

University of São Paulo
Luiz de Queiroz College of Agriculture

Ecological restoration through a phylogenetic perspective

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Dissertation presented to obtain the degree of Master in
Science. Area: Forest Resources. Option in: Conservation
of Natural Ecosystems

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versão revisada de acordo com a resolução CoPGr 6018 de 2011

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I dedicate this dissertation to my beloved parents,
Maria Lúcia and Ireno Mariano

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*Here is the means to end the great extinction spasm
The next century will, I believe, be the era of restoration in ecology*

Edward O. Wilson (1992)

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RESUMO

Restauração ecológica sob uma perspectiva filogenética

A restauração ecológica dos ecossistemas é vista como o caminho para mitigar e reverter o cenário mundial de perda de biodiversidade e serviços ecossistêmicos. A ciência da restauração ecológica, conhecida como ecologia da restauração, cresceu rapidamente ao longo dos anos e atualmente é uma disciplina que compreende diversas áreas do conhecimento científico e tem como objetivo desenvolver metodologias e estratégias para alcançar resultados que sejam significativos tanto para os humanos quanto para os outros seres vivos. Entre as diversas disciplinas que podem contribuir para a ecologia da restauração uma, especificamente, tem ganhado a atenção nas últimas décadas: a filogenética. A filogenética é o campo da biologia que estuda os graus de relações evolutivas entre um determinado grupo de organismos. Desde a década de 90 estas relações evolutivas têm sido incorporadas em métricas que avaliam a diversidade filogenética de uma comunidade. Esta dissertação tem como objetivo tratar deste tema e abordar a ecologia da restauração sob uma perspectiva filogenética. No primeiro capítulo, apresentamos uma revisão sistemática da literatura com o objetivo de identificar as tendências e lacunas de conhecimentos sobre estudos de filogenia na restauração de ecossistemas vegetais terrestres. Reconhecendo a ausência de estudos filogenéticos nos neotrópicos, no segundo capítulo, nós apresentamos o primeiro estudo em larga escala, que avaliou a diversidade filogenética de restaurações florestais nos trópicos, e discutimos o nível de recuperação da história evolutiva em ecossistemas tão diversos.

Palavras-chave: Diversidade filogenética, Ecologia da restauração, Filogenia, Floresta tropical, Mata Atlântica, Revisão sistemática

ABSTRACT

Ecological restoration through a phylogenetic perspective

Ecological restoration of ecosystems is seeing as the path to mitigate and reverse the currently scenario of biodiversity and ecosystem services losses. The science of ecological restoration, known as restoration ecology, grew rapidly over the years and is currently an interdisciplinary field that covers several areas of knowledge and seeks to outline restoration methodologies and strategies to achieve results that are significant for both nature and humans. Among the many disciplines that can contribute to restoration ecology one, specifically, is slowly gaining attention: phylogenetics. Phylogenetics is the field of biology focused in understanding the degrees of phylogenetic relationships among a given group of organisms. Since the 90s, these relationships were incorporated as measures of community diversity within the phylogenetic diversity metrics. This dissertation aims to look at ecological restoration through a phylogenetic perspective. In the first chapter, we performed a systematic review in order to identify the trends and gaps of phylogenetic studies in restoration ecology of terrestrial vegetation. Acknowledging the absence of phylogenetic studies in the neotropics we present, in the second chapter, the first large scale assessment of phylogenetic diversity in tropical forests restorations and discuss the level of evolutionary recovery in such highly diverse ecosystem.

Keywords: Atlantic Forest, Phylogeny, Phylogenetic diversity, Restoration ecology, Systematic review, Tropical forest

1. INTRODUCTION

Land use change, natural resources exploitation and the introduction of invasive species driven by anthropogenic activities are the main causes of biodiversity losses worldwide (Dirzo & Raven 2003). Deforestation, specifically, is the primary cause of plant species extinction and the largest source of CO₂ emission (IPCC 2019; Dirzo and Raven 2003). Many scientists recognized that we are living the Earth's sixth mass extinction, that is, three-quarters of species are being lost in a short geological period, and for the first time this phenomenal is being caused by one single species, the humans (Barnosky et al. 2011; Pellens & Grandcolas 2016; Dirzo & Raven 2003). The dangerous of uncontrolled human activity to species conservation is long known, yet, the lack of policies, governmental investment and support brought us to this dreadful scenario (Kerr & Currier 1995). The sixth mass extinction is the proof that, so far, humankind have failed in the attempts to conserve biodiversity. In that scenario, the ecological restoration of ecosystems is seeing as the path to mitigate and reverse the currently scenario of destruction (Montoya et al. 2012; Barral et al. 2015).

Ecological restoration can be defined as the process of recovering an ecosystem that has been degraded, damaged or destroyed (Gann et al. 2019). The field of science that applies ecological theories to the establishment of concepts, models and methodologies for restoration is called Restoration Ecology (Cairns & Heckman 1996). The first restorations activities emerged as a need to preserve mainly the soil and water resources through forest restoration (Brancalion et al. 2015). However, pioneer projects lacked scientific rigor, were based on trial and error experiences, required intense maintenance and applied a large percentage of exotic species (Rodrigues et al. 2009). In this way, the first record of forest restoration in the world was carried out in the Neotropics in 1862, in the Tijuca National Park, located in Rio de Janeiro city, Brazil. The city was experiencing a period of water scarcity, and the restoration of the forest, previously occupied by coffee plantations, was the solution to the problem. However, the project required intense maintenance for over 30 years and countless exotic species were planted (Brancalion et al. 2015). The use of ecological and scientific concepts in restoration only started with Aldo Leopold in 1935 in the United States (Brancalion et al. 2015).

Although the first studies started in the 1930s, restoration ecology is still a recent scientific field, and the articles published on this subject started to gain visibility only in the 1990s, especially after the foundation of the Society for Ecological Restoration (SER) in 1988 and the Restoration Ecology scientific journal, in 1993 (Young 2000; Young et al. 2005). Nowadays, restoration is being recognized by the politicians and world leaders as the main path to overcome global warming and

its effects. Acknowledging its importance, the United Nations established 2021 as the beginning of the Decade on Ecosystem Restoration, aiming to prevent, halt and reverse the degradation of ecosystems worldwide (United Nations 2020). These unprecedented goals can only be achieved through holistic and inclusive strategies, combining efforts from academic societies, Indigenous people, politician, non-profit agencies and corporations (Aronson et al. 2020).

Restoration ecology has evolved rapidly over the years and is currently an interdisciplinary field that covers several areas of knowledge and seeks to outline restoration methodologies and strategies to achieve results that are significant for both nature and humans (Perring et al. 2015). Among the many disciplines that can contribute to restoration ecology, one specifically, is slowly gaining attention: phylogenetics.

Phylogenetics is the field of biology focused on understanding the degrees of phylogenetic relationships among a given group of organisms, usually represented as a phylogenetic tree (Henning 1965). In 1991, the conservation biologist Vane-Wright proposed a novel metric for biodiversity measuring that encompass the phylogenetic relationship among species. The metric called taxonomic distinctness was based on the concept that species are not equivalent, and therefore should not be treated as equal units. That is, species should be weighted differently according to their evolutionary history. For example, when choosing between two species, one without close relatives and another one belonging to a widespread clade, the highest weight should be given to the first one, since it has a unique evolutionary history (Vane-Wright 1991). The same concept can be applied to the community level. Communities composed by phylogenetically distant species have higher phylogenetic diversity, when compared to those composed by closely related species, given the same richness. Therefore, the conservation of communities with higher phylogenetic diversity conserves a greater extend of the tree of life (Faith 1992; Isaac et al. 2007).

Since the first measure was proposed, the phylogenetic metrics usage grew rapidly, and today there are a myriad of metrics applied for different purposes (Tucker et al. 2017). The term phylogenetic diversity is generally used to denote biodiversity measures based on evolutionary relationships between species and represents one of the many components of biodiversity (Winter et al. 2013). Beyond biodiversity, phylogenetics have been widely applied within community ecology to infer about community assembly, organization, and species co-occurrence (Webb et al. 2002). Within restoration ecology, phylogenetic diversity have large potential to be applied (Hipp et al. 2015), especially with regard to the recovery of biodiversity (Turley & Brudvig 2016; Barber et al. 2017), understanding of community assembly (Schweizer et al. 2017; Verdú et al. 2009) and improvements of restoration techniques (Meira-Neto et al. 2020; Ribeiro et al. 2018; Schweizer et al. 2013).

Recognizing the several possibilities of phylogenetic application, this dissertation aims to address different aspects of phylogeny in the service of restoration. The conception of this work, started with the idea of the second chapter, and while we were looking for references for the construction of a conceptual base, we realized that, despite phylogeny being used as a tool by different sciences, its usage within the restoration ecology was very limited. Recognizing the lack of studies, we decided to carry out a systematic review of phylogenetic studies in restoration ecology of terrestrial vegetation in the first chapter of this dissertation. We address the trends and gaps of knowledge and identify the most used phylogenetic diversity metrics as well as the explanatory and response variables assessed in these studies. Finally, in the second chapter we present the first large scale assessment of phylogenetic diversity in tropical forest restorations and discuss the levels of evolutionary recovery that we found in such a highly diverse ecosystem.

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2. PHYLOGENETIC DIVERSITY AND RESTORATION ECOLOGY OF TERRESTRIAL ECOSYSTEMS: A SYSTEMATIC REVIEW

ABSTRACT

Phylogenetic diversity metrics encompass evolutionary relationships to estimate the diversity of a given community and its usage is slowly gaining attention within restoration ecology field. Yet, the contributions of phylogeny to restoration sciences still have a lot to grow and the synthetization of the knowledge acquired so far is fundamental for future developments. In this study, we systematically review the literature to assess the usage of phylogenetic diversity metrics in terrestrial restorations studies. Specifically, we answer what are the most used metrics, what are the global trends and gaps of phylogenetic diversity metrics usage and what are the explanatory and response variables of phylogenetic diversity metrics. Our search returned a total of 120 papers, of which 33 were included in the review. Most studies were carried out in the United States, followed by China and Brazil, and the most studied biomes were temperate broadleaf mixed forests (36.36%) and tropical and subtropical moist broadleaf forest (33.33%). Half of the papers were based on observational studies of restorations and the other half were experimental studies. Considering the studied taxa, 90.09% of papers assessed the phylogenetic diversity of plants, and the most studied life forms were grasses and trees. Standardized effect size of the mean pairwise distance (ses.MPD) and mean nearest taxonomic distance (ses.MNTD) metrics were the most frequent metrics used in restoration studies. The majority of studies used phylogenetic diversity as a response variable and restoration indicators (e.g., age, initial seed/seedling mixture and restoration impact) as explanatory variables. We identified a bias towards grassland studies and the absence of studies in highly diverse continents such as Africa and Oceania.

Keywords: Phylogeny; Phylogenetic metrics; Phylogenetic structure; Ecological restoration.

2.1. INTRODUCTION

Ecological restoration aim to conserve biodiversity and improve the provision of ecosystem services for human wellbeing (Gann et al. 2019). Restoration process involves the reconstruction of communities, therefore much of basic and applied knowledge in restoration ecology rely on established ecological principles and concepts, especially in those concerning community assembly process (Young et al. 2005). Phylogenetic diversity has been recognized by researchers as a new component largely applied in macroecology, community ecology and conservation biology (Tucker et al. 2019) that have a huge potential for application within restoration ecology (i.e. the science of ecological restoration) (Hipp et al. 2015; Verdú et al. 2012).

Phylogenetic diversity was first proposed 30 years ago as a metric to identify priority species for conservation based on phylogenetic relationships (Vane-Wright et al. 1991; Faith 1992). Since them, the number of studies and phylogenetic metrics grew steadily as well as the applicability of these metrics within many fields (Tucker et al. 2019; Cianciaruso 2011; Srivastava et al. 2012; Cadotte et al. 2010). These metrics are calculated through phylogenetic trees which represents the hypothesis of evolutionary relationships among species or entities (Winter et al. 2013). Biodiversity

measures based on evolutionary relationships are argued to be more inclusive than taxonomic ones, especially for rare, threatened and data deficient species (Purvis et al. 2000; Winter et al. 2013). Moreover, it can also describe, explain, or predict biological and ecological processes shaping community assembly (Tucker et al. 2017; Webb 2000; Webb et al. 2002).

Phylogeny in the service of restoration ecology showed large potential in studies concerning the evaluation of success, seedling survival, species selection and many others (Schweizer et al. 2016; Schweizer et al. 2013; Schweizer & Brancalion 2018; Verdú et al. 2012; Verdú & Pausas 2007; Williams et al. 2018; Faith et al. 2010). In facilitation experiments, for example, the survival rate of the facilitated plants are maximized as the phylogenetic distance of the neighboring species increases (Verdú et al. 2012). Phylogenetic distance also showed positive relationships with biomass productivity (Cadotte 2013) and ecosystem stability (Cadotte et al. 2012). Moreover, in grassland experiments, phylogenetic diversity was the best predictor of biomass production when compared to other community metrics (Cadotte et al. 2008, 2009). In tropical ecosystems, studies were particularly interested in using phylogenetic to enhance seedlings performance in enrichment planting (Schweizer et al. 2013; Schweizer & Brancalion 2018). These issues have been gradually addressed, yet, important questions still need to be answered, such as: i) how the phylogenetic diversity and structure of restored areas resemble the native ecosystems, ii) can phylogenetic diversity predict community assemblage's outcomes in restored sites, or iii) how can we build accessible phylogenetic tools for restoration practitioners (Hipp et al. 2015). All these questions need to be addressed, especially now that we are entering the United Nation Decade on Ecological Restoration, in which is expected the restoration of millions of hectares worldwide.

A few decades ago, the usage of phylogenetic tools and phylogenetic tree construction required a great effort, expertise and funding (Li et al. 2019; Hipp et al. 2015). However, the publications of resolved supertrees (Qian & Jin 2016; Gastauer & Meira-Neto 2017; Smith & Brown 2018; Jin & Qian 2019; Zanne et al. 2014; Wikstrom et al. 2001) and the development of software packages (Jin & Qian 2019; Qian & Jin 2016; Webb et al. 2008) are making the use of phylogenetic metrics accessible to scientist that are not familiar with genetic sequencing. For the next years, we expect greater collaboration between the two disciplines, therefore, it is fundamental to understand where the phylogeny has it been and where does it need to go in restoration ecology field. To answer these questions, we performed a systematic literature review searching for studies that evaluate the phylogenetic diversity in terrestrial restorations. Specifically, we aim to answer the following questions: 1) what are the most used phylogenetic metrics; 2) is there a global trend of phylogenetic diversity metrics usage in restoration ecology studies; 3) what are the gaps to the

applications of phylogenetic metrics in the restoration ecology; and 4) what are the explanatory and response variables of phylogenetic diversity metrics.

2.2. METHOS

We systematically searched for the relevant literature using the ISI Web of Science, Scopus and CAB Direct platforms, to retrieve publications with the following terms: "restor*" AND "phylo* diversit*" OR "phylo* ecology" OR "phylo* pattern*" OR "phylo* structur*" OR "phylo* beta" OR "phylo* distance". The search performed in July of 2020 spanned all years on record and returned a total of 412 papers. We removed the duplicates and followed the screening process (Appendix A) to select the papers in English that met all the eligibility criteria: (a) primary research papers; (b) papers that studied ecological restoration of terrestrial vegetation or papers that performed experiments concerning ecological restoration of terrestrial vegetation; and (c) papers that applied phylogenetic diversity metrics to assess the studied community. We considered ecological restoration as the process of assisting the recovery of an ecosystem that has been degraded, damaged, or destroyed (Gann et al. 2019). Therefore, we excluded the papers that only evaluated natural regenerated sites that do not involved any type of human intervention towards the recovery of the ecosystem. This process finally produced a database with 33 papers that assessed communities through phylogenetic metrics and met all the eligibility criteria (Appendix B). We analyzed these papers full texts to synthesize information about the following categories: (1) publication details, (2) restoration project characteristics, (3) study design, (4) phylogenetic metrics and (5) variables (Table 1).

