BIOMOD) e estes são combinados de diferentes maneiras, avaliações dos modelos também são realizadas (Hao et al., 2018).

Além do tipo de fonte de dados utilizados em cada método, outros parâmetros devem ser levados em consideração como a capacidade de incorporar variáveis contínuas e/ou categóricas na análise, a saída do resultado se é dada de forma contínua (apresentando probabilidades que variam de 0 a 1) ou se é apresentado de forma binária ("0" indicando áreas inadequadas ou ausência de espécies e "1" indicando áreas adequadas e presença de espécies) (Pearson, 2010). Deve-se também considerar se é possível avaliar a capacidade preditiva do modelo e a influência das variáveis na sua predição (Hallgren et al., 2019). O desempenho dos métodos deve ser avaliado de acordo com o objetivo do estudo e as possibilidades de aplicação dos modelos (Elith et al., 2006; Pearson et al., 2006).

O método MaxEnt não requer dados de ausência de espécies e é possível utilizar tanto variáveis contínuas como categóricas. A saída de seus resultados apresenta uma forma contínua, além disso o software calcula as estatísticas de validação do modelo e avalia a contribuição das variáveis ambientais para a previsão do modelo através do procedimento de jackknife (Phillips et al., 2006). Através do MaxEnt também podemos analisar predições climáticas passadas e futuras e entender como a biodiversidade respondeu ou responderá às mudanças climáticas (Merow et al., 2013). Este método foi avaliado e apresentou um bom desempenho em relação aos outros (Elith et al., 2006; Phillips et al., 2006; Pearson et al., 2007).

Após a escolha do método, deve-se dar atenção aos dados utilizados para gerar os modelos, como a seleção de registros de ocorrência e de variáveis ambientais, a escala e resolução utilizadas (Kramer-Schadt et al., 2013). Em relação aos pontos de ocorrência, deve-se evitar erros como usar registros de identificação incorreta de espécies ou dados imprecisos ou espacialmente tendenciosos, como por exemplo áreas mais pesquisadas ou de fácil acesso apresentará um maior número de registros de ocorrência (Phillips et al., 2009; Kramer-Schadt et al., 2013). Quanto às variáveis ambientais, deve-se dar preferência àquelas que têm um papel fisiológico ou comportamental direto na determinação da distribuição das espécies (Rodder et al., 2009) e deve-se evitar variáveis correlacionadas (Warren et al., 2014). As variáveis ambientais podem ser contínuas ou categóricas, na primeira cada pixel apresenta um valor da variável naquela área, já a categórica apresenta áreas classificadas por categoria, esta última é menos precisa e pode aumentar o erro (Warren et al., 2014).

Os modelos podem ser validados de duas formas: a dependente de limites de corte (*threshold*) como por exemplo através da Matriz de confusão e a validação independente de limite de corte que são áreas sob as curvas ROC (AUC – *area under curve*) (Liu et al., 2013). A seleção do limite de corte é realizada para que o resultado da modelagem passe a ter valores binários (0 e 1), e não contínuos, e possa ser utilizado na análise de matriz de confusão para saber se o modelo classificou corretamente as áreas de presença e ausência da espécie (Pearson, 2010). A "matriz de confusão" ou "matriz de contingência" avalia a relação entre o resultado que o modelo previu e a distribuição real da espécie, baseado nos registros de presença (Fielding e Bell, 1997). É um esquema que registra as frequências de cada um dos quatro tipos possíveis de previsão a partir da análise dos dados de teste: (a) verdadeiro positivo, (b) falso positivo, (c) falso negativo, (d) verdadeiro negativo (Fielding e Bell, 1997). O falso positivo e o falso negativo são erros, denominados de erro de comissão quando o programa indica uma área adequada para ocorrência da espécie e não há registro de ocorrência dela nesta área, e erro de omissão quando o programa não prevê a existência de uma área em que a espécie verdadeiramente ocorre (Reese et al., 2005). Através da matriz de confusão também pode-se estimar índices como sensibilidade e especificidade, o primeiro, testa se o modelo classifica corretamente o pixel como presença e o segundo se o pixel é corretamente classificado como ausência (Fielding e Bell, 1997). O limite de corte para a classificação dos pixels pode ser realizado de forma arbitrária, mas não é recomendado por não considerar questões ecológicas. Este limite pode tambéme ser definido a partir do menor valor previsto de probabilidade de presença da espécie, em que a partir desse valor as áreas vão ter valor de 1 (presença) e abaixo

de 0 (ausência), mas o limite mais indicado a ser utilizado é o que maximiza a concordância entre distribuições observadas e previstas (Liu et al., 2013). As taxas de erros são calculadas automaticamente por software projetado para modelagem de distribuição de espécies como, por exemplo, no MaxEnt (Merrow et al., 2013). O importante ao definir um limite de corte é saber qual o objetivo do estudo, pois um limiar baixo pode ser utilizado se a intenção é identificar áreas mais abrangentes para avaliação de impactos ou expandir áreas de ocorrência da espécie (Perason, 2010). Um limiar mais alto reduz o risco de escolher locais inadequados (Pearce & Ferrier, 2000), e é indicado quando se pretende identificar áreas para introdução ou reintrodução de espécies (Molloy et al., 2019).

Quando transformamos os resultados dos modelos que são contínuos em formas binárias, não são consideradas todas as informações fornecidas pelo modelo, uma forma mais robusta de se analisar os dados contínuos é através da validação independente de limite de corte (Fielding e Bell, 1997). Para esta validação são usados os resultados provenientes do teste AUC – a área sob a curva ROC (Receiver Operating Characteristic) que é a relação entre os índices de sensibilidade e especificidade (Pearce e Ferrier, 2000). A área sob a curva é medida para medir o desempenho preditivo do modelo (Swets, 1988). O AUC testa se o modelo classifica a presença com mais precisão do que uma previsão aleatória, o valor pode variar entre 0 – 1 e quanto mais próximo de 1 maior a sua capacidade preditiva (Fielding e Bell, 1997; Pearce e Ferrier 2000).

Apesar dos modelos darem previsões de distribuição, eles são muito úteis na identificação de áreas que se espera que a espécie ocupe, de áreas de distribuição real e que são desconhecidas e de áreas que são adequadas para a ocorrência da espécie e que não estão ocupadas (Pearson, 2010). A identificação de áreas adequadas para ocorrência de espécies pode direcionar novas amostragens e gerar novos registro de ocorrência (Fleishman et al., 2002; Bourg et al., 2005; Guisan et al. al., 2006), ações de extrema importância principalmente quando se trata de espécies ou ecossistemas ameaçados. No caso de áreas que são adequadas, mas que não foram registradas ocorrência da espécie, são importantes para possíveis projetos de reintrodução (Molloy et al., 2019), ou para ações de prevenção contra a ocupação por espécies invasoras (Peterson, 2003; Thuiller et al., 2005). Além disso, modelos de distribuição de espécies são ferramentas úteis para ajudar a entender quais impactos climáticos podem afetar os ecossistemas e quais medidas podem ser tomadas, previamente, para limitar seus efeitos (Gillson et al., 2013).

2.3 GENÉTICA DE PAISAGEM

Estudos relacionados à genética de paisagens são importantes para compreendermos como ocorrem as interações entre as características da paisagem e processos microevolutivos, como fluxo gênico, deriva genética e seleção (Manel et al., 2003). Este campo engloba estudos multidisciplinares como genética de populações, ecologia da paisagem e análises espaciais e temporais (Manel et al., 2003; Marko & Hart, 2011). É uma área de pesquisa importante para relacionar estudos de conservação da biodiversidade à fragmentação e perda de hábitats (Canale et al., 2012; Westphal et al., 2003), genética de populações (EsteS-Zumpf et al., 2010; Cushman e Lewis, 2010), biogeografia (Ben et al., 2013), mudanças climáticas (Brum et al., 2013), espécies invasoras (Hastings et al., 2005; Bossenbroek et al., 2001) e disseminação de doenças (Biek e Real, 2010).

O entendimento de como a diversidade genética e a estrutura populacional de espécies vem se comportando ao longo de sua distribuição geográfica é um dos pontos chaves para a determinação de planos de conservação da biodiversidade em longo prazo (Storfer et al., 2007; Cushman et al., 2012). Mudanças na configuração espacial e na qualidade de habitats podem influenciar na composição genética de uma população, principalmente quando causadas pela perda da conectividade entre populações naturais por atividades humanas (Wang et al., 2008; Ruiz-Lopez et al., 2016; Moraes et al., 2018). A redução da variabilidade genética e consequentemente perda do seu valor adaptativo é uma das consequências da perda de conectividade (Holderegger et al., 2006). Populações submetidas a condições de isolamento irão sofrer fortes ações relacionadas à deriva genética e consanguinidade, podendo aumentar o risco de uma extinção local (Ruiz-Lopez et al., 2016; Wang et al., 2017).

O aprimoramento das técnicas moleculares permitiu entender o quanto à fragmentação influencia na composição genotípica das populações (Storfer et al., 2007; Balkenhol et al., 2009; Bowman et al., 2016). Parâmetros genéticos como diversidade, níveis de endogamia, e medidas diretas e indiretas de fluxo gênico fornecem estimativas da resposta das populações à fragmentação do hábitat (Manel et al., 2003; Storfer et al. 2007). Podemos obter essas informações através de marcadores moleculares como os microssatélites, e identificar diferenças genéticas tanto entre indivíduos dentro de uma mesma população como entre populações distintas (Balloux, 2002). Apesar do uso de marcadores microssatélites ser uma técnica mais trabalhosa e custosa em relação às novas técnicas empregadas, estes marcadores permitem inferências mais precisas devido ao seu alto grau de polimorfismo (León Ortega & Gonzalez-Wangüemert, 2015; Tian et al., 2017; Srbek-Araujo et al., 2018). O polimorfismo é

avaliado através das frequências alélicas e/ou genotípicas dos locos analisados (Balloux, 2002). A identificação do número de alelos de uma população é obtida através da riqueza alélica e populações que apresentam alelos exclusivos são importantes para a manutenção da diversidade genética, pois irão ser responsáveis pela disseminação desses alelos a outras populações (Kalinowski, 2005; Ruiz-Lopez et al., 2016). A redução do valor adaptativo de um indivíduo ocorre quando há um acúmulo de alelos idênticos por descendência ocasionado pela endogamia resultante do isolamento de populações, seja por barreiras físicas naturais ou antrópicas, comportamentais ou ecológicas (Barrett e Schluter, 2007; Waits e Storfer, 2016).

O incremento dos dados moleculares aos de paisagem permitiu avaliar a dinâmica do fluxo gênico entre populações em um espaço geográfico, relacionando descontinuidades genéticas as características ambientais da paisagem (Manel et al., 2003). Parâmetros como o tamanho e a conectividade dos hábitats, heterogeneidade da matriz e a capacidade de cada espécie de atravessar a paisagem, assim como a diversidade e a distância genética são utilizados nas estimativas em genética de paisagem (Landguth et al., 2010; Cushman et al, 2012). Hipóteses são testadas para avaliar o que melhor explica os padrões de fluxo gênicos encontrados, as mais comumente analisadas são as de isolamento por distância (IBD) e isolamento por resistência (IBR) (Wright, 1943; McRae, 2006; Wan et al., 2018). O isolamento por distância relaciona a semelhança entre as populações e a distância geográfica, considerando que populações mais próximas geograficamente serão mais semelhantes geneticamente (Wright, 1943). No entanto, com o aumento da perda e fragmentação de hábitats, indivíduos de populações geograficamente próximas nem sempre conseguem migrar (Spear et al., 2010). Desta forma, o impedimento da dispersão entre populações não se dá devido à distância e sim às características da paisagem, então teremos um isolamento por resistência (McRae, 2006; Spear et al., 2010).

O isolamento por distância é testado através de matrizes de dissimilaridade, aplicando uma correlação, geralmente o teste de Mantel, entre a matriz de distância euclidiana e a de distâncias genéticas (F_{ST}) entre as populações estudadas (Manel et al., 2003; Cushman et al., 2012). Enquanto que o isolamento por resistência correlaciona uma matriz de resistência da paisagem à matriz de distância genética (McRae, 2006; Spear et al., 2010). As superfícies de resistência são normalmente criadas em um ambiente GIS rasterizado e são baseadas em funções biológicas como por exemplo a probabilidade de uma espécie se movimentar em diferentes tipos de cobertura do solo (O'Brien et al., 2006). A atribuição de valores à superfície de resistências pode ser realizada através de dados de campo, opinião de especialistas e

otimização de modelos (Spear et al., 2010). A forma mais comum é a opinião de especialistas e consultas à literatura específica (Murray et al., 2009), apesar de ser uma forma menos onerosa, a indicação de valores de resistência vai depender da experiência do pesquisador e da quantidade de informações disponibilizadas sobre a espécie em questão (Spear et al., 2010). Dados de campo, como radiotelemetria e dados de GPS, muitas vezes se tornam inviáveis e custosos, acarretando em tamanho de amostras pequenos, além disso incertezas na detecção de movimento tornam este método limitado (Spear et al., 2005; Chietkiewicz e Boyce, 2009). A otimização de modelos se destaca dentre as técnicas para criar superfícies de resistência e apesar das atribuições de valores ainda serem propostas por experts na área ou por consulta a literatura, múltiplas superfícies de resistências são criadas e comparadas estatisticamente para determinar qual superfície explica melhor o modelo (Cushman et al., 2006; Razgour, 2015).

A genética de paisagem trouxe um avanço importante nas avaliações sobre a conectividade de hábitats, permitindo avaliar o efeito da heterogeneidade espacial na estruturação genética de populações (Richardson et al., 2016; Bowman et al., 2016). Alguns pontos, no entanto, precisam ser levados em consideração quando se usa superfícies de resistências, o primeiro deles é que as superfícies de resistência são baseadas no movimento dos organismos e como nem sempre que há dispersão há fluxo gênico, temos que ter cautela com as conclusões dos estudos (Bohonak, 1999; Whitlock e McCauley, 1999). O sucesso no fluxo gênico vai depender da sobrevivência e da reprodução após a imigração para uma nova área (Richardson et al., 2016). Diferença nas características fisiológicas, morfológicas e comportamentais entre populações também podem influenciar na hora da escolha de dispersar, assim como a disponibilidade de recursos e a densidade populacional (Barrett e Schluter, 2007; Waits e Storfer, 2016). Neste caso, o movimento da espécie para outras populações estaria relacionado a questões adaptativas daquela população e não a permeabilidade da matriz (Baguette e Van Dyck 2007; Beier et al., 2008; Kadoya, 2009; Beier et al., 2009). Mas não há dúvidas que as características da paisagem podem modificar a taxa de movimento entre as populações e afetar o fluxo gênico entre elas (McRae, 2006; Dyer et al., 2010). Ferramentas que relacionem a configuração e estrutura da paisagem à conectividade para processos ecológicos são fundamentais para planejamentos efetivos e de longo prazo de conservação (Segelbacher et al. 2010; Bowman et al., 2016; Richardson et al., 2016).

Espécies que ainda não são classificadas como ameaçadas de extinção como a *S. libidinosus*, tem uma chance de não entrarem nesta categoria, se o status de conservação de suas populações for avaliado preventivamente. O entendimento sobre a forma como esses animais e as suas populações

interagem às consequências das mudanças climáticas e às alterações da paisagem, irá nortear as decisões quanto a gestão e conservação da espécie. As ferramentas aqui utilizadas para as análises populacionais vão nos dar essas informações e permitir avaliar e sugerir medidas de gestão e manejo das espécies aqui estudadas.

3. RED ALERT: HABITAT VIABILITY FOR PRIMATE CONSERVATION IN NORTHEAST SOUTH AMERICA

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3.1 INTRODUCTION

Brazil is home to 115 species of nonhuman primates (IUCN, 2019; Estrada et al., 2017; Costa-Araújo et al., 2019), of which, 21 occur in the Atlantic forest, Cerrado and Caatinga biomes in northeastern Brazil (IUCN, 2019). These three biomes have been extensively modified by centuries of human driven forest destruction for the development of agriculture, infrastructure and urbanisation. Half of the primate species in northeast Brazil are under threat, including four species classified as Endangered and six as Critically Endangered by IUCN (2019). Although a lot of attention has been, rightfully, devoted to the plight of the Brazilian Atlantic forest, very little attention has been given to the Cerrado and Caatinga. In particular, Caatinga is the most neglected biome in Brazil in terms of conservation action even though nearly half of it has already been lost (Beuchle et al., 2015). It is predicted that the Atlantic forest, Cerrado and Caatinga biomes will be severely affected in the future by continuing anthropogenic impacts in these rapidly developing areas, as well as by climate change (Marengo et al., 2017). Thus, in order to protect the primates in these biomes, it is important to determine which areas will be more severely affected and where new protected areas should be created to ensure that an effective network of protected areas is in place for the future survival of the primates (see Estrada et al., 2018).

In 2011 the *Instituto Chico Mendes de Conservação da Biodiversidade*, the national institution for biodiversity conservation in Brazil, developed a conservation action plan for the primates of Northeast Brazil (ICMBio-CPB, 2018). Six of the 21 primate species found in northeastern Brazil were included in this conservation action plan: red-handed howler monkey *Alouatta belzebul* Linnaeus, 1766, Caatinga howler monkey *Alouatta ululata* Elliot, 1912, blonde titi monkey *Callicebus barbarabrownae* Hershkovitz, 1990, Coimbra-Filho's titi monkey *Callicebus coimbrai* Kobayashi & Langguth, 1999, blonde capuchin *Sapajus flavius* Schreber, 1774 and yellow-breasted capuchin *Sapajus xanthosternos* Wied-Neuwied, 1826 . They are found in one or more of the three biomes occurring in the northeast, Atlantic forest, Cerrado and Caatinga. The main threats affecting these primates are habitat destruction and fragmentation, hunting and the pet trade (ICMBio-CPB, 2018; ICMBio, 2016). One of the actions proposed in the conservation action plan for the primates of northeastern Brazil is to determine more accurately the current distribution of all six species of primates and to evaluate how these distributions will be affected by future human activities and climate change (ICMBio-CPB, 2018). Such data are essential for planning future strategies that will set aside

enough suitable habitat for the survival of these species through creating new protected areas, connecting existing ones and restoring key habitats.

Spatial analysis approaches such as species distribution models and gap analysis are useful tools for assessing the impact of habitat loss and fragmentation on species (Beuchle et al., 2015; Titeux et al., 2017; Zwiener et al., 2018). Distribution models project potential suitable areas for a particular species based on presence location records and abiotic environmental data (Elith & Leathwick, 2009). Gap analysis is a method that assesses whether species or ecosystems are represented within existing protected areas, i.e. it identifies potential "conservation gaps" (Rodrigues et al., 2004). Both techniques provide information to guide more efficient management actions for the conservation of a greater number of species (Rodrigues et al., 2004), and, if integrated, improve the interpretation of impacts of global change scenarios on biodiversity (Titeux et al., 2017). Thus, the use of the combination of such techniques to set effective conservation goals is important because research and conservation efforts have traditionally focused on charismatic species and protected areas, leading to some species and their habitats being under considerable risk of extinction (Benzanson & McNamara, 2019).

Here we combine species distribution models and gap analysis to assess the long-term viability of suitable habitats for the conservation two of the six target species of the conservation action plan for the primates of northeastern Brazil: *A. belzebul* and *S. flavius*. We also included a third species, the bearded capuchin, *Sapajus libidinous* Spix, 1823, bearded capuchin, that, although not included in the national action plan, is strongly affected by habitat loss (Beuchle et al., 2015; Rylands & Kierulff, 2015), the illegal pet trade (Nascimento et al., 2013) and is hunted for traditional medicine purposes and as retaliation for crop raiding in Brazil (Torres Junior et al., 2016; Freire-Filho et al., 2018; Souto et al., 2018). These three species were chosen because they offer a good representation of the main biomes in northeastern Brazil, and therefore may help the conservation of these habitats. Thus, identifying suitable areas for the occurrence of our species may help the conservation of several other species that co-exist with them as they may serve as flagship species. Primate populations are currently in sharp decline, including the most charismatic, elusive and rare species. We i) estimate the current potential range of each species and project the effects of future climate change on their ranges; ii) evaluate the extent of suitable areas that overlap with existing protected areas and proposed priority areas for biodiversity conservation; and iii) assess how much forest cover still remains in the areas predicted as suitable for the occurrence of the species.

3.1.1 Study area and species

The study area comprises the known distribution area of the three target species, the Caatinga, Cerrado, Amazon and Atlantic forest biomes, encompassing mainly the northeast region of Brazil, but also areas in the north and in the center-west (Fig. 1). The Atlantic forest in northeastern Brazil is located at low altitudes (400m - 800m) (Tabarelli et al., 2010) with annual rainfall ranging from 1,800-2,000 mm (Rêgo & Hoeflich, 2001). The Caatinga and the Cerrado biomes are considered semiarid environments, characterized by a dry climate with annual precipitation values varying between 250 and 1200 mm (Ratter et al., 1997; Prado, 2003) and 750 and 2000 mm (Hunke et al., 2014), respectively. Annual precipitation in the Amazon rainforest biome ranges from 2000 to 3664 mm (Villar et al., 2009).

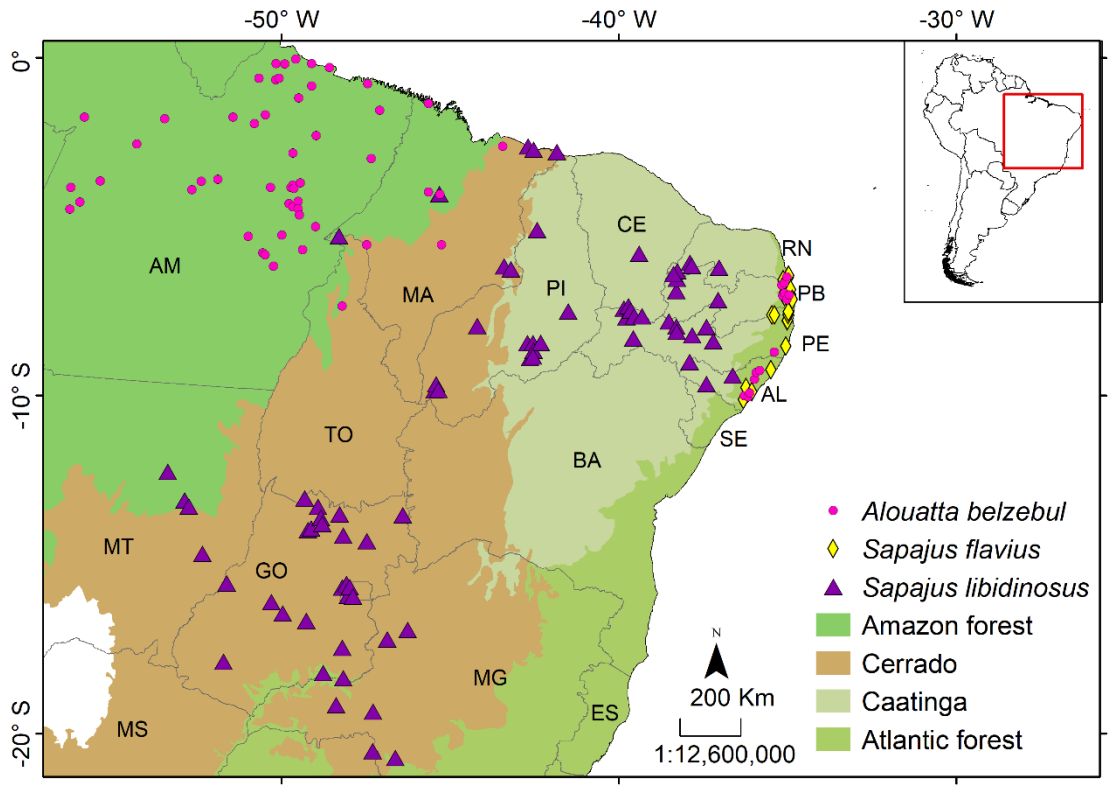

Figure 1.Occurrence records for *Alouatta belzebul*, *Sapajus flavius* and *S. libidinosus* presented over a map marking the main biomes and the Brazilian states included in our study area (RN-Rio Grande do Norte, PB-Paraíba, PE-Pernambuco, AL-Alagoas, SE-Sergipe, BA-Bahia, CE- Ceará, PI- Piauí, MA- Maranhão, MG- Minas Gerais, TO-Tocantins, GO- Goiás, AM- Amazônia, MT- Mato Grosso, MS- Mato Grosso do Sul, ES- Espírito Santo.

Alouatta belzebul has a disjunct distribution, occurring in the northeastern Atlantic forest and lower eastern Amazon in the states of Amapá, Pará, and Maranhão, Brazil (Veiga et al., 2008). It is considered as a folivorous–frugivorous species (Pinto et al., 2003) and

Vulnerable according to IUCN Red List due to a population decline of 30% in the past 30 years (Veiga et al., 2008). It is estimated that the population restricted to the Atlantic forest has only 200 individuals (Veiga et al., 2008).

Sapajus flavius occurs in the Atlantic forest and Caatinga of northeastern Brazil (de Oliveira et al., 2015; Martins et al. 2016). This species has a generalist diet (de Souza et al., 2019; Medeiros et al., 2019) and is classified as Critically Endangered by the IUCN due to habitat loss and fragmentation resulting from coastal development and sugar cane plantations (de Oliveira et al., 2015). It is recognised as one of the most endangered primates in the world (Mittermeier et al. 2012), though it is no longer in the top 25 most endangered primate species list.

Sapajus libidinosus inhabits dry forests in semiarid areas, including the Caatinga and Cerrado biomes (Rylands & Kierulff, 2015). Although classified as Least Concern by the IUCN (Rylands & Kierulff, 2015), the Brazilian government considers it as Near Threatened (ICMBio, 2016). However, this species is likely to become more threatened in the future due to its prevalence in the habitat loss (Beuchle et al., 2015; Rylands & Kierulff, 2015) and illegal pet trade (Nascimento et al., 2013).

4.2 METHODS

4.2.1 Species distribution modelling

We obtained occurrence data for the three target species from the Global Biodiversity Information Facility (www.gbif.org) and Species link (splink.cria.org.br). We also retrieved location records from the literature using the search terms *Sapajus*, *Sapajus libidinosus*, capuchin monkeys, *Cebus*, *Cebus libidinosus*, *flavius*, *Cebus flavius*, *Alouatta*, *Alouatta belzebul*, guariba, bugio, bugio-de-mãos-ruivas, macaco-prego, macaco-prego-galego, macaco-prego-da-caatinga, red-handed-howler-monkey, howler monkey, blonde capuchin monkey, bearded capuchin monkeys in ScienceDirect (www.sciencedirect.com), Web of Science (https://clarivate.libguides.com/webofscienceplatform/alldb), Periódicos Capes (www.periodicos.capes.gov.br) and Google Scholar (https://scholar.google.com.br/ . Finally, we collected new location data for *Sapajus libidinosus* during ten expeditions to nine localities in the state of Pernambuco, Brazil, between May 2016 and March 2017. All records were validated using satellite maps (Google Earth) to exclude records falling outside forested areas or the species ranges, which are likely the results of inaccurate coordinates.

Species distribution models were generated with MaxEnt v3.4.1 (Phillips et al., 2006). This tool uses a maximum entropy algorithm to select environmental variables that better explain species distribution using presence only data (Phillips et al., 2006). The background was delimited, for each species, as a buffer of 500 km generated around the minimum convex polygon of all known occurrence records (Appendix A). The climatic variables were obtained from WorldClim version 1.4 (Hijmans et al., 2005), Brazil ecoregions (http://mapas.mma.gov.br/i3geo/datadownload.htm), geomorphology databases (http://www.dpi. inpe.br/Ambdata/) and the slope layer was generated from the altitude layer (http://www.diva-gis.org/Data). To avoid collinearity, we only included variables that were not highly correlated ($r < 0.8$, Appendix B). Through Principal Component Analysis (Appendix C) we selected the most important variables to include in each species' model. These variables explained 80% of the distribution models. All variables were downloaded at (or converted) to a resolution of 30 arc-seconds (~ 1 km^2), which was the cell size for the analyses, using ArcGIS 10.1 (ESRI, Redlands, USA).

We reduced spatial autocorrelation among location records through an environmental heterogeneity rarefaction analysis using SDMTools box (Brown, 2014) in ArcGIS 10.1 (ESRI, Redlands, USA). A buffer of 10 km was created around each occurrence record, .and duplicate points within the zones of the buffers were randomly removed. If the records were within the same buffer, but in pixels with different environmental characteristics, they were retained. This procedure was performed to avoid a sampling bias, whereby clusters tend to give greater weight to environmental variables (Renner et al., 2015).

Models were projected into the future (2070) based on 13 General Circulation Models used in the 5th IPCC (Flato et al., 2013), ACCESS1-0, HadGem2-ES, Miroc-ESM, BCC-CSM1-1, CCSM4, CNRM-CM5, GFDL-CM3, GISS-E2-R, INMCM4, IPSL-CM5A-LR, MPI-ESM-LR, MRI-CGCM3, NorESM1-M. We selected the 2070 scenarios, which reflects how the climate will be towards the end of the century, because previous more recent time scales predictions would not provide an adequate parameter representation of the impact of climate change on the species studied here. We considered two representative concentration pathways, defined by the trajectory of greenhouse gas emissions and subsequent radiative forcing (Wayne, 2013): 4.5 W/m2 (moderate climate change scenario) and 8.5 W/m2 (severe climate change scenario). The continuous model output maps were converted into binary maps using the thresholding method that maximizes the sum of sensitivity and specificity (Liu et al., 2013). To incorporate model variability while avoiding biases due to outlier model outputs, we generated,

using ArcGIS 10.1 (ESRI, Redlands, USA), the final future maps for each scenario by adding the binary model outputs generated from 13 General Circulation Models and reclassifying the resulting map giving zero (unsuitable) to cells that were either identified by all models as unsuitable or identified as suitable by less or equal to three models, and one (suitable) to cells identified as suitable by more than three models. This means that suitable future areas were identified as suitable by > 25% of the GCM Maxent models (upper quantile).

Models were run with 1,500 iterations using the cloclog model output. We used the ENMeval package in R 3.4.3 (R Core Team, 2017) to evaluate and select the best model parameterization (regularization multiplier value and number of parameters) based on Akaike Information Criterion corrected for small sample sizes (AICc; Muscarella et al., 2014). The best fit model included three features (linear, quadratic and hinge) and a regularization multiplier of 1. The performance of the models was evaluated using ten-fold cross-validations and the Area Under the Receiver Operator Curve (AUC), a measure of the ability of the model to distinguish between presence locations and background/pseudoabsences. We compared model AUC scores with 100 null models, generated through resampling the Isothermality layer in ENMTools (Warren et al., 2010), to determine whether our models performed significantly better than random (Raes & ter Steege, 2007).

4.2.2 Gap Analysis

The gap and range change analyses were calculated using the reclassified binary maps and the South America Albers equal area conic projection system. We calculated the representativeness of predicted current and future suitable areas for each species by overlaying in ArcGIS 10.1 (ESRI, Redlands, USA) the outputs of our models with maps of Brazilian protected areas (ICMBio, 2017; MMA, 2018b), priority areas for biodiversity conservation (MMA, 2018a) and forest cover (IBGE, 2017). To highlight important protected areas and priority areas that will retain climatic suitability in the future we overlapped areas that were predicted to be suitable under both present and future conditions with existing protected areas and priority areas. We also overlapped priority areas and protected areas layers with our modelled suitable areas to identify relevant areas for the expansion or creation of protected areas. We also identified protected areas that are likely to be under threat due to hunting and other anthropogenic impacts by overlapping model outputs with a human settlement map (IBGE, 2017).

To classify the degree of protection of the areas predicted by our models to be suitable for our target species, we considered the following categories: *high protection status* – protected areas of integral protection biodiversity; *medium protection status* - protected areas of permanent protection that allow sustainable use of natural resources, except for environmental protection area; *low protection status* – protected areas allow settlement and development; and *unprotected* - areas not protected by any means but the environmental law.

The priority areas are a public policy instrument to support decision making, in an objective and participatory way, in the planning and implementation of actions such as the creation of protected areas, licensing, inspection and promotion of sustainable use. We considered areas occupied by forests as those with tree formations greater than five meters in height, including areas of dense forest, open forest, seasonal forest and mixed ombrophilous forest, as well as forested savanna, forested campinarana and mangroves (IBGE, 2017). Human settlements were defined as areas characterized by urban use, structured by buildings and road system, where non-agricultural artificial surfaces predominate (IBGE, 2017). This category includes metropolises, cities, towns, roads, services and transport, power grids, communications and associated land, areas occupied by industrial and commercial complexes, buildings, which may in some cases be located in periurban areas, indigenous villages and mining areas.

4.3 RESULTS

We gathered a total of 223 occurrence records for the three target species, 176 of which were retained after validation. These consisted of 66 records for *A. belzebul*, 33 for *S. flavius* and 77 for *S. libidinosus* (Appendix D).

All species distribution models had good predictive power (Table 1) and performed better than null models, AUC_{train} range: 0.61 - 0.80. Geomorphology, annual precipitation and ecoregion were the main environmental variables affecting habitat suitability for the target species (Table 1). The current model predicted suitable areas of 671.135 km^2, 47,183.5 km^2, and 1,059,360 km^2 for *A. belzebul*, S. *flavius* and *S. libidinosus*, respectively (Table 2, Fig. 2). Our future models predicted a reduction in the size of suitable areas under climate change for all species (Table 2; Fig. 3).

Gap analysis shows that only 24.39%, 8.05% and 9.42% of the areas predicted to be suitable for the *A. belzebul*, *S. flavius* and *S. libidinosus*, respectively, under current climatic

conditions fall within existing protected areas (Table 3, Fig. 4), and 72% of these areas are of low protection status. Approximately 88% of the areas predicted to be suitable are unprotected.

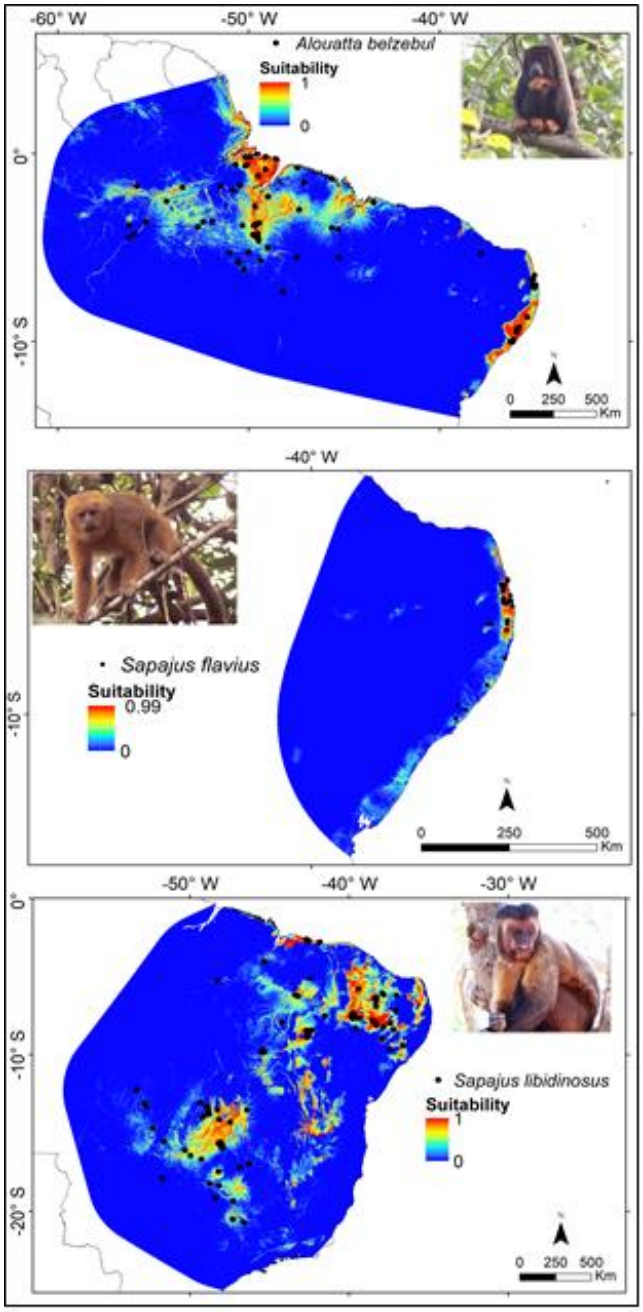

Figure 2. Maps showing predicted maps for the current distribution of suitable areas for the occurrence of three Brazilian primates: *Alouatta belzebul*, *Sapajus flavius* and *S. libidinosus*. Suitability ranges from low (0) in blue to high (1) in red.

Table 1. Results of the species distribution models for the three studied primates, number of location records included in the models (N), AUC scores and the percent contribution of the different environmental variables (Bio2 - Mean Diurnal Range ; Bio3- Isothermality ; Bio8- Mean Temperature of Wettest Quarter; Bio11- Mean Temperature of Coldest Quarter; Bio12- Annual Precipitation; Bio15- Precipitation Seasonality; Bio18- Precipitation of Warmest Quarter; Eco.- Ecoregion; Geom.- Geomorphology).

Species (N)	AUC train	AUC test	Environmental variables contribution									
			Bio2	Bio3	Bio8	Bio11	Bio12	Bio15	Bio18	Slope	Eco.	Geom.
***A. belzebul* (66)**	0.9143	0.8791	21.308	6.4176	-	3.9729	10.7661	7.9781	0.4382	3.6894	-	45.4297
***S. flavius* (33)**	0.9823	0.9736	0.6975	7.7803	0.1509	1.6525	37.4619	-	13.7553	3.0859	-	35.4157
***S. libidinosus* (77)**	0.8874	0.8278	4.4848	0.0623	-	0.365	3.3044	9.1066	-	6.9557	60.5284	15.1928

Table 2. Area predicted to be suitable for the species (km^2), considering current, future moderate and future severe scenarios for 2070 and including their geographical range (IUCN range: AF- Atlantic forest, CA – Caatinga, CE – Cerrado, AM -Amazon forest) and including their geographical range (IUCN range: AF- Atlantic forest, CA – Caatinga, CE – Cerrado, AM -Amazon forest) and future range loss.

