Biological Conservation 224 (2018) 178–187

Contents lists available at ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Landscape resistance influences effective dispersal of endangered golden lion tamarins within the Atlantic Forest

Andreia Magro Moraes[a,b,c,*], Carlos R. Ruiz-Miranda[a], Pedro M. Galetti Jr.[b], Bernardo Brandão Niebuhr[c], Brenda R. Alexandre[d], Renata L. Muylaert[c], Adriana D. Grativol[a], John W. Ribeiro[c], Arystene N. Ferreira[b], Milton Cezar Ribeiro[c]

[a] *Programa de Pós-graduação em Ecologia e Recursos Naturais, Instituto de Biociências e Biotecnologia, Universidade Estadual do Norte Fluminense, 28013-602 Campos dos Goytacazes, RJ, Brazil*

[b] *Laboratório de Biodiversidade Molecular e Conservação, Departamento de Genética e Evolução, Universidade Federal de São Carlos, 13565-905 São Carlos, SP, Brazil*

[c] *Laboratório de Ecologia Espacial e Conservação (LEEC), Instituto de Biociências, Universidade Estadual Paulista (UNESP), 13506-900 Rio Claro, SP, Brazil*

[d] *Programa de Pós-graduação em Ecologia, Departamento de Ecologia, Instituto de Biologia, Universidade Federal do Rio de Janeiro, 21941-590 Rio de Janeiro, RJ, Brazil*

ARTICLE INFO

Keywords:
Individual-based analyses
Isolation by resistance
Landscape genetics
Primate conservation
Sex-biased dispersal

ABSTRACT

Habitat fragmentation threatens tropical rainforests, which can significantly hinder dispersal in species such as arboreal primates. For conservation actions to be effective there must be an understanding of how landscape structure and biological traits shape dispersal. We assessed the effects of landscape, sex and population management (reintroductions and translocations) on gene flow of *Leontopithecus rosalia*, an endangered arboreal primate living in highly fragmented forests of Brazil. We genotyped 201 individuals using 14 microsatellite loci to answer three questions: (1) How far does *L. rosalia* disperse? (2) Is dispersal sex-biased? (3) What are the relative contributions of population management, distance, roads and landscape resistance to genetic kinship? We hypothesized that (1) gene flow decrease between more distant sites; (2) males disperse more than females; and (3) management and land-cover resistance (*i.e.* landscape resistance) are the variables that most influence genetic kinship. We found positive spatial population-structure up to 8 km. The spatial structure was similar between females and males suggesting that they equally contribute to gene flow. Management and landscape resistance best explained genetic kinship, showing that different land-cover types affect the dispersal at different degrees of landscape permeability. We advocate that maintaining more permeable landscapes is essential to ensure dispersal and gene flow of arboreal mammals. Conservation measures in tropical rainforests must take into account not only the habitat amount, but also the degree at which each land use – roads, urban areas, agriculture, pasture, isolated trees, and stepping stones – facilitates or impedes the species dispersal.

1. Introduction

Dispersal is among the main factors influencing population dynamics and viability. It is directly affected by landscape changes, particularly those associated to habitat fragmentation (*e.g.* inter-habitat distance, matrix composition and the presence of barriers), and by intrinsic characteristics of organisms such as sex, vagility through various land-cover types and dispersal strategies (Henriques-Silva et al., 2015; Nathan, 2008). The interplay of these external and organismal factors determines landscape connectivity: the capacity of landscapes to promote or impede animal movements (Arroyo-Rodríguez and Mandujano, 2009; Henriques-Silva et al., 2015; Nathan, 2008; Taylor et al., 1993). In fragmented landscapes, genetic connectivity may not be significantly hindered in species with high dispersal capacity – *e.g. Pardalotus striatus* and *Lichenostomus penicillatus* (Amos et al., 2012, 2014), *Procyon lotor* (Dharmarajan et al., 2014), and *Puma concolor* (Castilho et al., 2011) – whereas populations of less mobile species that rely on tree cover to move may become genetically differentiated – *e.g. Malurus cyaeneus* and *Lichenostomus melanops* (Amos et al., 2012, 2014), and *Mintonius gloydi* (Row et al., 2010).