The publication details category included year of publication and scientific journal where the paper was first published. Restoration project characteristics included the restoration technique applied in the studied area, country, and biome (according to Olson et al. 2011) where the study was conducted.

Within the study design category, we assessed the studied taxa, the existence of temporal monitoring and the use of reference and or control sites for comparisons. We also described whether the study was experimental or observational. We classified as experimental those studies where the scientists manipulated one or more variables to study its effects in the variable of interest. Whereas the observational studies, are those where the scientists made no manipulation, only observed the natural variation of the variable of interest (Gotelli & Elisson 2011).

In the phylogenetic metrics category, we identified all metrics used in the studies and classified according to the three phyllo-diversity dimensions proposed by Tucker et al. 2017:

richness, divergence and regularity. Richness metrics are calculated as the sum of phylogenetic differences within an assemblage; the divergence metrics compute the average phylogenetic difference among taxa in an assemblage; whereas the regularity metrics, quantify how regularly species are distributed along the phylogenetic tree and how evenly distant are species from each other (Tucker et al. 2017).

In order to calculate the phylogenetic diversity of a given community is necessary the construction of a dated hypothetical phylogenetic tree. Therefore, we evaluated the methodology applied to construct the phylogenetic trees, whether it was synthesis-based or purpose-based phylogenies. Purpose-based phylogenies are those constructed through genetic sequences whereas synthesis-based trees are constructed using a megaphylogeny as backbone (Li et al. 2019).

We also evaluated the response and explanatory variables of phylogenetic diversity used in the studies. We grouped the variables in ecological, restoration, landscape, environmental and topographic indicators. (Table 1). We further categorized the ecological indicators into composition, structure and function, following Gatica-Saavedra et al. 2017. The composition category encompasses richness, similarity, evenness, dominance, density, and abundance variables. The structure category refers to vegetation characteristics such as height, diameter, weight, traits, canopy cover, vegetation cover and litter structure. The function category encompass soil parameters, biomass, functional diversity, nutrient cycling and biological interactions (Ruiz-Jaen & Aide 2005; Gatica-Saavedra et al. 2017; Wortley et al. 2013). The restoration indicators included the variables related to restoration age, method and impact, seeds/seedlings mixtures and populations sources, years since last fire, disturbance level and seedlings performance. Landscape indicators comprehend distance to forest remnant, land use history and site size. The environmental indicators included precipitation, and temperature measurements, whereas the topographic indicators encompass measures such as slope and altitude.

Table 1. Description of the categories used to characterize the papers selected from the literature review.

Item	Category	Description
Publication details	Year of publication	Year of paper publication
	Journal of publication	Journal where the paper was published
Restoration project characteristics	Restoration technique	Restoration technique applied in the studied site.
	Country	Country where the study of conducted
	Biome	Biome where the study was conducted, according to Olson et al. 2011
Study design	Studied taxa	Description of the taxa assessed in the study
	Temporal monitoring	Existence and period (in months) of temporal monitoring in the study
	Use of reference/control sites	Usage of reference and or control sites for comparisons in the study
	Nature of the study	Whether the study was based on experimental or observational studies
Phylogenetic metrics	Phylogenetic metrics	Description of the phylogenetic metric used in the study. The metrics were classified according to the framework proposed by Tucker et al. (2017)
	Phylogenetic tree construction	Methodology applied to construct the phylogenetic tree, whether it was synthesis-based or purpose-based
Variables	Response and explanatory variables	Response and explanatory variables of phylogenetic diversity. The variables were grouped as ecological, restoration, landscape, environmental and topographic indicators.

2.3. RESULTS

The first paper based on phyllo-diversity dimensions was published in 2012, yet there is not a clear increase trajectory of publications (Figure 1). The Forest Ecology and Management journal concentrated most papers, followed by the Journal of Applied Ecology.

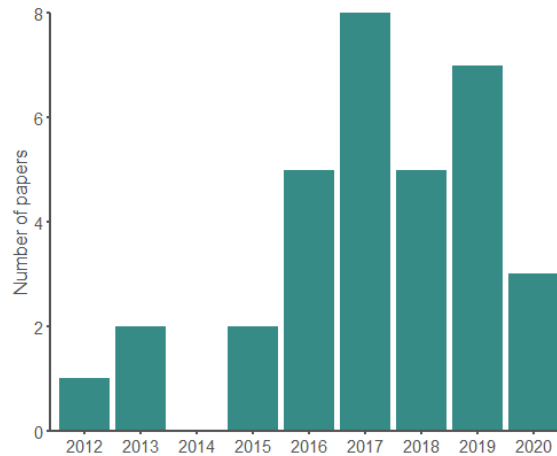


Figure 1. Number of studies based on phylogenetic diversity metrics in restored sites of terrestrial ecosystems per year.

Looking at the studied sites characteristics, we found papers conducted in 10 different countries (Figure 2 and 3A). The majority were carried out in the United States, followed by China and Brazil (Figure 3A). The most studied biomes were temperate broadleaf mixed forests (36.36%) and tropical and subtropical moist broadleaf forest (33.33%) (Figure 3B). Temperate grasslands and Mediterranean forest accounted for 12.12% and 9.09% of studies, respectively (Figure 3B). Whereas montane grasslands, savannas and temperate coniferous forest had only one study each. Regarding the restoration methods, 31 papers applied active restoration techniques such as seed sowing, total seedling plantings, enrichment planting and invasive species removing. Only three studies applied assisted restoration techniques.

Considering the studied taxa, 30 papers assessed the phylogenetic diversity of plants, two assessed fungal or bacteria and only one paper assessed fauna (only birds) diversity. Regarding the plant studies, the most studied life forms were grasses (66.67%), followed by trees (43.33%), shrubs (26.67%), herbs (20%) and lianas (6.67%).

Half of the papers were based on observational studies and the other half were experimental studies. Comparisons with reference sites were assessed in 53% of the observational studies and in 6.25% experimental studies, whereas comparisons with control sites were assessed in 43.75% of experimental studies. With respect to monitoring, 32.29% of the observational studies and 68.75% of the experimental studies assessed the phylogenetic diversity through time, of which, 36.37% assessed the sites before and after the restoration interventions. The average temporal monitoring was 40.83 months in observational studies and 57.66 months in experimental studies.

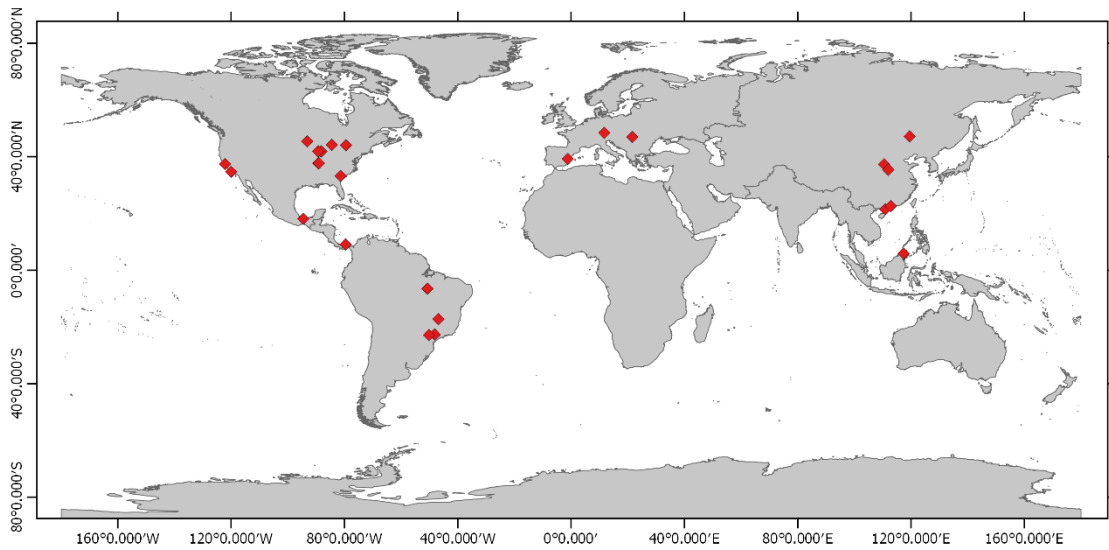


Figure 2. Distribution of the 33 studies based on phylogenetic diversity metrics in restored sites of terrestrial ecosystems across the world.

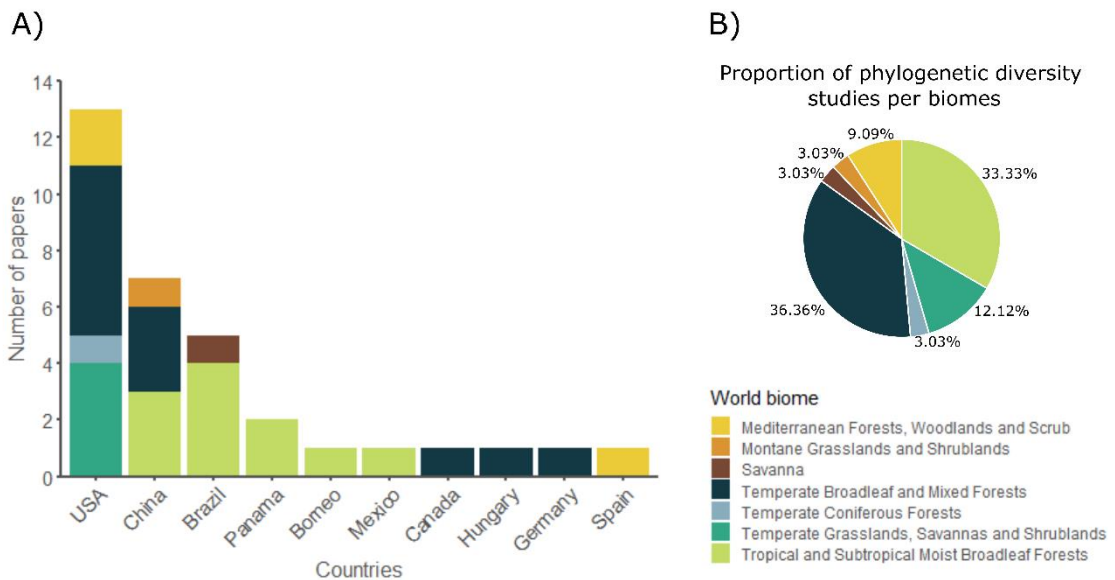


Figure 3. Distribution of phylogenetic diversity studies per biome (Olson et al. 2011), A) by country, B) total proportions.

Among the studies, we found 21 different phylogenetic diversity metrics, of which, 17 were alpha and four were beta (Table 2 and 3). Considering the dimensions of phylogenetic information proposed by Tucker et al. (2017), most metrics belonged to the divergence dimension, followed by richness and regularity. Four (Chao1 PD, DMANS, PAE and lnD) out of the 21 metrics were not classified by Tucker et al. (2017) (Table 2). The standardized effect size of mean pairwise distances (ses.MPD or NRI) and mean nearest taxonomic distances (ses.MNTD or NTI) were the most used alpha diversity metrics, applied in 15 and 12 studies, respectively. Whereas

MPD-based and MNTD-based β -diversity were the most used metrics when comparing assemblages. Three studies did not calculate any phylogenetic metric but applied the phylogenetic distance between species in their analysis (Table 3).

Table 2. Phylogenetic diversity alpha metrics applied in the papers selected from the literature review, its description, reference, number of papers, and classification (richness, divergence, and regularity) according to Tucker et al. (2017).

	Phylogenetic metric	Description	Reference	Number of papers	
Richness	Faith's PD	Sum of total branch lengths connecting species together	(Faith 1992)	8	
	ED	Evolutionary distinctiveness	(Isaac et al. 2007)	2	
Divergence	MPD = AvTD	Mean pairwise distance (MPD) Average taxonomic distinctness index (AvTD)	(Clarke & Warwick 1998; Webb et al. 2002; Webb 2000)	11	
	MPD.i	Mean phylogenetic distance between invasive species and the native community	(Bennett et al. 2013; Williams et al. 2018)	1	
	MNTD	Mean nearest taxonomic distance	(Webb 2000; Webb et al. 2002)	5	
	MNTD.i	Mean nearest taxonomic distance between invasive species and the native community	(Bennett et al. 2013; Williams et al. 2018)	1	
	sesMPD = -1 NRI	Standardized Mean pairwise distance	(Webb et al. 2002; Webb 2000)	15	
	sesMNTD = -1 NTI	Standardized Mean nearest taxonomic distance	(Webb et al. 2002; Webb 2000)	12	
	AvPD	Average phylogenetic diversity index	(Clarke & Warwick 2001)	1	
	WMDNS	Weighted mean distance to the native species	(Thuiller et al. 2010)	1	
	Regularity	VarTD	Variation in taxonomic distinctness index	(Clarke & Warwick 1998)	1
		IAC	Imbalance abundances of higher clades	(Cadotte et al. 2010)	1

Not classified by Tucker et al. (2017)	H _{ED}	Entropy measure of evolutionary distinctiveness	(Cadotte et al. 2010)	2
	Chao1 PD	Phylogenetic diversity	(Chao 1984)	1
	DMANS	Distance to the most abundant native species	(Thuiller et al. 2010)	1
	PAE	Phylogenetic evenness of the abundance distribution scaled by branch lengths	(Cadotte et al. 2010)	1
	lnD	Species phylogenetic position in a community	(Chang et al. 2015)	1

Table 3. Phylogenetic diversity beta metrics applied in the papers selected from the literature review, its description, reference, number of papers, and classification (richness, divergence, and regularity) according to Tucker et al. (2017).

	Phylogenetic metric	Description	Reference	Number of papers
Richness	Unifrac	Phylogenetic distance between sets of taxa in a phylogenetic tree	(Lozupone & Knight 2005)	1
	Jaccard's PD	Jaccard dissimilarity index for phylogenetic diversity	(Cardoso et al. 2014; Lozupone & Knight 2005)	1
Divergence	β -MPD = MPD _{ac}	MPD-based β -diversity	(Ricotta & Burrascano 2009; Swenson et al. 2011)	4
	β -MNTD = MNTD _{ac}	MNTD-based β -diversity	(Ricotta & Burrascano 2009; Swenson et al. 2011)	4

The phylogenetic diversity metrics were used as response variables in 21 papers and as explanatory variables in 12 papers. When phylogenetic diversity metrics were used as a response variable, the majority of studies (n=21) used restoration indicators (e.g., impact of restoration, restoration age, and initial seed/seedling mixture) as the explanatory variable. Functional indicators (e.g., biomass, predation, community stability and soil assessments), were the second most used explanatory variables (n=9), followed by composition, landscape and environmental indicators (four papers each) and structure and topographic indicators (three papers each) (Figure 4). On the other hand, when phylogenetic diversity metrics were used as an explanatory variable, the majority (n=7) of papers used functional indicators as a response variable, followed by compositional and restoration indicators (four papers each).

