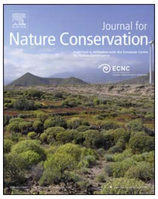
Journal for Nature Conservation 42 (2018) 28–35

Contents lists available at ScienceDirect

Journal for Nature Conservation

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



How effective are protected areas in conserving tree taxonomic and phylogenetic diversity in subtropical Brazilian Atlantic Forests?

Daniel Dutra Saraiva[a,*], Anita Stival dos Santos[a], Gerhard Ernst Overbeck[a,b], Eduardo Luís Hettwer Giehl[c], João André Jarenkow[a,b]

[a] Programa de Pós-Graduação em Botânica, Instituto de Biociências, Universidade Federal do Rio Grande do Sul (UFRGS), Av. Bento Gonçalves 9500, CEP 91501-970, Bloco IV, Prédio 43.433, Porto Alegre, RS, Brazil
[b] Departamento de Botânica, Instituto de Biociências, Universidade Federal do Rio Grande do Sul (UFRGS), Av. Bento Gonçalves 9500, CEP 91501-970, Bloco IV, Prédio 43.433, Porto Alegre, RS, Brazil
[c] Departamento de Ecologia e Zoologia, Universidade Federal de Santa Catarina (UFSC), Campus Universitário s/n, CEP 88040-900, Sala 05, Florianópolis, SC, Brazil

ARTICLE INFO

Keywords:
Beta diversity
Evolutionary history
Conservation targets
Spatial mismatch
Species richness
Systematic conservation planning

ABSTRACT

We assessed the effectiveness of a protected area (PA) network in representing tree taxonomic and phylogenetic uniqueness in subtropical Atlantic Forests (Rain, Mixed and Seasonal Forests). Using a network of plots distributed over ~95,000 km^2 in southern Brazil, we first map the distribution of species richness (SR), beta diversity (BD) and phylogenetic diversity (PD) across the extent of remaining forest in the region. We then tested whether areas of taxonomic and phylogenetic uniqueness are either over- or under-protected based on the existing PA network (3% coverage) and at least 10% coverage, and assessed whether protection is distributed equally for each uniqueness area type. Here, areas of taxonomic uniqueness were defined as those with higher contribution than the mean to the total BD, and areas of phylogenetic uniqueness as those with higher or lower PD than expected by chance given their SR, and sites exhibiting spatial congruence or mismatch between PD and SR. We found a high percentage of representation of both areas of uniqueness across the extent of remaining forest. However, our analyses showed that these areas are poorly and unequally captured by the PA network; they are on average less protected than expected based on at least 10% coverage and have high inequality of protection. Our results suggest that both beta diversity and evolutionary history of angiosperm trees are not adequately protected, and indicate relevant areas to extend the current PA network. We also emphasize the need to consider a multifaceted approach to maximize protection of the Atlantic Forest biodiversity.

1. Introduction

Protected areas (PAs) play a major role in biodiversity conservation in a world of increasing land-use change as they guarantee that natural ecosystems are not converted to other uses on the long term (Margules & Pressey, 2000; Pressey, Cabeza, Watts, Cowling, & Wilson, 2007). However, to ensure the long-term persistence of biodiversity within PAs, it is crucial that biodiversity is adequately represented and that effective management actions are implemented towards maintaining key ecological processes and mitigating climate and land-use changes (Turner & Pressey, 2009). Previous studies showed that PA networks in many countries are strongly biased towards areas that are unsuitable for animal husbandry, agriculture, or urban development and thus are unlikely to face human pressures, such as sites with difficult access or complex topographies, at high elevations or on less productive soils (Joppa & Pfaff, 2009; Scott et al., 2001; Thuiller et al., 2015). Thus, we can expect that PA networks will not contribute to the conservation of all species, as some types of ecosystems – and with that their species – will be underrepresented. This becomes even more relevant under climate change, as PA will contribute to conservation only if the distribution ranges of the species in question will continue to be contained within the PA networks (Hannah et al., 2007).

