



Natureza & Conservação

Brazilian Journal of Nature Conservation

Supported by Boticário Group Foundation for Nature Protection

<http://www.naturezaeconservacao.com.br>



Research Letters

Clade-specific impacts of human land use on primates



Fernanda T. Brum^{a,*}, Vanderlei J. Debastiani^a, Rafael Loyola^b, Leandro D.S. Duarte^a

^a Programa de Pós-Graduação em Ecologia, Universidade Federal do Rio Grande do Sul – UFRGS, Porto Alegre, RS, Brazil

^b Departamento de Ecologia, Universidade Federal de Goiás – UFG, Goiânia, GO, Brazil

ARTICLE INFO

Article history:

Received 30 August 2014

Accepted 22 September 2014

Available online 8 November 2014

Keywords:

Anthropogenic biomes
Human impact
Primate conservation
Principal coordinates of
phylogenetic structure – PCPS

ABSTRACT

Here we applied phylogenetically based conservation analyses using a novel multivariate approach to better evaluate the effects of human land use on different primate lineages worldwide. Using a $1^\circ \times 1^\circ$ grid, we obtained information on primate species distribution and the cover of six land use categories (Urban, Village, Cropland, Rangeland, Seminalural and Wild). We synthesized the phylogenetic composition into principal coordinates of phylogenetic structure. We correlated phylogenetic composition and land use in each region, and assessed statistical significance via null model. In America, the Atelidae clade was associated to areas with larger coverage of villages whereas Pitheciidae was found on areas with higher cover of wildlands. Moreover, we found some Atelidae, Callitrichidae and Pitheciidae species to be associated with seminatural areas, while other *Alouatta* and *Callicebus* species were more related with higher coverage of rangelands. In Madagascar, Lemuridae was negatively associated with wild areas. Africa did not show any statistically significant association between clades and land use. Asia had an intense association of some Cercopithecidae species with high coverage of villages. Primate lineages are currently facing different land use pressures, which would imply in the need of clade-specific conservation planning.

© 2014 Associação Brasileira de Ciência Ecológica e Conservação. Published by Elsevier Editora Ltda. All rights reserved.

Introduction

Approximately 75% of Earth's ice-free land has been altered by humans (Ellis and Ramankutty, 2008) and such alterations have modified global patterns of biodiversity. Over the last decades, increased information on human activities across the globe has enabled us to evaluate the effects

of such human activities on biodiversity at broad geographical scales (Brum et al., 2013; Harcourt and Parks, 2003; Pekin and Pijanowski, 2012). Commonly, these evaluations have been conducted using species as foci of the research (Davidson et al., 2012; Pekin and Pijanowski, 2012). However, phylogenetic relationships among taxa are also an important measure for conservation biology (Faith, 1992; Vane-Wright et al., 1991). Most phylogenetic approaches are limited because

* Corresponding author at: Phylogenetic and Functional Ecology Lab, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil.
E-mail address: ftbrum@gmail.com (F.T. Brum).

<http://dx.doi.org/10.1016/j.ncon.2014.09.009>

1679-0073/© 2014 Associação Brasileira de Ciência Ecológica e Conservação. Published by Elsevier Editora Ltda. All rights reserved.

they summarize phylogenetic diversity in a single metric, such as the phylogenetic diversity index (PD; Faith, 1992), which can obscure which clades are influenced by different sorts of threats. In fact, clades may be affected disproportionately by human disturbances, which, in turn, will determine the relationships among different regions of the phylogeny, providing clues for conservation interventions (Loyola et al., 2014). Here we applied phylogenetically based conservation analyses using a novel multivariate approach to better evaluate what threats impact different lineages.

Much of the variation in species' extinction risk is associated with spatial patterns of human threats and depends on how different species respond to threats (Purvis, 2000; Cardillo and Meijaard, 2012). Human land uses are unevenly distributed across the globe (Ellis and Ramankutty, 2008), and different types of land use can have different impacts on biodiversity. For example tropical regions, which shelter much of the global biodiversity, suffer from intense deforestation, condemning forest species to local extinction (Hansen et al., 2013). High human population densities in Asia lead to a direct conservation conflict between human populations and wild species, which result in increased hunting pressure (IUCN, 2013).