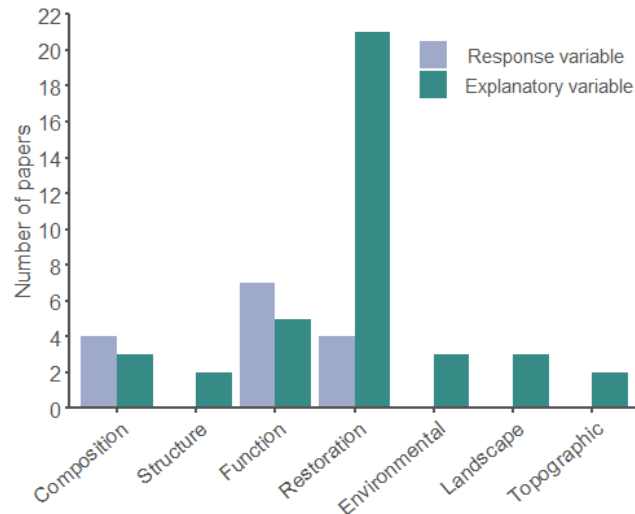


Figure 4. Number of papers that used each of the indicators category as response and/or explanatory variables in relation to phylogenetic diversity metrics.

2.4. DISCUSSION

We found that the number of studies that considered the phylogenetic diversity aspect in restoration of terrestrial vegetation is very limited and biased in terms of studied countries, taxon and metrics. Moreover, the explanatory and response variables were on its majority related to restorations characteristics and function indicators, respectively.

The first ecological restoration paper to assess phylogenetic diversity metric was published in 2012, more than twenty years after the first metric was proposed (Vane-Wright et al. 1991). Since then, the number of papers on this subject has not shown significant growth. This result demonstrates a lack of interaction between the two disciplines. We already expected this result since none of previous reviews concerning ecological indicators of restorations success had mentioned phylogenetic diversity metrics usage (Gatica-Saavedra et al. 2017; Ruiz-Jaen & Aide 2005; Wortley et al. 2013). In 2015, Hipp and collaborators had already highlighted the benefits of incorporating phylogeny in the service of restoration ecology and pointed out the methodological gaps and the inadequate communication across disciplines as possible factors for the low use of phylogeny in restoration studies. However, the collaboration among disciplines is still poor, at least for studies regarding the restoration of terrestrial vegetation, which is the subject of our study.

The concentration of studies in the United States corroborates with geographical biased towards North America found in previous restoration reviews (Wortley et al. 2013; Ruiz-Jaen & Aide 2005), which is correlated with the fact that high-income countries have more resources to invest in restoration research (Aronson et al. 2010). Contrastingly, we found no studies about phylogenetic in Africa and Oceania, which is a concerning result, since these are two continents

with high levels of biodiversity, endemism and ecological restoration opportunities (Myers et al. 2000; Brancalion et al. 2019; Campbell et al. 2017). Africa holds the top six tropical countries with the highest restoration opportunities, yet, the number of studies performed in this continent is inexpressive for many restoration subjects (Carlucci et al. 2020; Wortley et al. 2013; Gatica-Saavedra et al. 2017; Ruiz-Jaen & Aide 2005). Our results confirm the need for more investment and prioritization for studies in Africa. Recent efforts such as African Forest Landscape Restoration Initiative (AFR100) offer a great chance for increasing efforts on restoration studies focusing on phylogenetic approach. On the other hand, the absence of papers in Oceania was not expected given that Australia and Oceania are high-income countries. Such results highlight how phylogenetic diversity is still little explored, even in countries with a long expertise in restoration programs (Campbell et al. 2017; Saunders & Norton 2001; McDonald et al. 2018).

Beyond country biased, we also found an unbalanced distribution of studies across the biomes. On one hand, the high percentage of studies in tropical and subtropical moist broadleaf forests is a good sign. These biomes harbor the highest world's biodiversity, facing constant threats caused by human activities and have an enormous need for ecological restoration (Malhi et al. 2014; Brancalion et al. 2019). Approximately two thirds of global species are found in tropical forests, therefore, the use of phylogenetic diversity metrics to evaluate the level of evolutionary history of the communities that are being recovered in restored sites is essential. Conversely, highly diverse biomes such as tropical and subtropical grasslands-savannas-shrublands had only one assessment each. The absence of studies in those biome was not a surprise since non-forest ecosystems were historically neglected by restoration initiatives in these regions (Veldman et al. 2017; Buisson et al. 2020, 2019). The majority of conservation and restoration programs in the tropics are tree-oriented, aiming the mitigation of global warming effects through carbon storage (Overbeck et al. 2015; Veldman et al. 2015; Buisson et al. 2020; Locatelli et al. 2015; Shimamoto et al. 2014; Brancalion et al. 2018).

The large number of experimental studies was not a surprise since this is the dominant mode of inquiry in the restoration ecology field, differently from other disciplines such as conservation biology (Young 2000). Only half of the observational studies assessed reference sites for comparisons, although the Society for Ecological Restorations emphasizes the importance of a reference ecosystem as a model to characterize the approximate condition the site would be if degradation had no occurred (Gann et al. 2019).

Regarding the temporal monitoring, we found that half of the studies assessed phylogenetic diversity more than once. Ecological restoration is defined as a process and not a static event, a long and non-deterministic process open to stochastic events (Deluca et al. 2010;

Rodrigues et al. 2009). Therefore, temporal monitoring is fundamental to support adaptive management in ongoing restoration projects, assess restoration outcomes and evaluate whether the restoration target will be accomplished (Wortley et al. 2013; Rodrigues et al. 2009). In this context, phylogenetics can be particularly informative identifying the environmental factors shaping community assembly through time (Webb 2000). The phylogenetic structure of the community can indicate if environmental filtering or competition is the main ecological process shaping community composition and can help restorations practitioners adjusting the best techniques and methods to enhance restoration success (Webb 2000; Webb et al. 2002).

Only three studies focused in other organisms rather than plants, a worldwide tendency pointed out by previous studies (Young 2000; Guerra et al. 2020; Holl & Aide 2011). Although the role played by animals as dispersers, pollinators and grazers are recognized as fundamental to achieve restoration success (Dixon 2009; Beltrán & Howe 2020), the absence of fauna studies is still a major gap in restoration ecology (Guerra et al. 2020; Holl & Aide 2011). The one study in our review that assessed fauna, compared the phylogenetic diversity of logged forest restored sites (enrichment, vine and bamboo cutting) with naturally regenerating forests in Borneo (Cosset & Edwards 2017). The study found that the overall phylogenetic diversity of the understory bird community was the same between the restored and naturally regenerating forests. However, the overall bird community was lower in the restored forests. The authors believe that these results indicate that the main drivers of phylogenetic diversity changes are related to the understory community level. These are interesting findings, yet a more work needs to be done within that subject.

2.4.1. Phylogenetic metrics

Standardized effect size of mean pairwise distance (ses.MPD) and mean nearest taxonomic distance (ses.MNTD) were the most applied phylogenetic metrics. They are classified within the divergence dimension, and are used to answer questions about how closely related are the species within or between assemblage's phylogeny. The standardized effect sizes are calculated comparing the observed values of MPD and MNTD with null models generated from the regional species pool. These metrics were proposed by Webb in 2000, and are widely applied in many fields due to its ease interpretation and precedence in the literature (Tucker et al. 2017). Through these metrics it is possible to determine the structure (clustered or dispersed) of a community, as well as the ecological processes shaping community assemblages (Webb 2000). The studies found in our review applied these metrics to evaluate how disturbance, nitrogen supply, environmental factors,

seed mixes and seed population sources affect phylogenetic structure of tallgrass restorations (Brandt et al. 2019; Barber et al. 2019; Khalil et al. 2018, 2017).

The number of phylogenetic metrics grew rapidly over the years. There are approximately 70 different metrics, often mathematically similar to one another (Tucker et al. 2017). For those restoration scientists interesting in incorporate phylogenetic diversity in their studies, but are confused with the sea of different metrics, frameworks, such as proposed by Tucker et al. (2017) and others (Pavoine & Bonsall 2011; Ricotta 2007) help clarify the interpretation and similarities between all these metrics. These frameworks are fundamental to bridge the gap between the two disciplines.

Regarding the methods applied to construct phylogenies in restorations studies, we found that most studies used synthesis-based rather than purpose-based phylogenies. Purpose-based trees are constructed through genetic sequences, however only approximately 20% of vascular plants have been sequenced, according to GenBank (Jin & Qian 2019). Moreover, the construction of these purpose trees require great effort, expertise and funding (Li et al. 2019). Therefore, scientists commonly use megaphylogeny trees resolved at the family or genus level as a backbone (source tree) to construct their own synthesis-based phylogenies (Jin & Qian 2019; Li et al. 2019).

2.4.2. Explanatory variables

Most papers used restoration indicators as explanatory variables of phylogenetic diversity. The studies were mostly interested in evaluate the impact of restoration interventions in the phylogenetic diversity, assess how phylogenetic diversity varied over the years since restorations started and understand how the initial seed/seedling composition predict the phylogenetic diversity of restorations. The measurement of restoration impact and success is a major theme in restoration ecology (Gatica-Saavedra et al. 2017; Wortley et al. 2013; Ruiz-Jaen & Aide 2005), especially because this is an activity that requires large amount of time, effort and money, and we need to make sure that all the investment is worth (Holl & Howarth 2000; Rodrigues et al. 2009; Brancalion et al. 2012). Traditional success measurements involves the assessment of taxonomic diversity, composition and vegetation structure (Gatica-Saavedra et al. 2017; Wortley et al. 2013; Ruiz-Jaen & Aide 2005). However, phylogenetic approaches have a lot to contribute to success assessment, since it can correlate with ecosystems functioning (Srivastava et al. 2012).

As we said earlier, temporal monitoring is fundamental to support adaptive management, evaluate whether restoration targets will be accomplished in the near future and comprehend the changes in community assembly through time (Wortley et al. 2013; Rodrigues et al. 2009). The

studies that used restoration age as an explanatory variable of phylogenetics found contrasting results, with significant effects in communities phylogenetic structure in grassland experiments (Khalil et al. 2017, 2018; Gibson et al. 2019) but not significant in observational studies (Barak et al. 2017; Barber et al. 2019). Whereas, in tropical ecosystems, studies found that restoration age had significant effects on phylogenetic diversity (Li et al. 2018; Schweizer et al. 2015).

If we aim to restore ecosystems that recover the local evolutionary history, it is important to understand to what extent the initial composition affects the future phylogenetic diversity. Grassland studies found significant (Khalil et al. 2017) and not significant (Barber et al. 2019; Barak et al. 2017; Barber et al. 2017) effects of initial seed mix in phylogenetic diversity. In tropical trees, recent studies also found contrasting results, with positive (Schweizer et al. 2015) and negative (Li et al. 2018) influences of initial planting in phylogenetic patterns. These studies are extremely necessary in highly diverse ecosystems such as tropical forests. In the Brazilian Atlantic Forest for example, restoration practitioners use, on average, 80 species from different successional groups (fast and slow growing) to actively restore forest ecosystems (Rodrigues et al. 2009). However, we do not know if this richness is sufficient to guarantee the recovery of the local evolutionary history.

2.4.3. Response variables

When phylogenetic diversity was used as explanatory variable, the response variables were on its majority related to function indicators, such as biomass, predation, community stability and soil assessments. Ecological restoration is particularly interested in restoring ecosystems functionality, yet the measurement of functional diversity can be a difficult task due to the lack of species trait information or insufficient knowledge of how traits correspond to ecological services (Tucker & Cadotte 2013; Carlucci et al. 2020). In this context, phylogenetic diversity can be used as a useful and simple tool to assess the functionality of restored ecosystems. Some plant functional traits usually target as surrogates of ecosystem function in ecological restoration (Carlucci et al. 2020), such as woody density (Swenson & Enquist 2007; Chave et al. 2006; Hietz et al. 2017) and dispersal syndromes (Kuhlmann & Ribeiro 2016; Cortés-Flores et al. 2019) demonstrate strong phylogenetic signal (i.e. traits conservatism within the phylogeny). Yet, more effort needs to be done in order to identify the strength of these assumptions in different biomes and ecosystems.

2.4.4. Future directions

Our study demonstrated that phylogenetic diversity is still poorly applied within restoration ecology, although there are a number of opportunities and questions to be answered. We believe that the collaboration among scientists from different fields (i.e., phylogenetic, evolution, macroecology, conservation biology) is the path to fill this gap in a two-way street. The same way that other disciplines can help the development of restoration ecology, the experimental nature of restoration can help the elucidation of questions from these disciplines. We highlight the importance of expand the phylogenetic studies to a wider variety of biomes and ecosystems, especially the highly diverse ones, such as tropical forests. We also emphasize one important subject that we believe to be of great importance to be studied in the next years - on how phylogenetic can enhance ecological restoration success in a climate change scenario.

If on the one hand, restoration is seen as a path to mitigate global warming through carbon stocking, on the other, the future biophysical shifts (e.g., temperatures and sea level increase, changes in weather and precipitation patterns and higher incidence of extreme climatic events) caused by climate change has the potential to negatively impact the practice and outcomes of restoration (Harris et al. 2006). If global warming does not reduce within the next years, soon, in some regions, restorations based solely on historical references will be doomed to fail, since the past environmental characteristics will be completely different in the future (Harris et al. 2006). In that scenario, recent studies argue that conserving high phylogenetic diverse communities can enhance its evolutionary potential (i.e., potential of lineages adaptation and/or future diversification) in face of environmental changes (Tucker et al. 2019). Yet, the evidences for these assumptions are unclear and demands more research (Tucker et al. 2019; Winter et al. 2013).

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3. NO RECOVERY OF PLANTS EVOLUTIONARY HISTORY IN RESTORED TROPICAL FORESTS

ABSTRACT

Our study presents the first large scale evolutionary history assessment of restored sites in a highly diverse tropical ecosystem. The study was conducted in three Atlantic forest vegetation types (i.e., semideciduous, ombrophilous or mixed ombrophilous) where we evaluated both established and regenerating strata of 233 restoration assemblages (1 to 94 years old) and compared with 39 reference ecosystems. We used distinct phylogenetic diversity metrics to measure different depths of evolutionary relationships within the phylogenetic tree. We calculated the alpha metrics mean pairwise distance (MPD) to measure the overall evolutionary relationships and the mean nearest taxonomic distance (MNTD) to measure the recent (i.e., terminal nodes of the phylogenetic tree) evolutionary relationships. The measurements of distinct depth of the phylogenetic tree are important since different processes may act at different evolutionary time scales. To further comprehend the overall evolutionary history recovery, we combined the MPD results with the phylobetadiversity metric Unifrac and hypothesize six possible scenarios for the evolutionary history restoration assemblages. We found that the MNTD of restorations showed higher values than the reference ecosystems for all strata in all vegetation types. For the MPD and beta analysis, we found scenarios of loss and no recovery of evolutionary history in the semideciduous forests, partial recovery in the established stratum of ombrophilous and mixed ombrophilous forests and a false recovery of the regenerating stratum of mixed ombrophilous forests. We discuss each of these scenarios individually and address how the restoration age, species selection and dispersal can explain our findings.