Species	IUCN range	Distribution models	Area predicted to be suitable (km^2)	Range loss (%)
A. belzebul	AF, AM	Current	671135	-
		Future moderate	131792	80.36
		Future severe	40606.7	93.94
S. flavius	AF	Current	47183.5	-
		Future moderate	10331.4	78
		Future severe	1101.89	97.66
S. libidinosus	CA, CE	Current	1059360	-
		Future moderate	726892	31.38
		Future severe	486616	54

In our models, we overlapped areas predicted to be suitable for the occurrence of the three target species with government priority areas and forest cover layers. We found that 27% of the suitable areas for the three target species all together fall within government priority areas for conservation (10.4% in the Amazon forest, 9.8% in the Cerrado, 6.4% in the Caatinga and 0.82% in the Atlantic forest). Furthermore, we found that only 24% of the suitable areas are currently forested (17% in the Amazon forest, 3.9% in the Caatinga, 2.6% in the Cerrado and 0.5% in the Atlantic forest) (Table 3). Binary maps of current predictive distribution with their priority areas and forest cover are detailed in Appendix E and F, respectively.

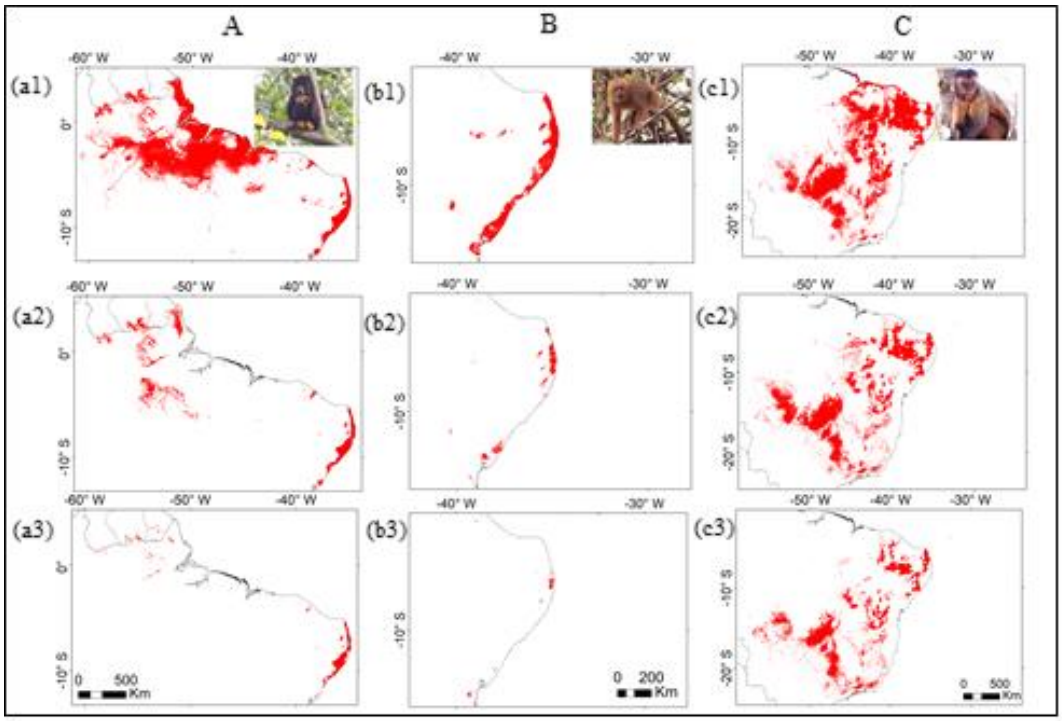

Figure 3. Binary maps of present and future predictive distribution for (A) *Alouatta belzebul*, (B) *Sapajus flavius* and (C) *Sapajus libidinosus*, under 1) current, 2) moderate future (2070 RCP 4.5) and 3) severe future (2070, RCP 8.5) scenarios. Future predictions are based on an ensemble of 13 GCMs for each scenario. Red indicates predicted suitable areas above the maximum training sensitivity plus specificity threshold.

In an attempt to identify relevant areas for the expansion or creation of protected areas as well as to identify potential connective spots between suitable areas, we overlapped government priority areas and protected areas layers with our modelled suitable areas. We found that 96.41%, 99% and 74.49% of the government priority areas within *A. belzebul*, *S. flavius* and *S. libidinosus* suitability areas, respectively, are outside protected areas (See Appendix G).

Table 3. Area predicted to be suitable for occurrence of the three primates and their representativeness in areas with different protections status (high, medium, low and unprotected), in priority areas for biodiversity conservation and in areas with forest cover.

Species	**Area predicted to be suitable (km^2)**	**Protection status (%)**				**Priority area for biodiversity conservation (%)**				**Forest cover area** (%)			
		High	***Medium***	***Low***	***Unprotected***	**Biome***				**Biome**			
						AF	**AM**	**CA**	**CE**	**AF**	**AM**	**CA**	**CE**
A. belzebul	671135	4.56	8.03	11.80	75.61	0.27	25.39	0.98	0.44	0.28	41.93	0.49	0.76
S. flavius	47183.5	0.44	0.48	7.13	91.95	1.76	-	8.07	-	6.61	-	1.70	-
S. libidinosus	1059360	2.32	0.35	6.75	90.58	1.09	0.80	10.12	15.22	0.57	1.29	6.17	3.88

*Biomes: AF- Atlantic forest, CA – Caatinga, CE – Cerrado, AM -Amazon forest

We found that 23% (93), 10.60% (43) and 73% (295) of protected areas will maintain climatically suitable under the moderate future climate change scenario for *A. belzebul*, *S. flavius* and *S. libidinosus*, respectively. These numbers decrease to 12.37% (50), 3.21% (13) and 66.83% (270) when we consider the more severe future scenario (see Appendix H for list of protected areas). Of all the protected areas identified as climatically suitability for the three primate species under present and future conditions, 13.85% (56) overlap with human settlements. For *S. flavius,* in particular, 32.88% of climatically suitable protected areas overlap with human settlements (see Appendix H). We also identified that 18.12% (91), 2.39% (12) and 87.84% (441) of government priority areas will maintain climatically suitable under the moderate future climate change scenario for *A. belzebul*, *S. flavius* and *S. libidinosus*, respectively. These numbers decrease to 4.98% (25), 0.39% (2) and 61.15% (357) when we consider the more severe future scenario (see Appendix G for list of government priority areas and conservation action for each area).

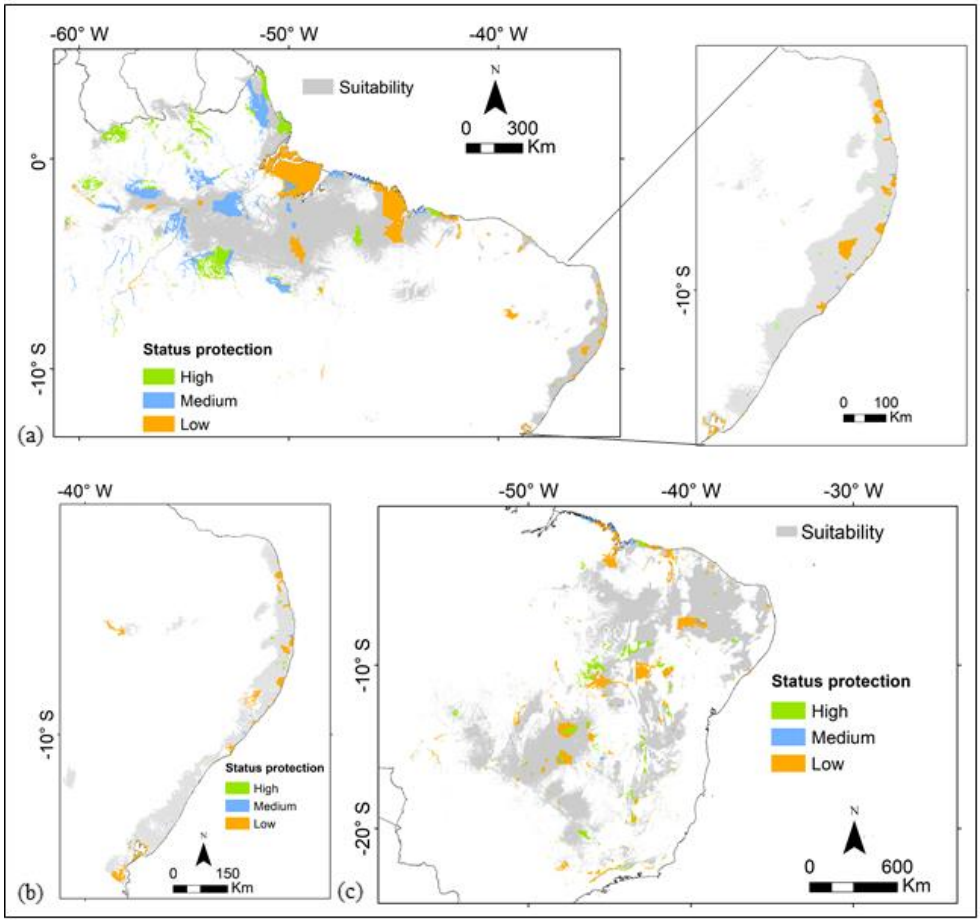

Figure 4. Predicted suitable areas for occurrence of (a) *Alouatta belzebul*, (b) *Sapajus flavius* and (c) *Sapajus libidinosus* in grey, and their overlap with protected areas of high (green), medium (blue) and low (red) protection status.

4.4 DISCUSSION

Our results show an alarming scenario for the future of the three primate species, whereby 88% of the areas predicted to be suitable for *A. belzebul*, *S. flavius* and *S. libidinosus* are unprotected. The remaining 12% of the suitable areas fall within protected areas, but 72% of those have low protection status. Only 27% of the overall areas predicted to be suitable for the occurrence of the three species overlap with priority areas for conservation, and only 24% is currently forested. Future models predict nearly a total loss of climatic suitability for the three species in tropical forests (Amazon and/or Atlantic forest) and loss of a quarter of suitable areas in the semi-arid regions (Caatinga and Cerrado).

The models presented in our study were able to distinguish between the habitats of the studied species. We found that habitat suitability for the target species is affected by geomorphology, annual precipitation and ecoregions, which together influence vegetation structure and composition (Shi-kui et al., 2019). Characteristics such as temperature variation and deciduous and semideciduous vegetation differentiate their habitat needs from other primates (Tatter et al., 1997; Prado, 2003). The availability of water and changes in soil composition also plays an important role by controlling the type of vegetation that can grow over different landscapes (El-Keblawy et al., 2015; Cowles et al., 2018).

Our results reflect the current situation of the protected areas system in Brazil, with high percent of areas classified as low protection status. Currently, the Atlantic forest has only 10.3% of its area under protection and only 2.6% falls within the high protection status (MMA, 2018b). An even more worrying scenario is observed in the Caatinga and Cerrado biomes, where 8% of the areas are protected and only 1.6% and 3%, respectively, are within the integral protection areas (MMA, 2018b). The Amazon stands out among other biomes with 28% of its area inside protected areas and 9% within integral protection areas (MMA, 2018b). In low protection status protected areas, extractive activities are allowed in accordance with applicable law, resulting in inadequate protection for those species at imminent risk of extinction (Schulze et al., 2018). In addition, some protected areas are referred to as "on paper protected areas" because they lack essential infrastructure or resources (Saout et al., 2013; Oliveira & Bernard, 2017). Despite problems related to the poor management of these areas, protected areas are relevant because they prevent the conversion of natural ecosystems (Geldmann et al., 2013) and allow the maintenance of a greater diversity and abundance of species than in unprotected areas (Gray et al., 2016).

We observed a lower percent overlap between habitat suitability for the primate species and government priority areas for biodiversity conservation in the northeastern Atlantic forest. This is because most of the Atlantic forest priority areas are concentrated in southern Brazil (MMA, 2018a). Only two government priority areas were considered in northeastern Brazil and these are located in the state of Bahia, in areas where the target species do not occur. Although government priority areas cover approximately a quarter of the territory of biomes like the Amazon, Caatinga and Cerrado, areas predicted as suitable for the three primate species in our study had a low representation within them (i.e. 6-10%). Nevertheless, because a high percentage of government priority areas within the modelled suitable areas are not within protected areas, it will be necessary to identify potential connectivity areas as well as areas for the expansion or creation of new protected areas in order to conserve these primate species. The government priority areas inside the suitable areas for the occurrence of the target species that will remain suitable under future climate change (see Appendix G) are potential sites for reintroducing confiscated individuals from the illegal wildlife trade, as long as these areas are under some level of legal protection.

The low percent of forest cover identified in areas predicted to be suitable for the three target species is mainly due to the high anthropogenic impact that biomes such as the Atlantic forest, Caatinga and Cerrado have suffered over the years. The northeastern Atlantic forest is highly fragmented (Ribeiro et al., 2011). According to Silva & Fialho (2013), in the Pernambuco Endemism Center, which includes the distribution of *A. belzebul* and *S. flavius*, 99% of the remnant forest fragments are smaller than 50 ha. The situation is no different for the Caatinga and Cerrado, where only 50% of the original vegetation remains (MMA, 2016; Strassburg et al., 2017). In addition, habitats remnants within the Atlantic forest and semi-arid zones are surrounded by an inhospitable and low permeability agricultural matrix (Portillo-Quintero & Sánchez-Azofeifa, 2010; Ribeiro et al., 2011). Areas of occurrence of the *S. flavius* are also affected by mining (eg, Bezerra et al., 2014). Although some species of primates are able to cross and benefit from non-forested matrices, like agricultural areas (Mandujano et al., 2004; Canale et al., 2013; Souza-Alves et al., 2019), anthropogenic areas increase conflict between humans and wildlife. Primates are threatened by dog attacks, contact with electricity, revenge from farmers because of crop raiding, as well as the illegal pet trade (Fuentes, 2006).

Our data corroborate with other studies that suggest that both the Amazon and the Atlantic forest will suffer significant biodiversity losses due to the combined effect of deforestation and climate change (Pires & Costa, 2013; Bellard et al., 2014). In the Amazon,

deforestation can alter the balance of the forest and transform it into a savanna environment (Costa & Pires, 2010). Future climate change projections indicate a 20% increase in aridity, both for the Amazon rainforest and for the northeast of Brazil (Franchito et al., 2014) and an increase in temperatures (Marengo et al., 2017). Biodiversity hotspots, such as the Cerrado and the Atlantic forest, are predicted to be adversely affected by future climate change and lose about 25% of their endemic species (Bellard et al., 2014) because they are projected to become arid lands (Franchito et al., 2014; Costa & Pires, 2010). It is believed that there will be changes in land use because of the projected decrease in herbaceous vegetation in the Cerrado and an increase in the extent of fragmentation and conversion to pasture in the Atlantic forest (Bellard et al., 2014). Changes in spatial configuration and habitat quality may affect the distribution and density of primate species (Estrada et al., 2017), as well as the quantity and quality of food resources available to them (Dunn et al., 2009, Morellato et al., 2016).

To suggest important areas for conservation action, we have identified protected areas that will maintain climate suitability in the future and may serve as a refuge for the species studied here. These areas had high representativeness in the suitability areas of *S. libidinosus*, but were very low in the suitability areas of *A. belzebul* and *S. flavius*. This indicates the importance of expanding or creating new protected areas for the latter two species, especially in the northeastern Atlantic forest. Even though the overall percentage of protected areas affected by urban settlements were relatively low in our study (i.e. 13.85%), the areas of *S. flavius* were the most impacted by human settlements (i.e. 32.88%). The existence of human settlements close to the suitable areas may result in hunting, even though there is no data available on current hunting pressure on *S. flavius*. Hunting has already been responsible for eradicating several primate populations in Brazil, including populations of capuchin monkeys (Estrada et al., 2018). In a scenario where primate extinction is mainly related to habitat loss (Estrada et al., 2018), the identification of areas for the maintenance of these populations is essential to assist conservation actions such as reintroduction or translocations (Molloy et al., 2019). Strengthening environmental policies and enforcing laws is key to preventing further destruction of forested areas, as well as hunting (Estrada et al., 2018; Brancalion et al., 2016). Therefore, our study is even more important given the present-day political context in Brazil, where the government is in favour of environmental exploitation and loosing conservation laws that are leading to more deforestation, fragmentation and habitat destruction in the country (see Ferrante & Fearnside, 2019).

Our study sounds a red alert regarding the conservation of Neotropical primates in general. We provide important information for the conservation of three primate species, two of which are part of the Brazilian Action Plan for the Conservation of Primates in Northeast Brazil. Even though the three target species inhabit areas considered to be of global conservation importance (Brooks et al., 2006), we identified a low percentage of protected areas and low forest cover in areas predicted to be suitable for these species, especially in the Atlantic forest. The Brazilian government designated priority areas for conservation, however, they still do not cover enough area for the maintenance of the primate populations studied here. Through identifying suitable areas for the occurrence of the target species under present and future conditions this study highlights areas where conservation efforts should focus to reduce habitat destruction and fragmentation. We believe that creating and maintaining protected areas may help to preserve forested areas and contribute to the survival of the species in the future. Thus, it is important that new priority areas are identified and implemented as protected areas urgently.

Our models show that future climate change may lead to substantial range losses for the studied primate species. This is extremely worrying as these changes can affect the establishment of populations and their ability to survive in these areas in the long term. Our results are valuable for assessing the conservation status of each species and establishing goals in action plans for the conservation of other species of primates inhabiting the same regions. Our findings and recommendations will be passed to key stakeholders to optimize future conservation actions.

Author contributions

Study design: BM, BB; Study fieldwork: BM; Data analysis and writing the article: BM, BB, OR, JSA, JB.

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Conflicts of interest

None.

Ethical standards

The study complies with Brazilian law (Fieldwork licence: SISBIO/ICMBio - 52404-1; License to interviews humans during fieldwork: Plataforma Brasil - CAAE-49198215.3.0000.5208 / Approval-1.266.360).

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4. MICROSATELLITE MARKERS FOR BEARDED CAPUCHINS (*SAPAJUS LIBIDINOSUS*): TRANSFERABILITY AND CHARACTERIZATION

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4.1 INTRODUCTION

Capuchin monkeys are classified into two distinct clades: tufted or robust capuchins (*Sapajus*) and the non-tufted or gracile capuchins (*Cebus*) (Lynch-Alfaro et al., 2012; Lima et al., 2018). The clades are differentiated by morphological, ecological and molecular characteristics (Lynch-Alfaro et al., 2012). The tufted form has specialized cranial and dental structures for the exploitation of hard foods items, and possess forelegs, hands and feet that are shorter than those of the non-tufted clade (Silva, 2001; Lynch-Alfaro et al., 2012). Additionally, the tufted capuchins make use of tools to obtain hard-to-access food items such as underground (e.g. roots) or encapsulated resources (e.g. palm nuts, cashew nuts) (Moraes et al., 2014). At present, eight species of tufted capuchin monkeys are recognized: *Sapajus apella*, *Sapajus cay*, *Sapajus flavius*, *Sapajus libidinosus*, *Sapajus macrocephalus*, *Sapajus nigritus*, *Sapajus robustus*, and *Sapajus xanthosternos* (IUCN, 2019). *Sapajus libidinosus* are Neotropical primates, distributed in Brazil throughout Cerrado areas in the central, north and south-eastern regions, and in Caatinga areas in the north-eastern region (Rylands & Kierulff, 2015). Although the *S. libidinosus* is not classified as a Threatened species (Rylands & Kierulff, 2015), it has been reclassified as "Near Threatened" by the Brazilian Red Book of Endangered species, owing to anthropogenic effects such as habitat loss and fragmentation of their habitats (Fialho et al., 2015; Rylands & Kierulff, 2015). Such impacts directly influence the viability of primate populations that rely on forest habitats to survive (Benchimol and Peres, 2013; Liu et al., 2017). Nevertheless, the lack of studies on population genetics in *S. libidinosus* limits our knowledge of how habitat loss is genetically affecting the species. Polymorphic markers are not yet available to study their diversity and population structure.

Microsatellite markers have been developed and tested on other capuchin monkeys such as *S. apella* (Escobar-Páramo, 2000), *C. capucinus* (Muniz & Vigilant, 2008) and *S. nigritus* (Tokuda et al., 2014). The characterization of genetic markers is a matter of great importance for population genetics studies, which are urgently required to assess gene flow and long-term viability of populations (Liu et al., 2014; León-Ortega & Gonzalez-Wangüemert, 2015; Tian et al., 2017; Srbek-Araujo et al., 2018). Microsatellite markers may also be useful in behavioural studies (Tokuda et al., 2018; Yewers et al., 2018; Hoogland et al., 2109). Such studies contribute to effective management and conservation strategies (Ruiz Lopez et al., 2016; Storfer et al., 2018).

This study will provide molecular markers that can be used in future genetic studies on *S. libidinosus* which need an urgent consideration in research and conservation agendas for the species and its habitat (e.g. Lynch-Alfaro et al., 2014). The use of primers transferability has become a more economical and efficient way of obtaining genetic information from species when compared to developing new primers (Oliveira et al., 2006; Buzatti et al., 2016). Thus, here we test for amplification and characterize 14 microsatellite loci in *S. libidinosus*. These microsatellites were previously isolated from *C. capucinus* (Muniz & Vigilant, 2008), which belongs to the same subfamily (i.e. Cebinae) of the *S. libidinosus* (Groves, 2016). The molecular markers tested here will help to advance conservation actions and genetic management of *S. libidinosus* populations.

4.2 MATERIAL AND METHODS

4.2.1 Sampling

We sampled individuals of *Sapajus libidinosus* from two localities in Pernambuco, north-eastern Brazil: 1) Serra do Pinheiro: -37.20 w, -8.38 s; 2) and in Serra do Estrago: -37.40 w, -7.96 s (Figure 1). We collected 22 faecal samples in September of 2016 in the and Serra do Estrago and 27 faecal samples in December 2016 in Serra dos Pinheiros. In each study area, we established food provision stations in order to attract the animals and consequently facilitate the collection of faeces. We monitored the provision stations using camera traps (model Bushnell 8MP) to confirm species identity as we did not habituate the animals (Figure 2). We also performed active searches in both areas to find the animals when they did not access the provision stations. We stored the faeces in Falcon tubes containing 50 ml of absolute alcohol in the field and then we froze them (-18°C) in the laboratory for up to 12 months prior to DNA extraction (Serra do Pinheiro samples were frozen for 12 months and Serra do Estrago samples for 9 months). Three blood samples from *S. libidinosus* individuals were used to ensure the right allele size in the genotyping. We obtained two of those faecal samples from free-living individuals from the municipality of Serra Talhada, Pernambuco, Brazil with the help of the National Center for Research and Conservation of Brazilian Primates (CPB). We obtained the third sample from a captive individual kept at the Dois Irmãos State Park Zoo in Recife, Pernambuco, during the routine health check-up of the individual. We kept the blood samples frozen before analysis.

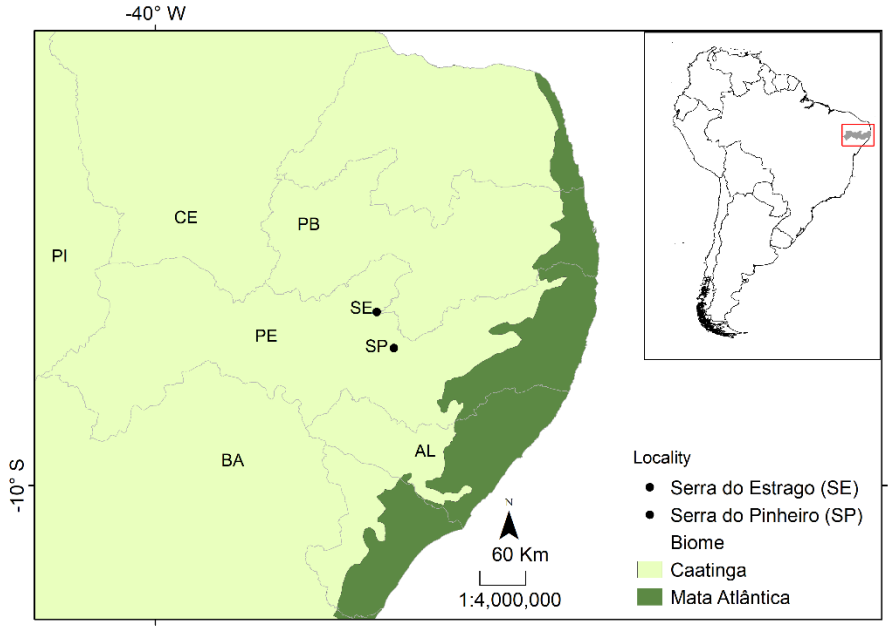

Figure 1. Location of the *S. libidinosus* sampled sites in the present study. The populations live in fragments of the Caatinga Biome, in the state of Pernambuco (PE), North-eastern Brazil. Serra do Pinheiro (SP): -37.20 w, -8.38 s, Serra do Estrago (SE): -37.40 w, -7.96 s. (PB- Paraíba, CE- Ceará, PI- Piauí, BA- Bahia, AL – Alagoas)

4.2.2 DNA extractions

We extracted the DNA from blood samples using a QIAamp DNA Mini Kit (Qiagen), following the QIAamp® DNA Mini and Blood Mini Handbook protocol for DNA Purification from Blood or Body Fluids (Spin Protocol).

DNA from faecal samples was extracted using a QIAamp DNA stool kit (Qiagen), specifically developed for faecal DNA purification (Di Fiore, 2003; Bradley et al., 2007). We used extraction protocols provided by Qiagen kits along with the adjusted protocols proposed by Di Fiore (2009) and Tokuda (2012). Briefly, the changes we made in the protocols were: 1) the DNA was extracted from approximately 100 mg of faeces; 2) faecal samples were incubated at room temperature in ASL buffer for 30 to 60 minutes, instead of 10 min; 3) the samples were incubated with proteinase K at 70 ºC for 30 minutes, instead of 10 minutes; and 4) we added 100 µl of buffer AE and samples were incubated at room temperature for 20 to 30 minutes, instead of 200 µl for 1 minute. The modified protocol was used for the samples with a low concentration of *S. libidinosus* DNA.

Figure 2. Camera trap image confirming the species identity. The image shows a group of *S. libidinosus* at Serra do Estrago, Pernambuco, Northeast Brazil.

4.2.3 Microsatellite amplification and analysis

We tested the transferability to *S. libidinosus* of 14 microsatellites (Ceb01, Ceb02, Ceb04, Ceb07, Ceb08, Ceb09, Ceb10, Ceb105, Ceb115, Ceb119, Ceb120, Ceb121, Ceb127, Ceb130: Muniz and Vigilant 2008) developed for *C. capucinus* and already tested for transferability on other Neotropical primate species (see Muniz and Vigilant 2008; Tokuda et al. 2014). The markers were tested in two steps. In the first, we used DNA extracts from the blood samples to test the amplification temperature gradient of each marker. The temperature gradient tested was between 54ºC and 64ºC. In each set of samples, we used negative controls to make sure the material was not contaminated. After identifying which markers amplified the blood DNA extracts, their annealing temperature and allele size, we tested these markers on stool DNA samples from *S. libidinosus* individuals from two localities. The Polymerase Chain Reactions (PCRs) mix contained 13 µL reaction volume and consisted for 2 µL DNA (5-63 ng/µL), 7.5 µL (2x) MyTaqMix (Bioline), 1.2 µL (6mg) bovine serum albumin, 0.3 µL (10µ/m) forward primer, 0.3 µL (10µ/m) reverse primer and 1.7 µL H_2O. We labelled each forward primer with the fluorochromes 6-FAM or HEX in the 5′ end. Amplifications were carried out under the following conditions: an initial denaturation step at 95°C for 1 min; 35 cycles at 95°C for 1min, annealing at 56-64°C for 45 s, and extension at 72°C for 1 min; and a final extension for 10 min at 72°C. The difference between the PCR protocols of the blood and faeces samples is that we used 1 µL of blood DNA extract and 2 µL for stool, adjusting only with the amount of water 2.7 µL and 1.7 µL, respectively. For both the blood and faeces samples, we used

negative controls to make sure the material was not contaminated. For stool samples, we also used a positive control (i.e. blood DNA extract) to confirm the amplification of the marker. We visualised amplified fragments on 2% agarose gels. We genotyped PCR products through Source BionScience (ABI Prism 3730), and allele sizes were scored using the program Geneious version 11.1.4 (Kearse et al. 2012).

We analysed the number of alleles per locus (N_A), observed heterozygosity (*H*o), expected heterozygosity (*H*e), probability of paternity exclusion (Q), identity index (*I*), polymorphic information content (PIC) and identity analysis, using CERVUS 3.0.7 software package (Kalinowski et al., 2007). We calculated the exact test of Hardy-Weinberg equilibrium using Arlequin v. 3.5.2.2 (Excoffier and Lischer, 2010), and the fixation index (Fis) for each locus using the Fstat v. 2.9.3.8 (Goldet, 2002), both analyses considering the Bonferroni correction of the confidence intervals (Rice, 1989). To test for evidence of null alleles, we used the program MICRO-CHECKER (Van Oosterhout et al., 2004). We performed these analyses in two ways: the first, considering samples from each locality separately and the second, considering samples of both localities together.

4.3 RESULTS

We managed to amplify six of the 14 microsatellite markers used (Ceb 130, Ceb 120, Ceb 105, Ceb 10, Ceb 4, Ceb 7) using the blood samples (Table 1). Subsequently, we tested the selected primers on the DNA extracted from the 49 faecal samples collected. We treated 11 faecal samples using the modified protocol for DNA extraction. Nine of those samples resulted in increased DNA concentration, demonstrating the effectiveness of the protocol. The remaining 38 samples were treated with the standard Qiagen protocol. Overall, we amplified the markers in 30 of the 49 samples collected, 15 in each locality. The mean proportion of amplified loci was 0.989 in Serra do Pinheiro, 0.956 in Serra do Estrago samples and 0.9722 considering the samples of both localities together. Ceb01, Ceb02, Ceb08, Ceb09, Ceb115, Ceb119, Ceb121, Ceb127 did not amplify in any sample. The number of alleles, the observed and the expected heterozygosities, the probability of paternity exclusion, the identity indexes and the polymorphic information contents are presented in Table 1. No loci showed evidence of null alleles and the identity test showed that there are no repeated individuals in the sample. No locus showed a significant deviation from the Hardy-Weinberg equilibrium in Serra do

Pinheiro, but in the Serra do Estrago, three loci presented a significant result Ceb130, Ceb120 and Ceb7 (Table 1). When we analysed the samples of both localities together, the HWE was also significant for the Ceb130, Ceb120 and Ceb7 loci. The Fis values showed negative and significant values (*p* smaller) for some loci, indicating an excess of heterozygosity (Serra do Pinheiro: Ceb7; Serra do Estrago: Ceb120 and Ceb7; samples from both localities together: Ceb130, Ceb10 and Ceb4) (Table 1).

Table 1: Genetic characterization, of the six microsatellite loci transferred to *Sapajus libidinosus* living in Serra do Pinheiro and Serra do Estrago in Sertânia municipality, Pernambuco State, north-eastern, Brazil. (N) number of individuals tested, (Ta) annealing temperature, (NA) number of alleles, (Ho) observed heterozygosity, (He) expected heterozygosity, (PIC) polymorphic information content, (Q) probability of paternity exclusion, (I) identity index, (HWE) Hardy–Weinberg equilibrium (p = 0.0083 after Bonferroni correction) and (Fis) fixation index (p = 0.00341 for localities separately, and p= 0.0083 for single population after Bonferroni correction); [c] combined probability, *significant; ***p* smaller significant, indicating excess heterozygosity).

Serra do Pinheiro samples												
Locus	GenBank ID	Ta ºC	N	Allele size range (pb)	N_A	Ho	He	PIC	Q	I	HWE	Fis
Ceb130	EU019215	64	15	210 - 282	7	0.933	0.869	0.820	0.679	0.046	0.23354	-0.077
Ceb120	EU019211	64	14	248 – 278	7	0.643	0.815	0.759	0.596	0.073	0.35481	0.217
Ceb105	EU019208	64	15	228 - 240	4	0.733	0.697	0.620	0.419	0.160	0.62538	-0.055
Ceb10	EU019203	59	15	238 - 250	4	0.800	0.605	0.543	0.355	0.215	0.47371	-0.339
Ceb7	EU019200	64	15	123 - 175	7	1.000	0.768	0.713	0.541	0.096	0.10861	-0.462**
Ceb4	EU019199	54	15	166 - 214	5	0.867	0.602	0.519	0.327	0.238	0.14529	-0.317
All loci	-	-	-	-	5.667	0.829	0.726	0.6621	0.9849[c]	0.000002[c]	-	-0.148
Serra do Estrago samples												
Locus	GenBank ID	Ta ºC	N	Allele size range (pb)	N_A	Ho	He	PIC	Q	I	HWE	Fis
Ceb130	EU019215	64	15	262 – 278	4	1.000	0.724	0.645	0.442	0.145	0.00009*	-0.400
Ceb120	EU019211	64	15	250 – 274	4	1.000	0.701	0.619	0.413	0.163	0.00165*	-0.448**
Ceb105	EU019208	64	15	224 – 272	5	0.667	0.653	0.580	0.384	0.188	0.23531	-0.022
Ceb10	EU019203	59	15	238 – 258	5	0.933	0.717	0.650	0.459	0.137	0.68687	-0.315
Ceb7	EU019200	64	13	127 – 167	4	1.000	0.618	0.515	0.315	0.244	0.00310*	-0.326**
Ceb4	EU019199	54	13	166 – 178	4	0.769	0.588	0.521	0.334	0.233	0.61242	-0.660
All loci	-	-	-	-	4.333	0.894	0.791	0.5883	0.9501[c]	0.000034[c]	-	-0.360
Serra do Pinheiro and Serra do Estrago samples together												
Locus	GenBank ID	Ta ºC	N	Allele size range (pb)	N_A	Ho	He	PIC	Q	I	HWE	Fis
Ceb130	EU019215	64	30	262 – 278	7	0.967	0.810	0.768	0.604	0.070	0.00163*	-0.197**
Ceb120	EU019211	64	29	250 – 274	9	0.828	0.775	0.728	0.557	0.090	0.00708*	-0.069
Ceb105	EU019208	64	30	224 – 272	6	0.700	0.668	0.606	0.41	0.169	0.43228	-0.049
Ceb10	EU019203	59	30	238 – 258	5	0.867	0.666	0.618	0.433	0.156	0.19439	-0.308**
Ceb7	EU019200	64	28	127 – 167	8	1.000	0.819	0.777	0.618	0.065	0.00000*	-0.371
Ceb4	EU019199	54	28	166 – 178	6	0.821	0.603	0.549	0.364	0.209	0.25641	-0.226**
All loci	-	-	-	-	6.667	0.8638	0.7235	0.6744	0.9857 [c]	0.000002 [c]	-	-0.198

4.4 DISCUSSION

We found that six of the 14 tested markers successfully amplified in the *S. libidinosus* samples and thus, we can effectively use them when designing future population genetic studies for the species, considerably reducing the costs of microsatellite marker isolation. The absence of null alleles demonstrates that the genotyping performed in this study does not present errors such as non-amplified alleles, stutter peaks or short allele dominance (large allele dropout) (Van Oosterhout et al., 2004). All markers tested were tetranucleotides and markers of this type are considered more consistent for allele identification through automated techniques (Di Fiore, 2003; Liu et al., 2008). Tokuda et al. (2014) tested eight (i.e. Ceb3, Ceb8, Ceb9, Ceb11, Ceb119, Ceb120, Ceb121, and Ceb130) of the primers developed for *C. capucinus* in 21 *S. nigritus* and only Ceb3, Ceb11 and Ceb130 amplified successfully. Despite amplifying successfully in *S. nigritus*, Ceb3 and Ceb11 loci showed only two alleles (Tokuda et al., 2014). On the other hand, Ceb130 showed a greater polymorphism with eight alleles for *S. nigritus* (Tokuda et al., 2014). Comparing the parameters of the Ceb130 locus, common to the three species tested, *C. capucinus* (Muniz & Vigilant, 2008), *S. nigritus* (Tokuda et al., 2014) and *S. libidinosus* (present study), we found differences in annealing temperature and size of the alleles. The annealing temperature ranged from 59ºC in *C. capucinus* (Muniz and Vigilant, 2008), to 60ºC in *S. nigritus* (Tokuda et al., 2014) and 64ºC in *S. libidinosus*. The size of alleles ranged from 182-218 in *C. capucinus* (Muniz and Vigilant, 2008) and 123-282 in *S. libidinosus*, and this information was not available for *S. nigritus*. Muniz & Vigilant (2008) developed primers for *C. capucinus* and tested the transferability of these primers to 23 Neotropical primate species. However, the number of individuals tested was very low in each species (only three species were tested using 10 individuals). Despite the low number of individuals, the species tested were polymorphic in at least two loci and species from the same family of *S. libidinosus* (i.e. *S. apella* n = 10 individuals, *C. olivaceus* n = 3 and *S. xanthosternos* n = 3) amplified the largest number of loci (Muniz & Vigilant, 2008), probably due to their phylogenetic proximity.