Arboreal primates are an example of animals whose dispersal is sensitive to forest connectivity (Arroyo-Rodríguez and Mandujano, 2009) and are threatened with extinction due to habitat fragmentation, particularly in the Neotropics (Estrada et al., 2017). However, few studies have investigated how primate dispersal is affected by distinct landscape attributes such as distance (*e.g.* Mandujano et al., 2004; Mickelberg, 2011), roads (*e.g.* Teixeira et al., 2013) and the structure of inter-habitat matrix (*e.g.* Pozo-Montuy et al., 2011; Silva et al., 2015).

---

* Corresponding author.
E-mail address: andreia_magro@hotmail.com (A.M. Moraes).

https://doi.org/10.1016/j.biocon.2018.05.023
Received 23 June 2017; Received in revised form 17 May 2018; Accepted 28 May 2018

Even landscape genetics studies investigating how human-modified landscapes affect the gene flow of arboreal primates under threat of extinction are rare in the literature (*e.g.* Blair and Melnick, 2012; Hagell et al., 2013). These studies are important because they enable the identification of landscape attributes that affect the behavior, survival and reproduction of species, and thus may facilitate the planning of conservation actions (Sork and Waits, 2010).

The golden lion tamarin (GLT), *Leontopithecus rosalia*, is an arboreal primate endangered mainly by habitat fragmentation. Conservation efforts have changed its IUCN threat status from 'critically endangered' to 'endangered' (Kierulff et al., 2008). Among the conservation measures implemented are reintroduction of captive-born individuals, translocation of isolated social groups to a continuous forest, and managing the species as a metapopulation (Kierulff et al., 2012; Ruiz-Miranda et al., 2010). A major current conservation challenge is that the region GLT inhabit – where animals were reintroduced and translocated – is highly fragmented. The low landscape connectivity and reduced gene flow may be the main threats to the long-term viability of their populations (Grativol et al., 2001). However, how or if the GLT disperse through human-modified landscapes is yet to be understood.

The extensive research on lion tamarins has focused mainly on within-fragment movements (*e.g.* Baker and Dietz, 1996; Dietz et al., 1997; Raboy and Dietz, 2004). Current knowledge of dispersal through the non-forest matrix is limited (*e.g.* Coelho, 2009; Dietz et al., 1997) and we lack information on how the modification of their habitat interferes in the behavior and strategies of dispersal. For example, sex-related dispersal strategies can be different in fragmented and continuous landscapes (*e.g. Alouatta caraya*; Oklander et al., 2010; *Leontopithecus rosalia*; Paula, 2013).

Golden lion tamarins also offer a great opportunity to evaluate the effects of landscape modifications on dispersal, because there has been an extensive collection of genetic samples at different spatial and temporal scales. Furthermore, since the founding of the reintroduced and translocated GLT populations (from 1983; Kierulff et al., 2012), the landscape where these populations occur remains relatively stable with little reduction in the forest cover (< 3%; Seabra, 2012). These small temporal changes reduce the probability of confounding the effects of historic landscape and current landscape on gene flow (Hall and Beissinger, 2014). The GLT conservation project also allows for the opportunity to evaluate the influence of population management on population genetic structure in landscape genetic studies (Moraes et al., 2017).

We used molecular tools to quantify the influence of landscape patterns on effective dispersal of endangered golden lion tamarin species. Genetic variability was accessed for different GLT populations distributed throughout their current range in southeastern Brazil. We asked three main questions (Fig. 1): (1) How far do GLT individuals disperse? (2) Are female dispersers more affected by landscape changes than male dispersers? (3) What are the relative contributions of population management, distance, roads (physical barriers) and landscape resistance to GLT genetic kinship? We hypothesized that:

1. Genetic kinship decreases with the distance between sites. This differentiation pattern is referred to as isolation by distance (Slatkin, 1985);
2. The negative correlation between genetic kinship and distance between sites is more pronounced in females than in males. Field studies suggest a sex-bias on the frequency of dispersal (Baker and Dietz, 1996);
3. Genetic kinship will be higher for animals within the same type of managed population (native or unmanaged, reintroduced and translocated). This is a result of management strategy: tamarins were translocated and reintroduced into separate areas devoid of wild tamarins (Kierulff et al., 2012);
4. Genetic kinship will be negatively correlated with distance, road presence, and landscape resistance; the influence of these factors will follow the order (from highest to lowest): population management, landscape resistance, roads and distance.