Conservation targets have been widely used in systematic conservation planning for setting priorities (Pressey, Cowling, & Rouget, 2003; Rodrigues et al., 2004; Soutullo, De Castro, & Urios, 2008), once they provide an initial reference to inform about the effectiveness of protection, the expansion of the PA network, and the importance of complementary PAs (Barr et al., 2011; Soutullo et al., 2008; Turner & Pressey, 2009). Information on the representation of biodiversity patterns within PAs (i.e. as quantitative estimates of how much of a given biodiversity aspect should be included within a network of PAs) is crucial for conservation targets, which more recently have been defined

---

* Corresponding author.
E-mail address: daniel.saraiva@bol.com.br (D.D. Saraiva).

https://doi.org/10.1016/j.jnc.2018.02.002
Received 31 October 2017; Received in revised form 25 January 2018; Accepted 6 February 2018

in terms of biodiversity persistence (Pressey et al., 2007). Conservation targets have been commonly formulated in terms of species richness (SR), rarity, endemism, and threat (Rodrigues et al., 2004; Williams et al., 1996). However, this may not be appropriate for setting conservation priorities: using only these traditional targets, we ignore the evolutionary and functional differences among species (Faith, 1992; Vane-Wright, Humphries, & Williams, 1991). Therefore, phylogenetic diversity (PD) is increasingly being used to include evolutionary relationships (and hence evolutionary history) among taxa in PA effectiveness assessments (e.g., Devictor et al., 2010; Daru, van der Bank, & Davies, 2015; Thuiller et al., 2015; Chen, Zhang, Jiang, Nielsen, & He, 2017). As extant PD comprises the raw material on which future evolutionary processes will operate (Rodrigues, Brooks, & Gaston, 2005), protecting as much evolutionary history as possible should maintain the evolutionary potential of biota, i.e., the capacity of species to respond adaptively to environmental changes (Faith, 1992; Forest et al., 2007; Laity et al., 2015; Vane-Wright et al., 1991; Vázquez & Gittleman, 1998). Under the assumption that closely related species share similar traits that are phylogenetically conserved on the phylogeny (Losos, 2008), prioritizing PD would lead at the same time to the protection of functional diversity (Zupan et al., 2014).

Importantly, prioritizing taxonomic diversity (TD) instead of evolutionary history may lead to different solutions in terms of spatial optimization of PA networks (Forest et al., 2007). Using TD, areas that contribute more than average to the total beta diversity of a region are particularly interesting for conserving uncommon species compositions (Legendre & De Cáceres, 2013), and conservation should target areas with high species turnover across the region (Socolar, Gilroy, Kunin, & Edwards, 2016). Regarding evolutionary history protection, areas with higher or lower PD than expected by chance given their SR are also important, as distinct phylogenetic signatures would be protected (Costion et al., 2015; Forest et al., 2007; Winter, Devictor, & Schweiger, 2013; Zupan et al., 2014). Areas with higher PD than expected based on SR are likely to contain a high proportion of evolutionarily distinct lineages, and hence a large amount of evolutionary history, while areas with lower PD than expected are likely to embrace a high proportion of species originated recently, which could potentially contribute to future evolutionary radiations (Collen et al., 2011; Davies & Buckley, 2011; Fritz & Rahbek, 2012; Mishler et al., 2014; Zupan et al., 2014). It has been hypothesized that areas with higher PD may indicate ancient refugia, where diversification has been slow and immigration of multiple lineages frequent, or biogeographic convergence zones that have experienced high diversification of multiple lineages together with high immigration of multiple lineages over time (Davies & Buckley, 2011; Fritz & Rahbek, 2012; Mishler et al., 2014). Conversely, areas with lower PD indicate recent evolutionary radiations, or large radiations of few lineages in habitat patches (Davies & Buckley, 2011; Fritz & Rahbek, 2012; Mishler et al., 2014). Because the same site may be highly diverse in both SR and PD, resulting in a high spatial congruence, mapping the spatial mismatch between them can reveal zones where few species (low SR) concentrates a high amount of evolutionary history (Laity et al., 2015). Spatial mismatch between PD and SR can be observed at different spatial scales and may reflect contrasting processes driving these facets or distinct evolutionary histories (Daru et al., 2015; Devictor et al., 2010; Strecker, Olden, Whittier, & Paukert, 2011).