The obtained heterozygosity values indicate that the study localities of *S. libidinosus* have a high genetic variation. These values show the reliability of the loci for paternity test use (Wang et al., 2015). Studies previously conducted for other primates consider indexes around 0.9660 and 0.9999 as being powerful for paternity testing (Chambers et al., 2004; Stevanovic et al., 2010; Wang et al., 2015). In our study, these values varied among localities and showed

good power of exclusion. The identity index indicates that the probability of identifying two different individuals as being of the same genotype is low, demonstrating the reliability of the studied sites for this type of estimation. Values between 0.01-0.0001 are sufficiently low and indicate that the chosen loci are effective to distinguish between individuals (Waits et al., 2001). One can also access genetic variability among genotypes by calculating PIC values for each of the six loci. The PIC value can range from 0 - 1.0, the closer to one, the greater the allele variability in a tested locality (Guo & Elston, 1999). This value is calculated by considering the number of known alleles and their frequency of distribution (Botstein et al., 1980, Guo & Elston, 1999). The PIC values indicated a high variability for the markers analysed here, in both our study sites. We found that the Ceb130 marker would be the most polymorphic marker followed by Ceb120, Ceb10 and Ceb4. Polymorphic markers are more useful for distinguishing individuals and understanding the relationships between them (Guo & Elston, 1999, Li et al., 2014). In the Serra do Pinheiro, there was no deviation from the HWE. However, three loci deviated from the HWE in the Serra do Estrago (Ceb130, Ceb120 and Ceb7) and also when analysing the samples from both localities together. Deviation from HWE can be an outcome from heterozygosity excesses (Cornuet & Luikartt, 1996), which was the case in our study. The species social system may have contributed to this result. The mating system of the study species is considered to be polygamous (Fialho et al., 2015), increasing the possibility of mating between the individuals of the group. They present a hierarchy of dominance maintained by males, but males disperse while females remain in the group (Verderane 2010). The study locations presented approximately 25 individuals (*unpublished data*), a common size for groups of capuchin monkeys. The standard size of *S. libidinosus* groups is 6 to 20 individuals (Rylands & Kierulff, 2015), although groups of 40 to 53 individuals have previously been recorded (Ferreira et al., 2009; Moraes et al., 2014).

It is worth pointing out that the DNA extracted from the faecal samples was “impure” primate DNA and despite the low concentrations (i.e. between 5 and 63 ng/µl), it was still possible to evaluate the efficiency of the primers tested. Some researchers recommend the multiple-tube approach in order to minimise the allelic dropout errors that may occur in low-concentration DNA from non-invasive samples (Gerloff et al., 1999; Kohn et al., 1999). However, due to few amounts of biological material and DNA we did not use the multiple-tube approach. Also, according to Morin et al. (2001) faecal DNA extracts with values higher than 201pg (0.201 ng) already guarantee high confidence (99% of certainty) and amplification precision of these extracts, being able to present allelic dropout in only 5.2% of samples. Due

to the absence of null alleles and the observed heterozygosity higher than expected heterozygosity, we believe that genotyping error due to allelic dropout (genotype a heterozygous as a homozygous) did not occur in the sample set. The low concentration of DNA in our samples could also be a result of the storage time of the samples. For logistical reasons, we had to store samples from Serra do Estrago for one year, and samples from Serra do Pinheiro for nine months before the DNA extractions. The type and time of storage of faecal samples are thought to influence the success of DNA extraction (Piggott & Taylor, 2003). There is no consensus on the best technique to be used, because often the type of storage will influence the choice of DNA extraction technique (Waits & Paetkau, 2005; Vallet et al., 2007). Other factors also need to be taken into account in order to obtain a good sample, such as the type of diet of the species and the site where it was collected (Broquet et al., 2007). Herbivorous animals present secondary metabolites that may inhibit DNA amplification (Broquet et al., 2007; Vallet et al., 2007). Good quality DNA samples (from blood and tissue) are difficult to collect for species that are threatened, elusive, rare, occupy inaccessible areas or occur at low densities (Salgado-Lynn et al., 2016). Thus, testing and using samples collected in a non-invasive manner became a relevant alternative for conservation genetics studies (Di Fiore, 2003; Broquet et al., 2007; Salgado-Lynn et al., 2016). The microsatellite markers transferred to *S. libidinosus* can be widely used in different fields in the future such as population genetics, molecular ecology, population structure, gene flow and landscape connectivity studies. Thus, this validation of such molecular tools will contribute to the development of effective conservation strategies for capuchin monkeys and other primates.

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5. HOW DOES LANDSCAPE AFFECT THE GENETIC STRUCTURE OF BEARDED CAPUCHIN POPULATIONS INHABITING A SEMI-ARID REGION IN NORTHEAST BRAZIL?

5.1 INTRODUCTION

One of the major challenges for conservationists today is to maintain biodiversity through mitigation of habitat loss (Asaad et al., 2016; Fonseca & Venticinque, 2018; Prévot et al., 2018). Anthropogenic activities are the leading cause of loss of natural vegetation and the consequent emergence of edge effects and spatial isolation of populations (Haddad et al., 2015; Pfeifer et al., 2017). Changes in habitat configuration may act as barriers or as conduits for the movement of individuals, depending on the ecological requirements and fitness of the organism in question (Banks et al., 2013; Pfeifer et al., 2017; Moraes et al., 2018; Wan et al., 2018). Such species movements across habitats may also depend on the distance between the fragments and the type of matrix found in the environment (Debinski, 2006; Fahrig, 2013). Changes in the dispersal behaviour of individuals and connectivity between forest fragments can lead to important ecological and evolutionary consequences (Parreira & Chikhia, 2015; Turbek et al., 2018), such as increased genetic drift and inbreeding (Spigler et al., 2016; Wang et al., 2017; Lino et al., 2018).

Habitat loss may result not only in declining species richness and abundance (Pimm et al., 2014; Newbold et al., 2015; Titeux et al., 2017), but may also in geographic isolation of populations in intensely fragmented habitats (Cushman et al., 2012; Bruggeman et al., 2010). Isolation of populations may occur due to the distance between them or the landscape characteristics (Wan et al., 2018). The first approach relates to the Isolation by Distance Hypothesis, which suggests that genetic distance between populations is positively correlated with geographic distance (Wright, 1943). This is considered a null model for studies of landscape genetics since only Euclidian distance between populations is evaluated. Habitat heterogeneity (effective distance) is not considered (Wan et al., 2000; Dileo et al., 2013). Another hypothesis that has been explored in the genetic analyses is Isolation by ResistanceHypothesis (McRae, 2006; Spear et al., 2010). In this case, we consider not only the distance between populations, but the landscape characteristics (Segelbacher et al., 2010, Waits et al., 2016). If the landscape does not permit gene displacement, it is considered to be highly resistant and a decrease in connectivity is expected among populations, even though populations are geographically close (McRae, 2006; Spear et al., 2010).

Landscape genetics is a relatively new approach to help understanding how geographical and environmental features influence genetic variation between and within populations (Manel et al., 2003; Manel & Holderegger, 2013; Richardson et al., 2016; Waits et al., 2016). Methods applied to landscape genetics have been widely used to evaluate the

effects of landscape composition, matrix configuration and quality on microevolutionary processes such as gene flow, drift and selection (Manel et al., 2003; Storfer et al., 2007; Balkenhol et al., 2016). These effects can be assessed in several ways, including distance isolation tests (Mantel, 1967), landscape indexes (Schumaker, 1996) and electrical circuit theory (McRae, 2006). The latter can be used to predict movement patterns, identify important habitat spots and movement corridors for conservation planning (McRae, 2006; McRae et al., 2008). Studies of how habitat heterogeneity influences population connectivity and its genetic variability has become an important tool to guide effective protection actions and creation of dispersal corridors (Schoville et al., 2012; Kahilainen et al., 2014; Waits et al., 2016).

Our study evaluated how landscape configuration has been influencing the genetic variability and composition of populations of bearded capuchins (*Sapajus libidinosus*), a primate that inhabits the Caatinga domain, a semi-arid region in North-eastern. The Caatinga domain is considered one of the largest semi-arid environments in the world (Moro et al., 2016). It presents vegetation formed by thorn scrub and seasonally dry forests and high rates of endemism of fauna and flora (Queiroz et al., 2017; Prado et al., 2005; Albuquerque et al., 2012). Despite its ecological importance, the Caatinga biome has already lost about 47% of its original area (MMA, 2011) and presents only 8% of its territory within protected areas (MMA, 2018). The biggest threats to Caatinga are related to human activities and include deforestation for agriculture and pasture expansion, charcoal production, men-caused wildfires and also climate change (Redo et al., 2013; Beuchle et al., 2015; Schulz et al., 2017).

Bearded capuchins are well-known for their high cognitive skills, which are believed to have helped their survival in such harsh environment (Moura & Lee, 2004; Moraes at al., 2014; Emidio & Ferreira, 2012). Bearded capuchin are categorized as Least Concern by the IUCN, however, its population decline is mainly linked to habitat loss, as well as trafficking (Rylands & Kierulff, 2015). Bearded capuchinsare social animals living in multi-male/multi-female groups ranging three to 40 individuals (Freese & Oppenheimer, 1981; Lynch & Rímoli, 2000; Mannu & Ottoni, 2009; Moraes et al., 2014). They present a hierarchy of dominance maintained by males, but the females are philopatric (i.e. while males disperse, females remain in the group) (Izar et al., 2012). These latter social characteristics are considered relevant for the maintenance of the genetic diversity of populations. The hierarchy of dominance by males can drastically reduce the effective size of the social group and increase the genetic differentiation between groups (Di Fiore, 2003). A male or a small set of males end up being responsible for most of the paternity within a social group for some time (Fragaszy et al., 2004). On the other hand, the

philopatry of females can cause a low diversity of mitochondrial DNA within the groups and larger inter-population differences (Di Fiore, 2003).

Here we tested three hypothesis considering the current scenario of substantial habitat loss for the bearded capuchins: i) The Isolation by Distance Hypothesis to find out whether the genetic distance between populations occurs as a function of geographic distance; ii) The Isolation by Resistance Hypothesis, to find out whether the genetic distance occurs as a function of the composition of the the matrix landscape. In other words, whether the more connected fragments, irrelated (positive) to greater genetic similarity between populations; iii) Whether genetic diversity varies according to the percentage of forest cover, fragment size and fragment connectivity. We would expect higher genetic diversity in areas with a higher percentage of forest cover, fragment size and connectivity.

5.2 METHODS

5.2.1 Sample collection

We collected 174 faecal samples from June 2016 to January of 2017 to obtain genetic material non-invasively from individuals belonging to six populations of bearded capuchins inhabiting six tropical dry forest fragments (samples per fragment, Serra do Pinheiro (SP)= 27, Serra do Estrago (SE) = 22, Serra da Maravilha (SM) = 51, Pedra Branca (PB) = 17, Serra do Almirante (SA) = 45, Serra das Tabocas (ST) = 12) in the state of Pernambuco (Figure 1). We selected the sites based on a literature survey and also through semi-structured interviews (Moraes et al., 2014) conducted with locals population in the area and researchers to find out where there were populations of bearded capuchins.

Because the animals were not habituated to human presence, we confirmed species identity in each site through analysis of images from baited camera trap stations (See Appendix I) and direct observations animals. We used dry corn inside PET bottles with small holes, papaya and banana as baits to help to attract the bearded capuchin monkeys. Camera traps Bushnell 8MP was set to take videos of the animals (videos lasting one minute at one-second intervals) for, at least, fifteen consecutive days in each site. The baited camera trap stations also proved to be useful for us to obtain the faecal samples and to confirm the presence of the speciesin the areas (Moraes et al *in press;* Chapter 2 in this thesis). We also performed active searches to obtain faeces in each fragment. We stored the collected faeces in plastic Falcon tubes containing 50 ml of absolute alcohol in the field. We then froze the samples (-18°C) in

the laboratory for up to 12 months before DNA extraction (Moraes et al *in press;* Chapter 2 in this thesis).

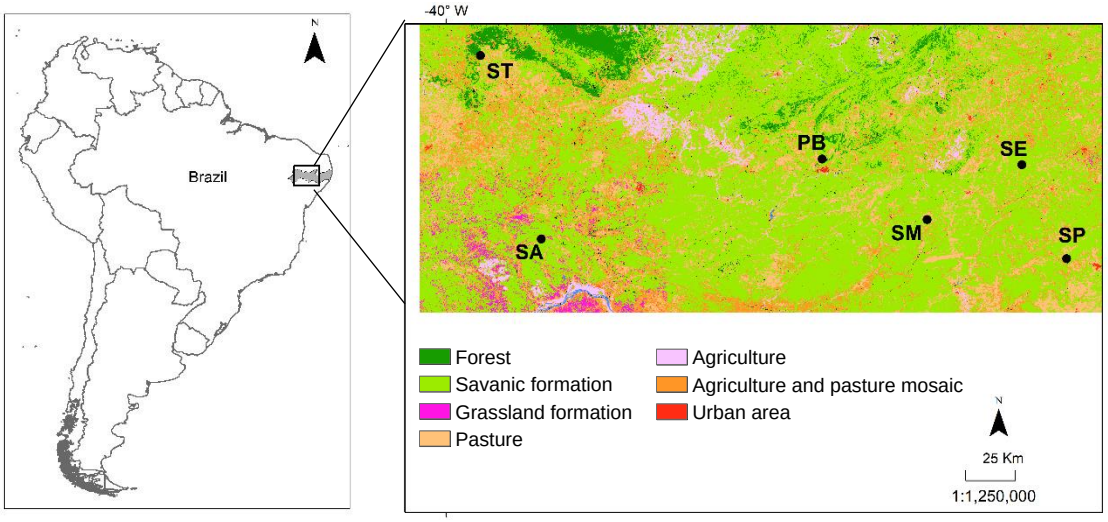

Figure 1. Location of sampling areas of *S. libidinosus* populations in the state of Pernambuco, northeastern Brazil.The image represents the land cover in the study area and was obtained from IBGE (2018). Serra do Pinheiro (SP): -37.20 w, -8.38 s, Serra do Estrago (SE): -37.40 w, -7.96 s, Serra da Maravilha (SM): -37.83 w, -8.20 s, Serra da Pedra Branca (PB): -38.30 w, -7.93 s, Serra do Almirante (SA): -39.57 w, -8.29 s), Serra das Tabocas (ST): -39.84 w, -7.47 s.

5.2.2 DNA extraction and microsatellite genotyping

We extracted the DNA from faecal samples using QIAamp DNA stool kit (Qiagen), developed specifically for faecal DNA purification (Di Fiore 2003; Bradley et al. 2007; see also outline details on the extraction protocols on Moraes et al. (*in press; and* Chapter 2 in this thesis) and Appendix J.

We used six microsatellites markers for genotyping (Ceb 130, Ceb 120, Ceb 105, Ceb 10, Ceb 4, Ceb 7: Muniz & Vigilant, 2008) developed for white-faced capuchin monkeys (*Cebus capucinus*) and previously tested on other Neotropical primates including the bearded capuchins (see Muniz & Vigilant, 2008; Tokuda et al., 2014; Moraes et al. *in press*; Chapter 2 in this thesis). Briefly, the Polymerase Chain Reaction (PCR) mix contained 13 µL reaction volume and consisted in 2 µL DNA (5-63 ng/µL), 7.5 µL (2x) MyTaqMix (Bioline), 1.2 µL (6mg) bovine serum albumin, 0.3 µL (10µ/m) forward primer, and 0.3 µL (10µ/m) reverse primer. We labelled each forward primer with the fluorochromes 6-FAM or HEX in the 5′ end. We performed amplifications under the following conditions: i) initial denaturation step at 95°C for 1 min; ii) 35 cycles at 95°C for 1min, annealing at 56-64°C for 45 s, and extension at 72°C for 1 min; and iii) a final extension for 10 min at 72°C. We visualised amplified fragments on

2% agarose gels. PCR products were genotyped by Source BioScience, and allele sizes were scored using the program Geneious version 11.1.4 (Kearse et al., 2012).

5.2.3 Genetic diversity, marker resolution and inbreeding

Genotyping errors, presence of null alleles and scoring errors due to stuttering were checked by Micro-Checker version 2.2.3 (Van Oosterhout et al., 2004). In order to verify the genetic diversity of each bearded capuchin populations, we inferred the mean number of alleles per locus (N_A), Observed Heterozygosity (*H*o), Expected Heterozygosity (*H*e), the Polymorphic Information Content (PIC) and Identity Analysis, using the software Cervus 3.0.7 (Kalinowski et al., 2007). We analysed the allelic diversity by calculating the mean allelic richness (Ar) and the proportion of private alleles (Pc) for each forest fragment in HP-RARE 1.0 (Kalinowski, 2005), using rarefaction for adjusted the estimates for sample size. It is expected that the greater the value of allelic richness, the greater the diversity of the region and the more gene flow is occurring between locations. While for the values of private alleles higher values are expected in isolated populations. Due to the low sharing of alleles with other locationsWe tested for deviation from Hardy–Weinberg Equilibrium (HWE) and Linkage Disequilibrium (LD) using the Arlequin v. 3.5.2.2 (Excoffier & Lischer, 2010). We performed the Exact test of Hardy–Weinberg Equilibrium with 10^6 steps in the Markov chain and 10^5 dememorization steps. Linkage Disequilibrium was performed using 10^4 permutations and five initial conditions for the expectation-maximization (EM) algorithm. Statistical significance levels were adjusted for multiple comparisons using a Bonferroni's correction (Rice, 1989).

The resolving power of the six microsatellite loci shared by the six populations were assessed using the PIC value. We classified each locus as highly informative (PIC> 0.5), reasonably informative (0.5> PIC> 0.25) or slightly informative (PIC <0.25) (Botstein et al., 1980). We estimated the inbreeding coefficient (F_{IS}) to assess if there was random mating in the samples, indicating whether the sampled locations belonged to distinct populations or not (Wright, 1965). The inbreeding coefficient was estimated using Fstat v. 2.9.3.2 (Goudet, 1995).

5.2.4 Genetic structure

We assessed the genetic structure the *Sapajus libidinosus* populations through Structure 2.3.4 software (Pritchard et al., 2000). A Bayesian algorithm that identifies genetically homogeneous groups of individuals, using an "ad hoc" ΔK statistic based on the rate of change in data logging probability between successive values of K, where K is the number of clusters

(Evanno et al., 2005). We set up the Structure software to identify if there were homogeneous groups among the six study populations, so we run the software with K ranging from 1 to 7. We used the admixture model, correlated allele frequencies and no location as prior information. The Monte Carlo Markov Chain (MCMC) was run for 100,000 steps, after a burn-in period of 100,000 steps. We performed ten independents run for each value of K. To access the number of clusters (K) that best fit the dataset, we run Structure Harvester software online (Earl & Vonholdt, 2012) to estimate the ΔK using Evanno et al. (2005) method.

To evaluate the spatial structure of populations, we used an individual-based Bayesian assignments test implemented in the R Geneland v 4.0.8 package (Guillot, 2005a). This test combines genetic data with geographic information from the samples and identifies genetic discontinuities between populations or individuals (Guillot et al., 2005a). We performed 10 independent run simulations of 50000 MCMC iterations, with a thinning value of 100. The number of populations (K) ranged from 1 to 7. We used the uncorrelated model, which considered independent allele frequencies, following Dirichlet distributions (D-Model) (Pritchard et al., 2000). According to Guillot et al. (2005b) this model provides the best results, avoiding the inference of spurious populations when compared to the correlated model (F-Model) (Falush et al., 2003). The correlated model does not indicate how differentiated the populations are (Guillot et al., 2005b). We also used the null alleles option enabled, for better inferences accuracy as recommended by Guillot et al. (2008). The number of distinct spatial groups were selected according to the highest average log posterior probability. These analyses were performed in RStudio 1.2.5 (RStudio Team, 2019), using *Geneland* package.

5.2.5 Genetic differentiation

We evaluated the genetic variation between populations through Analysis of Molecular Variance (AMOVA) (Excoffier et al., 1992). The analyses were performed using the Arlequin v.3.5.1.2 (Excoffiner & Lischer, 2010), with 20,000 random permutation and calculated with the stepwise mutation model (SMM) with R_{ST} (Slatkin, 1995). We analysed datatwo ways: the first considering each locality as a population and the second considering the clusters indicated by the result of the Structure and Geneland program. The coefficient of genetic differentiation was estimated within individuals, among populations, among groups, among populations within groups, among individuals within populations.

We also estimated the genetic differentiation between populations by calculating the pairwise F_{ST} (Weir & Cockerham, 1984) and R_{ST} (Slatkin, 1995) statistics, the first estimate takes into account the infinite alleles model (IAM; Kimura & Crow, 1964) and the second the Stepwise Mutation Model (Kimura & Otha, 1978), using Arlequin v 3.5.1.2 (Excoffier & Lischer, 2010). An F_{ST} or R_{ST} with values between 0-0.05 indicates a small differentiation, between 0.05-0.15 a moderate differentiation, between 0.15-0.25 a large differentiation and > 0.25 a very large differentiation (Wright, 1965).

5.2.6 Landscape genetics analysis

5.2.6.1 Isolation by distance hypothesis test

We evaluated whether geographic distance influenced the genetic distance between populations using the F_{ST} through a Mantel test (Reynolds et al., 1983). We calculated pairwise population genetic differentiation (F_{ST}) using Arlequin v 3.5.1.2 (Excoffier & Lischer, 2010). F_{ST} was estimated as $(H_T – H_S) / H_T$, where H_T is the total expected heterozygosity, and H_S is average expected heterozygosity across populations (Nei, 1977). Euclidian distances between pairs of population were calculated using software R. The significance of the correlationbetween the matrices along with the genetic structure $F_{ST} / (1-F_{ST})$ and the Euclidean geographical distance of the collection points with 10,000 iteractions were tested in the Arlequin v 3.5.1.2 (Excoffier & Lischer, 2010).

5.2.6.2 Landscape resistance analysis

We tested the Resistance Isolation Hypothesis to assess whether environmental variables affected the connectivity between the sampled populations of *S. libidinosus* (Storfer et al., 2007; Cushman et al., 2012). This analysis was performed using the Circuitscape 5.5.0 (McRae et al., 2013). This software uses electrical circuit theory to model connectivity in heterogeneous landscapes through the cumulative cost of movement due to landscape resistance and the result is a matrix of resistance distance between populations (McRae, 2006; McRae et al., 2008).

The analysis was performed by creating a resistance surface using the following layers: land use, forest cover, urbanization, human impact, permanent water, habitat suitability (Table 1). We have converted these layers into biologically relevant resistance values for *S. libidinosus*, based on the literature and expert opinions. The layers have a resolution of 1 km^2. Landscape

variables were assigned resistance costs ranging from one (no resistance to movement) to 100 (strong barrier to movement). Maps were processed in ArcGIS v10.1 (ESRI). We generate eight hypotheses of the effect of landscape variables on genetic connectivity (Table 1). The tested variables did not correlate with other variables used in the hypothesis test to avoid spurious inferences (Cushman et al., 2013).

To identify the landscape variables that most affected genetic differentiation among *S. libidinosus* populations, we adjusted linear mixed effects models using the maximum likelihood population (MLPE) parameterization. We used the genetic distance matrix (Pairwise F_{ST}) between populations as the dependent variable and the resistance matrix as the independent variable. Model adjustments were assessed using the Akaike (AICcmin) and Bayesian (BICew) information criteria values calculated from linear mixed-effect models within a 95% confidence interval (IC) (Burnham & Anderson, 2004). The analyses were performed in Software R (RStudio Team, 2019), using the *ggplot2* (Wickham, 2016), *lme4* (Bates et al., 2015) and *usdm* (Naimi et al., 2014) packages.

A first model was tested using six different cost surfaces generated for the land use layer (see Appendix L for details of each land use layer tested). Among these, we selected one layer to test the land use resistance and the genetic distance matrix. In a second model, we compared different forest variable models to select the best forest layer to take forward: Forest (1) vs non-forest (100) (binary layer), distance to forest (range 1 from 100 - Resistance decreases the closer to forested areas) and percent tree cover (range 1 from 100), being the last selected to test the model with the genetic distance. After selecting these variables, we tested each variable separately and the last two hypotheses, Barriers and Antropogenic, were tested by combining two layers, as shown in Table 1.

Table 1. Resistance layers used for to test the Resistance Isolation Hypothesis, and access the effect of landscape variables on genetic connectivity.

Hypothesis	Models Variables	Resistance layers
Land use	Land cover	Classification: Urban area (100), Agricultural (50), Livestock (100), Urban and forest mosaic (20), Native vegetation (1), Urban and savannah mosaic (20), Water (100) (see Appendix L 3 for description class and appendix M) (IBGE, 2018)
Vegetation	Percentage of forest cover	Resistance decreases as forest percentage increases (from 1 to 100) (Hansen et al. 2013)
Urbanization	Distance Urban area	Resistance increases the closer to urban areas (from 1 to 100) (generated from the land use layers and calculated in Arcgis 10.1)
Human impact	Footprint index	With 1 for lowest human footprint index and 100 for highest (Venter et al., 2018)
Permanent Water	Rivers	Water (100) and the rest (1)
Habitat suitability	Ecological niche modelling.	Resistance is lower in areas of high climatic suitability (1) and higher in unsuitable areas (100). (See chapter 1 of this thesis for Ecological niche modeling procedures).
Barriers	Percentage of forest cover + Rivers	
Antropogenic	Distance Urban area + Footprint index	

5.2.6.3 Landscape metric analyses

We adopted patch- and landscape-based perspectives because this is the most appropriate approach to study primate responses to habitat loss and fragmentation (Arroyo-Rodríguez & Mandrujano, 2009; Arroyo-Rodríguez & Fahrig, 2014). We considered that the spatial scale within which a given population is affected in a forest fragment is related to the dispersal ability of the individuals (Jackson & Fahrig, 2015).

For the data analysis, we first delimited the tropical dry forest fragments interpreting high-resolution (30 m) imagens obtained from *Projeto MapBiomas* version 4.0 (www.mapbiomas.org). On these images, we defined the scale of the effect of fragmentation

and degradation on *S. libidinosus* populations by setting a buffer of 5 km surrounding from the sampling point of the groups at each locality, covering an area of about 78,51 km^2. Buffer size was established based on species home range. Presotto et al. (2018) found that a group of *S. libidinosus* can walk approximately 1.5 km per day and form a 25 km route system covering a range of 3.54 km^2. In addition, the home range of capuchin monkey species variesfrom 80 to 900 ha (see Mittermeier et al., 2013). We used this buffer size due to cross-gap capacity of a capuchin monkey in the tropical dry forest. We expected that the response of individuals and groups to fragmentation, habitat loss and degradation must be restricted to a conservative estimate of their dispersal ability (within the landscape buffer). These landscape metrics were extracted in ArcGis 10.1 (ESRI) and are described in Table 2.

Table 2. Landscape metrics obtained from each of the six locations where *S. libidinosus* populations were sampled in the semiarid region of Pernambuco, Brazil. The images were obtained through MapBiomas and have a resolution of 30 x 30 m.

Metrics analysed	Description
Percentage of forest cover (savannah + forest area)	Percentage of forest cover (FC%) present within the 5 km buffer at each location. Buffer area (BA) = 78.51 km^2. We considered as total forest cover (AFCt) the sum of the areas classified as forest and savannah vegetation. The percentage was calculated as follows: FC% = (AFCt * 100) / BA.
Fragments size	The area in km^2 of the fragment in which the population was sampled (focal fragment).
Matrix connectivity	Sum of the total area (km^2) of forest cover inside the landscape buffer, excluding the area of the focal fragment) (Martensen *et al*. (2008, 2012) and Ribeiro *et al*. (2009).

Landscape metrics from each locality were related to the allelic richness and proportion of private alleles of *S. libidinosus* populations. In order to verify whether the genetic structure and landscape metrics were related, we performed a Multiple Linear Regression. Here, we run two models, with the first using the allelic richness and second one using the proportion of private alleles used as response variables, and percentage of forest cover, fragments size, and matrix connectivity as the predictor variable. We run Shapiro-Wilk tests with the residual values of both models to verify the normality (Model #1: W = 0.96147, p-value = 0.831; Model #2: W

= 0.91563, p-value = 0.4745). Furthermore, we also tested the homoscedasticity of variances for both models using Breusch-Pagan test (Model #1: BP = 5.9926, df = 3, p-value = 0.112; Model #2: BP = 5.8622, df = 3, p-value = 0.1185). In order to meet normality, we log-transformed the data when necessary. These analyses were performed in program RStudio 1.2.5 (RStudio Team, 2019), using *tidyverse* (Wickham, 2017) and *lmtest* (Hothorn et al., 2019) packages. Statistical significance was set at 0.05 probability level.

5.3 RESULTS

Six microsatellite markers used (Ceb 130, Ceb 120, Ceb 105, Ceb 10, Ceb 4, Ceb 7) were amplified in 74 (42.5%) of the samples collected (SP = 15, SE = 15, SM = 15, PB = 8. SA = 15, ST = 6). For these 74 individuals, the multilocus genotypes were 97% complete. A total of 59 alleles were detected from six microsatellite loci. The number of alleles observed at each locus varied from seven to 18.

5.3.1 Genetic diversity

Identity analysis did not detect any repeated individuals, so all samples were used in followed analyses. The mean allelic richness at the locus ranged from 2.6 to 3.42 (Table 3). The frequency of private alleles was higher in the Serra do Pinheiro population (0.72), while the Serra das Tabocas population (0.39) presented the lowest frequency. The observed mean heterozygosity and expected heterozygosity in the six populations ranged from 0.82 to 0.91 and 0.64 to 0.73, respectively (Table 3). The deviation of Hardy–Weinberg Equilibrium was observed only in the Serra do Estrago population for the Ceb 130, Ceb120 and Ceb7 loci. One pairs (Ceb130 and Ceb120) of loci showed evidence of linkage disequilibrium in two population (Study site: SE and SA). Once the binding patterns between loci are not consistent at all sites, all loci were used in the analyses.

The resolving power of the six microsatellites was classified as highly informative (PIC> 0.5) (Table 3). The values of inbreeding coefficient (F_{IS}) in the six populations were negative and presented ibreeding. Three population (SE, SA and ST), after Bonferroni correction, presented a significantly smaller *p*, suggesting that there is an excess of heterozygosity (Table 3).

Table 3. Genetic diversity based on six microsatellites loci measures for the six population of *Sapajus libidinosus* sampled in Caatinga forest fragments, in the state of Pernambuco, Brazil.

Pop	N	N_A	A_r	Pc	*Ho*	*He*	PIC	F_{IS}
SP	15	5.833	3.42	0.72	0.822	0.726	0.6621	-0.148
SE	15	4.667	2.95	0.67	0.855	0.695	0.5883	-0.360**
SM	15	5.833	3.42	0.49	0.858	0.7381	0.6693	-0.163
PB	8	4.167	3.09	0.50	0.854	0.7111	0.6047	-0.219
SA	15	5.000	2.72	0.43	0.822	0.6720	0.5922	-0.424**
ST	6	3.167	2.66	0.35	0.911	0.6407	0.5011	-0.491**

(N) Sample size per fragment, (NA) Mean number of alleles per locus, (Ar) Mean allelic richness, (Pc) Proportion of private alleles, (*Ho*) observed heterozygosity, (*He*) expected heterozygosity, (PIC) Polymorphic Information Content; (Fis) inbreeding coefficient; ** p smaller =0.001, indicating excess heterozygosity.

5.3.2 Population structure

Bayesian clustering approach, implemented with Structure Program, in the 10 independent simulations showed was maximized at K = 3, decreasing when K > 3 (Fig. 2a). The value ΔK was 32.41 when K=3. The three genetic clusters were 1- SP, SM, PB, ST; 2-SA and 3-SE populations (Figure 2b). The result of Structure analysis indicated that the population of *S. libidinosus* in Pernambuco state is divided into three subpopulations.

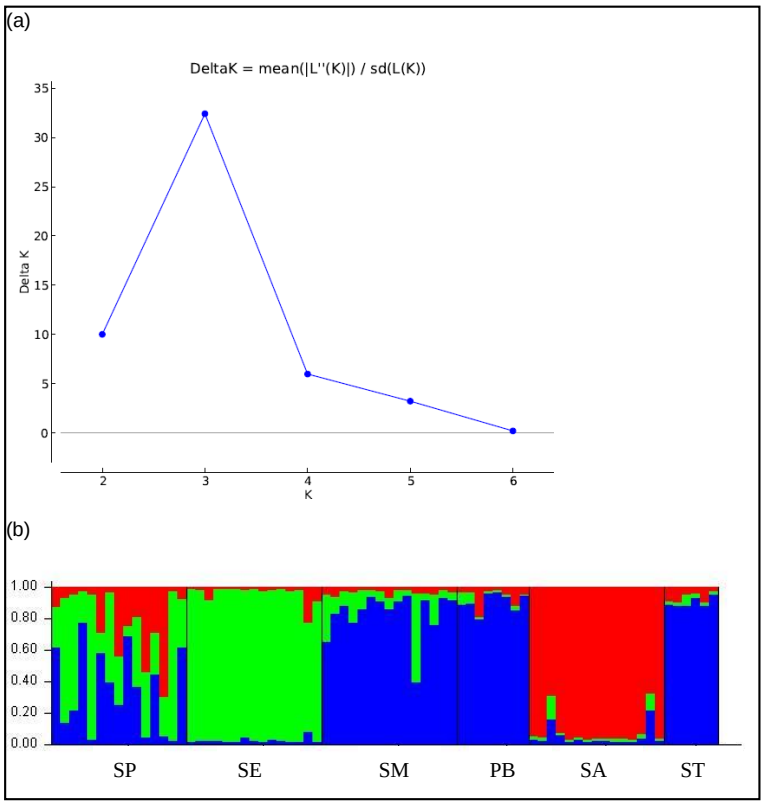

Figure 2. Results of Structure analysis. (a) Plot for detecting the number of K groups that best fit the data using Δ*K* estimative on a dataset of 74 faecal samples genotyped for six polymorphic microsatellites (1- Serra do Pinheiro, 2- Serra do Estrago, 3 – Serra da Maravilha, 4- Pedra Branca, 5- Serra do Almirante e 6 – Serra das Tabocas). The graphic was generated by the online program Structure harvester (Earl & Vonholdt, 2011) and shows the number of K = 3, decreasing when K> 3. (b) Distribution of the three genetic clusters generated by Structure software. The vertical lines are broken into coloured segments showing the proportion of each individual assigned to each of the inferred K. The numbers indicate the locations of each population, one cluster formed by Serra do Pinheiro (SP), Serra da Maravilha (SM), Pedra Branca (PB) and Serra das Tabocas (ST); a second cluster formed by Serra do Estrago (SE) and a third cluster formed by Serra do Almirante (SA). For (a) and (b) Structure (Pritchard et al., 2000) was set for 10 independent runs and K from 1 to 7.

Based on the higher average later probability, Geneland Program inferred the existence of three genetic groups, with spatial discontinuity between groups 1- SP, SM, PB, ST; 2- SE; 3- SA (Figure 3). The groups identified by Geneland were similar to those indicated by the analysis of the Structure program.

(a)

(b)

(c)

Figure 3. Spatial map of genetic discontinuity of *Sapajus libidinosus* populations, based on the Geneland analysis, considering the number population through highest average log posterior probability for 74 *S. libidinosus* individuals on six microsatellite loci. The posterior probability distribution suggested K=3 as the best fit for the data: (a) Serra do Pinheiro (SP), Serra da Maravilha (SM), Pedra Branca (PB) and Serra das Tabocas (ST); (b) Serra do Estrago (SE); (c) Serra do Almirante (SA). Red indicates a low probability of belonging to the genetic subpopulation and white indicates a high probability.

5.3.3 Genetic differentiation

The analysis of variance, considering the hierarchical levels of subdivision, showed that there is a significant difference between the six studied localities and among *S. libidinosus* individuals studied here (Table 4).

Table 4. Analysis of Molecular Variance (AMOVA) calculated with the Stepwise Mutation Model (SMM) at three (A) and four (B) hierarchical levels of subdivision. (A) Correspond to the six localities and (B) Correspond to the population clusters defined by Bayesian clustering analyses, Structure and Geneland.

Source of variation	df	Sum of square	Variance components	Percentage variation	*R* statistic (*p* value)
(A)					
Among populations	5	4743.799	37.84738	42.34811	0.00000**
Among individuals within populations	68	3874.122	7.46254	8.34997	0.03772*
Within individuals	74	3156.500	44.06214	49.30192	0.00000**
Total	145	11774.421	89.37206		
(B)					
Among groups	2	1917.348	-6.48142	-7.42713	0.57663
Among populations within groups	3	2826.452	42.22355	48.38443	0.00000**
Among individuals within populations	68	3874.122	7.46254	8.55141	0.04000*
Within individuals	74	3156.500	44.06214	50.49129	0.00000**
Total	145	11774.421	87.26682		

df, degrees of freedom. Statistical significance: * $P < 0.05$; ** $P < 0.001$

Genetic differentiation was also assessed by pairwise F_{ST} and R_{ST}. Statistical tests showed significant pairwise F_{ST} among all localities with $p < 0.001$ (Table 5). Values of pairwise F_{ST} ranged from 0.052 to 0.201. Genetic differentiation by R_{ST} did not show significant values between SP and SM, SE and SM, PB and ST localities and ranged from 0.029 to 0.847 (Table 5).

Table 5. Pairwise F_{ST} (above diagonal) and R_{ST} values (below diagonal) based on microsatellite genotyping data between the inferred localities of *S. libidinosus*.

Statistical significance: * $p < 0.001$; ** $p < 0.05$

Localities	Serra do Pinheiro	Serra do Estrago	Serra da Maravilha	Pedra Branca	Serra do Almirante	Serra das Tabocas
Serra do Pinheiro	-	0.06346*	0.07105*	0.10383 *	0.05873*	0.09130*
Serra do Estrago	0.12788**	-	0.11212*	0.19077 *	0.16517 *	0.20143 *
Serra da Maravilha	0.02907	0.06618	-	0.05211 *	0.14745 *	0.10992 *
Pedra Branca	0.62236*	0.74793*	0.38592*	-	0.14042 *	0.09404 *
Serra do Almirante	0.51367**	0.62154*	0.21872*	0.64301*	-	0.12619 *
Serra das Tabocas	0.62236	0.84759*	0.48804*	0.09512	0.80227*	-

5.3.4 Landscape genetics analysis

5.3.4.1 Analysis of Isolation by Distance

The genetic distance between the sampled localities was not related with the geographic distance (r = 0.274, p = 0.167). Pairwise F_{ST}/ (1-Fst) ranged from 0.058 to 0.201 and geographical distances spanned from 51.7 to 308.3 km (Table 6).