2. Material and methods

2.1. Study area and genetic data sampling

The study was conducted at São João River Basin (SJRB) and the União Biological Reserve (REBIO-União) region, located in southeastern Brazil, within the highly fragmented Atlantic Forest (Ribeiro et al., 2009). To ensure that the extent of the study area was large enough to evaluate the landscape influences on GLT populations (Anderson et al., 2010), we also analyzed a 5-km buffer beyond the boundaries of the area where the species occurs (Fig. 2). This size is based on a study that reported the maximum distance dispersed by GLT to be around 6 km (Mickelberg, 2011). The highway BR-101 cross the SJRB from west to east, dividing the GLT distribution region into two portions, and threatening species maintenance. The average linear distance between the habitat fragments above the BR-101 highway is 158 m and below this distance is 300 m. The BR-101 divide the landscape into to portions: (a) the northern portion comprises the most preserved area, with higher amounts of forest cover and less fragment isolation (Procópio-de-Oliveira et al., 2008); (b) the southern portion, where the Poço das Antas Biological Reserve (PDA) and other large and isolated populations of GLT occur (*e.g.* VR, Fig. 2).

We selected social groups from all of the management units (MU) in the SJRB and REBIO-União designated as REBIO-União, AVI, AVII, Imbaú and Serra (above BR-101) and PDA, VR and BE (below BR-101) (Fig. 2). The MUs are units established by the Golden Lion Tamarin Association (AMLD; *Associação Mico-Leão-Dourado*) and collaborating researchers, whose goal is to support the GLT management (Holst et al., 2006; Mickelberg, 2011). PDA and REBIO-União consist of public protected forests, while the MUs of AVI, AVII, Imbaú, Serra, BE and RV consist of forest fragments inside private areas. Descendants of the genetically unmanaged population (referred to as native individuals) are mainly distributed within the PDA and Serra. Descendants of the captive-born animals (N = 146) reintroduced to the wild in the period from 1984 to 2000 (referred to as reintroduced individuals) are mainly distributed within the AVI, AVII, Imbaú, RV, and BE. REBIO-União contains the descendants from six social groups that originated from four forest fragments on the coast of Rio de Janeiro State until the 90s, and that were translocated to REBIO-União in the period from 1994 to 1997 (referred to as translocated individuals) (Kierulff et al., 2012; Ruiz-Miranda et al., 2010).

Following a landscape genetics approach (Storfer et al., 2007), we simulated multi-path ecological corridors using the LSCorridors package (Ribeiro et al., 2017) to assist the choice of sampling locations of the social groups – more information on LSCorridors can be obtained at https://github.com/LEEClab/LS_CORRIDORS. As a result, we selected 48 social groups that had a minimum of two sampled individuals and covered various ranges of corridor costs – this step is best-described below in Spatial analysis section. In total, we sampled a mean of 4 (SD = 2.7) GLT individuals per social group captured in the study area during the period 2007–2009 (hereafter referred to as 'recent'). Of a total of 201 individuals sampled in the recent period, 152 were the same used in Moraes et al. (2017). Hair samples were collected by AMLD field team and were stored in silica gel until further genetic analysis. Capture procedures are described in detail elsewhere (Dietz et al., 1994). For each sampled individual with occurrence known in 2009, we obtained information about individual identification, sex, and social group based on field records from that year. Of those animals, only the adult individuals (aged > 2 years) were selected to reduce the influence of related individuals on the results – offspring tend to disperse out of the natal groups around two years of aged (Paula, 2013). We also analyzed the genotypes of GLTs living in the SJRB and REBIO-União in the period 1996–1997 (hereafter referred to as 'historic') – 78