Keywords: Atlantic forest; Community assembly; Ecological restoration; Phylogenetic diversity; Alpha diversity; Beta diversity; Phylogenetic diversity dimensions

3.1. INTRODUCTION

Ecological restoration can be defined as the process of recovering an ecosystem that has been degraded, damaged or destroyed (Gann et al. 2019). One of the main concerns in restoration ecology is to determine when a forest is recovered and what indicators should be evaluated in order to make that decision. The Society for Ecological Restoration (SER) suggest the evaluation of nine attributes to determine the ecological restoration success (SER 2004), among them, the taxonomic diversity is the most studied attribute (Ruiz-Jaen & Aide 2005; Wortley et al. 2013). However, in the past decades, new diversity components are being used within the conservation ecology science that have large potential for the restoration ecology field. Among them, the phylogenetic diversity approaches that measure the amount of communities evolutionary history (Purvis et al. 2000; Winter et al. 2013).

The phylogenetic diversity metrics encompass evolutionary relationships to estimate the diversity of a given community (Faith 1992; Vane-Wright et al. 1991; Webb 2000). These metrics are calculated through phylogenetic trees which represents the hypothesis of evolutionary relationships among species or entities (Winter et al. 2013). Each species in the tip of the tree reflect the accumulation of phenotypical, genetically and behavioral characteristics (Harvey & Pagel 1991).

Closely related species have similar characteristics to each other; on the other hand, species without closely relatives have unique and distinct attributes (Harvey & Pagel 1991; Tucker et al. 2017; Webb 2000). The more phylogenetically distinct are the species of a community, the higher its phylogenetic diversity. Since the early 90s, scientists have been studying the use of phylogeny applied to conservation strategies planning (Faith 1992; Vane-Wright et al. 1991; Redding & Mooers 2006; Hartmann & Andre 2013). However, although restoration aim to promote biodiversity conservation, phylogeny still need to be fully embraced by restoration ecology. The inadequate communication and methodological gaps are pointed as possible reasons for the lack of interaction between disciplines (Hipp et al. 2015). Nevertheless, we are now entering the United Nation Decade on Ecosystem Restoration (United Nations 2020), in which is expected the restoration of millions of hectares worldwide. It is time to evaluate what kind of ecosystems we (i.e., society, restoration practitioners and scientists) are recovering, and what we aimed, in terms of evolutionary history conservation.

Previous studies demonstrated loss of evolutionary history when comparing restored sites and natural remnants of tallgrass assemblages (Barak et al. 2017). In tropical ecosystems, phylogenetic diversity metrics were used to compare techniques (Schweizer & Brancalion 2018), evaluate success (Schweizer et al. 2015), measure the influence of environmental factors (Williams et al. 2018), competition (Verdú et al. 2012), fire (Verdú & Pausas 2007) and ecosystem services (Faith 2010) on restored sites. Moreover, phylogeny also demonstrated to be a useful tool in species selection for restorations practices aiming to optimize seedling performance (Schweizer & Brancalion 2020; Schweizer et al. 2013; Schweizer & Brancalion 2018). Yet, there is a need to understand how the phylogenetic diversity of restored sites resembles native ecosystems and how phylogenetic diversity predict community assemblage's outcomes in restorations (Hipp et al. 2015). The integration of phylogeny and restoration ecology is a fundamental theme for advancing science and practice beyond the traditional approaches.

Our goal was to evaluate if and how the evolutionary history of woody plant assemblages is being recovered in restored sites of the Brazilian Atlantic forest. Located in the neotropics, the Atlantic forest is a biodiversity hotspot with approximately 20 thousand species of plants and more than 1300 species of vertebrates with a high percentage of endemism (Myers et al. 2000). This ecosystem suffered an intense process of deforestation and land use change, remaining only 28% of its original vegetation cover (Rezende et al. 2018), threatening the survival of the local fauna and flora and the provision of ecosystem services (Emer et al. 2019; Silva & Tabarelli 2000; Mitchell et al. 2015). As a solution, is expected the restoration of millions Atlantic forest hectares in the next decades, pushed by the federal Native Vegetation Protection law (Rother et al. 2018; Brancalion et

al. 2016) and international and national agreements, such as Bonn Challenge and the Atlantic Forest Restoration Pact, respectively (Brancalion et al. 2013; Pinto et al. 2014; Melo et al. 2013). The Atlantic forest is the most studied Brazilian biome concerning ecological restoration (Guerra et al. 2020), yet, this is the first large scale study to assess its level of evolutionary history recovery.

To achieve our goal, we tested whether phylogenetic diversity of woody plants from active and assisted restored areas recovered the phylogenetic diversity of reference ecosystems (native forests). We evaluated both adults (hereafter established stratum), and the regenerating stratum from 233 restoration sites (from 1 to 94 years old). The study of the regenerating stratum is fundamental to understand the potential sustainability of the community over time. The young individuals of the present, under suitable conditions, will develop and compose the forest in the future in a process of natural succession (Chambers & MacMahon 1994).

We used distinct phylogenetic diversity metrics to measure different depths of evolutionary relationships within the phylogenetic tree. We calculated the mean pairwise distance (MPD) to measure the overall evolutionary relationships and the mean nearest taxonomic distance (MNTD) to measure the recent (i.e., terminal nodes of the phylogenetic tree) evolutionary relationships (Webb et al. 2002). The measurements of distinct depth of the phylogenetic tree is important since different processes may act at different evolutionary time scales (Mazel et al. 2016). For the recent evolutionary relationships, we expect to find higher values of MNTD in the restored sites when compared with reference ecosystems. This because, restoration projects in tropical forest select species that comprise as many families and genus as possible, therefore we expect to find many species without close relatives, which will inflate the MNTD.

To further comprehend the overall evolutionary history recovery we combined the MPD results with the phylobetadiversity metric Unifrac (Lozupone & Knight 2005) and hypothesize six possible scenarios, adapted from Sobral et al. (2016), for the evolutionary history recovery of established and regenerating stratum of restoration assemblages (Figure 5):

(1) Full Recovery: the species from the restoration and reference ecosystem share the same volume and position in the phylogenetic multidimensional space and, therefore, phylogenetic alpha diversity should be the same and phylogenetic beta diversity is near to zero.

(2) Recovery and gain: the species from the restoration occupy a higher volume but similar position in the multidimensional space when compared to the reference ecosystem. In this case, alpha diversity is higher in the restorations and dissimilarity is mainly explained by the nestedness-resultant component of phylogenetic beta diversity.

(3) Partial recovery: the species from the restoration occupy a lower volume but similar position in the multidimensional space when compared to the reference ecosystem. Alpha diversity

is higher in the reference ecosystem while phylogenetic dissimilarity is explained by the nestedness-resultant component of phylogenetic beta-diversity.

(4) False recovery: the species from the restoration and reference ecosystem share the same volume but have completely different positions within the phylogenetic multidimensional space. Alpha diversity is similar, and the beta diversity is mostly explained by its turnover component.

(5) Gain but no-recovery: the species from the restoration occupy a higher volume but in a different position of the multidimensional space when compared to the reference ecosystem. Alpha diversity is higher in the restoration and beta diversity is mainly due to the turnover component.

(6) Loss and no-recovery: the species from the restoration occupy a lower volume in a completely different position of the multidimensional space when compared to the reference ecosystem. Alpha diversity is higher in the reference ecosystem and phylogenetic dissimilarity arises mainly from turnover phenomenon.

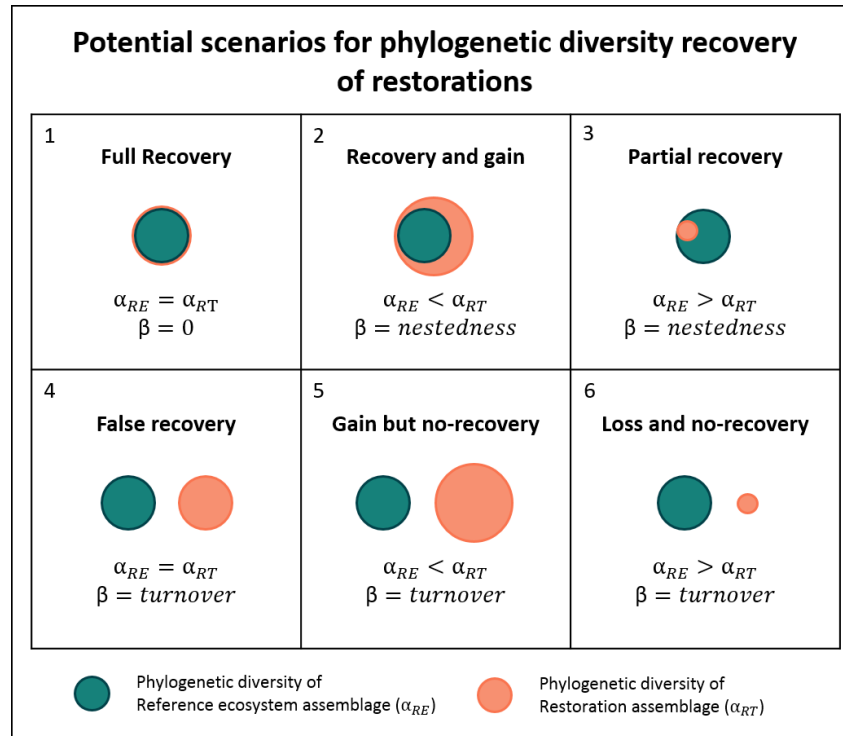


Figure 5. Potential scenarios for phylogenetic alpha (α) and beta (β) diversity of woody plant assemblages of restoration areas (adapted from Sobral et al. 2016). The circles represent the portion (volume and position) occupied by woody plants species from restoration (orange circles) and reference ecosystems (green circles) within the multidimensional phylogenetic space. Scenarios are described as follows: (1) Full Recovery: phylogenetic alpha diversity should be the same and phylogenetic beta diversity is near to zero. (2) Recovery and gain: alpha diversity is higher in the restores sites and dissimilarity is mainly explained by the nestedness-resultant component of phylogenetic beta diversity. (3) Partial recovery: alpha diversity is higher in the reference ecosystem while phylogenetic dissimilarity is explained by the nestedness-resultant component of phylogenetic beta-diversity. (4) False recovery: alpha diversity is similar, and the beta diversity is mostly explained by its turnover component. (5) Gain but no-recovery: alpha diversity is higher in the restoration and beta diversity is mainly due to the turnover component. (6) Loss and no-recovery: alpha diversity is higher in the reference ecosystem and phylogenetic dissimilarity arises mainly from turnover phenomenon.

3.2. METHODS

3.2.1. Study sites

We studied 233 restoration sites located along the Brazilian Atlantic Forest domain (Figure 6). Due to its long extension (latitude: 5° N to 33° S and longitude 35° W to 52° W), the Atlantic forest comprises a variety of vegetation types with different climatic and species compositional characteristics (IBGE 2012). The studied restored sites are located in three different vegetation types: 109 sites in the semideciduous forests (SF), 87 in the ombrophilous forests (OF) and 37 in the mixed ombrophilous forests (MOF). These forests differed on their floristic composition, which are strongly influenced by distinct environmental conditions (rainfall seasonality and temperature) (Oliveira-Filho & Fontes 2000; IBGE 2012). Furthermore, they also

differ from each other in terms of phylogenetic basis (Duarte et al. 2014), in which Amazonian lineages are largely present in the semideciduous and northern ombrophilous forests, whereas Andean-centered taxa strongly influences the mixed ombrophilous forests (Rambo 1951; Fiaschi & Pirani 2009; Safford 2007; Santos et al. 2007; IBGE 2012).

The semideciduous forests are characterized by the seasonal climate, which causes the partial fall of foliage during the cold and dry winter (IBGE 2012). About 20% to 50% of trees lose their leaves in this period. The summer is marked with high temperatures and intense rainfalls. Semideciduous forests are dominated by Amazonian genera such as *Parapiptadenia*, *Peltophorum*, *Cariniana*, *Lecythis*, *Handroanthus* and *Astronium* (IBGE 2012). The ombrophilous forests are associated with elevate temperatures and high levels of precipitations through the entire year. The vegetation is characterized by the presence of lianas and epiphytes in abundance (IBGE 2012). The mixed ombrophilous forests, also known as Araucaria forests, are typically from the highland plateau of southern Brazil, and its floristic composition is dominated by phylogenetically primitive genera such as *Drymis*, *Araucaria* and *Podocarpus*, which makes this vegetation type more phylogenetically distinct (IBGE 2012, Duarte et al. 2014).

We obtained the restoration data from the database of the Laboratory of Ecology and Forest Restoration, University of São Paulo, Brazil. This database contains information about woody plant species richness, composition, and abundance of more than 500 restoration projects sampled over the last decade, exciding 450.000 m² of sampling area. For our study, we selected the restoration sites with total sampling effort higher than 0.01 hectares restored through active (total seedling planting) and assisted methods (conduction of natural regeneration after clear cut and abandoning of pine and eucalyptus plantations and seedling planting for enrichment and densification). In the semi-deciduous forests, 97.25% of the sites were restored through active methods and 2.75% through assisted methods. In the ombrophilous forest, 87.35% were restored trough active and 12.64% through assisted method. Whereas in the mixed ombrophilous forests, all sites were restored trough assisted methods. Restoration sites age varied from 1 to 94 years, however, the majority (about 95%) ranged from 1 to 10 years old (Table 4) (Appendix H).

We split the restoration assemblages' data in two strata, the established stratum, representing the woody individuals with diameter at breast height (DBH \geq 5cm) higher than five centimeters, and the regenerating stratum representing the woody plant species with height higher than 0.50 centimeters and DBH $<$ 5. We did not consider as part of the regenerating strata the individuals that were planted during the restoration actions. Not all restored sites had information about the regenerating stratum; therefore, we conducted the regenerating stratum analysis for 178 restoration sites (Appendix G).

Table 4. Age average of the studied restoration sites in the two strata (regenerating and established), for three Atlantic forest vegetation types (semideciduous forest, ombrophilous forest and mixed ombrophilous forest).

	Age (years)	Semideciduous Forest	Ombrophilous Forest	Mixed Ombrophilous Forest
Established stratum	1 to 10	3.69 (n=97)	4.77 (n=87)	5.24 (n=37)
	11 to 20	12.71 (n=7)	0	0
	21 to 30	26 (n=2)	0	0
	41 to 50	46 (n=1)	0	0
	>50	74.5 (n=2)	0	0
Regenerating stratum	1 to 10	3.74 (n=67)	4.78 (n=74)	5.24 (n=37)
	11 to 20	12 (n=1)	0	0

n = number of restoration sites

For each restoration site, we selected the nearest native forest (distance ≤ 50 km) from the same vegetation type as a reference ecosystem to evaluate if the sites recovered the phylogenetic diversity present in the native sites. We obtained these data from the Neotropical Tree Communities database (TreeCo, version 4.0: available upon request at <http://labtrop.ib.usp.br/doku.php?id=projetos:treeco:start>), a Brazilian initiative comprising structure and diversity data from more than 2,000 Neotropical tree communities' surveys. The number of available native tree surveys is limited, and our selection returned 39 sites as reference ecosystems (Appendix F). Consequently, some restorations shared the same native forest as a reference ecosystem.

Woody plant species taxonomy and nomenclature follows The Plant List (<http://www.theplantlist.org>). We compared the species richness between reference ecosystem and restored sites through rarefaction curves, controlling for sampled efforts, using the *specaccum* function from the *vegan* R package (Oksanen et al. 2020).