Table 6. Genetic and geographical distances among six bearded capuchin populations sampled in the Caatinga forest fragment in the state of Pernambuco, Brazil. Genetic distance is represented by F_{ST}/ (1-Fst) (lower diagonal) and Euclidean geographic distance in km (upper diagonal).

Localities	Serra do Pinheiro	Serra do Estrago	Serra da Maravilha	Pedra Branca	Serra do Almirante	Serra das Tabocas
Serra do Pinheiro		51.71	71.94	131.12	260.97	308.27
Serra do Estrago	0.06346		54.45	99.36	241.63	274.66
Serra da Maravilha	0.07105	0.11212		60.17	191.83	236.48
Pedra Branca	0.10383	0.19077	0.05211		145.06	177.50
Serra do Almirante	0.05873	0.16517	0.14745	0.14042		96.09
Serra das Tabocas	0.09130	0.20143	0.10992	0.09404	0.12619	

5.3.4.2 Landscape Resistance Analysis

The best supported model was distance to urbanisation (AICc weight = 0.177) followed by habitat suitability (AICc weight = 0.168). Confidence intervals for both models did not overlap zero, supporting their effect on genetic connectivity (Table 7). Distance from urban areas was positively related to genetic distance, while habitat suitability was negatively related. Predicted movement density maps between populations based on landscape resistance due to distance from urban areas and habitat suitability are represented in Figure 4.

Table 7. Result of the Maximum Likelihood Population Effect (MLPE) analysis, in which we tested eight models to identify which environmental variable affects genetic connectivity among *S. libidinosus* populations in the Caatinga Biome, Pernambuco, Brazil.

Hypothesis	Models Variables	AIC	BIC	k	AICc	AICc weight	BIC weight	95% CI
1) Land use	Land cover	-92.797	-89.965	4	-88.797	0.152	0.142	
2) Vegetation	Percentage of forest cover	-92.890	-90.058	4	-88.890	0.160	0.148	
3) Urbanization	Distance Urban area	-93.101	-90.269	4	-89.101	**0.177**	**0.165**	**-0.011 - 0.020**
4) Human impact	Footprint index	-92.757	-89.925	4	-88.757	0.149	0.139	
5) Permanent Water	Rivers	-92.747	-89.915	4	-88.747	0.149	0.138	
6) Habitat suitability	Ecological niche modelling	-92.988	-90.156	4	-88.988	**0.168**	**0.156**	**-0.007- 0.005**
7) Barriers	Percentage of forest cover + Rivers	-91.645	-88.105	5	-84.978	0.023	0.056	
8) Antropogenic	Distance Urban area + Footprint index	-91.647	-88.107	5	-85.980	0.023	0.056	

AIC - Akaike information criterion; BIC- Bayesian information criteria; k - degrees of freedom; AICc- Akaike information criterion corrected for small sample size

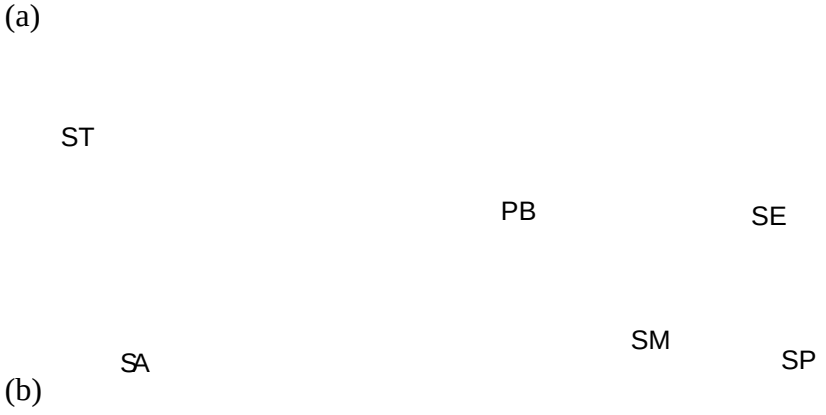

Figure 4. Predicted movement density maps between populations based on landscape resistance due to (a) Distance from urban areas and (b) Habitat suitability. Areas with the lowest movement are represented by the color blue and those with the highest movement by the color green. Localities: SP – Serra do Pinheiro, SE – Serra do Estrago, SM-Serra da Maravilha, PB-Pedra Branca, SA- Serra do Almirante, ST- Serra das Tabocas.

5.3.4.3 Landscape metric analyses

A multiple regression analysis tested whether allelic diversity (allelic richness and proportion of private alleles) was related to landscape metrics as a percentage of forest cover, fragment size and matrix connectivity. The first model tested the relationship between allelic richness and landscape metrics. Analysis indicated that the model explained 95% of the variability present in the data ($R^2 = 0.95$) and that the three predictors included in the model were significant. The percentage of forest cover ($b = -8.89$; $p = 0.032$) is negatively correlated to allelic richness, while fragment size ($\beta = 11.30$; $p = 0.032$) and matrix connectivity ($\beta = 11.27$; $p = 0.032$) are positively correlated. In the second model, we tested the relationship between the proportion of private alleles and landscape metrics and the test was not significant. Predictors explained only 9% of the variability present in the data ($R^2 = 0.09$) and did not show a significant relationship with the proportion of private alleles: percentage of forest cover ($\beta = 0.23$; $p = 0.94$), fragment size ($\beta = -1.25$; $p = 0.78$) and matrix connectivity ($\beta = -0.25$; $p = 0.72$).

5.4 DISCUSSION

Here we present the first study of genetic variation in *S. libidinosus*. Previous genetic studies with capuchin monkeys have evaluated historical phylogenetic and biogeographic issues (Lynch Alfaro et al., 2012; Lima et al., 2017; Lima et al., 2018). Here, we analyzed whether landscape characteristics may be influencing genetic diversity and gene flow in populations of *S. libidinosus* located in the various tropical dry forest fragments in the Caatinga biome in the state of Pernambuco, Brazil. Our results demonstrated that genetic diversity (allelic richness and heterozygosity) of six populations of *S. libidinosus* is similar, although there is significant genetic differentiation between them. Landscape genetics analyses indicated that urbanization and habitat suitability decrease the connectivity between populations and that genetic diversity is positively related to the connectivity and size of the fragments and negatively related to the percentage of forest cover.

5.4.1 Genetic diversity

Genetic diversity is a measure that assesses the genetic difference between individuals in a population (Osada, 2015) and provides the basis for maintaining the evolutionary potential and adaptive capacity of individuals (Romiguier et al., 2014). In our study, the mean values of heterozygosity showed high values (HO = 0.85 ± 0.032) when compared with other genetic studies of neotropical primates (ie Alouatta palliata Ho = 0.1 and A. pigra 0.45 Cortés-Ortiz et al. 2009 ;; Sapajus nigritus Ho = 0.57 Tokuda et al. 2014; Leonthopitecus chrysopygus Ho = 0.67 - 0.75 Ayala-Burbano et al. 2017). Regarding the allelic richness, the populations studied here presented lower values when compared to those found in cogeneric species, i.e. Sapajus nigritus Ar = 5.93 Tokuda et al. 2014. the population from Serra do Pinheiro presented the highest allelic richness and the highest proportion of private alleles. This population has a unique importance in maintaining heterozygosity, considering oppotunities for gene flowif through gene flow, it can spread its alleles. The population of Serra das Tabocas presented the lowest values of genetic diversity. This may be related both to the number of individuals sampled in this population (6), lower than intoin the other populations, as well as a low gene flow in the region. Allelic richness is reduced more than heterozygosity when a population's effective size decreases (Spencer et al., 2000). The decrease in allele richness may lead to a potential population reduction to adapt to future environmental changes (Greenbaum et al., 2014). It is an index that allows us to select and direct population management and conservation

programs that should be prioritized whether to maintain or increase allelic diversity (Petit et al., 1998; Leberg, 2002; Foulley & Ollivier, 2006 and Cabalero et al., 2010).

Polymorphic Information Content values were highly informative (PIC > 5) for all populations, confirming the potential of the markers used in the present study for the genetic characterization of populations (Botstein et al., 1980; Guo & Elston, 1999). In evaluating the inbreeding coefficient (F_{IS}), we found that there is no inbreeding, but three populations, Serra do Estrago, Serra do Almirante and Serra das Tabocas, showed significant values for excess heterozygosity. In Serra do Estrago, excess heterozygosity may have been one of the causes of the significant value for the Hardy – Weinberg Equilibrium deviation. According to Wright (1965), the F_{IS} is negative if there is systematic avoidance of consanguine mating within the subdivisions. Excess heterozygosity may be related to both the dynamics of male migration observed in S. *libidinosus* groups (Izar et al., 2012), decreasing the likelihood of close relatives mating (Melnick, 1987) or in some cases, may be related to a recent reduction in effective population size, a genetic bottleneck (Maruyama & Fuerst, 1985; Cornuet & Luikartt, 1996). The effect of the genetic bottleneck causes a reduction in allele numbers and heterozygosity, but the number of alleles is reduced more rapidly (Nei et al., 1975). Changes in heterozygosity values will depend on the time since the onset of the bottleneck, the effective proportion of population size before and after the onset of the bottleneck, the mutation rate of the locus, and the size of the gene sample (Maruyama & Fuerst, 1985).

5.4.2 Population structure

Our population structure analyzes consistently suggested the existence of three main genetic clusters along the study area (1- Serra do Pinheiro, Serra da Maravilha, Pedra Branca and Serra das Tabocas; 2- Serra do Estrago; 3- Serra do Almirante). When we look at the clusters presented by the results of Structure analysis, we find that groups 2 and 3 are more homogeneous, with low genetic representativeness in other populations. This suggests a low level of gene flow between populations and strong isolation (Balloux & Lugon-Moulin, 2002). Although genetic structuring also occurs in natural populations, unaffected by human activities, reducing dispersion efficiency in fragmented natural systems can lead to critical levels of habitat connectivity (Moraes et al., 2018; Wang et al., 2019) In small populations, the time to extinction drops sharply when this threshold is reached, because subject to genetic drift, these populations have their evolutionary potential affected due to the fixation of deleterious mutations (Wang et al., 2000; Higgins & Lynch, 2000, Charpentier et al., 2007). As

connectivity increases natural selection becomes more efficient against deleterious mutations and time to extinction increase (Higgins & Lynch, 2000). Habitat loss and fragmentation represent an important barrier to primate gene flow and may be one of the causes of gene flow disruption (Ruiz-Lopez et al., 2016; Wang et al., 2017). In relation to grouping 1, the population of Serra do Pinheiro presents a greater genetic variability among individuals. As reported above, this population also has the largest proportion of private alleles, reaffirming the importance of conservation actions in this area for maintaining the genetic diversity of *S. libidinosus*.

5.4.3 Genetic differentiation

Our results showed that although genetic diversity is similar across populations, there is genetic difference between them, as well as between individuals within each population and among all sampled individuals. Conversely, there was not variation between those groups suggested by genetic structure. The smallest genetic difference was found between the Serra do Pinheiro and Serra do Almirante (0.058) and Serra da Maravilha and Pedra Branca (0.0521) populations and the largest between Serra do Estrago and Serra das Tabocas (0.201). The Pairwise R_{ST} estimate did not show significant values between the populations of Serra do Pinheiro and Serra da Maravilha, Serra do Estrago and Serra da Maravilha, Pedra Branca and Serra das Tabocas, but shows a great genetic differentiation between the other populations. The F_{ST} and R_{ST} statistics use different models to calculate genetic differentiation, the first is based on allele frequency variations and the second takes into account allele size variations (Balloux & Lugon-Moulin, 2002). Genetic divergence between populations increases when the number of migrants to these populations decreases, that is, when gene flow decreases F_{ST} and R_{ST} values increase (Wright, 1965; Hartl & Clark, 1997). In cases, as in our study, where the migration rate is low among populations, the F_{ST} may underestimate genetic differentiation, which is the main problem affecting F statistics (Balloux & Lugon-Moulin, 2002). On the other hand, R_{ST} estimates vary widely and the F_{ST} estimate may outperform when it comes to data from populations with few loci for a small sample size (<50) (Gaggiotti et al., 1999).

In our study, although the values of F_{ST} and R_{ST} present different results, both indicate moderate to high genetic differences between populations, indicating low gene flow between populations. While the low genetic differentiation between some populations may reflect a past connection between them (Balloux & Lugon-Moulin, 2002). Spatial genetic differentiation between populations can also be influenced by social, mating and dispersal behavior (Di Fiore 2003). *Sapajus libidinosus* presents a social system of the dominance hierarchy. In addition,

males disperse and females are philopatric (Izar et al. 2012). Although male dispersion to neighbouring or widely separated groups every generation is sufficient to cause a decrease in genetic differentiation between populations (Wright, 1951), the male dominance hierarchy can cause differentiation to increase (Melnick, 1987). This dominance affects the frequency of paternity, so the gene samples in each cohort are not random (Dewsbury 1982; Fedigan 1983). Males who are subordinate have less access to fertile females and consequently leave fewer offspring (Cowlishaw & Dumbar, 1981; Di Fiore, 2003). In addition, the philopatric behavior of females causes a matrilineal aggregation to form, and the groups end up being formed by groups of relatives, where each group often has distinct allelic frequencies (Olivier et al., 1981).

5.4.4 Landscape genetics analysis

Landscape genetic analyses were performed to determine if landscape variables affect connectivity among *S. libidinosus* populations. Our results demonstrated that genetic differentiation between populations is not related to geographical distance, but to landscape resistance, percentage of forest cover, connectivity and fragment size. We found that urbanization is the main barrier to movement of *S. libidinosus* species in the caatinga, followed by the habitat suitability variable. We found that the genetic distance decreases in less urbanized areas and in areas of higher suitability habitat. In addition to landscape features, we also have to take into account the ability of species to move (Nathan et al., 2008). The maximum dispersal distance of the species *S. libidinosus* is not yet known and, therefore, we can not estimate the real capacity of the species to move in the current landscape configuration. Through the motion density map for the urbanization variable, we found that the populations studied are not connected. In the Caatinga biome, pasture and agricultural activities are the ones that most alter the landscape structure (Beuchle et al., 2015) and may have serious consequences for the genetic diversity of their populations (Fonseca et al., 2019). Although *S. libidinosus* species has greater habitat occupation flexibility compared to other primate species, areas with large agricultural and pasture areas are impervious to their dispersal (Mittermeier et al., 2013).

The proportion of habitat indicates the amount of habitat, but not its configuration, i.e. areas may have equal forest proportions, but may be fragmented (Jackson & Fahrig, 2016). Genetic diversity in these areas may be lower if the amount of habitat is continuous, as the fragment may maintain a larger number of connected populations within the same area, leading to a universally low genetic structure (Nei, 1977; Jackson & Fahrig, 2016). If this proportion of habitat is fragmented, but the distance between these fragments permits species dispersal, more

subpopulations may occur and increase the likelihood of genetic structure formation (Cushman et al., 2012; Wan et al., 2018). On the other hand, if the connectivity between these fragments is too low, with distances greater than the maximum dispersal distance of the species, these populations can probably become isolated and genetically disconnected and enter a process of diminishing genetic diversity, for example the inbreeding (Wang et al., 2017).

Our study demonstrates that low gene flow is occurring among *S. libidinosus* populations in Caatinga and that this discontinuity is related to landscape configuration, more specifically urbanization. LANDSCAPE genetic studies of an umbrella species such as *S. libidinosus* are extremely important to assess the health of this important ecosystem and outline actions to mitigate the effect of anthropogenic factors on their populations.

5.5 CONSERVATION IMPLICATIONS

The study showed that the populations of *S. libidinosus* evaluated here presented a good genetic diversity, despite the lower values for allelic richness. Despite the high diversity, it was found that urbanization has caused a break in connectivity between populations, which may lead to a future decrease in gene flow and, consequently, diversity. To avoid a loss of diversity, it is important that all populations are conserved, considering that most of the genetic variability is explained by the division of the samples into different populations. Within each population, the variability is less. Populations such as Serra do Almirante and Serra do Estrago, which had a more homogeneous genetic structure, and Serra do Pinheiro with greater variability, may have a wider distribution and which were not sampled in the present study.

It is worth noting that populations such as Serra das Tabocas and Pedra Branca are located within protected areas. The first in the Area de Proteção Ambiental da Chapada do Araipe and the second in the Parque Estadual da Mata da Pimenteira. The monitoring of these populations can be carried out by the managing institutions in each area. The other areas, Serra do Pinheiro, Serra do Estrago and Serra da Maravilha, are not protected and suffer great pressure from hunting, agricultural and livestock activities and deserve greater attention regarding their conservation.

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1. CONCLUSÕES GERAIS

O presente estudo foi de suma importância para a produção de novos conhecimentos a respeito da espécie *Sapajus libidinosus*. Apesar da espécie ainda não estar classificada como ameaçada de extinção, sendo considerada como "Least Concern" pela IUCN, os resultados obtidos no presente estudo demonstram que suas populações no bioma caatinga correm uma séria ameaça proveniente das alterações de seus hábitats. Dessa forma, o status de ameaça da espécie precisa ser urgentemente reavaliado. Destacamos, também, que o uso de técnicas não-invasivas como as usadas no presente estudo (i.e. câmeras traps para a coleta de dados comportamentais e ecológicos e o uso de material fecal para estudos moleculares) deve ser utilizado em futuros estudos sobre a espécie para minimizar estresse nas populações remanescentes.

A identificação de áreas potenciais para a ocorrência do *Sapajus libidinosus* e de outras duas espécies de primatas ameaçadas que ocorrem no nordeste brasileiro permitirá planejar ações de conservação mais direcionadas. Uma das primeiras ações seria a validação dessas áreas para o levantamento de novos registros de ocorrência. Os esforços também podem ser direcionados para reintroduções, translocações, formação de corredores e reflorestamento. As áreas previstas como climaticamente adequadas para a ocorrência das espécies e estão em áreas classificadas como prioritárias para a conservação da biodiversidade podem servir como base para a seleção de novas áreas protegidas ou para a expansão ou conexão de áreas protegidas existentes. As áreas de menor suscetibilidade às mudanças climáticas, indicadas nos resultados dos modelos futuros, podem ser tratadas como prioritárias para as ações de conservação a longo prazo, como translocações e reintrodução de indivíduos.

O uso do método de transferibilidade de marcadores genéticos como os microssatélites reduzem consideravelmente os custos e o tempo quando comparados com o desenvolvimento de marcadores específicos. Essas aplicações são importantes tendo em vista os orçamentos atualmente limitados de pesquisa e conservação no Brasil. Os marcadores aqui testados podem ser amplamente utilizados em diferentes campos, como ecologia molecular e genética de populações. Eles, favorecerão, principalmente os estudos de genética de populações da espécie *S. libidinosus*, que ainda são muito limitados. A metodologia empregada para a coleta e extração de DNA de amostras não-invasiva se mostrou eficiente e torna-se uma alternativa relevante para estudos de genética de conservação de primatas.

A configuração da paisagem em que os hábitats das populações de *S. libidinosus* se encontram, na caatinga pernambucana, possivelmente vem influenciando o fluxo gênico entre as populações. As populações se apresentam estruturadas, com uma alta a moderada diferenciação gênica entre elas. As áreas urbanizadas são o principal fator de divergência genética segundo as análises de isolamento por resistência, seguida das áreas de adequabilidade climática. Essas informações são importantes quando se pensa em planejamentos e ações de mitigação, tanto relacionadas a impactos antrópicos como a mudanças climáticas. Como se sabe, o nordeste brasileiro se mostra como uma das áreas potenciais a serem afetadas severamente pelas mudanças climáticas e o presente estudo aciona um alerta vermelho para o aprofundamento de pesquisas com a espécie nesta área. Outro ponto importante do estudo e que deve ser levado em consideração em ações de conservação é que, além da conectividade, o tamanho do fragmento que as populações de *S. libidinosus* habitam está relacionados positivamente com a diversidade genética. Apesar de ser o primeiro estudo de genética de populações realizado com a espécie *S. libidinosus*, resultados potenciais e aplicáveis ao planejamento de ações de conservação de curto e longo prazo para a espécie foram obtidos.

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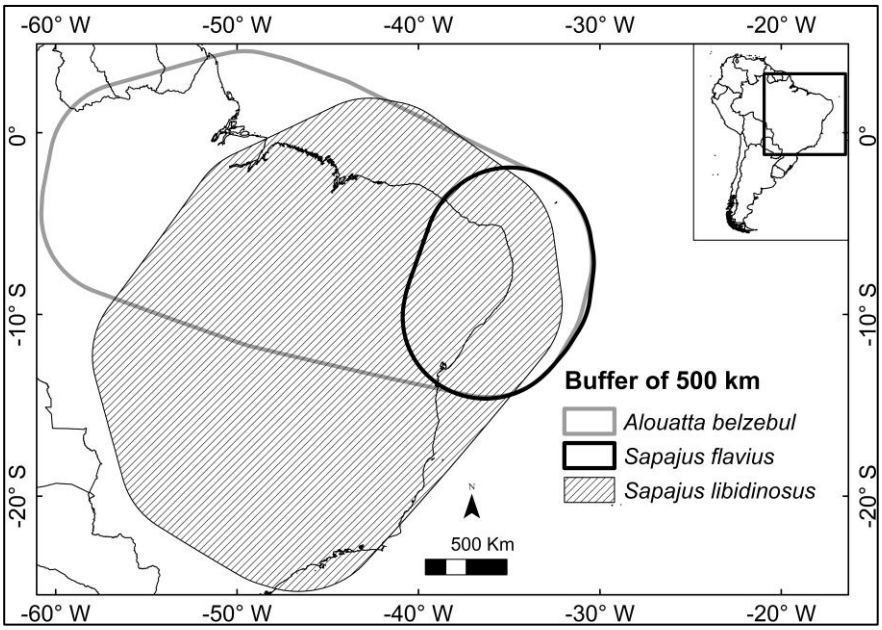
APÊNDICE A - STUDY AREA DELIMITED, FOR EACH SPECIES, BASED ON A 500 KM BUFFER GENERATED FROM THE MINIMUM CONVEX POLYGON OF THE OCCURRENCE RECORDS.

The gray line corresponds to the area of the red-handed-howler-monkeys *A. belzebul*, the black line to the blonde capuchins *S. flavius* and the striped area to bearded capuchins *S. libidinosus.*



APÊNDICE B - PEARSON'S CORRELATION RESULTS AMONG THE 19 CLIMATIC VARIABLES AVAILABLE IN THE WORLDCLIM DATABASE, ECOREGION (ECOR), GEOMORPHOLOGY (GEOM) AND SLOPE.

Correlation performed considering the occurrence extension of the species: a) *Alouatta belzebul*, b) *Sapajus flavius* and c) *Sapajus libidinosus.*

a) *Alouatta belzebul*

	bio1	bio10	bio11	bio12	bio13	bio14	bio15	bio16	bio17	bio18	bio19	bio2	bio3	bio4	bio5	bio6	bio7	bio8	bio9	slope	ecor.	geom.
bio1	1																					
bio10	**0.99**	1																				
bio11	**0.98**	**0.94**	1																			
bio12	0.11	0.07	0.18	1																		
bio13	0.46	0.39	0.55	0.77	1																	
bio14	-0.25	-0.22	-0.24	0.74	0.23	1																
bio15	0.55	0.48	0.6	-0.22	0.41	-0.69	1															
bio16	0.41	0.34	0.5	**0.84**	**0.98**	0.3	0.31	1														
bio17	-0.27	-0.24	-0.26	0.73	0.2	**0.99**	-0.72	0.28	1													
bio18	-0.4	-0.38	-0.41	0.47	0.05	0.61	-0.51	0.11	0.62	1												
bio19	0.41	0.34	0.5	**0.84**	**0.98**	0.3	0.31	1	0.28	0.11	1											
bio2	0.08	0.12	0.02	-0.63	-0.38	-0.58	0.27	-0.45	-0.57	-0.28	-0.45	1										
bio3	0.63	0.53	0.7	-0.17	0.28	-0.56	0.69	0.21	-0.58	-0.46	0.21	0.42	1									
bio4	-0.66	-0.53	-0.79	-0.31	-0.65	0.18	-0.61	-0.62	0.21	0.32	-0.62	0.17	-0.77	1								
bio5	**0.86**	**0.89**	0.79	-0.23	0.16	-0.45	0.53	0.09	-0.46	-0.49	0.09	0.53	0.61	-0.35	1							
bio6	**0.9**	**0.85**	**0.93**	0.35	0.61	-0.03	0.46	0.6	-0.06	-0.31	0.6	-0.34	0.5	-0.77	0.57	1						
bio7	-0.2	-0.12	-0.31	-0.63	-0.55	-0.4	-0.02	-0.61	-0.38	-0.11	-0.61	**0.91**	0.01	0.55	0.31	-0.6	1					
bio8	**0.83**	**0.82**	0.79	-0.22	0.19	-0.44	0.59	0.1	-0.47	-0.31	0.1	0.34	0.64	-0.48	**0.83**	0.63	0.08	1				
bio9	**0.91**	**0.88**	**0.92**	0.29	0.56	-0.09	0.45	0.54	-0.11	-0.4	0.54	-0.17	0.52	-0.69	0.68	**0.93**	-0.42	0.59	1			
slope	-0.26	-0.28	-0.22	0.04	0.03	0.01	-0.04	0.04	0.02	-0.02	0.04	-0.04	-0.07	0.03	-0.25	-0.19	-0.02	-0.29	-0.18	1		
ecor.	-0.13	-0.14	-0.09	0.67	0.35	0.68	-0.37	0.41	0.68	0.5	0.41	-0.54	-0.33	-0.04	-0.37	0.09	-0.47	-0.3	0.01	0.02	1	
geom.	0.07	0.06	0.06	-0.01	0.07	-0.1	0.13	0.06	-0.1	-0.07	0.06	0.02	0.07	-0.05	0.06	0.06	0	0.03	0.08	0.01	0.11	1

b) *Sapajus flavius*

	bio1	bio10	bio11	bio12	bio13	bio14	bio15	bio16	bio17	bio18	bio19	bio2	bio3	bio4	bio5	bio6	bio7	bio8	bio9	slope	ecor.	geom.
bio1	1																					
bio10	**0.99**	1																				
bio11	**0.98**	**0.94**	1																			
bio12	0.11	0.07	0.18	1																		
bio13	0.46	0.39	0.55	0.77	1																	
bio14	-0.25	-0.22	-0.23	0.74	0.23	1																
bio15	0.55	0.48	0.6	-0.22	0.41	-0.69	1															
bio16	0.41	0.34	0.5	**0.84**	**0.99**	0.3	0.31	1														
bio17	-0.27	-0.24	-0.26	0.73	0.2	**0.99**	-0.72	0.28	1													
bio18	-0.4	-0.38	-0.41	0.47	0.05	0.61	-0.51	0.11	0.61	1												
bio19	0.41	0.34	0.5	**0.84**	**0.99**	0.3	0.31	1	0.28	0.11	1											
bio2	0.08	0.12	0.01	-0.63	-0.38	-0.58	0.27	-0.46	-0.57	-0.28	-0.46	1										
bio3	0.63	0.53	0.7	-0.17	0.28	-0.56	0.69	0.21	-0.58	-0.46	0.21	0.42	1									
bio4	-0.66	-0.53	-0.79	-0.31	-0.65	0.18	-0.61	-0.62	0.21	0.32	-0.62	0.17	-0.77	1								
bio5	**0.86**	**0.89**	0.79	-0.23	0.16	-0.45	0.53	0.09	-0.46	-0.49	0.09	0.53	0.6	-0.35	1							
bio6	**0.9**	**0.85**	**0.93**	0.36	0.61	-0.03	0.46	0.6	-0.06	-0.31	0.6	-0.34	0.5	-0.77	0.57	1						
bio7	-0.2	-0.12	-0.31	-0.63	-0.55	-0.4	-0.02	-0.61	-0.38	-0.12	-0.61	**0.91**	0.01	0.55	0.31	-0.61	1					
bio8.	**0.83**	**0.82**	0.79	-0.21	0.19	-0.44	0.59	0.1	-0.47	-0.31	0.1	0.33	0.64	-0.48	**0.83**	0.63	0.07	1				
bio9	**0.91**	**0.88**	**0.92**	0.3	0.56	-0.09	0.45	0.54	-0.11	-0.4	0.54	-0.17	0.52	-0.69	0.68	**0.93**	-0.42	0.59	1			
slope	-0.26	-0.28	-0.22	0.04	0.03	0.01	-0.04	0.04	0.02	-0.02	0.04	-0.04	-0.06	0.03	-0.25	-0.19	-0.02	-0.29	-0.18	1		
ecor.	-0.13	-0.14	-0.09	0.68	0.35	0.69	-0.38	0.41	0.69	0.51	0.41	-0.54	-0.33	-0.04	-0.37	0.09	-0.46	-0.3	0	0.02	1	
geom.	0.07	0.07	0.07	-0.04	0.06	-0.13	0.16	0.06	-0.13	-0.1	0.06	0.04	0.08	-0.05	0.08	0.06	0.01	0.03	0.09	0.01	0.05	1

c) *Sapajus libidinosus*

	bio1	bio10	bio11	bio12	bio13	bio14	bio15	bio16	bio17	bio18	bio19	bio2	bio3	bio4	bio5	bio6	bio7	bio8	bio9	slope	ecor.	geom.
bio1	1																					
bio10	**0.97**	1																				
bio11	**0.98**	**0.91**	1																			
bio12	0.25	0.15	0.32	1																		
bio13	0.3	0.2	0.37	**0.92**	1																	
bio14	-0.21	-0.15	-0.23	0.25	0.05	1																
bio15	0.27	0.22	0.29	-0.2	0.13	-0.74	1															
bio16	0.3	0.2	0.38	**0.95**	**0.99**	0.06	0.08	1														
bio17	-0.19	-0.14	-0.2	0.3	0.09	**0.98**	-0.78	0.11	1													
bio18	-0.58	-0.55	-0.62	0.24	0.12	0.19	-0.31	0.15	0.2	1												
bio19	0.3	0.2	0.38	**0.95**	**0.99**	0.06	0.08	**1**	0.11	0.15	1											
bio2	-0.07	-0.1	-0.07	0.13	0.12	-0.5	0.24	0.15	-0.48	0.39	0.15	1										
bio3	0.64	0.51	0.71	0.24	0.35	-0.1	0.33	0.34	-0.08	-0.58	0.34	-0.15	1									
bio4	-0.75	-0.59	**-0.**87	-0.43	-0.47	0.25	-0.29	-0.48	0.22	0.57	-0.48	0.05	-0.78	1								
bio5	**0.88**	**0.86**	**0.86**	0.27	0.29	-0.4	0.3	0.31	-0.37	-0.39	0.31	0.35	0.4	-0.65	1							
bio6	**0.88**	**0.84**	**0.9**	0.16	0.22	0.01	0.17	0.21	0.02	-0.74	0.21	-0.48	0.73	-0.76	0.6	1						
bio7	-0.35	-0.32	-0.39	0.03	-0.02	-0.34	0.05	0.01	-0.33	0.6	0.01	**0.89**	-0.57	0.41	0.09	-0.74	1					
bio8	**0.91**	**0.94**	**0.83**	0.18	0.22	-0.14	0.19	0.22	-0.12	-0.39	0.22	0	0.47	-0.5	**0.83**	0.73	-0.21	1				
bio9	**0.96**	**0.9**	**0.98**	0.26	0.32	-0.19	0.26	0.32	-0.16	-0.68	0.32	-0.19	0.71	**-0.84**	**0.81**	**0.94**	-0.49	0.79	1			
slope	-0.4	-0.4	-0.36	-0.12	-0.13	0.07	-0.06	-0.13	0.05	0.14	-0.13	-0.05	-0.23	0.22	-0.37	-0.3	0.06	-0.41	-0.36	1		
ecor.	-0.36	-0.3	-0.4	0.08	0.03	0.3	-0.28	0.03	0.28	0.38	0.03	0.01	-0.42	0.41	-0.34	-0.4	0.21	-0.23	-0.42	0.14	1	
geom.	-0.09	-0.05	-0.12	-0.09	-0.07	0.07	0	-0.08	0.05	0.03	-0.08	-0.14	-0.12	0.16	-0.13	-0.05	-0.05	-0.07	-0.09	0.08	0.13	1

APÊNDICE C - PRINCIPAL COMPONENT ANALYSIS (PCA) RESULTS AMONG THE 19 CLIMATIC VARIABLES AVAILABLE IN THE WORLDCLIM DATABASE, ECOREGION (ECO.), GEOMORPHOLOGY (GEOM.) AND SLOPE FOR: A) *ALOUATTA BELZEBUL* B) *SAPAJUS FLAVIUS* AND C) *SAPAJUS LIBIDINOSUS*.