The Brazilian Atlantic Forest is a biodiversity hotspot that harbors high levels of diversity and endemism (Mittermeier, van Dijk, Rhodin, & Nash, 2004). This hotspot has been subject to several human pressures, such as farming, exotic tree monocultures, logging, urbanization, exotic species invasion, overhunting, and climate change (Tabarelli, Aguiar, Ribeiro, Metzger, & Peres, 2010). Because of this long history of degradation, only ~12% of the original forest remains in scattered and reduced patches (Ribeiro, Metzger, Martensen, Ponzoni, & Hirota, 2009). Although the Brazilian system of PAs covers 10.7% of its total area, only ~2% is effectively preserved in PAs of strict protection (IUCN categories I–IV; Fonseca, Lamas, & Kasecker, 2010; Ribeiro, Martensen, Metzger, & Fortin, 2011). In addition, the distinct forest physiognomies within the Atlantic Forest are unevenly protected, leading to an unequal representation of biodiversity in PAs (Bergamin et al., 2017; Metzger, 2009; Ribeiro et al., 2009). Despite the extremely worrying state of this hotspot, ecological information required to support conservation actions are still missing for most of the Atlantic region (de Lima et al., 2015).

Here, we used a multifaceted approach that integrates information on taxonomic and phylogenetic uniqueness to identify conservation gaps in protected coverage. Using a network of plots distributed along the three main physiognomies within the Atlantic Forest in southern Brazil (Rain, Mixed and Seasonal Forests), we first map the spatial distribution of tree TD and PD across the extent of remaining forest (i.e. a mosaic of old-growth and late-secondary forests), and then assessed the effectiveness of the current PA network in representing taxonomic and phylogenetic uniqueness in terms of coverage and equality of protection. Specifically, we tested whether areas of taxonomic and phylogenetic uniqueness (as defined below) are either over- or under-protected based on the existing PA network (3% coverage) and at least 10% coverage (under a random distribution of PAs), and assessed whether protection is distributed equally for each uniqueness area type. We defined areas of taxonomic uniqueness as those with higher contribution than the mean to the total beta diversity of the region (Legendre & De Cáceres, 2013), and areas of phylogenetic uniqueness as those with higher or lower PD than expected by chance given their SR (i.e. sites that make a higher or lower evolutionary contribution than SR alone), and sites exhibiting spatial congruence or mismatch between PD and SR (Devictor et al., 2010; Voskamp, Baker, Stephens, Valdes, & Willis, 2017; Zupan et al., 2014).

2. Methods

2.1. Dataset

Tree species data were provided by the forest inventory of Santa Catarina State (Portuguese acronym: IFFSC; http://www.iff.sc.gov.br), which consists of a network of 432 0.4-ha plots distributed in a total area of 95,717 km^2 in southern Brazil (Fig. 1). The IFFSC is a database financed by the State Government of Santa Catarina and the Brazilian Forest Service (SFB), and executed by the Regional University of Blumenau (FURB), the State University of Santa Catarina (UDESC), the Federal University of Santa Catarina (UFSC) and the Agricultural Research and Rural Extension Company of Santa Catarina (EPAGRI). The region covered by the IFFSC comprises the southern portion of the Brazilian Atlantic Forest hotspot (Mittermeier et al., 2004), where three main forest physiognomies are distributed from the sea level to the continental highlands, as follows: (1) Rain Forest (locally known as Dense Forest) in the coastal mountain range, (2) Mixed Forest (locally known as *Araucaria* Forest) on the highland, and (3) Seasonal Forest along the Uruguai river valley (Leite & Klein, 1990). We present a description of each physiognomy in Appendix A of the Supplementary Material.

The sampling design of the IFFSC is based on a 10 × 10 km grid across the entire territory of Santa Catarina, except for the Seasonal Forest where the grid was 5 × 5 km. This forest type is most reduced in cover and the 10 × 10 km grid would have led to a very low number of sample points. A central point was established at each intersection of the grid when a large forest remnant was found within a circle of 500 m (Vibrans, Moser, Lingner, & Gasper, 2012). From each central point, a set of four subunits of 1.000 m^2 (20 × 50 m) was pooled in a forest plot (0.4 ha). The subunits were allocated crosswise towards the four cardinal points, starting at a distance of 30 m away from the central point. The number of plots per forest type was proportional to the total remaining area of each type, with 202 (47%) located in the Rain Forest, 154 (36%) in the Mixed Forest and 76 (17%) in the Seasonal Forest (Fig. 1). Within each plot, all trees (including tree ferns and palms)