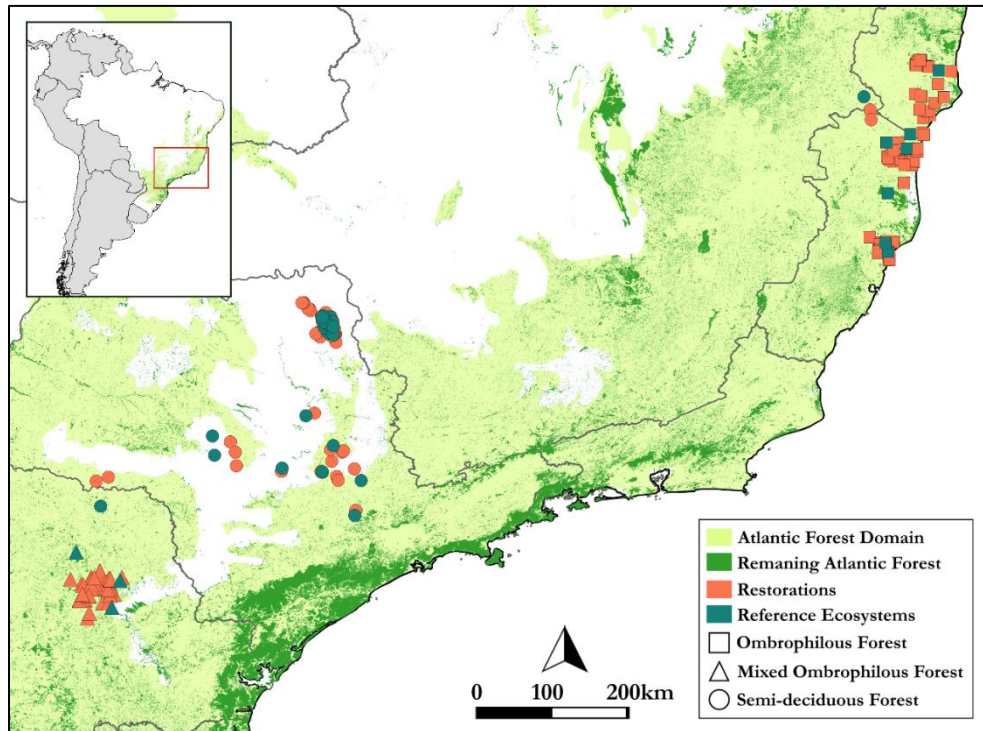


Figure 6. Location of the studied restoration sites and reference ecosystems; light green represents the original distribution and dark green represents the remaining Atlantic Forest domain.

3.2.2. Phylogenetic tree

To calculate the phylogenetic diversity metrics is necessary the construction of a phylogenetic tree. Because Atlantic Forest vegetation types have different patterns of alpha and beta phylogenetic diversity (Duarte et al. 2014), we built individual phylogenetic trees for each vegetation type (SF, MOF, OF). The phylogenies were built using the *phylo.maker* function from the V.Phylomaker R package (Jin & Qian 2019). The mega-tree GBOTB.extended.tree, the largest dated tree for vascular plants, comprising all families and more than 70 thousand species, was used as a backbone phylogeny (Jin & Qian 2019). Since we were only interested in evaluating the level of recovery of the local evolutionary history, all species exotic to the Atlantic forest domain were removed from the analysis.

We used the approach from scenario 3 to bind in the phylogenetic tree the species that were absent from the mega-tree (Qian & Jin 2016; Jin & Qian 2019). In this approach, when the genus is present in the mega-tree, the new tip is binded to the basal node of that genus. For absent genera, the new tip is inserted in the half point of the family branch (branch between the family root node and basal node); however, if the family branch length is longer than 2/3 of the whole family branch length (the branch from the family root node to the tip), the new genus is inserted in the upper 1/3 point of the whole family branch length (Jin & Qian 2019; Qian & Jin 2016).

3.2.3. Phylogenetic alpha diversity

For each restored site and reference ecosystem, we calculated the phylogenetic alpha diversity using the mean pairwise distance (MPD) and the mean nearest taxon distance (MNTD) metrics (Webb 2000). The MPD calculates the mean phylogenetic pairwise distance between all species in a sample and reflects the amount of evolutionary history within the entire phylogenetic tree. The MNTD calculates the mean phylogenetic distance from each species to its closest relative in a sample and reflects the recent phylogenetic relationships, near the tip of the phylogenetic tree (Webb 2000). We calculated the phylogenetic alpha diversity using the *picante* R package (Kembel et al. 2010).

In order to evaluate if the phylogenetic alpha diversity from the restored sites differed from the reference ecosystems, we used generalized linear models (GLM), considering the site type (reference ecosystems; established stratum and regenerating stratum from restoration sites) and vegetation type (SF, OF, MOF) as fixed components. However, our results showed strong heterogeneous residual variance violating the most important assumptions of linear regression, the homogeneity of variance (Zuur et al. 2009). The log transformed data also showed strong heterogeneity. Therefore, we decided to follow the approach described by Zuur et al. (2009), where we incorporate the heterogeneity into the model using the fixed variance structure. We applied different variances per type for each vegetation type thereby, each vegetation type can have a different variance. We fitted the model using the generalized least square (GLS) method in the *gls* function from *nlme* package (Pinheiro et al. 2020).

Our dataset is composed by restorations with different ages, therefore, we tested whether restoration age could influence the phylogenetic patterns. We performed the analysis with restorations from all ages and another one with only the restorations up to 10 years old, considering the number of restorations in such age range (Table 4). The final results did not vary, so we decided to carry on the analysis with all ages. We performed all the analysis in R environment (R Core Team, 2021).

3.2.4. Phylogenetic beta diversity

In order to find the level of evolutionary recovery in the restored sites we combined the results of the mean pairwise distance (MPD) with the phylobetadiversity metric UniFrac (Unic Fraction Metric). Both measures captures the total amount of evolutionary history within the entire

phylogenetic tree, differently from the MNTD which captures only recent phylogenetic relationships (Webb 2000; Lozupone & Knight 2005).

UniFrac is a metric derived from the Jaccard index of dissimilarity (Equation 1), which accounts for phylogenetic branch length information when comparing samples (Lozupone & Knight 2005). The results range from 0 to 1, where 0 indicates complete phylogenetic composition similarity and 1 the opposite (Lozupone & Knight 2005). UniFrac is a largely used phylobetadiversity metric, however, do not distinguish compositional differences arising from nestedness (species loss or gain) or turnover (species replacement) phenomena (Leprieur et al. 2012). In order to identify the degree to which the phylogenetic diversity is being recovered by restorations, we used the framework proposed by Leprieur et al. (2012), based on Baselga's approach (2010, 2012), in which the UniFrac metric is decomposed in turnover ($UniFrac_{turn}$) and nestedness ($UniFrac_{nest}$) additive components.

$$(1) \quad UniFrac = \frac{b+c}{a+b+c}$$

$$(2) \quad Unifrac = Unifrac_{turn} + Unifrac_{nest}$$

$$(3) \quad Unifrac_{turn} = \frac{2 \min(b,c)}{a+2 \min(b,c)}$$

$$(4) \quad Unifrac_{nest} = \frac{\max(b,c) - \min(b,c)}{a+b+c} \times \frac{a}{a+2 \min(b,c)}$$

Where, a is the sum of the branch length shared between species in communities B and C ; b is the sum of branch length from species present only in community B ; c is the sum of branch length from species present only in community C ; $\max(b, c)$ is the biggest number between b and c ; and $\min(b, c)$ is smallest number between b and c (Baselga 2010, 2012; Leprieur et al. 2012). The $UniFrac_{turn}$ measures the proportion of species replacement, if both communities had the same number of species, therefore is independent of species richness. Otherwise, $Unifrac_{nest}$ measures the dissimilarity between nested communities caused by the differences in species richness (Leprieur et al. 2012; Baselga 2010, 2012). We perform all the phylobetadiversity analysis using the “*beta.pd.decompo*” R function (Leprieur et al. 2012).

3.3. RESULTS

Our dataset contained a total of 1,287 woody plant species (1,181 identified at the species, 177 at the genus and 29 at the family level) belonging to 104 different families. In the restored sites, the richness varied from 2 to 75 species in the established stratum and from 2 to 76 in the regenerating stratum. In the reference ecosystems, the richness varied from 18 to 332. The richness of the reference ecosystem in the ombrophilous forests was higher than the restorations for both strata (Figure 7). Whereas in the semideciduous forests and mixed ombrophilous forests, the richness of the reference ecosystems was higher than the established stratum of restorations, but not greater than the regenerating stratum (Figure 7, Appendix C).

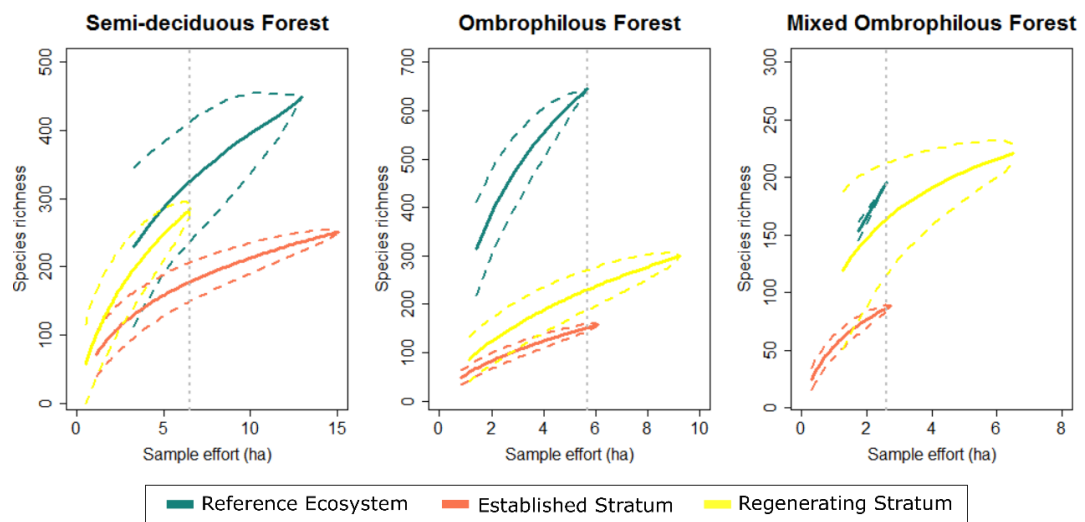


Figure 7. Rarefied richness for the reference ecosystems, established and regenerating strata of restorations in three vegetation types of the Brazilian Atlantic Forest. The dashed lines represent the 95% confidence interval level. The grey dotted vertical lines represents the richness comparison standardized to the smallest observed richness in each graph.

3.3.1. Phylogenetic alpha diversity

The mean pairwise distance (MPD) of the established and regenerating strata of restored sites was significantly lower than the reference ecosystems in the semideciduous and ombrophilous forests ($p < 0.001$). For the mixed ombrophilous forests the MPD from the reference ecosystems was significantly higher than the established strata of restorations ($p < 0.001$), but not significantly different from the regenerating strata ($p = 0.852$). For the mean nearest taxonomic distance (MNTD), the established and regenerating strata of restoration had significantly ($p < 0.001$) higher values than the reference ecosystems in all vegetation types.

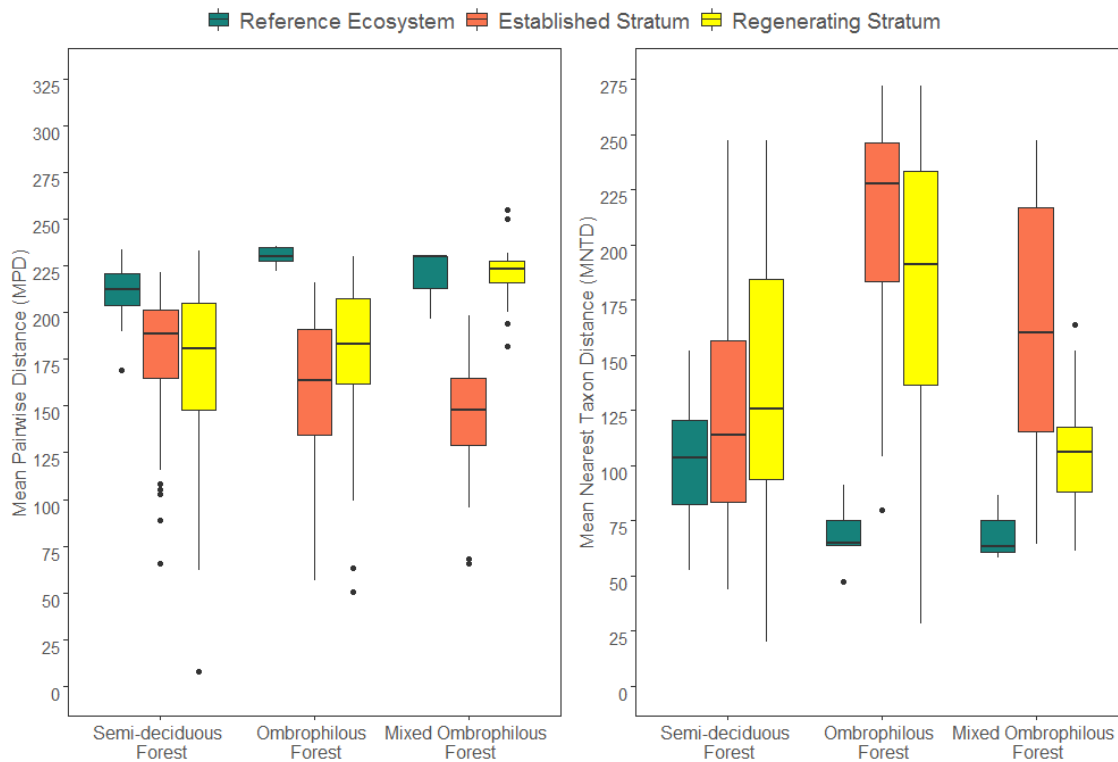


Figure 8. Observed values of Mean Pairwise Distance (MPD) and Mean Nearest Taxon Distance (MNTD) of the reference ecosystems, established and regenerating strata of restorations in three vegetation types of the Brazilian Atlantic Forest. The boxes indicate the 25th and 75th percentiles range, the line within the box marks the median. Lines below and above the boxes indicate the 10th and 90th percentiles. Dots indicate outliers outside the 10th and 90th percentiles.

3.3.2. Phylogenetic beta diversity

We found high phylogenetic dissimilarity between the reference ecosystems and restored sites, with Unifrac values higher than 0.70 in the three vegetation types, for both established and regenerating stratum (Table 5) (Appendix D and E). In the semideciduous forests, the largest contributor to dissimilarity between the reference ecosystems and the restored sites was the phylogenetic turnover (mean $\text{Unifrac}_{\text{turn}} > \text{mean Unifrac}_{\text{nest}}$), in both established and regenerating strata.

In the mixed ombrophilous forests, the dissimilarity between the restored sites and the reference ecosystems arises from nestedness in the established stratum (mean $\text{Unifrac}_{\text{turn}} < \text{mean Unifrac}_{\text{nest}}$) and from turnover in the regenerating stratum (mean $\text{Unifrac}_{\text{turn}} > \text{mean Unifrac}_{\text{nest}}$) (Table 5).

In the ombrophilous forests, we found nestedness dissimilarity patterns (mean $\text{Unifrac}_{\text{turn}} < \text{mean Unifrac}_{\text{nest}}$) between the established stratum of restored sites and the reference ecosystems.

Whereas, in the regenerating stratum we did not found a clear dissimilarity pattern, both nestedness and turnover patterns had similar values (mean $\text{Unifrac}_{\text{turn}} \approx \text{mean Unifrac}_{\text{nest}}$) (Table 5).

Table 5. Phylobetadiversity mean and standard deviation (minimum-maximum) value for the comparisons between reference ecosystems and restorations (established and regenerating strata) in the Atlantic Forest, Brazil.