The variable of greatest contribution in each pca is marked in bold. We use the number of pcas that explain 80% of the model distribution and select variables that are not correlated. Climatic variables wolrdclim selected: bio2 - mean diurnal range; bio3- isothermality; bio8- mean temperature of wettest quarter; bio11- mean temperature of coldest quarter; bio12- annual precipitation; bio15- precipitation seasonality; bio18- precipitation of warmest quarter.

a) *Alouatta belzebul*

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	···	PC22
bio1	0.318657	-0.02491	0.212553	0.015583	0.012562	-0.10031	-0.00916	0.076653	-0.00697	-0.06514	0.040166		-6.18E-16
bio10	0.29984	-0.03916	0.293931	-0.00513	0.024933	-0.15092	0.087511	0.131866	-0.0302	-0.06905	0.025513		1.17E-16
bio11	**0.32947**	0.004289	0.113786	0.039759	-0.00836	-0.06119	-0.09419	-0.02363	0.024493	-0.01139	0.023433		3.40E-16
bio12	0.059461	**0.371029**	0.012634	-0.21093	-0.05915	-0.02536	0.059202	-0.09672	0.111995	-0.15402	-0.17951		4.58E-16
bio13	0.210264	0.249412	-0.20457	-0.26776	-0.06425	0.070925	0.210515	0.027866	-0.01184	0.146678	-0.08186		5.57E-16
bio14	-0.10675	0.322554	0.276024	-0.05753	-0.03991	-0.14013	-0.06162	-0.18027	0.158269	0.415951	0.284627		-1.69E-16
bio15	0.239497	-0.13447	**-0.33942**	-0.07989	0.005069	0.218194	0.119634	0.25062	-0.21126	0.337912	0.641713		-1.32E-16
bio16	0.191645	0.279874	-0.1902	-0.24076	-0.05755	0.053639	0.207619	0.008348	0.019143	-0.04996	-0.14516		-0.70711
bio17	-0.11653	0.318685	0.282333	-0.05995	-0.03724	-0.15324	-0.05241	-0.1972	0.150999	0.338627	0.203137		-2.55E-16
bio18	-0.15207	0.205532	0.171566	-0.31748	-0.04878	0.260803	-0.39639	**0.542089**	0.246966	-0.35347	0.263705		5.43E-17
bio19	0.191645	0.279874	-0.1902	-0.24076	-0.05755	0.053639	0.207619	0.008348	0.019143	-0.04996	-0.14516		0.707107
bio2	0.008743	-0.32095	0.052429	**-0.48864**	-0.07321	-0.04786	-0.09979	-0.25696	-0.01326	-0.0226	0.053542		5.21E-17
bio3	0.248936	-0.13757	-0.18162	-0.1005	-0.07372	0.101781	**-0.49419**	-0.36849	0.166598	-0.12027	0.024033		6.26E-17
bio4	-0.27659	-0.08073	0.233666	-0.1076	0.064217	-0.1153	0.380438	0.270998	-0.11435	-0.1184	-0.0151		1.10E-16
bio5	0.255647	-0.17681	0.267384	-0.20643	-0.00345	-0.1789	0.10535	-0.0115	-0.06989	-0.02916	0.06257		7.07E-06
bio6	0.304794	0.107952	0.106629	0.243227	0.034576	-0.06157	-0.02509	0.084063	0.01168	-0.03132	0.034842		-8.43E-06
bio7	-0.10451	-0.2958	0.135677	-0.48067	-0.04327	-0.10206	0.130947	-0.1082	-0.08113	0.007944	0.02033		-7.30E-06
bio8	0.258432	-0.14318	0.215659	-0.06285	-0.02671	0.085462	-0.248	0.383427	-0.00017	0.472053	-0.47559		-8.81E-17
bio9	0.30321	0.063371	0.132834	0.142486	0.041081	-0.18596	0.124979	-0.09599	0.011426	-0.39031	0.275883		-1.47E-17

slope	-0.06413	0.029218	-0.4038	-0.06222	-0.12715	**-0.82013**	-0.24337	0.281946	-0.01137	0.017462	0.008331	-1.39E-17
eco.	-0.04138	0.301817	0.097066	-0.09772	0.215991	0.016301	-0.3268	-0.08924	-0.84833	-0.06738	-0.02528	-5.13E-18
geom.	0.032675	-0.00691	-0.11109	-0.14498	**0.946731**	-0.07956	-0.02078	0.0016	0.24292	0.053966	-0.01686	-2.90E-17

b) *Sapajus flavius*

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	···	PC22
bio1	0.318537	-0.02475	0.212294	0.015878	0.021098	-0.09991	-0.01085	0.076406	-0.00367	-0.06523	0.040036		-8.16E-15
bio10	0.299703	-0.03894	0.29295	-0.00539	0.045081	-0.15041	0.083057	0.133195	-0.02811	-0.06962	0.025782		4.16E-15
bio11	**0.329362**	0.004282	0.114491	0.040213	-0.01147	-0.06116	-0.09131	-0.02525	0.027516	-0.01155	0.023871		3.73E-15
bio12	0.059887	**0.37082**	0.011089	-0.21309	-0.04136	-0.02694	0.065528	-0.0949	0.117395	-0.15338	-0.179		1.07E-14
bio13	0.21042	0.249106	-0.20442	-0.2708	-0.04889	0.068643	0.211256	0.031263	-0.01918	0.145361	-0.08175		9.41E-15
bio14	-0.10648	0.323074	0.273852	-0.05925	-0.01851	-0.14155	-0.05341	-0.18227	0.15666	0.420637	0.282432		-3.35E-15
bio15	0.239466	-0.13491	-0.338	-0.0807	-0.00311	0.216778	0.108664	0.251912	-0.22349	0.336761	0.640441		1.88E-15
bio16	0.191834	0.279461	-0.19063	-0.2437	-0.04124	0.051544	0.209067	0.012182	0.016575	-0.05044	-0.144		-0.70711
bio1	-0.11626	0.319215	0.280059	-0.06175	-0.01385	-0.15444	-0.04474	-0.19904	0.149933	0.342783	0.201147		-2.99E-17
bio18	-0.15136	0.206155	0.170696	-0.3157	-0.05844	**0.257742**	-0.40041	0.538042	0.265154	-0.34441	0.264229		2.39E-16
bio19	0.191834	0.279461	-0.19063	-0.2437	-0.04124	0.051544	0.209067	0.012182	0.016575	-0.05044	-0.144		0.707107
bio2	0.007989	-0.32067	0.056284	**-0.48968**	-0.07006	-0.04743	-0.0941	-0.25853	-0.00961	-0.02353	0.053688		3.61E-16
bio3	0.249015	-0.13761	-0.1768	-0.09803	-0.11824	0.101614	**-0.47994**	-0.37582	0.177469	-0.11531	0.022006		-9.24E-17
bio4	-0.27682	-0.08023	0.229907	-0.10898	0.106628	-0.11392	0.365772	0.277001	-0.11719	-0.11902	-0.01587		7.25E-17
bio5	0.255243	-0.17666	0.268085	-0.20808	0.022449	-0.17813	0.102545	-0.01047	-0.06939	-0.03052	0.062611		-1.14E-05
bio6	0.304855	0.107677	0.105284	0.243508	0.035135	-0.06147	-0.02709	0.083045	0.013121	-0.02997	0.033973		1.36E-05
bio7	-0.10535	-0.29511	0.137543	-0.48235	-0.01888	-0.10119	0.130408	-0.10603	-0.08222	0.005114	0.021285		1.18E-05
bio8	0.258329	-0.14264	0.217948	-0.06108	-0.0465	0.083229	-0.24816	**0.37855**	-0.00405	0.472182	-0.47802		-3.73E-16
bio9	0.303192	0.063282	0.131111	0.141782	0.061503	-0.18412	0.121885	-0.0942	0.01573	-0.38858	0.278316		9.00E-17
slope	-0.0636	0.027666	**-0.39977**	-0.06536	-0.12327	-0.82526	-0.24299	0.274342	-0.00836	0.017384	0.007898		-2.37E-17
eco.	-0.04201	0.302434	0.100797	-0.09001	0.172331	0.024965	-0.35498	-0.09581	-0.84478	-0.08341	-0.02767		2.12E-17
geom.	0.036103	-0.02093	-0.14413	-0.11978	**0.950125**	-0.0422	-0.09262	-0.00657	0.213095	0.058988	-0.02874		4.40E-17

c) *Sapajus libidinosus*

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	···	PC22
bio1	-0.32002	-0.05325	0.000453	-0.17604	-0.04753	0.080626	0.020746	-0.05752	0.023184	-0.06934	0.02763		7.20E-16
bio10	-0.29465	-0.08436	0.024728	-0.28572	-0.10716	0.094174	0.068674	-0.20445	0.059178	0.082326	-0.06312		1.14E-15
bio11	**-0.32839**	-0.02615	0.001655	-0.06693	-0.00574	0.092285	-0.00879	0.086105	-0.06033	-0.08733	0.170472		-1.46E-15
bio12	-0.12243	**0.458621**	-0.01236	0.014282	0.027852	0.02702	-0.091	0.036214	-0.1597	-0.05604	-0.0672		2.17E-14
bio13	-0.15111	0.415428	-0.07918	0.167772	-0.0787	-0.0553	0.071749	-0.14985	-0.00721	0.14503	-0.08367		2.31E-14
bio14	0.076816	0.202116	0.431988	-0.18696	0.065156	0.024497	-0.08553	0.012324	0.264169	0.298199	0.344108		-6.42E-16
bio15	-0.11397	-0.16167	-0.31031	**0.353164**	-0.19103	-0.13553	0.27083	-0.28839	0.335299	0.285025	0.508551		4.30E-15
bio16	-0.15042	0.426918	-0.08376	0.137094	-0.05469	-0.03157	0.032589	-0.09893	-0.04596	0.081458	-0.10205		-0.70711
bio17	0.068028	0.223187	0.426682	-0.196	0.089849	0.028688	-0.12646	0.046193	0.215097	0.232581	0.20787		-5.03E-16
bio18	0.208169	0.260453	-0.14047	-0.18856	0.002599	-0.05743	-0.09116	-0.29728	0.232954	-0.71631	0.347996		2.67E-16
bio19	-0.15042	0.426918	-0.08376	0.137094	-0.05469	-0.03157	0.032589	-0.09893	-0.04596	0.081458	-0.10205		0.707107
bio2	0.032222	0.078208	**-0.47019**	-0.1894	0.110906	0.075557	-0.1886	0.357232	0.289295	0.125942	-0.00768		1.72E-16
bio3	-0.25423	-0.00921	0.077476	0.284894	0.122125	-0.10398	-0.05146	**0.355444**	0.652666	-0.15773	-0.28665		1.95E-16
bio4	0.28967	-0.04169	0.013685	-0.20959	-0.11011	-0.07603	0.090379	-0.41448	0.192632	0.241123	-0.42389		2.88E-16
bio5	-0.27378	-0.0256	-0.19504	-0.29288	-0.00393	0.162806	-0.10267	0.049704	-0.095	0.145605	0.152371		-4.28E-06
bio6	-0.30015	-0.08825	0.204073	0.027014	-0.02683	0.03216	0.032106	-0.05389	-0.06184	-0.08502	0.061038		6.30E-06
bio7	0.142649	0.088515	-0.42038	-0.28221	0.030174	0.097949	-0.12721	0.109485	-0.00336	0.229732	0.053025		5.04E-06
bio8	-0.27067	-0.04961	-0.01231	-0.35548	-0.10252	0.069738	0.087163	-0.26033	0.295893	-0.1192	-0.29217		-2.80E-16
bio9	-0.32399	-0.05548	0.052824	-0.04052	-0.01759	0.067064	-0.02338	0.040244	-0.13158	-0.03015	0.11388		5.43E-17
slope	0.131454	0.004472	0.026251	0.295871	-0.08081	**0.920262**	-0.08418	-0.13032	0.120744	-0.02794	-0.03569		-2.87E-17
eco.	0.144265	0.163984	0.050347	-0.19994	-0.33316	0.136621	**0.765713**	0.419475	0.020485	-0.09769	0.034555		1.82E-17
geom.	0.041263	-0.02504	0.066304	0.025842	**-0.86898**	-0.11357	-0.44561	0.157679	0.017319	-0.02134	-0.0061		7.36E-17

APÊNDICE D - OCCURRENCE RECORDS USED TO GENERATE THE POTENTIAL DISTRIBUTION PATTERNS OF THE SPECIES ALOUATTA BELZEBUL, SAPAJUS FLAVIUS AND THE SAPAJUS LIBIDINOSUS FOR THE NORTHEASTERN REGION OF BRAZIL.

n	Species	Long	Lat	State	Locality	Author	Register
1	*Alouatta belzebul*	-56.28	-4.48	PA	MG08128	Meloro et al. 2014a	Museum collection
2	*Alouatta belzebul*	-56.25	-3.83	PA	Parque Nacional dos Tapajós	Branch, 1983	Direct observation
3	*Alouatta belzebul*	-55.98	-4.27	PA	MG13261	Meloro et al. 2014a	Museum collection
4	*Alouatta belzebul*	-55.85	-1.75	PA	MG00502	Meloro et al. 2014b	Museum collection
5	*Alouatta belzebul*	-55.38	-3.65	PA	Santa Cruz	Meloro et al. 2014a	Museum collection
6	*Alouatta belzebul*	-54.3	-2.55	PA	MG05158	Meloro et al. 2014a	Museum collection
7	*Alouatta belzebul*	-53.47	-1.8	PA	MN11603	Meloro et al. 2014a	Museum collection
8	*Alouatta belzebul*	-52.67	-3.9	PA	Margem do Rio Xingú	Gregorin, 2006	Museum collection
9	*Alouatta belzebul*	-52.38	-3.65	PA	Cachoeira do espelho	Gregorin, 2006	Museum collection
10	*Alouatta belzebul*	-51.9	-3.6	PA	Rio Bacajá	Gregorin, 2006	Museum collection
11	*Alouatta belzebul*	-51.45	-1.75	PA	Estação científica Ferreira Pena	Bobadilla and Ferrari, 2000	Direct observation
12	*Alouatta belzebul*	-51	-5.28	PA		Meloro et al. 2014a	Museum collection
13	*Alouatta belzebul*	-50.82	-1.95	PA	Rio pracupy (Portel)	Gregorin, 2006	Museum collection
14	*Alouatta belzebul*	-50.68	-0.6	AP	MG22521	Meloro et al. 2014a	Museum collection
15	*Alouatta belzebul*	-50.57	-5.77	PA	National Forest of Tapirape-Aquiri	Monteiro et al. 2013	Direct observation
16	*Alouatta belzebul*	-50.5	-5.83	PA	Serra dos Carajás, área de cobre	Bonvincino et al. 1989	Museum collection
17	*Alouatta belzebul*	-50.48	-1.68	PA	Ferreira Penna Scientific Station	de Souza et al. 2002	Direct observation
18	*Alouatta belzebul*	-50.33	-3.83	PA	Fazenda Arataú	Bobadilla and Ferrari, 2000	Direct observation
19	*Alouatta belzebul*	-50.25	-6.17	PA	Serra do cobre e serra do manganês	Gregorin, 2006	Museum collection
20	*Alouatta belzebul*	-50.18	-0.65	PA	Igarapé cururu	Gregorin, 2006	Museum collection
21	*Alouatta belzebul*	-50.17	-0.17	PA	Faz. São Luiz	Fernandes, M.E.B.,1994	Museum collection
22	*Alouatta belzebul*	-50.08	-0.6	PA		Meloro et al. 2014a	Museum collection
23	*Alouatta belzebul*	-50	-5.25	PA	Reserva Natural de Tucuruí	Estalrrich et al. 2016	Direct observation
24	*Alouatta belzebul*	-49.91	-0.18	PA	N. da I de marajó, Chaves, Ig Tapereba	Fernandes, 1994	Museum collection
25	*Alouatta belzebul*	-49.78	-4.32	PA		Meloro et al. 2014a	Museum collection
26	*Alouatta belzebul*	-49.73	-3.83	PA	Vale do Caraípe	Gregorin, 2006	Museum collection

27	*Alouatta belzebul*	-49.67	-2.82	PA	Santo Antônio	Gregorin, 2006	Museum collection
28	*Alouatta belzebul*	-49.67	-4.42	PA	Usina Hidrelétrica Tucuruí	Gregorin, 2006	Museum collection
29	*Alouatta belzebul*	-49.67	-3.77	PA	MG12385	Meloro et al. 2014a	Museum collection
30	*Alouatta belzebul*	-49.65	-3.86	PA	Ilha de Germoplasma	Camargo & Ferrari, 2007a	Direct observation
31	*Alouatta belzebul*	-49.58	-0.03	PA	I. Mexicana	Fernandes, 1994	Museum collection
32	*Alouatta belzebul*	-49.52	-4.25	PA	Tucurui hydroelectric reservoir	Bastos et al. 2010	Direct observation
33	*Alouatta belzebul*	-49.52	-4.47	PA		Meloro et al. 2014a	Museum collection
34	*Alouatta belzebul*	-49.5	-1.18	PA	Ponta de Pedras, F. São Joaquim, R. arari	Fernandes, 1994	Museum collection
35	*Alouatta belzebul*	-49.48	-4.65	PA	MG12142	Meloro et al. 2014a	Museum collection
36	*Alouatta belzebul*	-49.45	-3.7	PA	Rio Tocantins	Meireles et al. 1992	Museum collection
37	*Alouatta belzebul*	-49.38	-5.68	PA	Itupiranga	Gregorin, 2006	Museum collection
38	*Alouatta belzebul*	-49.12	-0.83	PA	Ponta de Pedras, Rio Ariri	Gregorin, 2006	Museum collection
39	*Alouatta belzebul*	-49.12	-0.17	PA	Igarapé Taperebá	Gregorin, 2006	Museum collection
40	*Alouatta belzebul*	-49	-5	PA	Reservatório Tucuruí	Armada et al. 1987	Capture
41	*Alouatta belzebul*	-48.98	-2.30	PA	Piratuba	Gregorin, 2006	Museum collection
42	*Alouatta belzebul*	-48.58	-0.28	PA	Livramento	Gregorin, 2006	Museum collection
43	*Alouatta belzebul*	-48.22	-7.35	TO	Araguaína	Gregorin, 2006	Museum collection
44	*Alouatta belzebul*	-47.48	-5.53	MA	Imperatriz	Gregorin, 2006	Museum collection
45	*Alouatta belzebul*	-47.45	-0.77	PA	Maracanã	Gregorin, 2006	Museum collection
46	*Alouatta belzebul*	-47.35	-2.98	PA	MG09209	Meloro et al. 2014a	Museum collection
47	*Alouatta belzebul*	-47.10	-1.55	PA	Ourém	Gregorin, 2006	Museum collection
48	*Alouatta belzebul*	-45.65	-3.97	MA	MN23198	Meloro et al. 2014a	Museum collection
49	*Alouatta belzebul*	-45.65	-1.35	MA	MG01021	Meloro et al. 2014a	Museum collection
50	*Alouatta belzebul*	-45.32	-4.03	MA	Boa Vista	Meloro et al. 2014a	Museum collection
51	*Alouatta belzebul*	-45.27	-5.53	MA	Aldeia São Pedro	Gregorin, 2006	Museum collection
52	*Alouatta belzebul*	-43.45	-2.62	PA	Miritiba	Meloro et al. 2014a	Museum collection
53	*Alouatta belzebul*	-36.30	-10.01	AL	Mata da Usina Coruripe 1	Fialho et al. 2014	Survey and Interview
54	*Alouatta belzebul*	-36.18	-10.04	AL	Mata da Usina Coruripe 3	Fialho et al. 2014	Survey and Interview
55	*Alouatta belzebul*	-36.13	-9.92	AL	Usina Sinimbu	Fialho et al. 2014	Direct observation
56	*Alouatta belzebul*	-35.98	-9.52	AL	RPPN Santa Tereza	Fialho et al. 2014	Survey and Interview

57	*Alouatta belzebul*	-35.93	-9.32	AL	Murici	Gregorin, 2006	Museum collection
58	*Alouatta belzebul*	-35.84	-9.26	AL	Estação Ecológica Murici	Langguth et al. 1987	Museum collection
59	*Alouatta belzebul*	-35.40	-8.71	PE	Engenho Sacramento	Fialho et al., 2014	Survey
60	*Alouatta belzebul*	-35.18	-6.73	PB	Rebio Guaribas	Fialho et al. 2014	Survey
61	*Alouatta belzebul*	-35.15	-7.04	PB	RPPN Pacatuba	Langguth et al. 1987	Museum collection; Direct observation
62	*Alouatta belzebul*	-35.10	-6.96	PB	Dois Rios	Oliveira & Oliveira, 1993	Interview
63	*Alouatta belzebul*	-35.10	-6.67	PB	Guaribas	Ayres, 1997	NA
64	*Alouatta belzebul*	-35.02	-7.15	PB	Açude dos Reis	Oliveira & Oliveira, 1993	Interview, Direct observation
65	*Alouatta belzebul*	-35.02	-6.49	RN	Mata Pituba	Ludwig et al. 2016	Survey
66	*Alouatta belzebul*	-34.96	-7.03	PB	RPPN Engenho Gargaú	Oliveira & Oliveira, 1993	Interview, Direct observation
67	*Sapajus flavius*	-36.31	-10.11	AL	Mata dos Macacos (Usina Coruipe)	Fialho et al. 2014	Survey and Interview
68	*Sapajus flavius*	-36.24	-9.76	AL	Usina Porto Rico	Fialho et al. 2014	Survey and Interview
69	*Sapajus flavius*	-36.06	-9.88	AL	Junco (Usina Caete)	Fialho et al. 2014	Survey and Interview
70	*Sapajus flavius*	-35.50	-9.23	AL	Santa Justina (Usina Santo Antonio)	Fialho et al. 2014	Survey and Interview
71	*Sapajus flavius*	-35.47	-7.61	PE	Oito Porcos (Serra dos Mascarenhas)	Fialho et al. 2014	Survey and Interview
72	*Sapajus flavius*	-35.39	-7.61	PE	Agua Azul (Usina Cruanji)	Fialho et al. 2014	Survey and Interview
73	*Sapajus flavius*	-35.13	-6.61	PB	Estacao Ecologica Estadual do Pau Brasil	Fialho et al. 2014	Survey and Interview
74	*Sapajus flavius*	-35.13	-6.56	PB	ASPALAN		Direct observation
75	*Sapajus flavius*	-35.13	-6.57	PB	Estacao Experimental de Camaratuba-Fazenda Jacana	Fialho et al. 2014	Survey and Interview
76	*Sapajus flavius*	-35.11	-6.76	PB	Rio Vermelho	Fialho et al. 2014	Survey and Interview
77	*Sapajus flavius*	-35.11	-6.73	PB	Grupiuna	Fialho et al. 2014	Survey and Interview
78	*Sapajus flavius*	-35.10	-6.96	PB	Dois Rios	Fialho et al. 2014	Survey and Interview
79	*Sapajus flavius*	-35.09	-7.02	PB	Sucupira-Sao Joao-Jacuipe	Fialho et al. 2014	Survey and Interview
80	*Sapajus flavius*	-35.09	-7.06	PB	Bruxaxa	Fialho et al. 2014	Survey and Interview
81	*Sapajus flavius*	-35.08	-6.65	PB	Cajarana-Aguas Claras	Fialho et al. 2014	Survey and Interview

82	*Sapajus flavius*	-35.08	-6.93	PB	Italiana	Fialho et al. 2014	Survey and Interview
83	*Sapajus flavius*	-35.07	-6.96	PB	Capitao-Sucupira-Pau Brasil	Fialho et al. 2014	Survey and Interview
84	*Sapajus flavius*	-35.06	-6.64	PB	Jardim	Fialho et al. 2014	Survey and Interview
85	*Sapajus flavius*	-35.05	-8.53	PE	Usina Salgado	Fialho et al. 2014	Survey and Interview
86	*Sapajus flavius*	-35.05	-6.6	PB	Estacao Experimental de Camaratuba	Lynch Alfaro et al. 2014	Direct observation
87	*Sapajus flavius*	-35.01	-7.78	PE	Mata dos Macacos (Usina Sao Jose)	Fialho et al. 2014	Survey and Interview
88	*Sapajus flavius*	-35.01	-7.08	PB	Pau de Ze Bedias-Oiteiro	Fialho et al. 2014	Survey and Interview
89	*Sapajus flavius*	-35.00	-7.77	PE	Mata dos Macacos	Fialho et al. 2014	Direct observation
90	*Sapajus flavius*	-34.99	-7.60	PE	Bujari	Fialho et al. 2014	Survey and Interview
91	*Sapajus flavius*	-34.98	-6.50	PB	Mata da Cristal	Bastos et al. 2015	Direct observation
92	*Sapajus flavius*	-34.98	-6.44	RN	RPPN Senador Antonio Farias	Fialho et al. 2014	Survey and Interview
93	*Sapajus flavius*	-34.98	-7.51	PB	Corrego do Inferno	Fialho et al. 2014	Survey and Interview
94	*Sapajus flavius*	-34.97	-6.44	PB	Millennium	Fialho et al. 2014	Survey and Interview
95	*Sapajus flavius*	-34.96	-7.03	PB	RPPN Engenho Gargaú	Oliveira & Oliveira, 1993	Coleção, Entrevista e visualização
96	*Sapajus flavius*	-34.92	-6.99	PB	Fazenda Pau Brasil 1	Fialho et al. 2014	Survey and Interview
97	*Sapajus flavius*	-34.92	-7.01	PB	Fazenda Pau Brasil 2	Fialho et al. 2014	Survey and Interview
98	*Sapajus flavius*	-34.91	-6.86	PB	APA Mamanguape	Fialho et al. 2014	Survey and Interview
99	*Sapajus flavius*	-34.86	-7.15	PB	Buraquinho	Fialho et al. 2014	Survey and Interview
100	*Sapajus libidinosus*	-53.38	-12.25	MT	MZ 10716	Cárceres et al. 2014	Museum collection
101	*Sapajus libidinosus*	-52.88	-13.10	MT	MZ 06964	Cárceres et al. 2014	Museum collection
102	*Sapajus libidinosus*	-52.75	-13.28	MT	MZ 06961	Meloro et al. 2014b	Museum collection
103	*Sapajus libidinosus*	-52.35	-14.68	MT	MZ 06713	Meloro et al. 2014b	Museum collection
104	*Sapajus libidinosus*	-51.72	-17.88	GO	MZ 07905	Meloro et al. 2014b	Museum collection
105	*Sapajus libidinosus*	-51.63	-15.55	GO	MZ 02364	Meloro et al. 2014b	Museum collection
106	*Sapajus libidinosus*	-50.30	-16.11	GO		Lima et al. 2017	GenBank
107	*Sapajus libidinosus*	-49.97	-16.45	GO	MZ 11095	Meloro et al. 2014b	Museum collection
108	*Sapajus libidinosus*	-49.31	-13.04	GO	Fazenda Santa Tereza,	Mendes et.al. 2015	Direct observation
109	*Sapajus libidinosus*	-49.27	-16.67	GO	MZ 19618	Meloro et al. 2014b	Museum collection

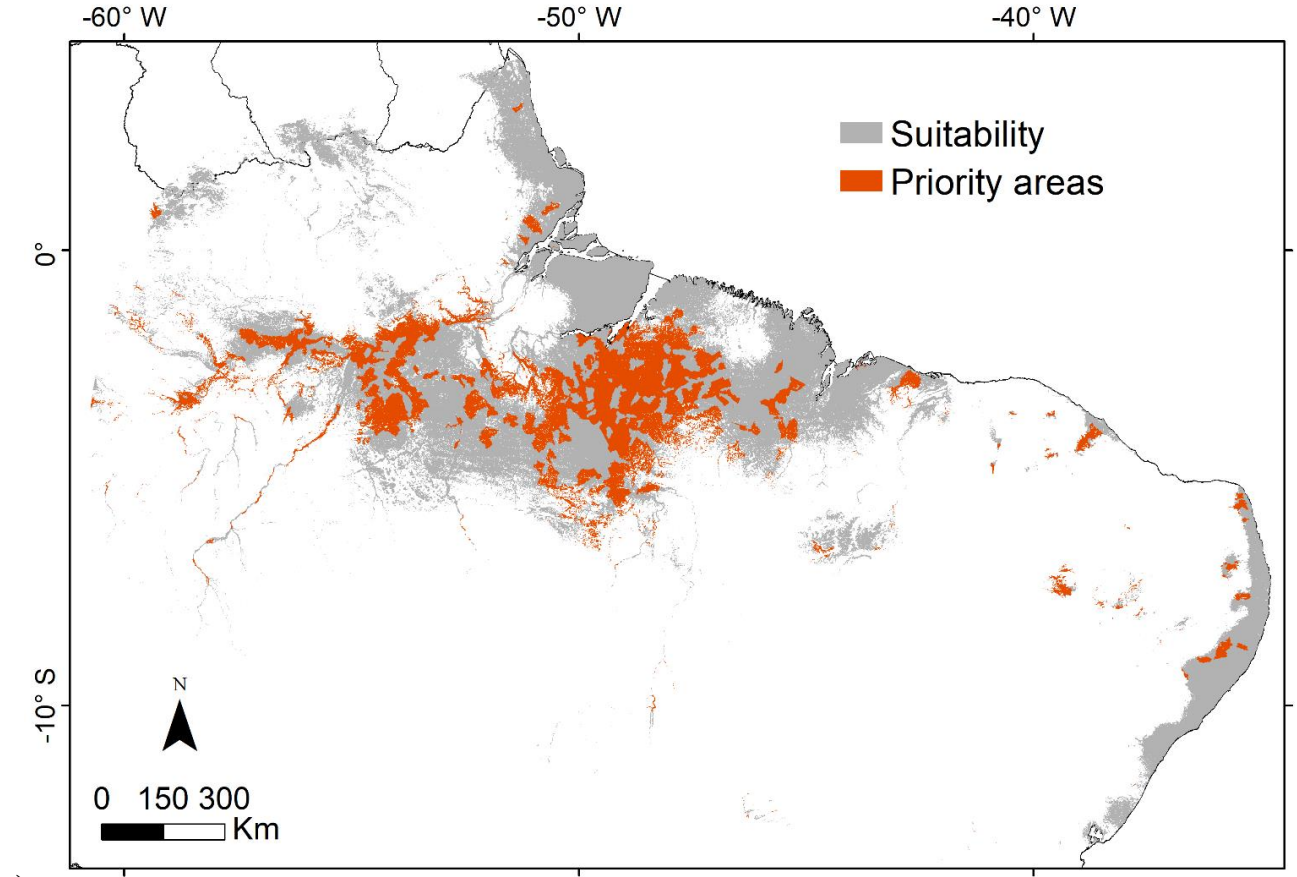
110	*Sapajus libidinosus*	-49.22	-13.98	GO	Fazenda Jatobá	Mendes et.al. 2015	Direct observation
111	*Sapajus libidinosus*	-49.12	-13.94	GO	Mara Rosa - Fazenda Lambari	Mendes et.al. 2015	Direct observation
112	*Sapajus libidinosus*	-48.93	-13.28	GO	Fazenda São Judas Tadeu	Mendes et.al. 2015	Direct observation
113	*Sapajus libidinosus*	-48.84	-13.62	GO	Fazenda Nossa Senhora da Aparecida	Mendes et.al. 2015	Direct observation
114	*Sapajus libidinosus*	-48.80	-13.80	GO	Fazenda Bom sucesso	Mendes et.al. 2015	Direct observation
115	*Sapajus libidinosus*	-48.77	-18.21	GO	Parque Estadual Mata Atlântica (MASP)	Rocha et al. 2015	Sightings and vocalization
116	*Sapajus libidinosus*	-48.38	-19.17	MG	Estação Ecológica do Panga	Bruna et al. 2016	Direct observation
117	*Sapajus libidinosus*	-48.30	-5.28	TO		Lima et al. 2017	GenBank
118	*Sapajus libidinosus*	-48.28	-13.51	GO	Reserva Particular da SAMA	Mendes et.al. 2015	Direct observation
119	*Sapajus libidinosus*	-48.20	-17.46	GO	Goiano Federal Institute - Urutai Campus	da Costa Estrela et al. 2015	Direct observation
120	*Sapajus libidinosus*	-48.20	-15.68	DF	Brasilandia	Lynch Alfaro et al. 2012	Museum collection
121	*Sapajus libidinosus*	-48.17	-18.37	GO	MZ 01430	Cárceres et al. 2014	Museum collection
122	*Sapajus libidinosus*	-48.17	-14.14	GO		Lima et al. 2017	GenBank
123	*Sapajus libidinosus*	-48.08	-15.57	DF	PARNA de Brasília	Sabbatini et al. 2007	Direct observation
124	*Sapajus libidinosus*	-48.03	-15.92	DF	Fazenda Sucupira Embrapa	Vilela, 2007	Direct observation
125	*Sapajus libidinosus*	-47.98	-15.67	DF	Parque Nacional de Brasília	Sabbatini et al. 2007	Direct observation
126	*Sapajus libidinosus*	-47.89	-15.94	DF	Reserva Ecológica do IBGE	Vilela, 2007	Direct observation
127	*Sapajus libidinosus*	-47.48	-14.31	GO	Fazenda Olhos D'água	Mendes et.al. 2015	Direct observation
128	*Sapajus libidinosus*	-47.30	-20.53	SP	Fazenda Santa Gemma	Freitas et al. 2008	Survey
129	*Sapajus libidinosus*	-47.29	-19.35	MG	Galheiros-Mata da Zilda	Neri, 1997	Interview
130	*Sapajus libidinosus*	-46.87	-17.22	MG	NA	Lynch Alfaro et al. 2012	Museum collection
131	*Sapajus libidinosus*	-46.63	-20.73	MG	Faz. Mata da Mandioca	Kinzey, 1982	NA
132	*Sapajus libidinosus*	-46.41	-13.54	GO	São Domingos	Mendes et.al. 2015	Direct observation
133	*Sapajus libidinosus*	-46.27	-16.94	MG	Fazenda Tres Rios	Lessa et al. 2012	Direct observation
134	*Sapajus libidinosus*	-45.47	-9.85	PI	Guibués – Fazenda Boa Vista	Hinely, 2006	Direct observation
135	*Sapajus libidinosus*	-45.42	-9.66	PI	Fazenda Boa Vista	Haslam et.al. 2014	Direct observation
136	*Sapajus libidinosus*	-45.35	-9.83	PI	Fazenda Boa Vista	Silva, 2010	Photograph
137	*Sapajus libidinosus*	-45.32	-4.03	MA	MZ 02488	Meloro et al. 2014b	Museum collection

138	*Sapajus libidinosus*	-44.20	-7.93	PI		Lima et al. 2017	GenBank
139	*Sapajus libidinosus*	-43.40	-6.17	RN	Serrinha dos Pintos	Ferreira, 2009	Interview
140	*Sapajus libidinosus*	-43.20	-6.25	RN	João Dias	Ferreira, 2009	Interview
141	*Sapajus libidinosus*	-42.72	-8.45	PI	PARNA Serra da Capivara	Falótico et al. 2016	Direct observation
142	*Sapajus libidinosus*	-42.69	-2.62	MA	Estuário do Rio Preguiças	Lynch Alfaro et al. 2014	Direct observation
143	*Sapajus libidinosus*	-42.63	-8.88	PI	Parna Serra da Capivara	Haslam & Falótico, 2015	Direct observation
144	*Sapajus libidinosus*	-42.55	-8.45	PI	PARNA Serra da Capivara	Cardoso, 2014	Direct observation
145	*Sapajus libidinosus*	-42.53	-8.67	PI	Parque Nacional da Serra da Capivara	Moura, 2015	Direct observation
146	*Sapajus libidinosus*	-42.53	-2.71	MA	Estuário do Rio Novo	Lynch Alfaro et al. 2014	Direct observation
147	*Sapajus libidinosus*	-42.43	-5.09	PI		Lima et al. 2017	GenBank
148	*Sapajus libidinosus*	-42.32	-8.43	PI	PARNA Serra da Capivara	Moura, 2007	Direct observation
149	*Sapajus libidinosus*	-41.84	-2.78	MA	Povoado de vassouras	Silva, 2010	Photograph
150	*Sapajus libidinosus*	-41.50	-7.50	PI	Parna Serra da capivara	Moura & Lee, 2004	Direct observation
151	*Sapajus libidinosus*	-39.86	-7.42	PE	Serra das tabocas	Bárbara Moraes (current study)	Direct observation
152	*Sapajus libidinosus*	-39.78	-7.68	PE	Timorante, Serra Da Luveja, Pedra Da Ventania	Oliveira, 2015	Museum collection
153	*Sapajus libidinosus*	-39.72	-7.35	PE	Exú – Fazenda Catareno	Oliveira & Langguth, 2006	Museum collection
154	*Sapajus libidinosus*	-39.65	-7.47	PE	Faz. Mangueira	Bárbara Moraes (current study)	Direct observation
155	*Sapajus libidinosus*	-39.57	-8.30	PE	Serra do Almirante	Bárbara Moraes (current study)	Direct observation
156	*Sapajus libidinosus*	-39.55	-7.65	PE	Cariri mirim	Oliveira & Langguth, 2006	Museum collection
157	*Sapajus libidinosus*	-39.40	-5.79	CE	Fazenda Vila Nova	Silva, 2010	Photograph
158	*Sapajus libidinosus*	-39.32	-7.65	PE	Sítio Boi, Morro Redondo	Oliveira & Langguth, 2006	Museum collection
159	*Sapajus libidinosus*	-38.52	-7.80	PE	Santa Rita, Fazenda Saco Velho	Bárbara Moraes (current study)	Direct observation
160	*Sapajus libidinosus*	-38.30	-6.90	PB	Serra da Boa Vista	Silva, 2010	Museum collection
161	*Sapajus libidinosus*	-38.30	-7.96	PE	Serra Talhada	Moraes et al. 2014	Direct observation
162	*Sapajus libidinosus*	-38.29	-8.10	PE	Serra do Ramalhete	Bárbara Moraes (current study)	Direct observation
163	*Sapajus libidinosus*	-38.28	-6.53	PB	Serra Branca	Silva, 2010	Museum collection
164	*Sapajus libidinosus*	-38.27	-6.32	RN	José da Penha	Ferreira, 2009	Interview
165	*Sapajus libidinosus*	-37.91	-9.00	PE	Sítio do sr. Virgílio	ICMBio (comunicação pessoal)	Direct observation

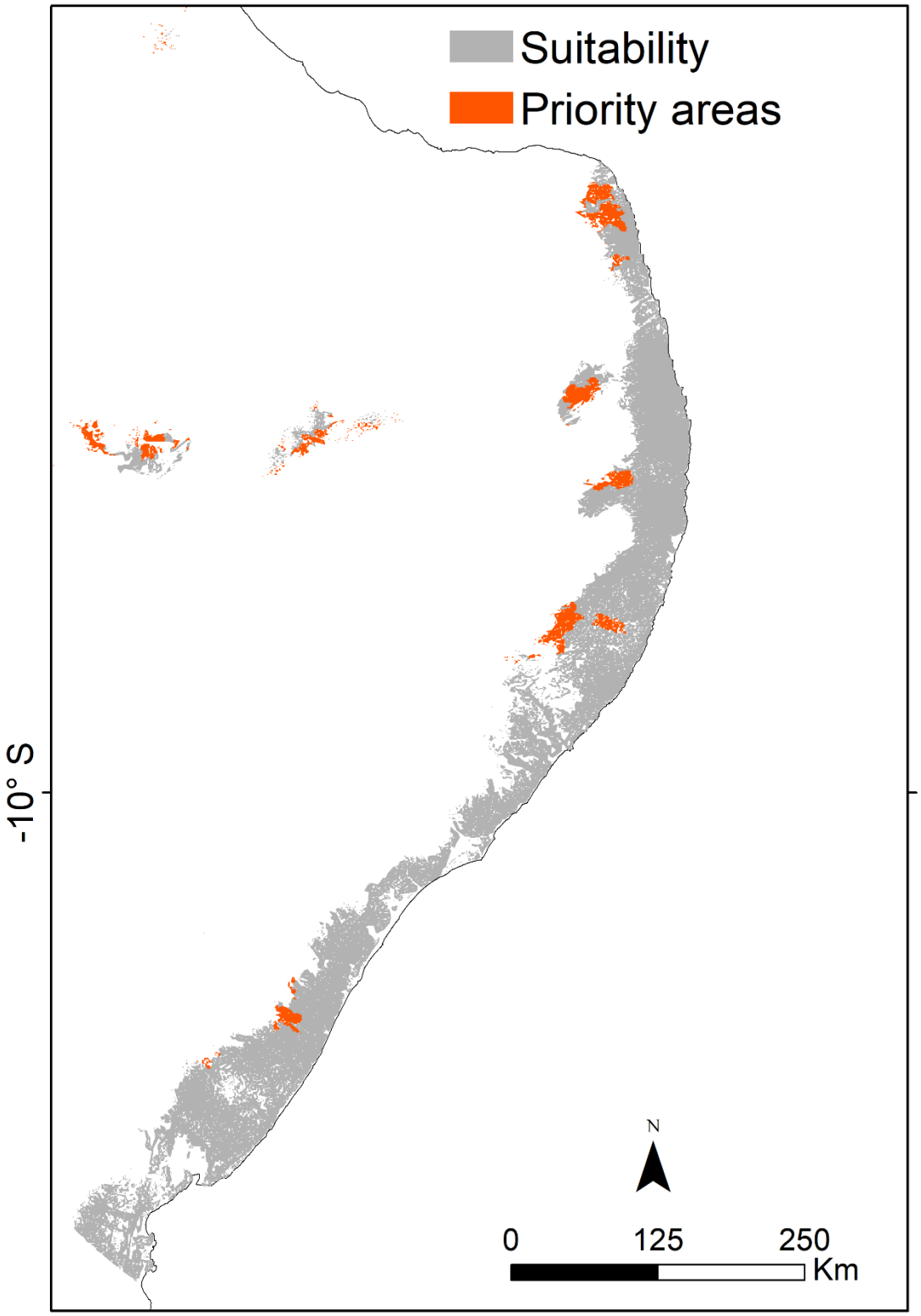
166	*Sapajus libidinosus*	-37.90	-6.07	RN	Martins	Ferreira, 2009	Direct observation
167	*Sapajus libidinosus*	-37.83	-6.15	RN	Frutuoso Gomes	Ferreira, 2009	Interview
168	*Sapajus libidinosus*	-37.83	-8.21	PE	Serra das Maravilhas	Bárbara Moraes (current study)	Direct observation
169	*Sapajus libidinosus*	-37.41	-9.66	AL	Serra das Ponteiras,	Canale et. al. 2009	Interview, vestiges
170	*Sapajus libidinosus*	-37.40	-7.96	PE	Serra do Estrago	Bárbara Moraes (current study)	Direct observation
171	*Sapajus libidinosus*	-37.20	-8.39	PE	Serra dos Pinheiros	Bárbara Moraes (current study)	Direct observation
172	*Sapajus libidinosus*	-37.06	-7.16	PB	Grota do Adenino, Serra do Firmino	Silva, 2010	Photograph
173	*Sapajus libidinosus*	-37.04	-6.21	RN	Jucurutu	Emidio & Ferreira, 2012	Direct observation
174	*Sapajus libidinosus*	-36.63	-9.40	AL		Oliveira & Langguth, 2006	Museum collection
175	*Sapajus libidinosus*	-42.55	-8.83	PI	PARNA Serra da Capivara no Boqueirão da Pedra Furada	Falótico & Ottoni, 2016	Direct observation
176	*Sapajus libidinosus*	-38.39	-6.40	RN	Serra do Estreito (RN)	Emidio & Ferreira, 2012	Direct observation

APÊNDICE E - MAP INDICATING SUITABILITY AREAS FOR OCCURRENCE OF A) ALOUATTA BELZEBUL, B) SAPAJUS FLAVIUS AND C) SAPAJUS LIBIDINOSUS AND THEIR RELATION WITH GOVERNMENT PRIORITY AREAS.