Phylogenetic relatedness may influence how species respond to human impacts. Closely related species are likely to show high trait similarity (Felsenstein, 1985) and, consequently, could respond similarly to threats. In other words, species with high extinction risk sharing the same phylogenetic affinities and ecological traits may be more prone to go extinct. In contrast, unrelated species might respond differently to human threats. As a result, it may be useful to consider phylogenetic relatedness in conservation assessments and planning (Corey, 2010; Cardillo and Meijaard, 2012; Hidasi-Neto et al., 2013; Loyola et al., 2014).

One common way to quantify phylogenetic relatedness is to use diversity metrics based on phylogenetic distance. The most frequently used metric is Faith's PD (Faith, 1992), which sums the branch lengths of the phylogenetic tree connecting all species within a community (Faith, 1992). However, phylogenetic diversity metrics synthesize phylogenetic information into one single value. As a consequence, other aspects of phylogenetic diversity are neglected. Hence, it is important to not only know how much diversity is found in a given location, but what that diversity is, especially since different lineages likely respond to different threats (Davidson et al., 2012; Pekin and Pijanowski, 2012). To address this shortcoming we used a metacommunity phylogenetics approach, which describes the distribution of different phylogenetic lineages across a set of communities using fuzzy sets defined by species' phylogenetic similarities (Pillar and Duarte, 2010; Duarte, 2011). By using this approach, we could assess the main anthropogenic pressure acting on individual lineages.

Primates represent an important case study on which to apply our methods because nearly half of all the world's primates are currently threatened (IUCN, 2013). Primates are mainly threatened by habitat destruction, hunting (for food and other purposes) and live capture for export or local trade (Chapman and Peres, 2001; Mittermeier et al., 2012). Not surprisingly, the mechanisms underlying the increased extinction risk in primates are directly linked to human

population growth and social-economic activities (Chapman and Peres, 2001; Harcourt and Parks, 2003; Benchimol and Peres, 2013). While much has been done on the impact of human activities on primate species, only few studies evaluated how these impacts influence phylogenetic diversity beyond simply quantifying loss of phylogenetic diversity (Sechrest et al., 2002; Spathelf and Waite, 2007).

In this paper, we did a broad-scale evaluation on the association between land use and primate phylogenetic composition to answer the following question: what human impacts have the strongest influence on primate clades in each continent and Madagascar? For this, we evaluated if there is an association between the distribution of primate lineages and particular types of land use. We discuss the potential threats that most likely impact each clade.

Methods

Primate occurrence data

We obtained primate species occurrences by overlapping the range maps from the Global Mammal Assessment (IUCN, 2013) on to a $1^\circ \times 1^\circ$ grid. Only cells with presences were used for further analysis. We split the occurrence data per continent; Madagascar was analyzed separately from continental Africa, due to its historical isolation, which generated a completely distinct biota in this island (Lehman and Fleagle, 2006). We used primate species composition in each cell for further analyses.

Phylogenetic composition

We used the phylogenetic hypothesis from Perelman et al. (2011), which includes phylogenetic relationship between 186 primate species from 61 genera and estimated divergence time for each node in MYA. Species were arranged as polytomies inside the node of the genera, and genera and species absent in Perelman's phylogeny were inserted based on literature information (see Supplementary Material). The phylogeny used in the analyses contained 416 primate species, from 72 genera, and the branch lengths were dated in MYA. Then we assessed the phylogenetic composition of primate clades in each continent and Madagascar performing the phylogenetic fuzzy-weighting method developed by Pillar and Duarte (2010), using the package SYNCSA (Debastiani and Pillar, 2012) and *ape* (Paradis et al., 2004) in the R software. This method uses phylogenetic similarities between taxa to scale-up the phylogenetic relationships from taxa to the site level. First, pairwise phylogenetic distances between species were taken from the phylogeny, and then transformed into a phylogenetic similarity matrix (S_P) ranging from 0 to 1. Then, phylogenetic similarities in S_P were used to weigh primate species composition in each cell, using a fuzzy set algorithm (see Pillar and Duarte, 2010 for details). This procedure generated a matrix P of species by cells containing primate species composition weighted by phylogenetic relationships. Each value in matrix P is the probability of a given species to occur in a cell given its phylogenetic similarities to the species that were actually found in the cell. We then performed a principal

Download English Version:

<https://daneshyari.com/en/article/4400812>

Download Persian Version:

<https://daneshyari.com/article/4400812>

[Daneshyari.com](https://daneshyari.com)