	Restoration sites					
	Established stratum			Regenerating stratum		
	Unifrac	$\text{Unifrac}_{\text{turn}}$	$\text{Unifrac}_{\text{nest}}$	Unifrac	$\text{Unifrac}_{\text{turn}}$	$\text{Unifrac}_{\text{nest}}$
Semideciduous	0.83 ± 0.08	0.59 ± 0.13	0.25 ± 0.15	0.86 ± 0.07	0.64 ± 0.14	0.22 ± 0.15
Forest	(0.56-0.99)	(0.17-0.86)	(0-0.75)	(0.71-0.98)	(0.31-0.86)	(0.01-0.53)
Ombrophilous	0.94 ± 0.03	0.31 ± 0.17	0.63 ± 0.19	0.90 ± 0.04	0.44 ± 0.14	0.46 ± 0.16
Forest	(0.85-0.98)	(0-0.67)	(0.22-0.97)	(0.75-0.97)	(0.17-0.70)	(0.10-0.78)
Mixed						
Ombrophilous	0.87 ± 0.06	0.35 ± 0.11	0.52 ± 0.12	0.72 ± 0.08	0.45 ± 0.08	0.28 ± 0.12
Forest	(0.67-0.94)	(0.09-0.59)	(0.33-0.79)	(0.53-0.86)	(0.27-0.62)	(0.09-0.53)

3.3.1. Scenarios of phylogenetic recovery

Considering the MPD and beta diversity results into the six hypothetical scenarios that we proposed, in the semideciduous forests we found loss and no-recovery ($\text{MPD}_{\text{reference}} > \text{MPD}_{\text{restorations; } \beta=\text{turnover}}$) of the phylogenetic diversity for both established and regenerating strata. In the mixed ombrophilous restorations we found partial recovery ($\text{MPD}_{\text{reference}} > \text{MPD}_{\text{restorations; } \beta=\text{nestedness}}$) of the MPD in the established stratum, whereas in the regenerating stratum, we found a false recovery ($\text{MPD}_{\text{reference}} = \text{MPD}_{\text{restorations; } \beta=\text{turnover}}$). In the ombrophilous restorations we found partial recovery ($\text{MPD}_{\text{reference}} > \text{MPD}_{\text{restorations; } \beta=\text{nestedness}}$) of the MPD in the established stratum. In the regenerating stratum, the phylobetadiversity pattern was unclear, therefore we could not determine the recovery scenario.

3.4. DISCUSSION

The phylogeny has been widely applied in the study of ecosystems stability (Cadotte et al. 2012), species interaction (Verdú et al. 2012), biomass production (Cadotte 2013; Satdichanh et al. 2019) and community assemblage process (Gerhold et al. 2015). However, it is still poorly used in the field of restoration ecology, especially in the tropical forests (Hipp et al. 2015). Our study presents the first large scale assessment of the evolutionary outcomes of restorations in a highly

diverse tropical ecosystem. Results demonstrate that the restored sites are not recovering the phylogenetic diversity of woody plants found in reference ecosystems, regardless the vegetation type (i.e., semideciduous, ombrophilous or mixed ombrophilous) and strata (i.e., regenerating or established).

3.4.1. Alpha diversity

Regarding the more recent evolutionary relationships (MNTD), the restored sites showed higher values than the reference ecosystems for all strata in all vegetation types, corroborating with our hypothesis. Such pattern indicates that neighboring species are more phylogenetically distant in the restored sites. This result can be explained by the intense diversification process that made the Atlantic Forest the biodiversity center for some plants clades. In such highly diverse ecosystem, it is common to find many species within the same genus (Stehmann et al. 2009). For example, the *Eugenia* and *Myrcia* genus, from the Myrtaceae family, encompass 241 and 132 different woody plant species on the Atlantic forest, respectively (Stehmann et al. 2009). On the other hand, in the restoration projects, the practitioners select a few sets of species from the nursery's stocks trying to comprise as many genera as possible. Consequently, we might find fewer species for each genus in the restored sites, which makes the species far from their closest neighbors. In our data set, for example, we found 41 *Eugenia* species in the reference ecosystems, but only 15 in the restored sites.

The same pattern of species underrepresentation by clade was found in Atlantic forest nurseries, where less than 30% of Melastomataceae and Rubiaceae species were available (Vidal et al. 2019). These families, together with Myrtaceae and Fabaceae, are the richest woody plants clades in the Atlantic forest (Lucas & B unger 2015; Stehmann et al. 2009). Species belonging to rich clades have, on average, lower distribution range size (Le o et al. 2020), considering that the nurseries production depends on seed collection from tree matrices, species with lower distribution might be difficult and costly to be found. Such factors may cause its absence from nurseries stocks, highlighting the need of well-structured seed supply chain and the combination of several harvesting strategies to enhance the diversity of seedlings for restorations (Brancalion et al. 2012).

Assuming that distantly related species have different evolutionary potential (resilience to environmental changes), having communities with distantly related species raises the probabilities of having species with high evolutionary potential (Winter et al. 2013). Consequently, increases the ability of the restored communities to respond to climate changes. On the other hand, if the lineages are represented by only a few species on the tip of the phylogeny, and these species are occasionally extinct, then an entire unique evolutionary history is lost with it. Our results emphasize

the importance of combining phylogenetic diversity knowledge to the species selection in restoration initiatives aiming the community resilience facing climate changes.

Concerning the mean pairwise distance (MPD), we found phylogenetic diversity of restored sites lower than the reference ecosystems for all strata in all vegetation types, except for the regenerating strata of the mixed ombrophilous forests. Considering that MPD measures the amount of the overall evolutionary relationships within the phylogenetic tree, lower MPD values means that the species in the restored sites are more closely related to each other than the reference ecosystems (Tucker et al. 2017; Webb 2000). That is, combining both MPD and MNTD results we have: higher clades, such as families and orders, more closely related (MPD), yet, within the clades, the genus and species are distantly related from each other (MNTD).

The combination of mean pairwise distance and phylobetadiversity results to assess the scenarios of evolutionary recovery are described below.

3.4.2. Scenarios of phylogenetic recovery

We found high levels of dissimilarity in all vegetation types, demonstrating that, in terms of evolutionary relationships, the studied restored sites are phylogenetically far from the reference ecosystems. The partitioning of the beta diversity into nestedness and turnover helped us in the understanding of the mechanisms behind these differences. The nestedness tell us that the dissimilarity between the restored sites and the reference ecosystems arises mainly due to differences in phylogenetic diversity, that is, communities share at least one branch within the phylogeny (Baselga 2010; Leprieur et al. 2012). On the other hand, the turnover phenomena is independent of total branch length differences between the two compared communities and represents the substitution of lineages (Leprieur et al. 2012; Baselga 2010, 2012).

The nestedness pattern was found only for the established stratum of the ombrophilous and mixed ombrophilous forests. Fitting the scenario of partial recovery (Figure 5, scenario 3) of the evolutionary relationships (MPD). In the ombrophilous forests, the sites were restored mainly through active methods (total seedlings planting) and the scenario of partial recovery of the phylogenetic diversity can be a result of poor species selection for seedling plantings. Within the studied region, the nurseries have, on average, less than 60 seedlings species available for purchase (Almeida et al. 2007). Most nurseries collect their own propagules within nearby distances which can limit the number of species acquired (Vidal et al. 2019; Silva et al. 2016), purchase from additional sources, such as freelance seed harvest professionals and cooperatives can increase considerably the nurseries species richness (Brancalion et al. 2012).

We also need to highlight that these sites are still very young, five years-old on average. In such communities, the established strata are mostly represented by the fast-growing species that were actively planted during the restoration actions. The majority of Atlantic Forest active restorations combine the use of fast-growing and slow-growing species in two planting lines (Nave & Rodrigues 2006; Rodrigues et al. 2009). The fast-growing, pioneer species are planted in the “filling line” with the goal to promote fast canopy cover and suppress the exotic weeds. On the other hand, the slow-growing species are planted in the “diversity line” with the goal to slowly replace the fast-growing species in the established stratum and introduce more functional diversity to the ecosystem (Nave & Rodrigues 2006; Rodrigues et al. 2009). Having in mind that this system was probably applied in the studied restored sites, we expect that, as years will pass by, the species from the established stratum will die and leave space to the slow-growing species and enhance the community phylogenetic diversity. However, there are no study in the literature that evaluate how this restoration method influences the assemblage’s phylogenetic diversity over time.

The regenerating strata of the mixed ombrophilous forest showed a turnover of phylogenetic composition. In terms of mean pairwise distance, this was the only strata that exhibit similar phylogenetic diversity to that of reference ecosystem. This pattern can be described as a false recovery (Figure 5, scenario 4) of the evolutionary history, where the restoration sites hold the same amount of alpha phylogenetic diversity as the reference ecosystems but is composed by distinct clades and lineages. These results are remarkably interesting because we observed a partial recovery in the established strata of these restorations.

The mixed ombrophilous forest were restored through assisted methods, which involved the conduction of natural regeneration and seedling planting for enrichment and densification. In terms of seedling species availability, previous studies performed in the mixed ombrophilous forests domain also found limited availability and variability of species pool in nurseries in the region of Araucaria forest, with restorations practitioners using on average 21 species in their plantings, with very low percentage of rare and threatened taxon (Shaw 2019; Hoffmann et al. 2015). On the other hand, the process of natural regeneration depends exclusively from species dispersion from adjacent forest fragments and the condition of partial and false recovery could be explained by seed dispersal and/or recruitment limitation. Seed dispersal limitation results from a failure of enough seeds to reach specific sites (Muller-Landau et al. 2002; Rother et al. 2013). These limitations promoted by the absence of seed dispersers, especially large frugivorous, are one of the main bottlenecks in the early years of natural regeneration (Reid et al. 2015). The small and isolated mixed ombrophilous forest remnants makes even harder the movement of seed dispersers across the landscapes (Ribeiro et al. 2009). Even if the seeds reach the restored sites, pressures such as

seed predation, herbivory, pathogen attack and competition with invasive species can affect seedling recruitment and growth (Muller-Landau et al. 2002; Rother et al. 2013).

We also found the turnover phenomena in both strata of the semideciduous forests, fitting the scenario of loss and no recovery of the old evolutionary relationships (Figure 5, scenario 6). The replacement of lineages between restored sites and reference ecosystems draws our attention to a much more alarming situation of phylogenetic recovery. The turnover phenomena indicates that the unique evolutionary relationships are being lost and replaced by foreign lineages.

In the semideciduous region, the sites were also restored through active methods (total seedlings planting) and would be expected the use of native species in the restorations, as a compliance with the Federal Native Vegetation Protection Law (Brancalion et al. 2016; Soares-Filho et al. 2014). Moreover, these sites are all located within São Paulo state, which possess one of the most stringent Brazilian legislation for legally mandatory restoration (Chaves et al. 2015). The legislation suggests a minimum of 80 species belonging to different shade tolerance groups, dispersion syndromes, successional stages and threatened levels for the implantation of restoration plantings. However, once seedlings are planted, they are subject to various biotic and abiotic factors, such as flood, drought (Engelbrecht et al. 2005; Martínez-Garza et al. 2013), predation (Garcia et al. 2020; Rother et al. 2013) and competition (González & Fisher 1994), influencing survival rate and shaping the community composition over the years. The average seedlings survival rate in restorations is 60% (Palma & Laurance 2015), which may be even lower for late-successional species in tropical forests (Román-Dañobeytia et al. 2012). In this context, phylogeny proved to be an interesting tool to increase seedlings survival rate in restoration enrichment plantations (Schweizer & Brancalion 2020; Schweizer et al. 2013; Schweizer & Brancalion 2018; Webb et al. 2006). Moreover, the study of phylogenetic relationships and trait conservation could help the identification of assembly process shaping seedlings survival and community composition (Webb et al. 2002).

3.4.3. Implications for restoration practices

Phylogenetic diversity measures were born with the purpose of helping with the agony of choosing biodiversity conservation priorities (Vane-Wright et al. 1991). That is, if we had to choose between two communities to conserve we should choose the one with more distantly related species, in other words, the community with more evolutionary history (Vane-Wright et al. 1991). This approach would be particularly useful in the process of selecting species for restoration planting; selecting a group of species with high phylogenetic diversity would guarantee the

conservation of more evolutionary history, which per se it is an important accomplishment. Moreover, the use of phylogenetic approach in species selection can enhance seedling survival rate in restored sites using enrichment planting (Schweizer et al. 2013).

Here we demonstrated that the evolutionary history of woody plants is being lost in the Brazilian Atlantic Forest restored sites, regardless the vegetation type and strata. If we aim to use restored ecosystems for biodiversity conservation purpose, we should start looking at phylogenetic diversity as a measure of restoration success. More studies like this are needed to understand the extent to each evolutionary history is being recovered in restored ecosystems. Especial attention needs to be given to long-term studies, to comprehend how phylogenetic diversity can inform about community assembly patterns and process and especially how phylogenetic diversity change over time. Now that we are entering the United Nations Decade on Ecosystem Restoration, we need to address the evolutionary history that we recovered so far, and what we want for future restorations.

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4. FINAL CONSIDERATIONS

In this dissertation, we aimed at looking to ecological restoration through a different perspective. Through the two chapters, we investigated the extend and advantages of phylogenetic usage in restoration ecology, presented a practical example and highlighted the gaps of knowledge between the collaboration of these two sciences.

In the first chapter, we conducted a systematic review to identify trends and gaps of knowledge of phylogenetics usage in restoration ecology, and as expected, we found a very limited number of studies. Our results demonstrated that so far, the science neglected the importance of conserving the evolutionary history in restoration as well as the importance of evolutionary history to answer important issues in restoration practice. So far, most studies were concentrated in the United States and in the restoration of grassland ecosystems. These findings highlight the importance of studies in highly diverse ecosystems such as the tropical forests.

The low number of studies in the tropics brought an extra motivation for the study that we conducted in the second chapter of this dissertation. We performed the first large scale study that assessed the phylogenetic diversity of restored sites in the Atlantic Forest. In general, we found that restorations are not completely recovering the evolutionary history of the local community, yet, we emphasized that the majority of studied sites are very young so we believe that, in the future, the slow-growing species will develop and with the arrival of new species through dispersal the assemblages phylogenetic diversity may potentially enhance.

Based on our results, we recommend that future studies should i) monitor the phylogenetic diversity of restoration over the years, ii) evaluate how different restoration methods affect the assemblage' phylogenetic diversity, iii) identify the relationship between the main ecosystem services provided by restorations, functional traits and phylogenetic diversity. In the near future, we expect to publish our results in peer-reviewed journals so our findings become available to the scientific public and contribute to the development of restoration ecology and practice.

APPENDICES

APPENDIX A. Eligibility screening process applied. Modified from Collaboration for Environmental Evidence (2018).

Title, Abstract and keywords meets all eligibility criteria?

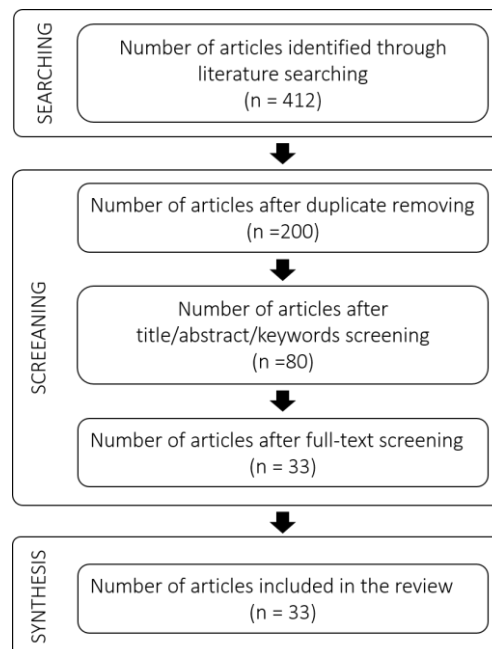
No Not included in the review

Yes or unclear 2

Full text meets all eligibility criteria?