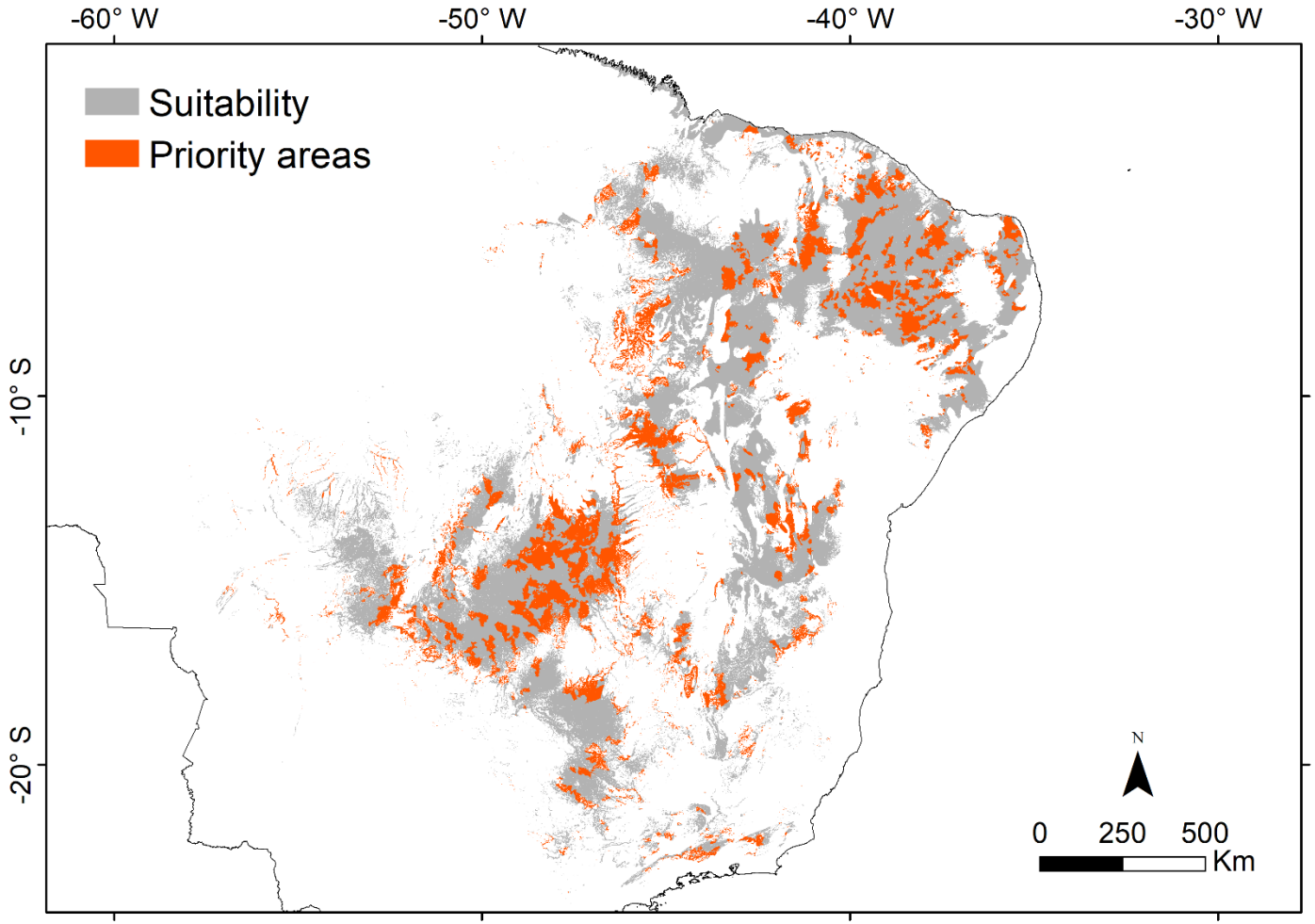
Priority areas for biodiversity conservation are established by brazil government based on biodiversity indices, threat level and ecoregions, among other criteria.



a)



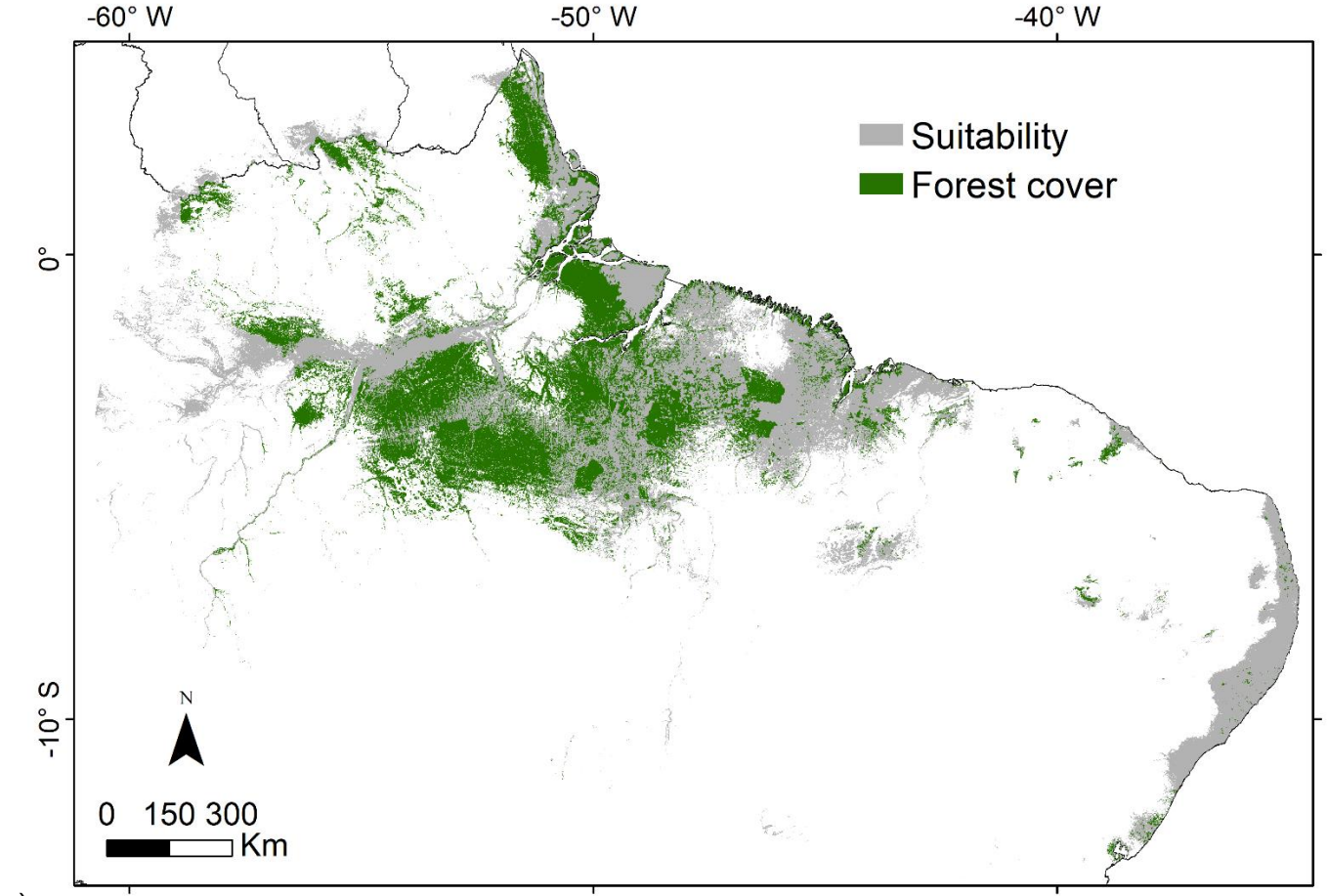
b)


-60° W
-50° W
-40° W
-30° W
-10° S
-20° S
Suitability
Priority areas
N
0
250
500
Km

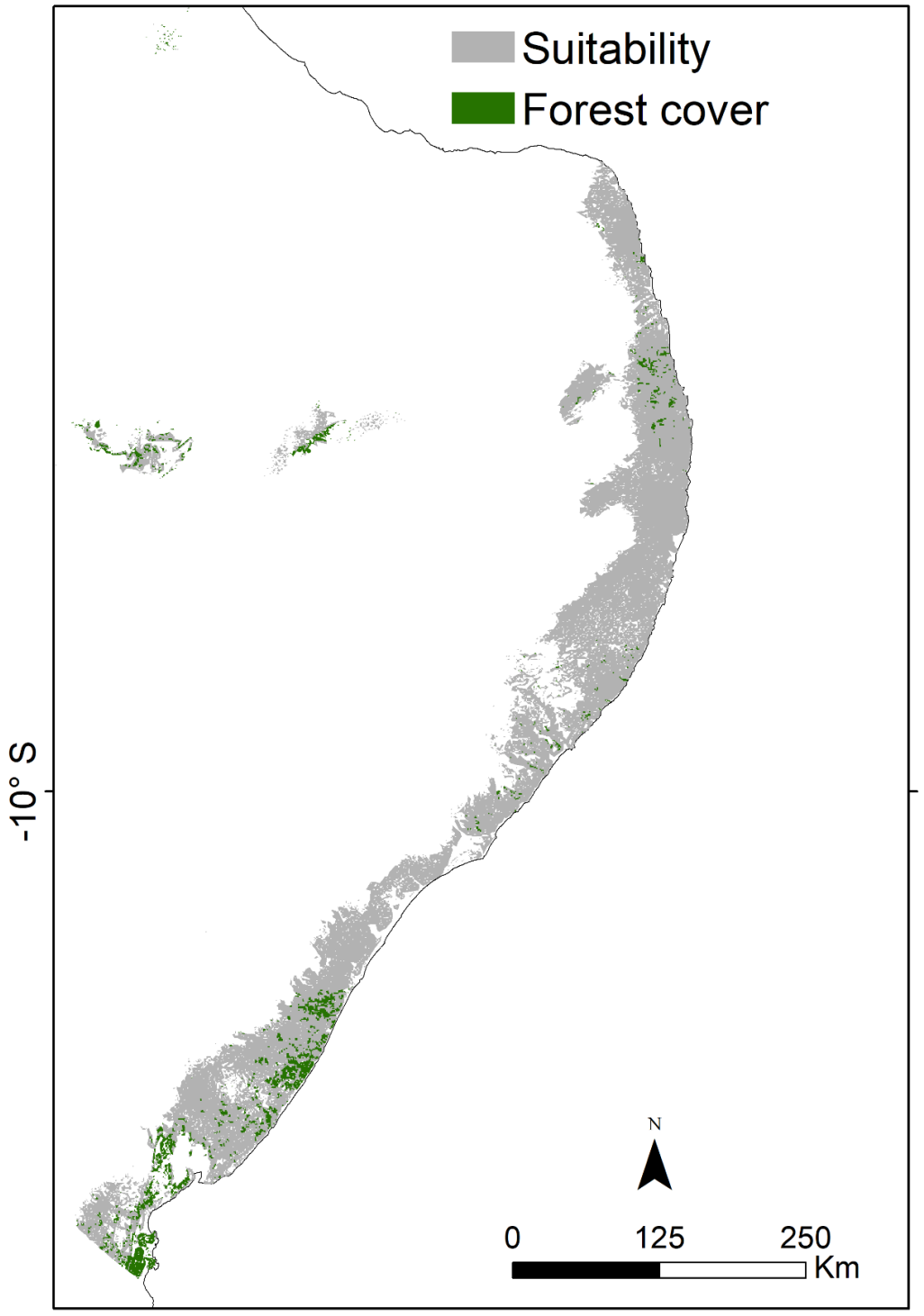
c)

APÊNDICE F - MAP INDICATING SUITABILITY AREAS FOR OCCURRENCE OF A) ALOUATTA BELZEBUL, B) SAPAJUS FLAVIUS, C) SAPAJUS LIBIDINOSUS AND THEIR RELATION WITH FORESTED AREAS.

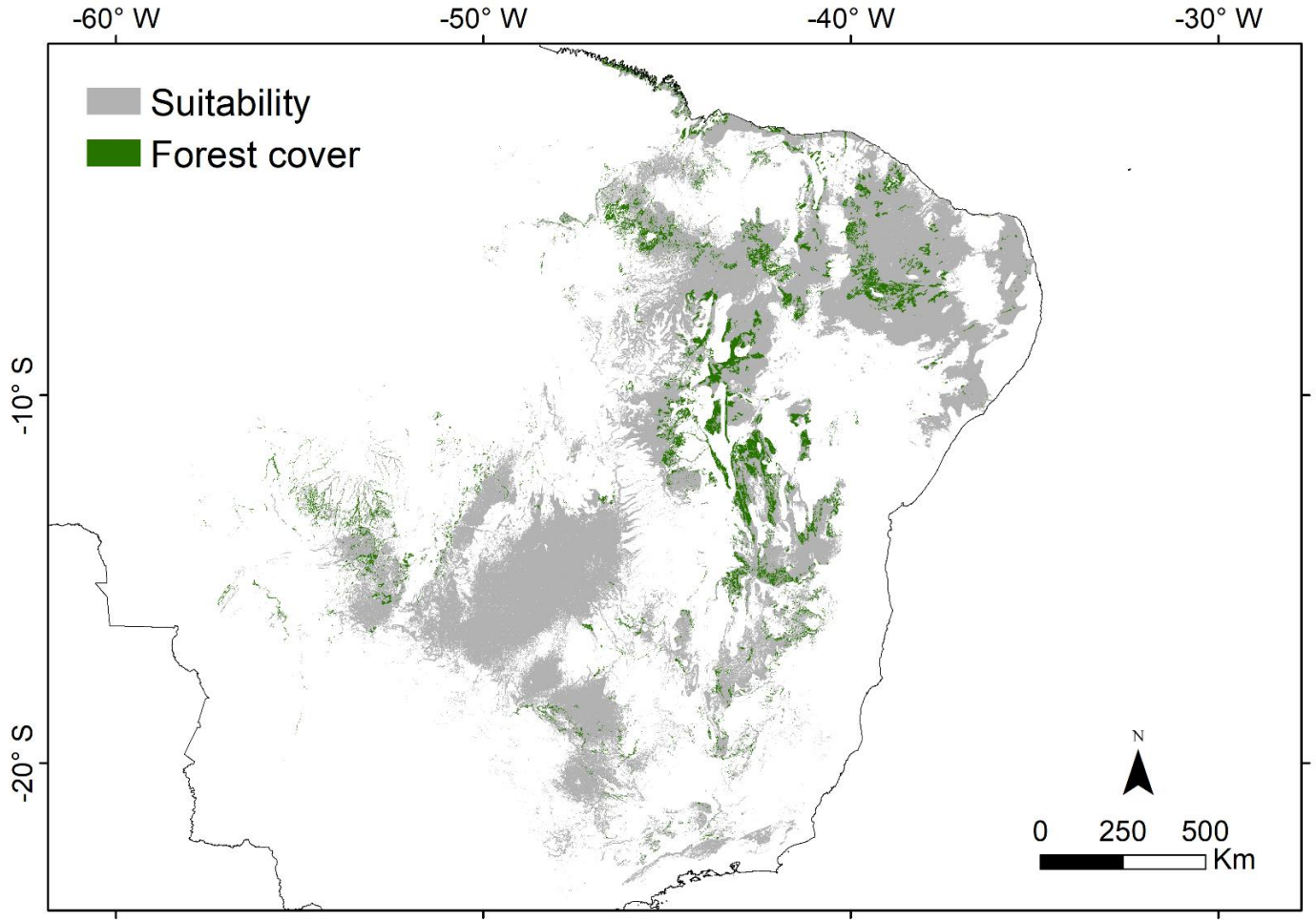
According to o ibge (2017), areas occupied by forests are those with tree formations greater than 5 meters in height, including areas of dense forest, open forest, seasonal forest and mixed ombrophilous forest, as well as forested savanna, forested campinarana and mangroves.



a)



b)


-60° W
-50° W
-40° W
-30° W
-10° S
-20° S
Suitability
Forest cover
N
0 250 500
Km

c)

APÊNDICE G - LIST OF GOVERNMENT PRIORITY AREAS FOR CONSERVATION THAT CURRENTLY EXIST IN AREAS PREDICTED BY OUR MODELS AS SUITABLE FOR THE FUTURE OCCURRENCE OF (1) ALOUATTA BELZEBUL, (2) SAPAJUS FLAVIUS, AND (3) SAPAJUS LIBIDINOSUS.

We considered the presence of priority areas in a moderate and severe future scenario. We also list the actions for conservation of these areas. This information was collected in studies conducted with the participation of researchers, managers and representatives of various brazilian institutions and conducted by the brazilian ministry of environment between 2012 and 2018 (mma, 2018a). Some government priority areas are inside officially protected areas in brazil and we highlighted them in the column “inside protected areas”.

N	Priority areas	Biome	Biological importance	Conservation Actions	Future climate suitability		Inside protected áreas?
					Moderate	Severe	x = yes; - = no
1	AMZ-010	Amazon	High	Supervision and control of illegal activities	2	-	-
2	AMZ-114	Amazon	Very high	Restoration of degraded areas	1, 3	3	-
3	AMZ-115	Amazon	Extremely high	Restoration of degraded areas	1	-	x
4	AMZ-116	Amazon	Extremely high	Restoration of degraded areas	1, 3	1, 3	-
5	AMZ-117	Amazon	High	Restoration of degraded areas	1	-	-
6	AMZ-118	Amazon	Very high	Restoration of degraded areas	1	-	-
7	AMZ-119	Amazon	High	Restoration of degraded areas	1	-	-
8	AMZ-120	Amazon	Extremely high	Restoration of degraded areas	1	-	-
9	AMZ-122	Amazon	High	Restoration of degraded areas	1, 3	-	-
10	AMZ-124	Amazon	Extremely high	Restoration of degraded areas	1	-	-
11	AMZ-148	Amazon	Extremely high	Monitoring and Management	1	-	-
12	AMZ-195	Amazon	Extremely high	Protected Area Extension	1	-	-
13	AMZ-020	Amazon	Extremely high	Protection of relevant geological formation / Recognition	1	-	-
14	AMZ-202	Amazon	Extremely high	Reconhecimento de TI	1	1	-
15	AMZ-024	Amazon	Extremely high	Restoration of degraded areas	1	-	-
16	AMZ-294	Amazon	Extremely high	Searches	1	-	x
17	AMZ-313	Amazon	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	1	-	x
18	AMZ-317	Amazon	High	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	1	-	-
19	AMZ-367	Amazon	High	Supervision and control of illegal activities	1	-	-

20	AMZ-368	Amazon	High	Supervision and control of illegal activities	1	-	-
21	AMZ-369	Amazon	High	Supervision and control of illegal activities	1	-	-
22	AMZ-424	Amazon	Extremely high	Regularization of degrading activity	1	-	-
23	AMZ-426	Amazon	Extremely high	Protection of relevant geological formation / Recognition	1, 3	1, 3	x
24	AMZ-491	Amazon	Extremely high	Supervision and control of illegal activities	1	-	-
25	AMZ-507	Amazon	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	1	-	-
26	AMZ-512	Amazon	Extremely high	Supervision and control of illegal activities	1	-	-
27	AMZ-532	Amazon	Extremely high	Monitoring and Management	1	-	-
28	AMZ-533	Amazon	Extremely high	Monitoring and Management	1	-	-
29	AMZ-546	Amazon	Extremely high	Regularization of degrading activity	1	1	-
30	AMZ-547	Amazon	Very high	Regularization of degrading activity	1	1	-
31	AMZ-548	Amazon	High	Regularization of degrading activity	1	-	-
32	AMZ-549	Amazon	Extremely high	Regularization of degrading activity	1	-	-
33	AMZ-055	Amazon	Extremely high	Protection of relevant geological formation / Recognition	1	-	-
34	AMZ-566	Amazon	Extremely high	Creation of sustainable use protected areas	1	-	-
35	AMZ-567	Amazon	Extremely high	Strengthening management tools	1	-	x
36	AMZ-581	Amazon	Extremely high	Strengthening the value chains of socio-biodiversity products	1	-	x
37	AMZ-617	Amazon	Extremely high	Strengthening the value chains of socio-biodiversity products	1	1	-
38	AMZ-618	Amazon	High	Strengthening the value chains of socio-biodiversity products	1	-	-
39	AMZ-702	Amazon	Extremely high	Regularization of degrading activity	1	1	-
40	AMZ-711	Amazon	Extremely high	Restoration of degraded areas	1, 3	3	x
41	AMZ-718	Amazon	Muito High	Restoration of degraded areas	1	-	-
42	AMZ-728	Amazon	High	Restoration of degraded areas	1	-	-
43	AMZ-777	Amazon	Extremely high	Restoration of degraded areass	1	-	-
44	AMZ-008	Amazon	Very high	Strengthening the value chains of socio-biodiversity products	1	-	-
45	AMZ-824	Amazon	Very high	Restoration of degraded areas	1	-	-
46	AMZ-825	Amazon	Extremely high	Restoration of degraded areas	1	-	-
47	AMZ-826	Amazon	Extremely high	Restoration of degraded areas	1	-	-
48	AMZ-827	Amazon	High	Restoration of degraded areas	1	-	-
49	AMZ-846	Amazon	Very high	Restoration of degraded areas	1	-	-
50	AMZ-849	Amazon	High	Restoration of degraded areas	1	-	-
51	AMZ-850	Amazon	High	Restoration of degraded areas	1	-	-
52	AMZ-857	Amazon	Extremely high	Restoration of degraded areas	1	-	-
53	AMZ-858	Amazon	High	Restoration of degraded areas	1	1	-
54	AMZ-859	Amazon	Extremely high	Restoration of degraded areas	1	1	-

55	AMZ-867	Amazon	Very high	Supervision and control of illegal activities	1	-	-
56	AMZ-901	Amazon	Extremely high	Restoration of degraded areas	1	-	-
57	AMZ-902	Amazon	High	Restoration of degraded areas	1	-	-
58	AMZ-903	Amazon	Extremely high	Strengthening the value chains of socio-biodiversity products	1	1	-
59	AMZ-909	Amazon	High	Restoration of degraded areas	1	-	x
60	AMZ-143	Amazon	Very hig	Monitoring and Management	3	-	
61	AMZ-216	Amazon	Very hig	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	-	-
62	AMZ-217	Amazon	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	-
63	AMZ-304	Amazon	Extremely high	Monitoring and Management	3	-	-
64	AMZ-313	Amazon	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	-	-
65	AMZ-334	Amazon	High	Regularization of degrading activity	3		-
66	AMZ-335	Amazon	Very hig	Regularization of degrading activity	3	3	-
67	AMZ-338	Amazon	Very hig	Regularization of degrading activity	3	-	-
68	AMZ-339	Amazon	Very hig	Regularization of degrading activity	3	-	-
69	AMZ-340	Amazon	Very hig	Regularization of degrading activity	3	-	-
70	AMZ-342	Amazon	Extremely high	Regularization of degrading activity	3	-	-
71	AMZ-343	Amazon	High	Regularization of degrading activity	3	-	-
72	AMZ-344	Amazon	Extremely high	Regularization of degrading activity	3	-	-
73	AMZ-345	Amazon	Very hig	Regularization of degrading activity	3	-	-
74	AMZ-347	Amazon	High	Regularization of degrading activity	3	-	-
75	AMZ-370	Amazon	Very hig	Supervision and control of illegal activities	3	-	-
76	AMZ-371	Amazon	Very hig	Supervision and control of illegal activities	3	-	-
77	AMZ-374	Amazon	Very hig	Supervision and control of illegal activities	3	-	-
78	AMZ-413	Amazon	High	Supervision and control of illegal activities	3	3	-
79	AMZ-525	Amazon	High	Monitoring and Management	3	-	-
80	AMZ-527	Amazon	Very hig	Monitoring and Management	3	-	-
81	AMZ-529	Amazon	High	Monitoring and Management	3	-	-
82	AMZ-531	Amazon	Extremely high	Monitoring and Management	3	3	-
83	AMZ-541	Amazon	Extremely high	Supervision and control of illegal activities	3	-	-
84	AMZ-641	Amazon	High	Creation of sustainable use protected areas	3	3	-
85	AMZ-713	Amazon	Extremely high	Restoration of degraded areas	3	-	x

86	AMZ-795	Amazon	High	Restoration of degraded areas	3	3	x
87	AMZ-797	Amazon	High	Restoration of degraded areas	3	3	-
88	AMZ-798	Amazon	High	Restoration of degraded areas	3	3	-
89	AMZ-799	Amazon	Extremely high	Restoration of degraded areas	3	3	-
90	AMZ-801	Amazon	Very hig	Restoration of degraded areas	3	-	-
91	AMZ-802	Amazon	Extremely high	Restoration of degraded areas	3	-	-
92	AMZ-803	Amazon	High	Restoration of degraded areas	3	-	-
93	AMZ-804	Amazon	High	Restoration of degraded areas	3	-	-
94	AMZ-806	Amazon	Very hig	Restoration of degraded areas	3	-	-
95	AMZ-807	Amazon	Very hig	Restoration of degraded areas	3	-	-
96	AMZ-808	Amazon	Extremely high	Restoration of degraded areas	3	-	-
97	AMZ-816	Amazon	Extremely high	Restoration of degraded areas	3	-	-
98	AMZ-847	Amazon	Extremely high	Restoration of degraded areas	3	3	-
99	AMZ-089	Amazon	High	Creation of sustainable use protected areas	3	-	-
100	AMZ-009	Amazon	Extremely high	Regularization of degrading activity	3	-	-
101	AMZ-090	Amazon	High	Creation of sustainable use protected areas	3	-	-
102	AMZ-091	Amazon	Very hig	Creation of sustainable use protected areas	3	-	-
103	MA263	Atlantic Forest	Very high	Creation of Integral Protection protected area	1, 2	-	x
104	MA264	Atlantic Forest	Very high	Environmental regularization of rural properties	1, 2	-	-
105	MA262	Atlantic forest	Extremely high	Creation of Integral Protection protected area	1	-	-
106	MA145	Atlantic forest	High	Environmental regularization of rural properties	3	3	x
107	MA148	Atlantic forest	High	Environmental regularization of rural properties	3	3	-
108	MA155	Atlantic forest	Very high	Environmental regularization of rural properties	3	3	-
109	MA159	Atlantic forest	Extremely high	Municipal Plan for Conservation and Recovery of the Atlantic Forest	3	3	x
110	MA168	Atlantic forest	High	Environmental regularization of rural properties	3	3	-
111	MA180	Atlantic forest	High	Municipal Plan for Conservation and Recovery of the Atlantic Forest	3	3	-
112	MA186	Atlantic forest	Very high	Municipal Plan for Conservation and Recovery of the Atlantic Forest	3	3	-

113	MA211	Atlantic forest	Extremely high	Species protection	3	3	-
114	MA217	Atlantic forest	High	Watershed Management Plans	3	3	-
115	MA218	Atlantic forest	High	Restoration of degraded areas	3	3	-
116	MA219	Atlantic forest	High	Environmental regularization of rural properties	3	3	-
117	MA222	Atlantic forest	High	Restoration of degraded areas	3	3	-
118	MA225	Atlantic forest	High	Environmental regularization of rural properties	3	3	-
119	MA229	Atlantic forest	Very high	Undefined category protected area creation	3	3	-
120	MA107	Atlantic forest	Very high	Protected Area Extension	3	3	x
121	MA134	Atlantic forest	Very high	Restoration of degraded areas	3	3	-
122	MA143	Atlantic forest	Extremely high	Protected Area Extension	3	3	x
123	MA142	Atlantic forest	Extremely high	Municipal Plan for Conservation and Recovery of the Atlantic Fores	3	-	-
124	MA152	Atlantic forest	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	-
125	MA161	Atlantic forest	High	Searches	3	3	-
126	MA153	Atlantic forest	Very high	Endangered Species Recovery and Management	3	3	x
127	MA163	Atlantic forest	Extremely high	Inspection and control of illegal activities	3	3	-
128	MA170	Atlantic forest	Very high	Inspection and control of illegal activities	3	3	x
129	MA174	Atlantic forest	Extremely high	Endangered Species Recovery and Management	3	3	-
130	MA173	Atlantic forest	High	Protected Area Creation	3	3	-

131	MA176	Atlantic forest	High	Endangered Species Recovery and Management	3	3	-
132	MA177	Atlantic forest	Extremely high	Endangered Species Recovery and Management	3	3	-
133	MA183	Atlantic forest	Extremely high	Restoration of degraded areas	3	3	-
134	MA184	Atlantic forest	Extremely high	Sustainable Tourism Development	3	3	-
135	MA190	Atlantic forest	High	Protected Area Creation	3	3	-
136	MA200	Atlantic forest	Extremely high	Environmental regularization of rural properties	3	3	-
137	MA201	Atlantic forest	High	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	-
138	MA202	Atlantic forest	High	Limitation / Regularization of degrading activities	3	3	-
139	MA203	Atlantic forest	Very high	Endangered Species Recovery and Management	3	3	-
140	MA207	Atlantic forest	Extremely high	Sustainable Management	3	3	-
141	MA206	Atlantic forest	High	Sustainable Tourism Development	3	3	-
142	MA209	Atlantic forest	Very high	Environmental regularization of rural properties	3	3	x
143	MA214	Atlantic forest	High	Endangered Species Recovery and Management	3	3	-
144	MA224	Atlantic forest	High	Limitation / Regularization of degrading activities	3	3	-
145	MA230	Atlantic forest	High	Restoration of degraded areas	3	3	-
146	MA151	Atlantic forest	Extremely high	Searches	3	3	x
147	MA137	Atlantic forest	Very high	Limitation / Regularization of degrading activities	3	3	x
148	MA195	Atlantic forest	Extremely high	Development of financial support mechanisms	3	3	-

149	MA205	Atlantic forest	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
150	MA234	Atlantic forest	Very high	Restoration of degraded areas	3	3	-
151	MA238	Atlantic forest	Very high	Endangered Species Recovery and Management	3	3	-
152	MA240	Atlantic forest	High	Restoration of degraded areas	3	3	-
153	MA243	Atlantic forest	Very high	Restoration of degraded areas	3	3	-
154	MA236	Atlantic forest	Very high	Protected Area Extension	3	3	x
155	MA156	Atlantic forest	High	Environmental regularization of rural properties	3	3	x
156	MA146	Atlantic forest	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
157	MA131	Atlantic forest	Extremely high	Environmental regularization of rural properties	3	3	x
158	MA226	Atlantic forest	High	Restoration of degraded areas	3	3	x
159	Fortaleza e Costa Oeste	Caatinga	Extremely high	Undefined category protected area creation	1, 2, 3	1, 2, 3	x
160	Mato Grande	Caatinga	Extremely high	Creation of Integral Protection protected area	1, 2, 3	1, 3	-
161	Macaí-ba	Caatinga	Extremely high	Undefined category protected area creation	1, 2, 3	1	-
162	Brejos Paraibano	Caatinga	Extremely high	Undefined category protected area creation	1, 2, 3	1, 2, 3	-
163	Parque Poeta	Caatinga	High	Restoration of degraded areas	1, 2, 3	1	-
164	Araripe	Caatinga	Very high	Undefined category protected area creation	1, 2, 3	3	x
165	Serra do Mascarenhas	Caatinga	Very high	Creation of Integral Protection protected area	1, 2, 3	1, 3	x
166	Jacobina	Caatinga	Extremely high	Creation of Integral Protection protected area	2, 3	3	x
167	Explanada	Caatinga	High	Caatinga sustainable management for livestock	1, 2, 3	3	-
168	Moraújo	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	3	x
169	Itapipoca	Caatinga	Very high	Restoration of degraded areas	1, 3	1, 3	-
170	Meruoca	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	3	x
171	Santa Quitéria	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	3	-
172	Canindé	Caatinga	Very high	Restoration of degraded areas	1, 3	1, 3	x
173	Chorozinho	Caatinga	Extremely high	Restoration of degraded areas	1, 3	1, 3	-

174	Bica do Ipú	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	3	x
175	Serra do Machado	Caatinga	Very high	Undefined category protected area creation	1, 3	1, 3	-
176	Itatira sul	Caatinga	Very high	Restoration of degraded areas	1, 3	1, 3	-
177	Monolitos de Quixadá	Caatinga	Extremely high	Undefined category protected area creation	1, 3	3	-
178	Vera Cruz	Caatinga	Extremely high	Restoration of degraded areas	1, 3	-	-
179	Curimatau	Caatinga	Extremely high	Undefined category protected area creation	1, 3	1, 3	-
180	Remigio	Caatinga	High	No actions recommended by selection workshop	1, 3	1, 3	-
181	Serra da Mina	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	3	-
182	Serra do Teixeira	Caatinga	Very high	Creation of Integral Protection protected area	1, 3	1, 3	-
183	Serra da Matinha	Caatinga	High	Creation of Integral Protection protected area	1, 3	3	-
184	Serra Talhada	Caatinga	Extremely high	Creation of Integral Protection protected area	1, 3	1	x
185	Serra das Pias	Caatinga	Extremely high	No actions recommended by selection workshop	1, 3	3	-
186	Lençóis	Caatinga	Very high	Restoration of degraded areas	1, 3	3	x
187	Catimbau	Caatinga	Extremely high	Creation of Integral Protection protected area	1, 3	3	-
188	Tabuleiro Costeiro	Caatinga	High	Undefined category protected area creation	3	-	x
189	Granja	Caatinga	Very high	Creation of Integral Protection protected area	3	3	x
190	Marco	Caatinga	Very high	Creation of sustainable use protected areas	3	3	-
191	Acaraú	Caatinga	High	Biological Inventory	3	3	-
192	Irauçuba/Tejuçuoca	Caatinga	Very high	Creation of Integral Protection protected area	3	3	-
193	Carnaubal/Arabé	Caatinga	High	Restoration of degraded areas	3	3	x
194	Guaraciaba do Norte	Caatinga	Extremely high	No actions recommended by selection workshop	3	-	-
195	Opala	Caatinga	High	Undefined category protected area creation	3	3	x
196	Nova Russas	Caatinga	Extremely high	Restoration of degraded areas	3	3	-
197	Apudi Mossoró	Caatinga	High	Restoration of degraded areas	3	-	-
198	Pedra Grande	Caatinga	High	Restoration of degraded areas	3	-	-
199	Sertão	Caatinga	Extremely high	Creation of sustainable use protected areas	3	3	x
200	Prata Velha do Piauí-	Caatinga	Very high	No actions recommended by selection workshop	3	-	-
201	Jardim dos Angicos	Caatinga	High	No actions recommended by selection workshop	3	3	-
202	Chapada do Apodi	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	-
203	Sítio dos Padres	Caatinga	High	No actions recommended by selection workshop	3	-	-
204	Pedra Branca	Caatinga	High	Creation of Integral Protection protected area	3	3	-
205	Serra do Pereiro	Caatinga	High	Creation of Integral Protection protected area	3	3	x
206	Solonopolis	Caatinga	High	Creation of Integral Protection protected area	3	-	-
207	Alto dos Coqueiros	Caatinga	Extremely high	Creation of Integral Protection protected area	3	-	-
208	Soltas 2	Caatinga	Very high	No actions recommended by selection workshop	3	-	-
209	Soltas 1	Caatinga	Very high	No actions recommended by selection workshop	3	-	-
210	Mombaça sul	Caatinga	High	Restoration of degraded areas	3	3	-

211	Macaíba	Caatinga	Extremely high	Undefined category protected area creation	3	3	-
212	Nascentes do Poti 2	Caatinga	High	Undefined category protected area creation	3	3	-
213	Nascente do Potengi	Caatinga	High	Creation of Integral Protection protected area	3	3	-
214	São Francisco	Caatinga	Extremely high	Undefined category protected area creation	3	-	-
215	Palmeirais	Caatinga	High	Restoration of degraded areas	3	3	-
216	Serra Augusto Severo	Caatinga	High	Creation of Integral Protection protected area	3	3	-
217	Monte Alegre	Caatinga	Extremely high	Restoration of degraded areas	3	3	-
218	Ponta de Orós	Caatinga	High	No actions recommended by selection workshop	3	-	-
219	Valença	Caatinga	Very high	Undefined category protected area creation	3	3	-
220	Serra de Santana	Caatinga	High	Creation of Integral Protection protected area	3	3	-
221	Serra de Martins	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	-
222	Nascentes do Poti 3	Caatinga	Very high	Restoration of degraded areas	3	3	-
223	Caiada	Caatinga	Very high	Undefined category protected area creation	3	3	-
224	Baixão do Coco	Caatinga	Extremely high	No actions recommended by selection workshop	3	-	-
225	Chapada São José - MA/PI	Caatinga	High	Undefined category protected area creation	3	3	-
226	Jucurutu	Caatinga	Very high	Undefined category protected area creation	3	3	-
227	Lagoas do Jacu	Caatinga	Extremely high	Restoration of degraded areas	3	3	
228	Tucuns	Caatinga	Extremely high	No actions recommended by selection workshop	3	3	
229	Santa Cruz	Caatinga	High	Restoration of degraded areas	3	3	
230	Santo Antonio 1	Caatinga	Extremely high	Restoration of degraded areas	3	3	
231	Trussu	Caatinga	High	Creation of Integral Protection protected area	3	3	
232	Lima Campos	Caatinga	Very high	Restoration of degraded areas	3	3	
233	Timbauba	Caatinga	Very high	Restoration of degraded areas	3		
234	Picuí	Caatinga	High	Restoration of degraded areas	3	3	
235	Serra de Luis Gomes	Caatinga	High	Creation of Integral Protection protected area	3	3	
236	Santo Antonio 2	Caatinga	Extremely high	Restoration of degraded areas	3	3	
237	Acari	Caatinga	High	Undefined category protected area creation	3	-	
238	Campestre	Caatinga	Extremely high	No actions recommended by selection workshop	3	3	
239	Japi	Caatinga	Extremely high	No actions recommended by selection workshop	3	3	
240	Parambú/Cococi	Caatinga	High	Creation of Integral Protection protected area	3	3	
241	Rio Canindé	Caatinga	Very high	No actions recommended by selection workshop	3	-	
242	Caico	Caatinga	High	Undefined category protected area creation	3	3	
243	Riacho dos Cavalos	Caatinga	High	Undefined category protected area creation	3	-	
244	Cap. De Campo	Caatinga	Extremely high	No actions recommended by selection workshop	3	-	
245	Serra Negra	Caatinga	High	Undefined category protected area creation	3	3	
246	Serido	Caatinga	High	Environmental Education	3	3	x

247	SEM NOME	Caatinga	Very high	Reforestation	3	3	
248	Serra do Comissário	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
249	Caipu	Caatinga	Very high	No actions recommended by selection workshop	3	3	
250	Açude do Xixa	Caatinga	High	No actions recommended by selection workshop	3	3	
251	Gurgueia	Caatinga	Extremely high	Creation of Integral Protection protected area	3	-	
252	Serra de São José de Espinharas	Caatinga	Extremely high	Restoration of degraded areas	3	-	
253	Serra de Santa Catarina	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
254	São Romão/Cajazeiras	Caatinga	Very high	No actions recommended by selection workshop	3	3	
255	Serra de Santa Luzia	Caatinga	High	Creation of Integral Protection protected area	3	3	
256	Oeiras/Lagoa Tabuleiro	Caatinga	Very high	No actions recommended by selection workshop	3	3	
257	Salitre 1	Caatinga	High	Restoration of degraded areas	3	3	x
258	Parque Poeta	Caatinga	High	Restoration of degraded areas	3	3	x
259	Gurinhém	Caatinga	Extremely high	Undefined category protected area creation	3	3	
260	Pico do Jabre	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	
261	Salitre 2	Caatinga	Very high	Restoration of degraded areas	3	3	x
262	Bonito de Santa Fé/Piranhas	Caatinga	Extremely high	Creation of sustainable use protected areas	3	3	
263	Olho D'Ã¡gua	Caatinga	High	Undefined category protected area creation	3	-	
264	Gesseiro	Caatinga	Extremely high	Restoration of degraded areas	3	3	x
265	Borda do Araripe	Caatinga	High	Restoration of degraded areas	3	3	x
266	Queimadas	Caatinga	Very high	Undefined category protected area creation	3	-	
267	Jatobá	Caatinga	Extremely high	Restoration of degraded areas	3	3	
268	Conceição	Caatinga	Extremely high	Restoration of degraded areas	3	3	
269	Araripina	Caatinga	Very high	Restoration of degraded areas	3	3	x
270	Pau Branco	Caatinga	High	Undefined category protected area creation	3	3	
271	Brejo Santo	Caatinga	Extremely high	Restoration of degraded areas	3	3	x
272	Ipubi-Trindade	Caatinga	Very high	Restoration of degraded areas	3	3	x
273	Monteiro	Caatinga	Very high	Restoration of degraded areas	3	3	
274	Floresta Nacional de Negreiros	Caatinga	High	Strengthen protected area management	3	3	x
275	Pajeú	Caatinga	High	Creation of Integral Protection protected area	3	3	
276	Serra do Capim	Caatinga	High	Undefined category protected area creation	3	3	
277	Rio Itaueira	Caatinga	High	Creation of sustainable use protected areas	3	-	
278	Periperi	Caatinga	High	No actions recommended by selection workshop	3	-	
279	Complexo de Serras Livramento	Caatinga	High	Creation of Integral Protection protected area	3	3	

280	Serras do Almirante e Boqueirão	Caatinga	High	Undefined category protected area creation	3	3	
281	Serra da Capivara	Caatinga	Very high	No actions recommended by selection workshop	3	-	x
282	Serra da Canoa	Caatinga	Very high	Undefined category protected area creation	3	3	x
283	Floresta	Caatinga	High	Undefined category protected area creation	3	3	
284	Caboclo	Caatinga	High	Creation of Integral Protection protected area	3	3	
285	Ibimirim	Caatinga	Very high	No actions recommended by selection workshop	3	3	
286	Serra do Açude Saco II	Caatinga	High	Creation of Integral Protection protected area	3	3	x
287	Lajedo/Cachoeirinha	Caatinga	Extremely high	No actions recommended by selection workshop	3	3	
288	Sertão de Itaparica	Caatinga	Very high	Undefined category protected area creation	3	3	
289	Afluentes do Piauí	Caatinga	High	Restoration of degraded areas	3		
290	Águas Belas	Caatinga	Extremely high	No actions recommended by selection workshop	3	3	
291	Curaça	Caatinga	Very high	Creation of Integral Protection protected area	3	3	x
292	Iati-Santana do Ipanema	Caatinga	Extremely high	Creation of sustainable use protected areas	3	3	x
293	Riacho da Melancia	Caatinga	High	Creation of Integral Protection protected area	3	-	
294	Cajueiro/Guaribas	Caatinga	High	No actions recommended by selection workshop	3	3	
295	Juazeiro	Caatinga	Extremely high	Creation of Integral Protection protected area	3	-	
296	Riacho Terra do Sol	Caatinga	High	Creation of Integral Protection protected area	3	-	x
297	Canions do São Francisco	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
298	Serra da Mão	Caatinga	High	Creation of Integral Protection protected area	3	3	
299	Santa Brígida	Caatinga	High	Creation of sustainable use protected areas	3	3	
300	Porteiras - Serra do Monte Santo	Caatinga	High	Undefined category protected area creation	3	3	
301	Boqueirão da Onça	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	x
302	Pilão Arcado 1	Caatinga	Very high	Biological Inventory	3		x
303	Serra dos Manões	Caatinga	High	Undefined category protected area creation	3	3	
304	Porto da Folha	Caatinga	Very high	Undefined category protected area creation	3	3	
305	Serra da Guia	Caatinga	High	Undefined category protected area creation	3	3	
306	Traipu - São Bras	Caatinga	Very high	Restoration of degraded areas	3	3	
307	Tibiri - Borda da mata	Caatinga	Extremely high	Caatinga sustainable management for livestock	3	3	
308	Sitio do Quinto	Caatinga	Very high	Creation of sustainable use protected areas	3	3	
309	Barra do Riachinho	Caatinga	High	Biological Inventory	3	3	x
310	Serra da Fumaça	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	
311	Coronel João As	Caatinga	Very high	Creation of sustainable use protected areas	3	3	
312	Nossa Senhora Aparecida	Caatinga	High	Restoration of degraded areas	3	3	

313	São Miguel do Aleixo	Caatinga	Extremely high	Undefined category protected area creation	3	3	
314	Serra do Pinhão	Caatinga	Extremely high	Undefined category protected area creation	3	3	
315	Complexo Serra dos Macacos	Caatinga	Very high	Creation of sustainable use protected areas	3	3	
316	Itapicuru	Caatinga	Very high	Restoration of degraded areas	3	3	
317	Cascudo Preto	Caatinga	Very high	Biological Inventory	3	3	
318	Ilha	Caatinga	Very high	Biological Inventory	3	3	
319	Morro do Chapéu	Caatinga	Very high	Creation of sustainable use protected areas	3	3	x
320	Rio Real	Caatinga	Very high	Biological Inventory	3	3	
321	Vereda do Bonito	Caatinga	High	Creation of Integral Protection protected area	3	3	
322	Seabra	Caatinga	Extremely high	Creation of sustainable use protected areas	3	3	
323	Oliveira dos Brejinhos	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
324	Ibotirama	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
325	Brotas de Macaúbas	Caatinga	High	Creation of Integral Protection protected area	3	3	
326	Itaberaba	Caatinga	Extremely high	Creation of sustainable use protected areas	3	3	
327	Ibiquera	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
328	Itaete	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	
329	Marcionílio Souza	Caatinga	Very high	Creation of sustainable use protected areas	3	3	
330	Chapada Diamantina Sul	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	x
331	Floresta Nacional Sincora	Caatinga	Extremely high	Inspection	3	3	x
332	Brumado	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	
333	Tanhaçu	Caatinga	Very high	Restoration of degraded areas	3	3	
334	Manga	Caatinga	Extremely high	Creation of Integral Protection protected area	3	3	x
335	Belo Campo	Caatinga	Very high	Inspection	3	3	
336	Espinosa Norte	Caatinga	Extremely high	Inspection	3	3	
337	Condeuba	Caatinga	Very high	Creation of Integral Protection protected area	3	3	
338	Jaiba	Caatinga	Very high	Restoration of degraded areas	3	3	
339	Aiuaba	Caatinga	Very high	Restoration of degraded areas	3	3	
340	Capivara	Caatinga	Extremely high	Undefined category protected area creation	3	3	
341	Guaraçiaba do Norte	Caatinga	Extremely high	No actions recommended by selection workshop	-	3	
342	Olho D'água	Caatinga	High	Undefined category protected area creation	-	3	
343	Alto Araguaia	Cerrado	Very high	Undefined category protected area creation	1, 3	3	
344	Carste Arcos e Pains	Cerrado	Very high	Restoration of degraded areas	1, 3	3	
345	Almas	Cerrado	Extremely high	Protected Area Creation	3	3	x
346	Alpinopolis	Cerrado	Very high	Restoration of degraded areas	3	3	x
347		Cerrado	Very high	Protected Area Creation	3		

348	Alto Rio Taquari	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	
349	Araguacu	Cerrado	Extremely high	Regularization of degrading activity	3	3	x
350	Araxa	Cerrado	Very high	Regularization of degrading activity	3	3	
351	Barra do Garcas	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
352	Barreirinhas	Cerrado	High	Land use planning	3	3	x
353	Bela Vista	Cerrado	High	Restoration of degraded areas	3	3	x
354	Bonito	Cerrado	High	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	-	
355	Buritizeiro	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
356	Caiaponia	Cerrado	Very high	Protected Area Creation	3	3	
357	Campos Gerais	Cerrado	Very high	Restoration of degraded areas	3	3	
358	Carinhana	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
359		Cerrado	Very high	Restoration of degraded areas	3	-	
360	Cavernas de Candeias	Cerrado	High	Regularization of degrading activity	3	3	
361	Cavernas de Unaí	Cerrado	High	Regularization of degrading activity	3	3	
362	Cavernas Peruacu	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	x
363	Chapada da Contagem	Cerrado	Extremely high	Protected Area Creation	3	3	
364	Conceição do Tocantins	Cerrado	Extremely high	Protected Area Creation	3	3	x
365	Coribe	Cerrado	Very high	Creation of Integral Protection protected area	3	-	
366	Corinto	Cerrado	Very high	Development of financial support mechanisms	3	3	x
367	Córrego Fundo	Cerrado	Very high	Creation of Integral Protection protected area	3	-	
368	Corrego Sítio Felipe	Cerrado	High	Land use planning	3	3	
369	Correntina	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
370	Corumba	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
371	Cotegipe	Cerrado	Very high	Creation of Integral Protection protected area	3	3	x
372	Cristais	Cerrado	Very high	Restoration of degraded areas	3	3	x
373	Cristalina	Cerrado	Extremely high	Regularization of degrading activity	3	3	x
374	Cristopolis	Cerrado	Very high	Creation of Integral Protection protected area	3	-	x
375	Curvelo	Cerrado	Very high	Restoration of degraded areas	3	-	
376	Diamantina	Cerrado	Extremely high	Strengthening the value chains of socio-biodiversity products	3	-	
377	Doverlândia	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
378	Entorno Estação Ecológica Serra Geral do Tocantins	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	

379	Entorno Parque Estadual Serra Dourada	Cerrado	Very high	Restoration of degraded areas	3	3	
380	Entorno Parque Nacional Nascentes do Parnaíba	Cerrado	Extremely high	Protected Area Creation	3	3	
381	Entorno Parque Nacional Serra das Confusoes I	Cerrado	High	Land use planning	3	3	x
382	Entorno Refúgio de Vida Silvestre Veredas	Cerrado	Extremely high	Expansion of protected areas of integral protection	3	3	x
383	Entorno Terra Indígena Areoes III	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	-	
384	Entorno Terra Indígena Bacuruzinho	Cerrado	Extremely high	Protected Area Creation	3	-	x
385	Entorno Terra Indígena Kanela – Terra Indígena Porquinhos	Cerrado	Very high	Land use planning	3	-	
386	Entorno Terra Indígena Kraolandia	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
387	Entorno Terra Indígena Merure	Cerrado	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
388	Entorno Terra Indígena Sangradouro / Volta Grande	Cerrado	Very high	Restoration of degraded areas	3	3	x
389	Entorno Terra Indígena Xerente	Cerrado	Extremely high	Land use planning	3	3	
390	Entrono Parque Nacional Chapada dos Veadeiros	Cerrado	Very high	Regularization of degrading activity	3	3	x
391	Felixlândia	Cerrado	Very high	Creation of sustainable use protected area	3		x
392	Formosa	Cerrado	Very high	Regularization of degrading activity	3	3	
393	Formosa do Rio Preto	Cerrado	Very high	Creation of sustainable use protected area	3	3	x
394	Formoso	Cerrado	Very high	Development of financial support mechanisms	3	3	
395	Furnas	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
396	Ibia	Cerrado	High	Restoration of degraded areas	3	3	

397	Itapetininga	Cerrado	Extremely high	Restoration of degraded areas	3	3	x
398	Itarare	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
399	Itirapina	Cerrado	High	Restoration of degraded areas	3	3	x
400	Iuiu	Cerrado	Very high	Regularization of degrading activity	3	3	x
401	Jaborandi	Cerrado	Very high	Creation of Integral Protection protected area	3	3	x
402	Jacuba - Corrente	Cerrado	Very high	Restoration of degraded areas	3	-	
403		Cerrado	Very high	Restoration of degraded areas	3	-	
404	Jataí	Cerrado	Very high	Restoration of degraded areas	3	3	x
405	Jequitaí	Cerrado	Very high	Creation of Integral Protection protected area	3	3	x
406	João Pinheiro	Cerrado	High	Restoration of degraded areas	3	3	x
407	Lagoa do Tocantins	Cerrado	Very high	Land use planning	3	3	x
408	Lagoas do Rio São Francisco	Cerrado	Very high	Creation of Integral Protection protected area	3	3	x
409	Lajeado	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	x
410	Lizarda	Cerrado	Extremely high	Protected Area Creation	3	3	
411	Mambai	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
412	Matoes	Cerrado	High	Land use planning	3	3	
413	Muquem de São Francisco	Cerrado	High	Restoration of degraded areas	3	3	
414	Nascente Urucui	Cerrado	Extremely high	Creation of sustainable use protected area	3	3	x
415	Nascentes do Rio Paraguai	Cerrado	Extremely high	Restoration of degraded areas	3	3	
416	Nioaque	Cerrado	Extremely high	Protected Area Creation	3	3	x
417	Niquelandia	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
418	Nova Xavantina	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
419	Pandeiros Concha e Gibão	Cerrado	Extremely high	Protected Area Extension	3	3	
420	Pedregulho	Cerrado	Very high	Restoration of degraded areas	3		
421	Peruaçu	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
422	Piranhas	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
423	Pirenópolis	Cerrado	Extremely high	Protected Area Creation	3	3	
424	Porto Nacional	Cerrado	High	Regularization of degrading activity	3	3	
425	Pouso Alto	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	

426	Riacho do Bano	Cerrado	Very high	Restoration of degraded areas	3	3	x
427	Riacho do Ramalho	Cerrado	Very high	Creation of Integral Protection protected area	3	3	x
428	Riacho dos Machados	Cerrado	Very high	Creation of sustainable use protected area	3	3	
429	Riacho Pedra-Branca	Cerrado	High	Creation of Integral Protection protected area	3	3	
430	Riacho Tucum	Cerrado	High	Implementation of Rural Environmental Registry	3	3	x
431	Ribeirao Aquidauana	Cerrado	Extremely high	Restoration of degraded areas	3	3	
432	Ribeirao Barreiro	Cerrado	Very high	Fomento ao uso sustentavel	3		
433	Ribeirao Cachoeira	Cerrado	Extremely high	Restoration of degraded areas	3		
434	Ribeirao Mutum	Cerrado	Very high	Restoration of degraded areas	3		
435	Ribeirao Ponte de Pedra	Cerrado	Extremely high	Restoration of degraded areas	3	3	
436	Ribeirao Serrote	Cerrado	Very high	Restoration of degraded areas	3	3	x
437	Ribeirao Ticororo	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
438	Rio Apa	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	x
439	Rio Aquidaba	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	
440	Rio Areial	Cerrado	Extremely high	Restoration of degraded areas	3	3	
441	Rio Arica-Acu	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
442	Rio Arinos	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	x
443	Rio Arrojado	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
444	Rio Caracol	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
445	Rio Corrente	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
446	Rio Correntes	Cerrado	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	
447	Rio Corumba	Cerrado	Extremely high	Strengthening the value chains of socio-biodiversity products	3	3	
448	Rio Coxim	Cerrado	High	Restoration of degraded areas	3	3	x
449	Rio Coxipo	Cerrado	Very high	Restoration of degraded areas	3	3	x
450	Rio Cristalino	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
451	Rio da Prata	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
452	Rio Galhão	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	
453	Rio Miranda	Cerrado	Very high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	

454	Rio Miranda - Pantanal	Cerrado	Extremely high	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	
455	Rio Parnaiba - Balsas	Cerrado	High	Land use planning	3	3	
456	Rio Parnaiba II	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	
457	Rio Perdido	Cerrado	Very high	Restoration of degraded areas	3	3	
458	Rio Pindaiba	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
459	Rio Piraim	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
460	Rio Ponte Alta	Cerrado	Extremely high	Protected Area Creation	3	3	x
461	Rio Ponte de Pedra	Cerrado	Extremely high	Restoration of degraded areas	3	3	
462	Rio Santa Tereza	Cerrado	High	Land use planning	3	3	x
463	Rio São Domingos	Cerrado	Very high	Restoration of degraded areas	3	3	x
464	Rio São Lourenco	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
465	Rio São Marcos	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	
466	Rio São Valerio	Cerrado	High	Strengthening the value chains of socio-biodiversity products	3	3	x
467	Rio Sapão	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
468	Rio Sapucaí	Cerrado	High	Restoration of degraded areas	3	3	x
469	Rio Sono	Cerrado	Very high	Land use planning	3	3	
470	Rio Sucuriiju	Cerrado	Extremely high	Protected Area Creation	3	3	
471	Rio Taboco	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
472	Rio Taquari	Cerrado	Extremely high	Restoration of degraded areas	3	3	
473	Rio Taruma	Cerrado	High	Creation of sustainable use protected area and integral protection	3	3	
474	Rio Trairas	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	x
475	Rio Turvo - GO	Cerrado	Very high	Restoration of degraded areas	3	3	
476	Rio Turvo - SP	Cerrado	High	Restoration of degraded areas	3	3	
477	Rio Urucui-Vermelho	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
478	Rio Urucuia	Cerrado	Very high	Protected Area Creation	3	3	
479	Rio Verde	Cerrado	Extremely high	Strengthening the value chains of socio-biodiversity products	3	3	
480	Riozinho	Cerrado	Extremely high	Protected Area Creation	3		
481	Santa Cruz de Goiás	Cerrado	Very high	Restoration of degraded areas	3	3	
482	Santa Maria da Vitoria	Cerrado	High	Regularization of degrading activity	3	3	
483	Santuário São Miguel	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
484	São Bartolomeu	Cerrado	High	Restoration of degraded areas	3	3	
485	São Desiderio	Cerrado	Very high	Creation of Integral Protection protected area	3	3	

486	São Domingos	Cerrado	High	Integrated and participatory management of protected areas, ecological corridors and territories of traditional peoples and communities	3	3	
487	São José dos Dourados	Cerrado	High	Restoration of degraded areas	3	3	x
488	São Pedro	Cerrado	High	Protected Area Extension	3	3	x
489	São Romão	Cerrado	Very high	Regularization of degrading activity	3	3	x
490	Serra da Prata	Cerrado	Very high	Protected Area Creation	3	3	
491	Serra de Caldas	Cerrado	Extremely high	Protected Area Creation	3	3	
492	Serra de São Bartolomeu	Cerrado	Very high	Strengthening the value chains of socio-biodiversity products	3	3	
493	Serra do Cabral	Cerrado	Extremely high	Creation of Integral Protection protected area	3	3	
494	Serranópolis	Cerrado	Very high	Restoration of degraded areas	3	3	
495	Tapira	Cerrado	High	Creation of Integral Protection protected area	3	3	x
496	Três Lagoas	Cerrado	Extremely high	Restoration of degraded areas	3	3	x
497	Unaí	Cerrado	Very high	Restoration of degraded areas	3	3	
498	Unaí II	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
499	Uruaçu	Cerrado	Very high	Restoration of degraded areas	3	3	x
500	Vazante Riozinho	Cerrado	Very high	Creation of Integral Protection protected area	3	3	
501	Felixlandia	Cerrado	Very high	Creation of sustainable use protected	-	3	x
502	Peruaçu	Cerrado	Extremely high	Creation of Integral Protection protected area	-	3	

APÊNDICE H - LIST OF PROTECTED AREAS THAT CURRENTLY EXIST IN AREAS PREDICTED BY OUR DISTRIBUTION MODELS AS SUITABLE FOR THE FUTURE OCCURRENCE OF (1) *ALOUATTA BELZEBUL*, (2) *SAPAJUS FLAVIUS*, AND (3) *SAPAJUS LIBIDINOSUS*.

We considered the presence of protected areas in a moderate and severe future scenario. We also identified protected areas located in human settlements, which we marked with "x".

N	Protected areas	Category	Brazilian State	Future climate suitability		Located in human settlements
				Moderate	Severe	
1	Reserva Particular do Patrimônio Natural Cachoeira	Sustainable use	Alagoas	1	1	-
2	Reserva Particular do Patrimônio Natural Santa Fé	Sustainable use	Alagoas	1	1	-
3	Reserva Particular do Patrimônio Natural Mata do Cedro	Sustainable use	Alagoas	1	1	-
4	Reserva Particular do Patrimônio Natural Salvador Lyra	Sustainable use	Alagoas	1	1	-
5	Reserva Particular do Patrimônio Natural Quebra Carro	Sustainable use	Alagoas	1	1	-
6	Reserva Particular do Patrimônio Natural Saint Michel 2	Sustainable use	Alagoas	1	1	-
7	Área de Proteção Ambiental Da Marituba do Peixe	Sustainable use	Alagoas	1	1	X
8	Reserva Particular do Patrimônio Natural Saint Michel 1	Sustainable use	Alagoas	1	1	-
9	Área de Proteção Ambiental de Santa Rita	Sustainable use	Alagoas	1	-	X
10	Reserva Particular do Patrimônio Natural Saint Michel 3	Sustainable use	Alagoas	1	1	-
11	Reserva Particular do Patrimônio Natural Madeiras	Sustainable use	Alagoas	1	1	-
12	Área de Proteção Ambiental de Muricí	Sustainable use	Alagoas	1	1	-
13	Reserva Extrativista Marinha da Lagoa do Jequiá	Sustainable use	Alagoas	1	1	-
14	Área de Proteção Ambiental de Piaçabuçu	Sustainable use	Alagoas	3	1, 3	-
15	Reserva Particular do Patrimônio Natural Cachoeira	Sustainable use	Alagoas	3	3	-
16	Área de Proteção Ambiental da Marituba do Peixe	Sustainable use	Alagoas	3	3	-
17	Reserva Particular do Patrimônio Natural Jader Ferreira Ramos	Sustainable use	Alagoas	3	3	-
18	Reserva Particular do Patrimônio Natural Madeiras	Sustainable use	Alagoas	3	3	-
19	Estação Ecológica de Murici	Integral protection	Alagoas	1	1	X
20	Refúgio de Vida Silvestre dos Morros do Caraunã e do Padre	Integral protection	Alagoas	3	3	-

21	Floresta Estadual do Amapá	Sustainable use	Amapá	1	1	-
22	Reserva de Desenvolvimento Sustentável do Rio Iratapuru	Sustainable use	Amapá	1	-	-
23	Floresta Nacional do Amapá	Sustainable use	Amapá	1	-	-
24	Reserva Biológica do Lago Piratuba	Integral protection	Amapá	1	-	-
25	Parque Nacional do Cabo Orange	Integral protection	Amapá	1	-	-
26	Parque Nacional Montanhas do Tumucumaque	Integral protection	Amapá	1	1	-
27	Estação Ecológica de Maracá-Jipioca	Integral protection	Amapá	1	-	-
28	Reserva Particular do Patrimônio Natural do Jequitibá	Sustainable use	Bahia	1, 2	1, 2	-
29	Área de Proteção Ambiental Plataforma continental do Litoral Norte	Sustainable use	Bahia	1	1	-
30	Área de Proteção Ambiental Bacia do Rio de Janeiro	Sustainable use	Bahia	1	-	X
31	Área de Proteção Ambiental Lagoas de Guarajuba	Sustainable use	Bahia	1	1	X
32	Área de Proteção Ambiental Baía de Todos os Santos	Sustainable use	Bahia	1	1	X
33	Área de Proteção Ambiental Bacia do Cobre/São Bartolomeu	Sustainable use	Bahia	1, 3	1, 3	X
34	Área de Proteção Ambiental Marimbus / Iraquara	Sustainable use	Bahia	1	-	-
35	Reserva Particular do Patrimônio Natural Limoeiro	Sustainable use	Bahia	2	-	-
36	Área de Proteção Ambiental Caminhos ecológicos da Boa Esperança	Sustainable use	Bahia	2	2	-
37	Reserva Extrativista Marinha da Baia do Iguapé	Sustainable use	Bahia	1	1	-
38	Área de Proteção Ambiental Lagoa de Itaparica	Sustainable use	Bahia	3	3	-
39	Área de Proteção Ambiental Serra do Barbado	Sustainable use	Bahia	3	3	-
40	Área de Proteção Ambiental de São Desidério	Sustainable use	Bahia	3	3	-
41	Área de Proteção Ambiental Bacia do Rio de Janeiro	Sustainable use	Bahia	3	3	-
42	Área de Proteção Ambiental Serra Branca / Raso da Catarina	Sustainable use	Bahia	3	3	-
43	Área de Proteção Ambiental Lago de Sobradinho	Sustainable use	Bahia	3	3	-
44	Área de Proteção Ambiental Do Rio Preto	Sustainable use	Bahia	3	3	X
45	Área de Proteção Ambiental Dunas e Veredas do Baixo Médio São Francisco	Sustainable use	Bahia	3	3	X
46	Área de Proteção Ambiental Marimbus / Iraquara	Sustainable use	Bahia	3	3	X
47	Monumento Natural dos Canions do Subaé	Integral protection	Bahia	2	-	-

48	Parque Nacional da Chapada da Diamantina	Integral protection	Bahia	1, 3	3	-
49	Parque Estadual da Serra dos Montes Altos	Integral protection	Bahia	3	3	-
50	Estação Ecológica do Rio Preto	Integral protection	Bahia	3	3	-
51	Refúgio de Vida Silvestre da Serra dos Montes Altos	Integral protection	Bahia	3	3	
52	Parque Estadual das Sete Passagens	Integral protection	Bahia	3	3	-
53	Parque Estadual do Morro do Chapéu	Integral protection	Bahia	3	3	-
54	Refúgio de Vida Silvestre das Veredas do Oeste Baiano	Integral protection	Bahia	3	3	-
55	Parque Nacional do Boqueirão da Onça	Integral protection	Bahia	3	3	-
56	Refúgio de Vida Silvestre da Ararinha Azul	Integral protection	Bahia	3	3	-
57	Floresta Nacionalcontendas do Sincorá	Sustainable use	Bahia	3	3	-
58	Floresta Nacional de Cristópolis	Sustainable use	Bahia	3	3	-
59	Área de Proteção Ambiental do Boqueirão da Onça	Sustainable use	Bahia	3	3	-
60	Área de Proteção Ambiental da Ararinha Azul	Sustainable use	Bahia	3	3	-
61	Parque Natural Municipal da Macaqueiras	Integral protection	Bahia	3	3	-
62	Área de Proteção Ambiental das Nascentes do Rio Vermelho	Sustainable use	Bahia/ Goiás	3	3	-
63	Parque Nacional Grande Sertão Veredas	Integral protection	Bahia/ Minas Gerais	3	3	-
64	Estação Ecológica Serra Geral do Tocantins	Integral protection	Bahia/Tocantins	3	3	-
65	Área de Proteção Ambiental do Estuário do Rio Ceará - Rio Maranguapinho	Sustainable use	Ceará	1	-	X
66	Área de Proteção Ambiental da Serra da Aratanha	Sustainable use	Ceará	1, 2	1, 2	-
67	Área de Relevante Interesse Ecológico do Sítio Curió	Sustainable use	Ceará	1	-	X
68	Área de Relevante Interesse Ecológico do Cambeba	Sustainable use	Ceará	1	-	X
69	Área de Proteção Ambiental do Rio Pacoti	Sustainable use	Ceará	1	-	-
70	Área de Proteção Ambiental da Bica do Ipú	Sustainable use	Ceará	1	-	X
71	Área de Proteção Ambiental da Serra do Baturité	Sustainable use	Ceará	1	1, 2	-
72	Floresta Nacional do Araripe-Apodi	Sustainable use	Ceará	1, 2, 3	-	-
73	Reserva Extrativista do Batoque	Sustainable use	Ceará	1	-	-
74	Área de Proteção Ambiental Serra da Meruoca	Sustainable use	Ceará	1, 3	3	-
75	Área de Proteção Ambiental da Serra da Aratanha	Sustainable use	Ceará	3	3	-

76	Área de Relevante Interesse Ecológico das Águas Emendadas dos Inhamuns	Sustainable use	Ceará	3	3	-
77	Área de Proteção Ambiental do Rio Pacoti	Sustainable use	Ceará	3	-	-
78	Área de Proteção Ambiental da Bica do Ipú	Sustainable use	Ceará	3	3	-
79	Área de Proteção Ambiental da Serra de Baturité	Sustainable use	Ceará	3	3	-
80	Parque Natural Municipal das Dunas da Sabiaguaba	Integral protection	Ceará	1	-	X
81	Parque Estadual das Carnaúbas	Integral protection	Ceará	3	3	-
82	Monumento Natural Sítio Cana Brava	Integral protection	Ceará	3	3	-
83	Parque Estadual Sítio Fundão	Integral protection	Ceará	3	3	-
84	Monumento Natural Sítio Riacho do Meio	Integral protection	Ceará	3	3	-
85	Parque Estadual do Cocó	Integral protection	Ceará	3	-	X
86	Estação Ecológica do Castanhão	Integral protection	Ceará	3	3	-
87	Parque Nacional de Ubajara	Integral protection	Ceará	3	3	-
88	Área de Proteção Ambiental do Lago Paranoá	Sustainable use	Distrito Federal	3	3	-
89	Área de Relevante Interesse Ecológico Cruls	Sustainable use	Distrito Federal	3	3	-
90	Área de Relevante Interesse Ecológico da Granja do Ipê	Sustainable use	Distrito Federal	3	3	-
91	Área de Relevante Interesse Ecológico do Torto	Sustainable use	Distrito Federal	3	3	-
92	Área de Relevante Interesse Ecológico do Córrego Cabeceira do Valo	Sustainable use	Distrito Federal	3	3	-
93	Área de Relevante Interesse Ecológico do Córrego Mato Grande	Sustainable use	Distrito Federal	3	3	-
94	Área de Relevante Interesse Ecológico Parque JK	Sustainable use	Distrito Federal	3	3	-
95	Área de Proteção Ambiental da Bacia dos Ribeirões do Gama e Cabeça de Veado	Sustainable use	Distrito Federal	3	3	-
96	Área de Relevante Interesse Ecológico da Vila Estrutural	Sustainable use	Distrito Federal	3	3	-
97	Área de Relevante Interesse Ecológico Dom Bosco	Sustainable use	Distrito Federal	3	3	-
98	Área de Proteção Ambiental de Cafuringa	Sustainable use	Distrito Federal	3	3	X
99	Área de Relevante Interesse Ecológico Santuário de Vida Silvestre do Riacho Fundo	Sustainable use	Distrito Federal	3	3	-
100	Área de Relevante Interesse Ecológico do Bosque	Sustainable use	Distrito Federal	3	3	-
101	Área de Relevante Interesse Ecológico Paranoá Sul	Sustainable use	Distrito Federal	3	3	-

102	Reserva Biológica do Cerradão	Sustainable use	Distrito Federal	3	3	-
103	Parque Distrital Salto do Tororó	Integral protection	Distrito Federal	3	3	-
104	Reserva Biológica do Guará	Integral protection	Distrito Federal	3	3	-
105	Reserva Biológica do Rio Descoberto	Integral protection	Distrito Federal	3	3	-
106	Refúgio de Vida Silvestre da Mata Seca	Integral protection	Distrito Federal	3	3	-
107	Estação Ecológica de Águas Emendadas	Integral protection	Distrito Federal	3	3	-
108	Monumento Natural do Conjunto Espeleológico do Morro da Pedreira	Integral protection	Distrito Federal	3	3	-
109	Reserva Biológica do Gama	Integral protection	Distrito Federal	3	3	-
110	Estação Ecológica do Jardim Botânico	Integral protection	Distrito Federal	3	3	X
111	Parque Nacional de Brasília	Integral protection	Distrito Federal	3	3	X
112	Reserva Biológica da Contagem	Integral protection	Distrito Federal	3	3	-
113	Área de Relevante Interesse Ecológico Capetinga - Taquara	Sustainable use	Distrito Federal	3	3	-
114	Área de Relevante Interesse Ecológico Floresta da Cicuta	Sustainable use	Distrito Federal	3	3	-
115	Floresta Nacionalde Brasília	Sustainable use	Distrito Federal	3	3	-
116	Monumento Natural Estadual Serra das Torres	Integral protection	Espírito Santo	3	3	-
117	Monumento Natural dos Pontões Capixabas	Integral protection	Espírito Santo	3	3	-
118	Área de Proteção Ambiental João Leite	Sustainable use	Goiás	3	3	X
119	Área de Proteção Ambiental dos Pireneus	Sustainable use	Goiás	3	3	X
120	Área de Proteção Ambiental Serra da Jibóia	Sustainable use	Goiás	3	3	-
121	Área de Relevante Interesse Ecológico Águas de São João	Sustainable use	Goiás	3	-	-
122	Área de Proteção Ambiental da Serra das Galés da Portaria	Sustainable use	Goiás	3	3	-
123	Área de Proteção Ambiental do Encantado	Sustainable use	Goiás	3	3	-
124	Área de Proteção Ambiental Pouso Alto	Sustainable use	Goiás	3	3	X
125	Área de Proteção Ambiental da Serra Dourada	Sustainable use	Goiás	3	3	X
126	Área de Proteção Ambiental Serra Geral de GoIás	Sustainable use	Goiás	3	3	-
127	Parque Estadual do Descoberto	Integral protection	Goiás	3	3	X
128	Parque Estadual dos Pirineus	Integral protection	Goiás	3	3	-
129	Parque Estadual de Paraúna	Integral protection	Goiás	3	3	-

130	Parque Estadual Altamiro de Moura Pacheco	Integral protection	Goiás	3	3	-
131	Parque Estadual da Serra Dourada	Integral protection	Goiás	3	3	-
132	Parque Estadual da Serra de Caldas Novas	Integral protection	Goiás	3	3	X
133	Parque Estadual da Mata Atlântica	Integral protection	Goiás	3	3	-
134	Parque Estadual de Terra Ronca	Integral protection	Goiás	3	3	-
135	Parque Nacional da Chapada dos Veadeiros	Integral protection	Goiás	3	-	-
136	Reserva Extrativista de Recanto das Araras de Terra Ronca	Sustainable use	Goiás	3	3	-
137	Floresta Nacional da Mata Grande	Sustainable use	Goiás	3	-	-
138	Floresta Nacional de Silvânia	Sustainable use	Goiás	3	3	-
139	Reserva Extrativista Lago do Cedro	Sustainable use	Goiás	3	-	-
140	Parque Natural Municipal das Orquídeas José Pinheiro de Souza	Integral protection	Goiás	3	3	-
141	Parque Natural Municipal Ribeirão da Prata	Integral protection	Goiás	3	3	-
142	Parque Natural Municipal Eli Bastos	Integral protection	Goiás	3	3	-
143	Parque Natural Municipal do Setor Santa Cruz	Integral protection	Goiás	3	3	X
144	Área de Proteção Ambiental da Bacia do Corrego Capao Grande	Sustainable use	Goiás	3	3	-
145	Área de Relevante Interesse Ecológico da Cabeceira do Córrego Mahana	Sustainable use	Goiás	3	3	-
146	Área de Perservação Ambiental do Córrego da Lagoa	Sustainable use	Goiás	3	3	-
147	Área de Proteção Ambiental do Limoeiro	Sustainable use	Goiás	3	3	-
148	Área de Relevante Interesse Ecológico Serra Bonita de Adelandia	Sustainable use	Goiás	3	3	-
149	Área de relevante interesse Ecológico Mata das Perobas Tim Ferreira	Sustainable use	Goiás	3	-	-
150	Área de Proteção Ambiental do Planalto Central	Sustainable use	Goiás/ Distrito Federal	3	3	X
151	Área de Proteção Ambiental da Bacia do Rio Descoberto	Sustainable use	Goiás/ Distrito Federal	3	3	X
152	Área de Proteção Ambiental das Reentrâncias Maranhenses	Sustainable use	Maranhão	1, 3	-	X
153	Reserva Biológica do Gurupi	Integral protection	Maranhão	1	-	-
154	Parque Nacional da Chapada das Mesas	Integral protection	Maranhão	3	3	-
155	Parque Nacional das Nascentes do Rio Parnaíba	Integral protection	Maranhão / Piauí/ Bahia	3	-	-