No Not included in the review

Yes Included in the review



Collaboration for Environmental Evidence. 2018. Guidelines and Standards for Evidence synthesis in Environmental Management. Version 5.0 (Pullin AS, Frampton GK, Livoreil B & Petrokofsky G, Eds). Available from www.environmentalevidence.org/information-for-authors [accessed November 2020].

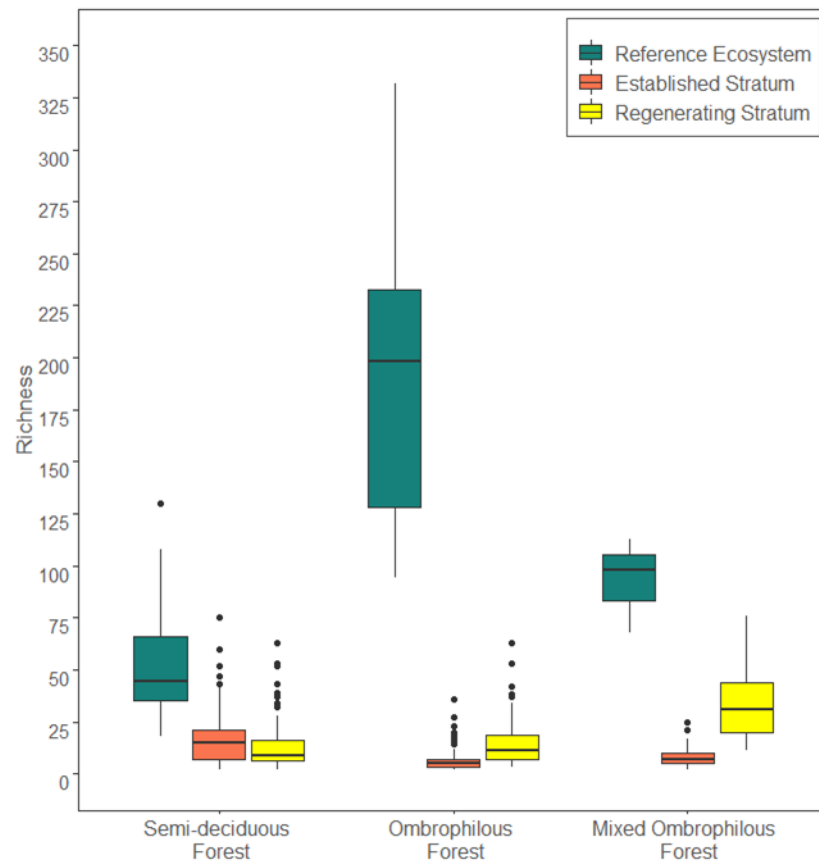
APPENDIX B. List of papers included in the systematic review.

- Barak RS, Williams EW, Hipp AL, Bowles ML, Carr GM, Sherman R, Larkin DJ (2017) Restored tallgrass prairies have reduced phylogenetic diversity compared with remnants. *Journal of Applied Ecology* 54:1080–1090
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- Gibson DJ, Shupert LA, Liu X (2019) Do no harm: efficacy of a single herbicide application to control an invasive shrub while minimizing collateral damage to native species. *Plants* 8:426
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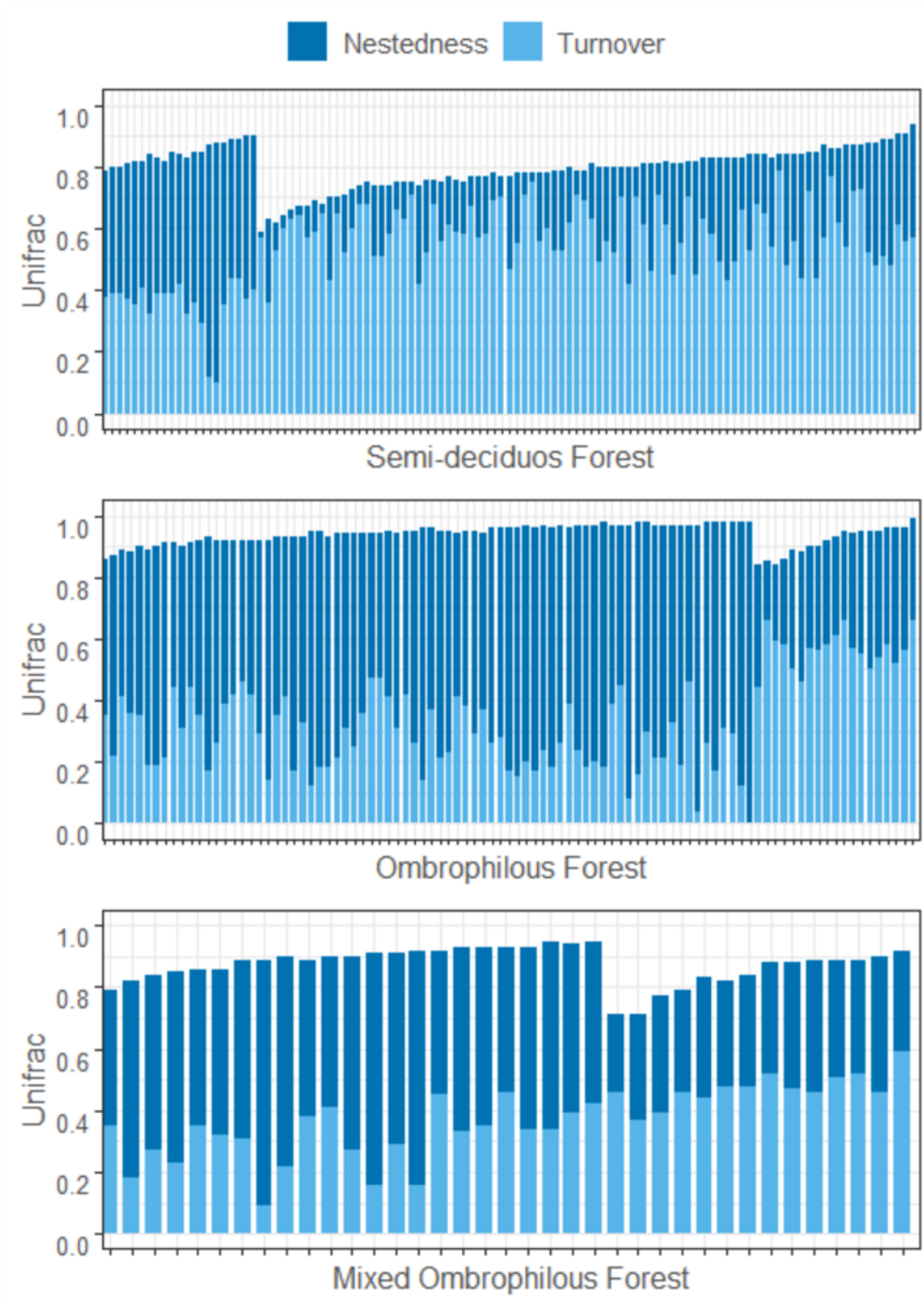
- Khalil MI, Gibson DJ, Baer SG, Willand JE (2018) Functional diversity is more sensitive to biotic filters than phylogenetic diversity during community assembly. *Ecosphere* 9:e02164
- Li L, Cadotte MW, Martínez-Garza C, Peña-Domene M, Du G (2018) Planting accelerates restoration of tropical forest but assembly mechanisms appear insensitive to initial composition. *Journal of Applied Ecology* 55:986–996
- Navarro-Cano JA, Ferrer-Gallego PP, Laguna E, Ferrando I, Goberna M, Valiente-Banuet A, Verdú M (2016) Restoring phylogenetic diversity through facilitation. *Restoration Ecology* 24:449–455
- Qin H, Wang Y, Zhang F, Chen J, Zhang G, Dong G (2016) Application of species, phylogenetic and functional diversity to the evaluation on the effects of ecological restoration on biodiversity. *Ecological Informatics* 32:53–62
- Qin H, Dong G, Zhang F (2019) Relative roles of the replacement and richness difference components of beta diversity following the ecological restoration of a mountain meadow, north China. *Ecological Informatics* 52:159–165
- Qin H, Dong G, Zhang Y, Zhang F, Wang M (2017) Patterns of species and phylogenetic diversity of *Pinus tabuliformis* forests in the eastern Loess Plateau, China. *Forest Ecology and Management* 394:42–51
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- Zhang Z, Liu M, Liu X, Zhou G (2018) A new vegetation index based on multitemporal sentinel-2 images for discriminating heavy metal stress levels in rice. *Sensors* 18:1–15
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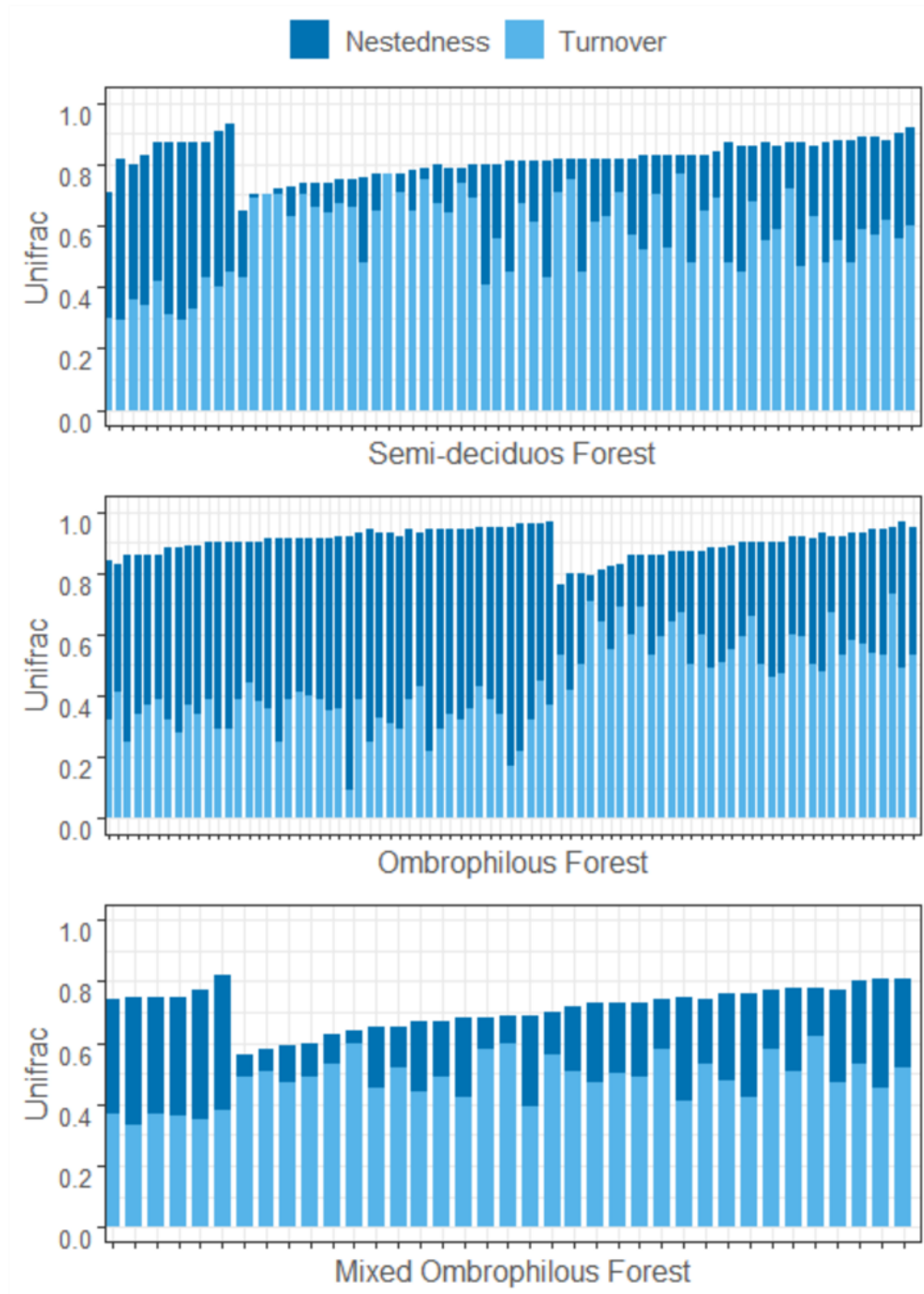
APPENDIX C. Taxonomic richness of the reference ecosystems, established and regenerating strata of restorations in three vegetation types of the Brazilian Atlantic Forest.



APPENDIX D. Phylobetadiversity Unifrac values and its nestedness and turnover components for all pairwise comparisons between reference ecosystems and established stratum of restorations in three vegetation types of the Atlantic Forest, Brazil.



APPENDIX E. Phylobetadiversity *Unifrac* values and its nestedness and turnover components for all pairwise comparisons between reference ecosystems and regenerating stratum of restorations in three vegetation types of the Atlantic Forest, Brazil.



APPENDIX F. Information about the studied reference ecosystems sites of the Atlantic Forest, Brazil.

ID	State	Effort (ha)	Vegetation type	Abundance	Richness	Exotic species percentage	MNTD	MPD
forestT3711	MG	1	FES	1048	72	8.86	52.48	169.14
forestT714	PR	2.5	FES	1977	77	2.53	73.69	220.94
forestB1	SP	0.1	FES	118	38	7.32	116.64	230.16
forestB10	SP	0.1	FES	106	30	9.09	108.07	196.38
forestB11	SP	0.1	FES	120	42	8.7	118.22	221.13
forestB12	SP	0.1	FES	145	36	10	120.23	213.37
forestB13	SP	0.1	FES	112	40	18.37	126.26	233.22
forestB14	SP	0.07	FES	255	18	5.26	151.64	204.41
forestB15	SP	0.1	FES	145	41	6.82	101	215.45
forestB16	SP	0.1	FES	122	37	7.5	102.72	209.05
forestB17	SP	0.1	FES	70	19	20.83	121.11	189.97
forestB18	SP	0.1	FES	136	29	25.64	126.01	201.73
forestB2	SP	0.1	FES	101	41	8.89	118.38	233.73
forestB3	SP	0.1	FES	98	49	5.77	84.37	210.91
forestB4	SP	0.1	FES	116	31	11.43	104.8	201.17
forestB5	SP	0.1	FES	130	49	5.77	75.6	217.54
forestB6	SP	0.1	FES	88	32	0	90.42	202.38
forestB8	SP	0.1	FES	147	54	3.57	103.96	222.64
forestB9	SP	0.1	FES	157	33	10.81	147.09	212.89
forestT1350	SP	3.2	FES	3577	108	7.69	73.2	215.21
forestT1477	SP	0.4	FES	519	65	8.45	123.44	204.06
forestT1484	SP	0.6	FES	697	97	4.9	83.91	207.8
forestT1505	SP	1	FES	1065	108	3.57	61.13	214.61
forestT1618	SP	1	FES	1188	67	4.29	78.3	209.54
forestT1631	SP	0.6	FES	509	47	2.08	123.64	202.68
forestT3172	SP	0.43	FES	759	130	4.41	77.8	223.58
forestT3593	SP	0.44	FES	657	52	7.14	85.46	211.64

ID	State	Effort (ha)	Vegetation type	Abundance	Richness	Exotic species percentage	MNTD	MPD
forestT5994	SP	0.12	FES	152	66	0	84.87	228.91
forestT3723	BA	1	FOD	1896	238	5.18	64.81	235.77
forestT4573	BA	0.5	FOD	690	136	3.55	91.27	234.9
forestT10	ES	1	FOD	1470	231	4.94	64.65	225.92
forestT4636	ES	0.96	FOD	1939	332	3.49	47.33	228.55
forestT4637	ES	0.5	FOD	747	205	1.91	63.67	230.65
forestT49	ES	1.12	FOD	1756	192	2.54	64	235.74
forestT5550.3	ES	0.31	FOD	415	104	4.59	74.06	222.23
forestT5550.6	ES	0.31	FOD	383	94	3.09	77.71	229.6
forestT571	PR	1	FOM	1475	113	4.24	58.04	230.63
forestT743	PR	1	FOM	1176	98	2.97	63.27	229.77
forestT806	PR	0.59	FOM	862	68	6.85	86.58	196.28

APPENDIX G. Information about the studied restoration sites of the Atlantic Forest, Brazil. Regenerating stratum.