156	Área de Proteção Ambiental Serra da Tabatinga	Sustainable use	Maranhão/ Piauí	3	3	-
157	Área de Proteção Ambiental Nascentes do Rio Paraguai	Sustainable use	Mato Grosso	3	3	-
158	Área de Proteção Ambiental do Salto Magessi	Sustainable use	Mato Grosso	3	-	-
159	Área de Proteção Ambiental da Chapada dos Guimarães	Sustainable use	Mato Grosso	3	3	-
160	Área de Proteção Ambiental das Cabeceiras do Rio Cuiabá	Sustainable use	Mato Grosso	3	3	-
161	Parque Estadual do Xingu	Integral protection	Mato Grosso	3	-	-
162	Monumento Natural Morro de Santo Antônio	Integral protection	Mato Grosso	3	3	-
163	Parque Estadual Serra Azul	Integral protection	Mato Grosso	3	3	X
164	Reserva Biológica Culuene	Integral protection	Mato Grosso	3	3	-
165	Estação Ecológica do Rio Ronuro	Integral protection	Mato Grosso	3	3	-
166	Parque Estadual Águas do Cuiabá	Integral protection	Mato Grosso	3	3	-
167	Parque Estadual de Águas Quentes	Integral protection	Mato Grosso	3	3	-
168	Estação Ecológica da Serra das Araras	Integral protection	Mato Grosso	3	3	-
169	Parque Nacional da Chapada dos Guimarães	Integral protection	Mato Grosso	3	3	-
170	Área de Proteção Ambiental Municipal do Aricá-Açu	Sustainable use	Mato Grosso	3	3	-
171	Parque Natural Municipal de Piraputangas	Integral protection	Mato Grosso do Sul	3	3	-
172	Área de Proteção Ambiental Fernão Dias	Sustainable use	Minas Gerais	3	3	X
173	Reserva de desenvolvimento Sustentável Veredas do Acari	Sustainable use	Minas Gerais	3	3	-
174	Área de Proteção Ambiental Águas Vertentes	Sustainable use	Minas Gerais	3	3	-
175	Área de Proteção Ambiental da Bacia Hidrográfica do Rio Machado	Sustainable use	Minas Gerais	3	3	-
176	Área de Proteção Ambiental Sul-RMBH	Sustainable use	Minas Gerais	3	3	-
177	Área de Proteção Ambiental Serra São José	Sustainable use	Minas Gerais	3	3	-
178	Área de Proteção Ambiental do Alto do Mucuri	Sustainable use	Minas Gerais	3	3	-
179	Área de Proteção Ambiental Bacia do Rio Pandeiros	Sustainable use	Minas Gerais	3	3	-
180	Reserva Particular do Patrimônio Natural Ecocerrado Brasil	Sustainable use	Minas Gerais	3	3	-
181	Área de Proteção Ambiental Cachoeira das Andorinhas	Sustainable use	Minas Gerais	3	3	-
182	Área de Proteção Ambiental Serra do Sabonetal	Sustainable use	Minas Gerais	3	3	-
183	Reserva Particular do Patrimônio Natural Gruta do Carimbado	Sustainable use	Minas Gerais	3	3	X

184	Área de Proteção Ambiental Cochá e Gibão	Sustainable use	Minas Gerais	3	3	-
185	Parque Estadual Nova Baden	Integral protection	Minas Gerais	3	3	-
186	Parque Estadual Caminho dos Gerais	Integral protection	Minas Gerais	3	3	-
187	Parque Estadual Serra Negra	Integral protection	Minas Gerais	3	3	-
188	Parque Estadual do Itacolomi	Integral protection	Minas Gerais	3	3	-
189	Monumento Natural Estadual Pico do Ibituruna	Integral protection	Minas Gerais	3	3	-
190	Parque Estadual Serra da Boa Esperança	Integral protection	Minas Gerais	3	3	-
191	Parque Estadual Mata Seca	Integral protection	Minas Gerais	3	3	-
192	Parque Estadual do Limoeiro	Integral protection	Minas Gerais	3	3	-
193	Parque Estadual Rio Corrente	Integral protection	Minas Gerais	-	3	-
194	Monumento Natural Estadual Várzea do Lageado e Serra do Raio	Integral protection	Minas Gerais	3	3	-
195	Parque estadual Rio Preto	Integral protection	Minas Gerais	3	3	-
196	Parque Estadual Verde Grande	Integral protection	Minas Gerais	3	3	-
197	Parque Estadual Biribiri	Integral protection	Minas Gerais	3	3	X
198	Parque Estadual Serra do Intendente	Integral protection	Minas Gerais	3	3	-
199	Refúgio Estadual de Vida Silvestre Libélulas da Serra de São José	Integral protection	Minas Gerais	3	3	-
200	Parque Estadual Grão Mogol	Integral protection	Minas Gerais	3	3	-
201	Parque Estadual Sete Salões	Integral protection	Minas Gerais	3	3	-
202	Parque Estadual da Serra do Cabral	Integral protection	Minas Gerais	3	3	-
203	Estação Ecológica de Sagarana	Integral protection	Minas Gerais	3	3	-
204	Parque Estadual de Montezuma	Integral protection	Minas Gerais	3	3	-
205	Estação Ecológica de Acauã	Integral protection	Minas Gerais	3	3	-
206	Parque Estadual Pico do Itambé	Integral protection	Minas Gerais	3	3	-
207	Parque Estadual Pau Furado	Integral protection	Minas Gerais	3	3	-
208	Parque Estadual Lagoa do Cajueiro	Integral protection	Minas Gerais	3	3	-
209	Parque Estadual Serra Nova	Integral protection	Minas Gerais	3	3	-
210	Parque Estadual Serra das Araras	Integral protection	Minas Gerais	3	3	-

211	Parque Nacional Cavernas do Peruaçu	Integral protection	Minas Gerais	3	3	-
212	Parque Nacional das Sempre-vivas	Integral protection	Minas Gerais	3	3	-
213	Estação Ecológica de Pirapitinga	Integral protection	Minas Gerais	3	3	-
214	Parque Nacional da Serra do Cipó	Integral protection	Minas Gerais	3	3	-
215	Parque Nacional da Serra do Gandarela	Integral protection	Minas Gerais	3	3	-
216	Reserva Biológica da Mata Escura	Integral protection	Minas Gerais	3	3	-
217	Parque Nacional da Serra da Canastra	Integral protection	Minas Gerais	3	3	-
218	Área de Proteção Ambiental Cavernas do Peruaçu	Sustainable use	Minas Gerais	3	3	-
219	Área de Proteção Ambiental da Pedreira	Sustainable use	Minas Gerais	3	3	-
220	Reserva de Desenvolvimento Sustentável Nascentes Geraizeiras	Sustainable use	Minas Gerais	3	3	-
221	Reserva Biológica da Serra de Santa Rita Mitzi Brandão	Integral protection	Minas Gerais	3	3	-
222	Parque Natural Municipal da Serra de São Domingos	Integral protection	Minas Gerais	3	3	X
223	Parque Natural Municipal do Tabuleiro	Integral protection	Minas Gerais	3	3	-
224	Parque Natural Municipal da Lajinha	Integral protection	Minas Gerais	3	3	X
225	Parque Natural Municipal Elci Rolla Guerra	Integral protection	Minas Gerais	3	-	-
226	Área de Proteção Ambiental do Boqueirão da Mira	Sustainable use	Minas Gerais	3	3	-
227	Área de Proteção Ambiental Serra do Timóteo	Sustainable use	Minas Gerais	3	3	X
228	Área de Proteção Ambiental Uruana de Minas	Sustainable use	Minas Gerais	3	3	-
229	Área de Proteção Ambiental do Itacuru	Sustainable use	Minas Gerais	3	3	-
230	Área de Proteção Ambiental Córrego da Mata	Sustainable use	Minas Gerais	3	3	-
231	Reserva Biológica Municipal da Mata do Bispo	Integral protection	Minas Gerais	-	3	-
232	Parque Nacional de Itatiaia	Integral protection	Minas Gerais / Rio de Janeiro	3	3	-
233	Área de Proteção Ambiental Bacia do Paraíba do Sul	Sustainable use	Minas Gerais/ Rio de Janeiro/ São Paulo	3	3	-
234	Área de Proteção Ambiental da Serra da Mantiqueira	Sustainable use	Minas Gerais/Rio de Janeiro/ São Paulo	3	3	-
235	Floresta Estadual de Iriri	Sustainable use	Pará	1	-	-
236	Floresta Estadual do Trombetas	Sustainable use	Pará	1	-	-

237	Área de Proteção Ambiental Triunfo do Xingú	Sustainable use	Pará	1		-
238	Área de Proteção Ambiental de São Geraldo do Araguaia	Sustainable use	Pará	1	-	-
239	Floresta Estadual do Paru	Sustainable use	Pará	1	1	-
240	Área de Proteção Ambiental do Igarapé Gelado	Sustainable use	Pará	1	-	-
241	Floresta Nacional de Mulata	Sustainable use	Pará	1	1	-
242	Reserva Extrativista Marinha de Tracuateua	Sustainable use	Pará	1	-	-
243	Reserva Extrativista Marinha de Gurupi-Piriá	Sustainable use	Pará	1, 3	-	-
244	Floresta Nacional do Tapirapéaquiri	Sustainable use	Pará	1	-	-
245	Floresta Nacional do Itacaiunas	Sustainable use	Pará	1	-	-
246	Reserva Extrativista Rio Xingú	Sustainable use	Pará	1	-	-
247	Floresta Nacional de Altamira	Sustainable use	Pará	1	-	-
248	Reserva Extrativista Marinha de Caeté-Taperaçu	Sustainable use	Pará	1, 3	-	-
249	Reserva Extrativista Tapajós-Arapiuns	Sustainable use	Pará	1	-	-
250	Floresta Nacional do Tapajós	Sustainable use	Pará	1	-	-
251	Floresta Nacional de Carajás	Sustainable use	Pará	1, 3	3	-
252	Reserva Extrativista Riozinho do Anfrísio	Sustainable use	Pará	1	-	-
253	Reserva Extrativista Rio Iriri	Sustainable use	Pará	1	-	-
254	Área de Proteção Ambiental de Alter do Chão	Sustainable use	Pará	-	1	-
255	Área de Proteção Ambiental da Serra do Saubal	Sustainable use	Pará	-	1	-
256	Área de Proteção Ambiental de São Geraldo do Araguaia	Sustainable use	Pará	3	-	-
257	Reserva Biológica do Tapirapé	Integral protection	Pará	1	-	-
258	Estação Ecológica da Terra do Meio	Integral protection	Pará	1	1	-
259	Parque Nacional da Serra do Pardo	Integral protection	Pará	1	-	-
260	Parque Nacional dos Campos Ferruginosos	Integral protection	Pará	1, 3	3	-
261	Parque Nacional do Jamanxim	Integral protection	Pará	1	-	-
262	Parque Natural Municipal Veredas dos Carajás	Integral protection	Pará	1	-	-
263	Parque Estadual da Serra dos Martírios / Andorinhas	Integral protection	Pará	3	-	-
264	Reserva Extrativista Marinha de Araí• -Peroba	Sustainable use	Pará	3	-	X

265	Estação Ecológica do Jari	Integral protection	Pará / Amapá	1	1	-
266	Área de Proteção Ambiental Roncador	Sustainable use	Paraíba	2	-	-
267	Área de Proteção Ambiental da Barra do rio Mamanguape	Sustainable use	Paraíba	1, 2	1, 2	X
268	Área de Relevante Interesse Ecológico Manguezais da Foz do rio Mamanguape	Sustainable use	Paraíba	1, 2	1, 2	-
269	Área de Relevante Interesse Ecológico da Barra do Rio Camaratuba	Sustainable use	Paraíba	2	1	-
270	Floresta Nacional da Restinga de Cabedelo	Sustainable use	Paraíba	1	1	X
271	Refúgio de Vida Silvestre Mata do Buraquinho	Integral protection	Paraíba	2	-	X
272	Parque Estadual Pico de Jabre	Integral protection	Paraíba	-	2	-
273	Reserva Biológica Guaribas	Integral protection	Paraíba	1, 2,3	1	-
274	Parque Estadual do Poeta e Repentista Juvenal de Oliveira	Integral protection	Paraíba	3	3	-
275	Reserva Extrativista Acaú-Goiana	Sustainable use	Paraíba / Pernambuco	1,2	1, 2	-
276	Área de Proteção Ambiental Aldeia-Beberibe	Sustainable use	Pernambuco	1, 2	1, 2	X
277	Área de Proteção Ambiental de Guadalupe	Sustainable use	Pernambuco	1, 2	1	X
278	Área de Relevante Interesse Ecológico Ipojuca-Merepe	Sustainable use	Pernambuco	1	-	-
279	Área de Proteção Ambiental de Santa Cruz	Sustainable use	Pernambuco	1, 2	1, 2	X
280	Área de Proteção Ambiental de Sirinhaém	Sustainable use	Pernambuco	1, 2	1	X
281	Refúgio de Vida Silvestre Mata do Amparo	Integral protection	Pernambuco	2	-	-
282	Refúgio de Vida Silvestre Matas de Siriji	Integral protection	Pernambuco	2, 3	3	-
283	Refúgio de Vida Silvestre Mata de São João da Várzea	Integral protection	Pernambuco	2	-	X
284	Refúgio de Vida Silvestre Mata de Miritiba	Integral protection	Pernambuco	2	-	-
285	Refúgio de Vida Silvestre Serra do Cumaru	Integral protection	Pernambuco	2	-	-
286	Refúgio de Vida Silvestre Mata Jaguaribe	Integral protection	Pernambuco	2	-	-
287	Refúgio de Vida Silvestre Mata do Engenho São João	Integral protection	Pernambuco	2	-	-
288	Refúgio de Vida Silvestre Mata do Curado	Integral protection	Pernambuco	2	-	X
289	Refúgio de Vida Silvestre Mata do Engenho Macaxeira	Integral protection	Pernambuco	2	-	-
290	Refúgio de Vida Silvestre Mata de Mussaíba	Integral protection	Pernambuco	2	-	X
291	Refúgio de Vida Silvestre Mata Santa Cruz	Integral protection	Pernambuco	2	-	-

292	Parque Estadual Dois Irmãos	Integral protection	Pernambuco	2	-	X
293	Estação Ecológica de Caetés	Integral protection	Pernambuco	2	-	X
294	Refúgio de Vida Silvestre Mata do Urucu	Integral protection	Pernambuco	2	-	-
295	Refúgio de Vida Silvestre Mata do Quizanga	Integral protection	Pernambuco	2	-	-
296	Refúgio de Vida Silvestre Mata Lanço dos Canções	Integral protection	Pernambuco	2	-	X
297	Refúgio de Vida Silvestre Matas de Água Azul	Integral protection	Pernambuco	2, 3	-	-
298	Refúgio de Vida Silvestre Mata da Usina São José	Integral protection	Pernambuco	2	2	-
299	Parque Natural Municipal Professor João Vasconcelos Sobrinho	Integral protection	Pernambuco	1, 2	2	-
300	Parque Nacional do Catimbau	Integral protection	Pernambuco	1, 3	3	-
301	Reserva Biológica de Saltinho	Integral protection	Pernambuco	1	1	-
302	Parque Natural Municipal do Forte de Tamandaré	Integral protection	Pernambuco	1	1	X
303	Parque Estadual Mata da Pimenteira	Integral protection	Pernambuco	3	3	-
304	Refúgio de Vida Silvestre Tatu-bola	Integral protection	Pernambuco	3	3	-
305	Monumento Natural Pedra do Cachorro	Integral protection	Pernambuco	3	3	-
306	Estação Ecológica Serra da Canoa	Integral protection	Pernambuco	3	-	-
307	Reserva Biológica de Serra Negra	Integral protection	Pernambuco	3	3	-
308	Floresta Nacional de Negreiros	Sustainable use	Pernambuco	3	3	-
309	Área de Proteção Ambiental da Costa dos Corais	Sustainable use	Pernambuco / Alagoas	1, 2	1	X
310	Reserva Biológica de Pedra Talhada	Integral protection	Pernambuco / Alagoas	1, 3	1, 3	-
311	Parque Nacional da Serra das Confusões	Integral protection	Piauí	3	3	-
312	Estação Ecológica de Uruçui-una	Integral protection	Piauí	3	3	-
313	Parque Nacional da Serra da Capivara	Integral protection	Piauí	3	3	-
314	Área de Proteção Ambiental Serra da Ibiapaba	Sustainable use	Piauí/Ceará	3	3	X
315	Área de Proteção Ambiental da Chapada do Araripe	Sustainable use	Piauí/Ceará/Pernambuco	1, 2, 3	2, 3	X
316	Reserva Particular do Patrimônio Natural Agulhas Negras	Sustainable use	Rio de Janeiro	3	3	-
317	Reserva Particular do Patrimônio Natural Santo Antônio	Sustainable use	Rio de Janeiro	3	3	-
318	Reserva Particular do Patrimônio Natural Chalé Club do Alambary	Sustainable use	Rio de Janeiro	3	3	-

319	Reserva Particular do Patrimônio Natural Jardim de Mukunda	Sustainable use	Rio de Janeiro	3	3	-
320	Reserva Particular do Patrimônio Natural Pedra Branca	Sustainable use	Rio de Janeiro	3	3	-
321	Reserva Particular do Patrimônio Natural Fazenda Miosótis	Sustainable use	Rio de Janeiro	3	3	-
322	Reserva Particular do Patrimônio Natural Reserva Ecológica de Guapiaçu 3	Sustainable use	Rio de Janeiro	3	3	-
323	Área de Proteção Ambiental Da Bacia do Rio Macacu	Sustainable use	Rio de Janeiro	3	3	-
324	Área de Proteção Ambiental Macaé de Cima	Sustainable use	Rio de Janeiro	3	3	-
325	Reserva Particular do Patrimônio Natural Dois Peões	Sustainable use	Rio de Janeiro	3	3	-
326	Reserva Particular do Patrimônio Natural Sítio Grande	Sustainable use	Rio de Janeiro	-	3	-
327	Refúgio de Vida Silvestre Estadual do Médio Paraíba	Integral protection	Rio de Janeiro	3	3	-
328	Parque Estadual do Desengano	Integral protection	Rio de Janeiro	3	3	-
329	Monumento Natural Estadual da Serra da Beleza	Integral protection	Rio de Janeiro	3	3	-
330	Parque Estadual da Pedra Selada	Integral protection	Rio de Janeiro	3	3	-
331	Refúgio de Vida Silvestre Estadual da Lagoa da Turfeira	Integral protection	Rio de Janeiro	3	3	-
332	Parque Estadual da Serra da Concórdia	Integral protection	Rio de Janeiro	3	3	-
333	Área de Proteção Ambiental da Bacia do Rio São João/mico-leão-dourado	Sustainable use	Rio de Janeiro	3	3	-
334	Parque Natural Municipal Montanhas de Teresópolis	Integral protection	Rio de Janeiro	3	3	-
335	Parque Natural Municipal Fazenda Santa Cecília do Ingá	Integral protection	Rio de Janeiro	3	3	-
336	Refúgio de Vida Silvestre do Chaua	Integral protection	Rio de Janeiro	3	3	-
337	Parque Natural Municipal da Cachoeira da Fumaça e Jacuba Parfumaça	Integral protection	Rio de Janeiro	3	3	-
338	Parque Natural Municipal do Livramento	Integral protection	Rio de Janeiro	3	3	-
339	Área de Proteção Ambiental da Lagoa de Cima	Sustainable use	Rio de Janeiro	3	3	-
340	Área de Proteção Ambiental Carapiá	Sustainable use	Rio de Janeiro	3	3	-
341	Área de Proteção Ambiental Bemposta	Sustainable use	Rio de Janeiro	3	3	-
342	Área de Proteção Ambiental Santa Fé	Sustainable use	Rio de Janeiro	3	3	-
343	Área de Relevante Interesse Ecológico- Ilhas do Rio Paraíba do Sul	Sustainable use	Rio de Janeiro	3	3	-
344	Área de Proteção Ambiental da Serra da Bolívia	Sustainable use	Rio de Janeiro	3	3	-

345	Área de Proteção Ambiental de Engenheiro Passos Apaep	Sustainable use	Rio de Janeiro	3	3	-
346	Área de Proteção Ambiental Waldeir Gonçalves - Serra do Itaóca	Sustainable use	Rio de Janeiro	3	3	-
347	Área de Proteção Ambiental do Sana	Sustainable use	Rio de Janeiro	3	3	-
348	Área de Proteção Ambiental de Jenipabu	Sustainable use	Rio Grande do Norte	1, 2	1	-
349	Área de Proteção Ambiental Piquiri-uma	Sustainable use	Rio Grande do Norte	1, 2	1	-
350	Área de Proteção Ambiental Bomfim/Guaraíra	Sustainable use	Rio Grande do Norte	1, 2	1	-
351	Floresta Nacional de Nísia Floresta	Sustainable use	Rio Grande do Norte	1, 2	1	-
352	Reserva de Desenvolvimento Sustentável Estadual Ponta do Tubarão	Sustainable use	Rio Grande do Norte	3		-
353	Área de Proteção Ambiental Piquiri-Una	Sustainable use	Rio Grande do Norte	3	3	-
354	Parque Natural Municipal da Cidade do Natal Dom Nivaldo Monte	Integral protection	Rio Grande do Norte	1, 2	1	-
355	Estação Ecológica do Seridó	Integral protection	Rio Grande do Norte	3	-	-
356	Área de Proteção Ambiental Bonfim/Guaraíra	Sustainable use	Rio Grande do Note	3	3	-
357	Área de Proteção Ambiental Corumbataí Botucatu Tejupa Perímetro Botucatu	Sustainable use	São Paulo	3	3	-
358	Reserva Particular do Patrimônio Natural Santa Rita de Cassia	Sustainable use	São Paulo	3	3	-
359	Reserva Particular do Patrimônio Natural Serrinha	Sustainable use	São Paulo	3	3	-
360	Área de Proteção Ambiental Sapucaí Mirim	Sustainable use	São Paulo	3	3	-
361	Área de Proteção Ambiental Corumbataí, Botucatu e Tejupá Perímetro Corumbataí	Sustainable use	São Paulo	3	3	-
362	Área de Proteção Ambiental Cabreuva	Sustainable use	São Paulo	3	3	-
363	Área de Proteção Ambiental do Banhado	Sustainable use	São Paulo	3	3	-
364	Área de Proteção Ambiental Campos do Jordão	Sustainable use	São Paulo	3	3	-
365	Reserva Particular do Patrimônio Natural Gigante do Itaguaré	Sustainable use	São Paulo	3	3	-
366	Área de Proteção Ambiental Tietê	Sustainable use	São Paulo	3	3	-
367	Área de Proteção Ambiental ibitinga	Sustainable use	São Paulo	3	3	-
368	Área de Proteção Ambiental Silveiras	Sustainable use	São Paulo	3	3	-
369	Floresta Estadual Edmundo Navarro de Andrade	Sustainable use	São Paulo	3	-	-
370	Área de Relevante Interesse Ecológico da Pedra Branca	Sustainable use	São Paulo	3	3	-

371	Reserva Particular do Patrimônio Natural Pedra da Mina	Sustainable use	São Paulo	3	3	-
372	Reserva Particular do Patrimônio Natural Toca da Paca	Sustainable use	São Paulo	3	3	-
373	Área de Proteção Ambiental Piracicaba Juqueri Mirim Área I	Sustainable use	São Paulo	3	3	-
374	Área de Proteção Ambiental Piracicaba Juquerí-mirim Área II	Sustainable use	São Paulo	3	3	-
375	Parque Estadual das Furnas do Bom Jesus	Integral protection	São Paulo	3	3	-
376	Estação Ecológica de Paulo de Faria	Integral protection	São Paulo	3	3	-
377	Estação Ecológica Jataí	Integral protection	São Paulo	3	3	-
378	Estação Ecológica Mata do Jacaré	Integral protection	São Paulo	3	3	-
379	Parque Estadual de Itaberaba	Integral protection	São Paulo	3	3	-
380	Parque Estadual de Vassununga	Integral protection	São Paulo	3	3	-
381	Estação Ecológica do Noroeste Paulista	Integral protection	São Paulo	3	3	-
382	Estação Ecológica de Itirapina	Integral protection	São Paulo	3	3	-
383	Monumento Natural Estadual da Pedra do Baú	Integral protection	São Paulo	3	3	-
384	Estação Ecológica de Mogi-Guaçu	Integral protection	São Paulo	3	3	-
385	Floresta Nacional de Ipanema	Sustainable use	São Paulo	3	3	-
386	Monumento Natural Municipal do Pico do Itaguaré	Integral protection	São Paulo	3	3	-
387	Parque Natural Municipal do Banhado	Integral protection	São Paulo	3	3	-
388	Parque Natural Municipal do Trabiju	Integral protection	São Paulo	3	3	-
389	Parque Natural Municipal Augusto Ruschi	Integral protection	São Paulo	3	3	-
390	Área de Proteção Ambiental - Pedregulho	Sustainable use	São Paulo	3	3	-
391	Área de Proteção Ambiental de Campinas	Sustainable use	São Paulo	3	3	-
392	Floresta Nacional do Ibura	Sustainable use	Sergipe	1	-	-
393	Reserva Biológica de Santa Isabel	Integral protection	Sergipe	1	1	-
394	Parque Nacional Serra de Itabaiana	Integral protection	Sergipe	1, 3	1, 3	-
395	Refúgio de Vida Silvestre Mata do Junco	Integral protection	Sergipe	3	3	-
396	Área de Proteção Ambiental Lago de Peixe/Angical	Sustainable use	Tocantins	3	-	-
397	Área de Proteção Ambiental Jalapão	Sustainable use	Tocantins	3	3	-
398	Área de Proteção Ambiental Lago de São Salvador do Tocantins, Paranã e Palmeirópolis	Sustainable use	Tocantins	3	-	-

399	Área de Proteção Ambiental Serra do Lajeado	Sustainable use	Tocantins	3	3	-
400	Área de Proteção Ambiental Lago de Santa Isabel	Sustainable use	Tocantins	3	-	-
401	Parque Estadual do Jalapão	Integral protection	Tocantins	3	3	-
402	Parque Estadual do Lajeado	Integral protection	Tocantins	3	3	-
403	Monumento Natural das Árvores Fossilizadas	Integral protection	Tocantins	3	-	-

APÊNDICE I - IMAGES OF TRAP CAMERAS INSTALLED IN THE LOCATIONS STUDIED

Pedra Branca, Municipality Serra Talhada, Pernambuco, Brazil. colocar data

Serra do Estrago, Municipality Sertânia, Pernambuco, Brazil

Serra da Maravilha, Municipality Betânia, Pernambuco, Brazil

APÊNDICE J – RESULT MOLECULAR ANALYSIS

Genetic characterization, annealing temperature and GenBank accession number of the six microsatellite loci transferred to bearded capuchins, *Sapajus libidinosus,* living in Serra do Pinheiro and Serra do Estrago in Sertânia municipality, Pernambuco State, north-eastern, Brazil. *N- number of individuals, Ta – Temperature, (NA*) Number of alleles, (*Ho*) observed heterozygosity, (*He*) expected heterozygosity, (*Q*) probability of paternity exclusion, (*I*) identity index, (PIC) Polymorphic Information Content; (HWE) Hardy–Weinberg equilibrium (p=0.008, after Bonferroni correction); inbreeding coefficient (Fis) (p= 0.001 after Bonferroni correction) p= [c] combined probability; *significant (p=0.008, after Bonferroni correction).

Serra do Pinheiro fragment												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	15	210 - 282	7	0.933	0.869	0.679	0.046	0.820	0.23354	-0.077
Ceb120	EU019211	64	14	248 - 278	7	0.643	0.815	0.596	0.073	0.759	0.35481	0.217
Ceb105	EU019208	64	15	228 - 240	4	0.733	0.697	0.419	0.160	0.620	0.62538	-0.055
Ceb10	EU019203	59	15	238 - 250	4	0.800	0.605	0.355	0.215	0.543	0.47371	-0.339
Ceb7	EU019200	64	15	123 - 175	7	1.000	0.768	0.541	0.096	0.519	0.10861	-0.317
Ceb4	EU019199	54	15	166 - 214	5	0.867	0.602	0.327	0.238	0.713	0.14529	-0.462
All loci	-	-	-	-	5.667	0.829	0.726	0.9849 [c]	0.000002 [c]	0.6621	-	-0.148

Serra do Estrago fragment												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	15	262 - 278	4	1.000	0.724	0.442	0.145	0.645	0.00009*	-0.400
Ceb120	EU019211	64	15	250 - 274	4	1.000	0.701	0.413	0.163	0.619	0.00165*	-0.448**
Ceb105	EU019208	64	15	224 - 272	5	0.667	0.653	0.384	0.188	0.580	0.23531	-0.022
Ceb10	EU019203	59	15	238 - 258	5	0.933	0.717	0.459	0.137	0.650	0.68687	-0.315
Ceb7	EU019200	64	13	127 - 167	4	1.090	0.618	0.315	0.244	0.521	0.00310*	-0.660
Ceb4	EU019199	54	13	166 - 178	4	0.769	0.588	0.334	0.233	0.515	0.61242	-0.326
All loci	-	-	-	-	4.333	0.894	0.791	0.9501 [c]	0.000034 [c]	0.5883	-	-0.360**
Serra da Maravilha fragment												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	15	210 - 278	7	0.933	0.777	0.559	0.088	0.725	0.7238	-0.210
Ceb120	EU019211	64	13	262 - 278	5	0;615	0.742	0.494	0.118	0.678	0.0141	0.176
Ceb105	EU019208	64	15	228 - 240	4	0.933	0.756	0.483	0.120	0.683	0.9148	-0.206
Ceb10	EU019203	59	15	242 - 254	4	0.867	0.660	0.370	0.193	0.576	0.2598	-0.328
Ceb7	EU019200	64	15	123 - 231	10	1.000	0.864	0.682	0.045	0.818	0.1848	-0.163
Ceb4	EU019199	54	15	146 - 178	5	0.800	0.630	0.339	0.225	0.537	0.0096	-0.282
All loci	-	-	-	-	-	0.858	0.7381	0.9847 [c]	0.0000002 [c]	0.6693	-	-0.163

Serra da Pedra Branca fragmente												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	8	206 - 270	3	1.000	0.700	0.362	0.193	0.582	0.5103	-0.474
Ceb120	EU019211	64	8	258 - 278	4	0.875	0.725	0.411	0.164	0.618	0.2740	-0.225
Ceb105	EU019208	64	8	228 - 240	3	0.875	0.658	0.333	0.220	0.544	0.7758	-0.361
Ceb10	EU019203	59	8	242 - 262	5	0.750	0.733	0.442	0.149	.0636	0.4893	-0.024
Ceb7	EU019200	64	8	115 - 159	6	1.000	0.808	0.547	0.093	0.723	0.6507	-0.258
Ceb4	EU019199	54	8	158 - 198	4	0.625	0.642	0.325	0.235	.0525	1.000	-0.028
All loci	-	-	-	-	4.167	0.854	0.7111	0.9571[c]	0.000022 [c]	0.6047	-	-0.219
Serra do Almirante fragment												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	15	266 - 274	4	0.867	0.724	0.450	0.435	0.650	0.0042	-0.576**
Ceb120	EU019211	64	15	254 - 274	5	0.733	0.706	0.440	0.446	0.634	0.4639	-0.375
Ceb105	EU019208	64	15	212 - 240	6	0.800	0.662	0.380	0.478	0.576	0.0044	-0.418
Ceb10	EU019203	59	15	238 – 246	4	0.867	0.669	0.389	0.472	0.590	0.0128	-0.523
Ceb7	EU019200	64	15	123 - 191	4	0.933	0.582	0.268	0.541	0.465	0.0049	-0.640
Ceb4	EU019199	54	15	134 - 186	7	0.733	0.690	0.460	0.452	0.637	0.5224	-0.066
All loci	-	-	-	-	5	0.822	0.6720	0.9538 [c]	0.00002 [c]	0.5922	-	-0.424**

Serra das Tabocas fragment												
Loci	GenBank ID	Ta (ºC)	N	Allele size range (pb)	N_A	*Ho*	*He*	*Q*	*I*	PIC	HWE	Fis
Ceb130	EU019215	64	6	206 - 266	3	1.000	0.621	0.276	0.535	0.477	0.0912	-0.714
Ceb120	EU019211	64	5	262 - 274	2	0.800	0.533	0.182	0.606	0.365	0.4288	-0.600
Ceb105	EU019208	64	6	232 - 240	3	0.833	0.621	0.276	0.535	0.477	0.3931	-0.389
Ceb10	EU019203	59	5	238 – 246	3	1.000	0.644	0.288	0.526	0.492	0.1747	-0.667
Ceb7	EU019200	64	6	123 – 167	5	1.000	0.803	0.502	0.410	0.692	0.0232	-0.277
Ceb4	EU019199	54	6	166 - 178	3	0.833	0.621	0.304	0.528	0.505	0.6350	-0.389
All loci	-	-	-	-	3.167	0.911	0.6407	0.894 [c]	0.000224 [c]	0.5011	-	-0.491**

APÊNDICE L - LANDSCAPE GENETIC ANALYSIS

Land use classification and definitions according to IBGE (2018)

Class	Definition
Urban area	Areas where non-agricultural anthropogenic surfaces predominate. These are those structured by buildings and road system, which include the metropolises, cities, towns, indigenous villages and quilombola communities, areas of highways, services and transport, energy networks, communications and associated land, areas occupied by industrial complexes and buildings and buildings that may in some cases be located in peri-urban areas. Also in this class are areas where mining or extraction of mineral substances by mining or mining takes place.
Agricultural	An area characterized by temporary, semi-perennial and permanent crops, irrigated or not, being the land used for the production of food, fiber and agribusiness commodities. Includes all cultivated areas, including fallow or floodplain. It can be represented by heterogeneous agricultural zones or large areas of plantations. Also includes aquaculture tanks.
Livestock	Areas intended for grazing cattle and other animals, with cultivated herbaceous vegetation (brachiaria, ryegrass, etc.) or field vegetation (natural), both presenting high-intensity anthropogenic interference. These interferences may include planting; land clearing (relocation and shattering); mechanical or chemical weeding (herbicide application); harrowing; liming; fertilizing; among others that misrepresent the natural cover
Urban and forest mosaic	An area characterized by the mixed occupation of agriculture, pasture and / or forestry associated or not with forest remnants, in which it is not possible to individualize its components. It also includes areas with natural and anthropogenic, mechanical or non-mechanical disturbances that make it difficult to characterize the area.
Forest	The area occupied by forests. Forestry is considered to be tree formations greater than 5 meters in height, including areas of Dense Ombrophylous Forest, Open Ombrophilous Forest, Seasonal Forest, and Mixed Ombrophilous Forest. It includes other features due to its size greater than 5 m in height, such as Forest Savannah, Forest Campinarana, Forest Savannah-Steppe, Mangroves, and Buritizais, according to the Technical Land Use Manual (IBGE, 2013).
Grasslands	Area characterized in grasslands. Grasslands are understood to be the different categories of physiognomically very diverse vegetation of the forest, that is, those characterized by a predominantly shrub stratum, sparsely distributed over a grassy woody stratum. This category includes Savannas, Steppes, Steppe Savannas, Pioneer Formations, and Ecological Refuge. They are scattered throughout different phytogeographic regions, comprising different primary typologies: plateau steppes, coastal mountain ranges and coastal (restinga) hydro-sandy fields, according to the Technical Manual for Land Use (IBGE, 2013). These areas may be subject to grazing and other low-intensity anthropogenic interferences such as unmanaged pasture areas in Rio Grande do Sul and Pantanal.
Urban and Grasslands mosaic	An area characterized by the mixed occupation of agriculture, pasture and / or forestry associated or not with grasslands remnants, in which it is not possible to individualize its components. It also includes areas with natural and anthropogenic, mechanical or non-mechanical disturbances that make it difficult to characterize the area.
Water	Includes all inland waters, such as rivers, streams, canals, and other linear water bodies. It also encompasses naturally enclosed water bodies (natural lakes) and artificial reservoirs (artificial water reservoirs built for irrigation, flood control, water supply and power generation).

APÊNDICE M - LAND USE COST LAYERS

Land use cost layers used to perform Mixed-Effects Models (RLME) Linear Regression analysis to choose the variable that best explains the genetic distance between populations.

Class	Resistance cost					
	Land.a	Land.b	Land.c	Land.d	**Land.e**	Land.f
Urban area	100	100	100	100	**100**	100
Agricultural	50	50	50	20	**50**	50
Livestock	100	80	100	100	**100**	50
Urban and forest mosaic	80	80	50	80	**20**	80
Native vegetation	1	1	1	1	**1**	1
Urban and savannah mosaic	80	80	50	80	**20**	80
Water	100	100	100	100	**100**	100

The land use that best explained the genetic distance between populations was Land.e. This cost layer was used to test the models.