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration479	forestT3711	ES	0.4	FES	Active	5	306	13	7.14	35.2	80.79	133.99
restoration71	forestT3711	ES	0.04	FES	Assisted	5	227	28	3.45	20.96	114.63	219.26
restoration103	forestB5	SP	0.08	FES	Active	2	14	3	0	1.48	215.91	124.32
restoration104	forestB1	SP	0.05	FES	Active	2	15	3	25	0.74	229.24	119.13
restoration105	forestB1	SP	0.16	FES	Active	3	79	7	12.5	0.99	230.54	158.81
restoration106	forestB17	SP	0.08	FES	Active	5	46	9	10	1.54	224.02	184.93
restoration107	forestB1	SP	0.14	FES	Active	4	83	12	20	1.65	196.81	182.68
restoration108	forestB1	SP	0.03	FES	Active	6	62	27	12.9	0.12	129.62	213.25
restoration115	forestB13	SP	0.04	FES	Active	3	13	6	0	4.03	222.09	182.79
restoration116	forestB18	SP	0.11	FES	Active	6	13	8	0	0.6	152.04	194.43
restoration118	forestB18	SP	0.03	FES	Active	6	44	25	0	1.02	99.71	222.04
restoration120	forestB13	SP	0.03	FES	Active	4	111	52	14.75	0.82	69.99	220.4
restoration121	forestT3172	SP	0.26	FES	Active	12	74	15	21.05	15.3	136.12	206.54
restoration122	forestT3172	SP	0.09	FES	Active	8	7	6	25	16.05	209.31	199.44
restoration124	forestB9	SP	0.03	FES	Active	3	85	43	8.51	0.4	74.2	209.38
restoration126	forestB2	SP	0.04	FES	Active	5	13	5	16.67	3.38	247.2	180.55
restoration127	forestB2	SP	0.13	FES	Active	3	42	7	30	2.37	148.51	148.33
restoration128	forestB5	SP	0.06	FES	Active	1	12	7	12.5	5.34	187.33	179.64
restoration133	forestB2	SP	0.07	FES	Active	5	11	4	0	11.93	97.4	100
restoration137	forestB16	SP	0.14	FES	Active	1	55	10	9.09	1.13	135.43	192.34
restoration138	forestB16	SP	0.23	FES	Active	4	57	16	0	1.16	125.69	200.38
restoration139	forestB12	SP	0.03	FES	Active	6	25	15	16.67	1.25	154.78	214.26
restoration141	forestB3	SP	0.06	FES	Active	2	19	5	0	0.92	240.71	147.93
restoration143	forestB3	SP	0.03	FES	Active	5	129	53	14.52	1.09	86.97	223.02
restoration181	forestB10	SP	0.05	FES	Active	4	20	9	25	6.08	169.52	187.35
restoration215	forestB16	SP	0.16	FES	Active	3	65	15	6.25	2.97	133.39	202.65

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration216	forestB9	SP	0.07	FES	Active	1	12	4	0	6.75	138.57	144.54
restoration221	forestB15	SP	0.34	FES	Active	5	97	16	5.88	2.35	108.39	212.96
restoration225	forestB2	SP	0.03	FES	Active	4	98	39	7.14	0.95	100.76	217.65
restoration226	forestB13	SP	0.11	FES	Active	2	15	8	20	4.12	190.53	178.05
restoration227	forestB5	SP	0.07	FES	Active	4	18	6	0	1.54	87.11	150.56
restoration229	forestB11	SP	0.25	FES	Active	3	154	22	4.35	21.3	75.83	161.44
restoration233	forestB11	SP	0.07	FES	Active	4	13	7	0	20.83	119.08	171.58
restoration241	forestB11	SP	0.14	FES	Active	4	41	14	6.67	23.37	114.02	192.88
restoration245	forestB11	SP	0.3	FES	Active	4	74	19	13.64	34.49	104.69	186.24
restoration250	forestB11	SP	0.19	FES	Active	4	37	14	12.5	34.96	104.13	180
restoration252	forestB11	SP	0.07	FES	Active	4	14	7	0	33.57	64.01	122.59
restoration255	forestB11	SP	0.08	FES	Active	2	7	3	25	34.95	158.23	87.96
restoration261	forestB8	SP	0.08	FES	Active	1	15	6	14.29	12.89	60.04	132.83
restoration263	forestB4	SP	0.07	FES	Active	4	11	3	25	1.28	78.27	62.2
restoration265	forestB11	SP	0.1	FES	Active	4	18	9	18.18	0.83	130.2	181.07
restoration266	forestB16	SP	0.03	FES	Active	6	52	32	5.88	2.07	127.52	224.3
restoration391	forestT3593	SP	0.1	FES	Active	3	11	5	16.67	33.66	83.2	134
restoration392	forestT1350	SP	0.12	FES	Active	2	40	11	8.33	25.93	47.22	117.1
restoration393	forestT3593	SP	0.07	FES	Active	2	41	11	21.43	28.9	183.63	169.26
restoration495	forestB4	SP	0.03	FES	Active	3	146	53	7.02	1.38	85.83	217.42
restoration497	forestB17	SP	0.03	FES	Active	8	84	37	9.76	1.46	94.99	233.17
restoration498	forestB6	SP	0.03	FES	Active	7	76	33	10.81	1.04	106.68	229.94
restoration499	forestB11	SP	0.12	FES	Active	4	50	15	6.25	1.3	135.82	199.89
restoration500	forestB10	SP	0.03	FES	Active	6	92	38	11.63	1.58	92.05	224.52
restoration502	forestB13	SP	0.12	FES	Active	4	17	8	0	2.68	143.78	195.75
restoration503	forestB13	SP	0.13	FES	Active	4	28	11	15.38	3.26	97.7	196.56
restoration507	forestB14	SP	0.03	FES	Active	6	87	34	12.82	0.54	104.72	219.37
restoration509	forestB9	SP	0.05	FES	Active	1	10	3	0	2.55	237.27	112.48

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration510	forestB13	SP	0.12	FES	Active	3	29	11	15.38	2.53	88.17	180.41
restoration514	forestB13	SP	0.16	FES	Active	4	61	16	11.11	1.7	104.58	204.16
restoration515	forestB8	SP	0.05	FES	Active	3	7	4	0	3.7	231.2	164.07
restoration517	forestB5	SP	0.11	FES	Active	5	42	8	11.11	3.75	185.35	147.34
restoration519	forestB5	SP	0.08	FES	Active	3	10	4	20	2.56	88.71	86.95
restoration521	forestB8	SP	0.1	FES	Active	1	12	5	37.5	2.76	190.64	174.21
restoration522	forestB16	SP	0.1	FES	Active	4	19	6	25	0.49	147	154.97
restoration524	forestB13	SP	0.12	FES	Active	2	33	7	12.5	0.92	62.15	132.38
restoration525	forestB5	SP	0.02	FES	Active	2	7	4	20	2.58	225.91	153.9
restoration526	forestB5	SP	0.13	FES	Active	3	35	6	14.29	2.1	125.2	134.8
restoration527	forestB2	SP	0.02	FES	Active	2	4	2	0	1.4	20.11	7.54
restoration530	forestB8	SP	0.05	FES	Active	3	5	4	20	3.5	231.95	180.53
restoration568	forestB15	SP	0.03	FES	Active	5	161	63	7.35	0.9	96.4	230.66
restoration109	forestT3723	BA	1.06	FOD	Active	1	1405	34	8.11	33.88	163.73	170.75
restoration110	forestT3723	BA	0.53	FOD	Active	1	273	22	8.33	31.39	131.86	197.93
restoration112	forestT3723	BA	0.55	FOD	Active	1	471	18	0	30.72	171.52	176.56
restoration114	forestT3723	BA	0.94	FOD	Active	1	763	29	3.33	30.25	168.54	127.65
restoration535	forestT3723	BA	0.06	FOD	Assisted	5	146	21	8.7	47.67	136.03	219.31
restoration538	forestT3723	BA	0.14	FOD	Assisted	5	319	37	7.5	39.55	106.71	217.59
restoration545	forestT3723	BA	0.04	FOD	Assisted	5	82	10	0	19.73	179.51	162.61
restoration555	forestT3723	BA	0.08	FOD	Active	5	260	17	0	14.88	28.09	63.25
restoration557	forestT3723	BA	0.05	FOD	Assisted	5	95	12	7.69	46.02	217.89	213.24
restoration558	forestT3723	BA	0.31	FOD	Assisted	5	265	27	12.9	32.76	104.25	208.89
restoration560	forestT3723	BA	0.33	FOD	Assisted	5	604	38	5	32.26	74.55	214.09
restoration562	forestT3723	BA	0.2	FOD	Assisted	5	141	19	17.39	30.29	219.62	203.15
restoration564	forestT3723	BA	0.04	FOD	Active	5	89	12	7.69	44.85	72.76	118.99
restoration101	forestT49	ES	0.95	FOD	Active	5	1750	63	5.97	19.62	37.99	157.52
restoration28	forestT4636	ES	0.02	FOD	Assisted	5	140	4	20	2.45	255.55	172.32

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration31	forestT4636	ES	0.03	FOD	Assisted	5	61	6	14.29	2.78	258.68	105.04
restoration32	forestT4636	ES	0.04	FOD	Assisted	5	45	10	16.67	9.5	241.29	164.96
restoration33	forestT4636	ES	0.06	FOD	Assisted	5	176	8	11.11	12.79	145.66	163.44
restoration34	forestT4636	ES	0.02	FOD	Assisted	5	53	9	18.18	12.56	184.85	169.52
restoration36	forestT4636	ES	0.09	FOD	Assisted	5	111	14	6.67	11.11	112.45	170.94
restoration37	forestT4636	ES	0.03	FOD	Assisted	5	93	7	30	11.49	257.76	120.23
restoration38	forestT4636	ES	0.02	FOD	Assisted	5	17	4	20	11.49	190.51	179.54
restoration40	forestT4636	ES	0.02	FOD	Assisted	5	245	26	0	12.32	114.27	216.62
restoration404	forestT5550.3	ES	0.03	FOD	Assisted	5	59	10	0	26.38	216.95	207.7
restoration405	forestT5550.3	ES	0.01	FOD	Assisted	5	45	5	16.67	24.75	213.35	111.88
restoration409	forestT49	ES	0.03	FOD	Assisted	5	104	11	0	26.73	109.72	152.72
restoration41	forestT4636	ES	0.04	FOD	Assisted	5	236	34	2.86	7.95	104.74	193.44
restoration410	forestT49	ES	0.02	FOD	Assisted	5	119	13	7.14	9.03	109.22	184.78
restoration411	forestT49	ES	0.03	FOD	Assisted	5	39	6	0	10.48	256.9	161.91
restoration419	forestT49	ES	0.03	FOD	Assisted	5	120	6	0	20.97	234.25	182.03
restoration42	forestT4636	ES	0.05	FOD	Assisted	5	119	6	25	6.16	259.06	193.23
restoration420	forestT49	ES	0.01	FOD	Assisted	5	20	3	0	23.49	271.79	50.29
restoration424	forestT49	ES	0.02	FOD	Assisted	5	103	12	7.69	23.61	206.63	194.93
restoration428	forestT5550.3	ES	0.02	FOD	Assisted	5	56	6	0	24.75	198.47	196.02
restoration44	forestT4636	ES	0.03	FOD	Assisted	5	49	15	11.76	14.02	211.1	196.4
restoration442	forestT49	ES	0.13	FOD	Assisted	5	260	14	6.67	25.94	237.7	148.61
restoration443	forestT49	ES	0.04	FOD	Assisted	5	159	15	0	24.11	207.29	194.1
restoration444	forestT49	ES	0.03	FOD	Assisted	5	126	8	0	19.62	163.75	173.31
restoration445	forestT49	ES	0.02	FOD	Assisted	5	99	9	0	19.62	71.56	168.3
restoration451	forestT49	ES	0.02	FOD	Assisted	5	42	6	0	20.64	253.35	159.18
restoration455	forestT49	ES	0.07	FOD	Assisted	5	35	6	0	16.22	252.67	206.59
restoration456	forestT49	ES	0.27	FOD	Assisted	5	182	14	12.5	14.99	216.46	161.83
restoration458	forestT49	ES	0.31	FOD	Assisted	5	157	9	10	15.39	190.81	199.12

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration46	forestT4636	ES	0.07	FOD	Assisted	5	145	18	10	12.03	184.38	228.05
restoration461	forestT49	ES	0.02	FOD	Assisted	5	16	11	0	10.14	205.24	224.2
restoration464	forestT49	ES	0.03	FOD	Assisted	5	59	12	7.69	13.93	179.14	207.58
restoration468	forestT5550.3	ES	0.04	FOD	Assisted	5	49	8	11.11	19.66	179.93	135.56
restoration470	forestT5550.3	ES	0.03	FOD	Assisted	5	29	15	0	22.75	179.09	230.09
restoration472	forestT5550.3	ES	0.05	FOD	Assisted	5	137	21	4.55	14.24	142.94	198.52
restoration473	forestT5550.3	ES	0.03	FOD	Assisted	5	19	4	20	14.8	231.49	108.04
restoration475	forestT49	ES	0.03	FOD	Assisted	5	85	8	0	24.06	199.17	209.17
restoration489	forestT10	ES	0.16	FOD	Assisted	5	290	14	12.5	26.9	164.75	209.05
restoration49	forestT4637	ES	0.02	FOD	Assisted	5	45	6	14.29	2.35	234.13	117.67
restoration50	forestT4637	ES	0.05	FOD	Assisted	5	66	8	20	2.5	253.11	196.4
restoration57	forestT4637	ES	0.05	FOD	Assisted	5	85	23	8	7.57	177.28	221.37
restoration63	forestT4637	ES	0.09	FOD	Assisted	5	301	11	21.43	23.61	243.27	194.65
restoration64	forestT4637	ES	0.02	FOD	Assisted	5	28	6	0	10.95	240.5	98.98
restoration66	forestT4637	ES	0.02	FOD	Assisted	5	53	12	7.69	9.5	154.44	217.37
restoration67	forestT4637	ES	0.02	FOD	Assisted	5	47	11	8.33	7.4	206.51	220.68
restoration69	forestT4637	ES	0.01	FOD	Assisted	5	12	4	0	11.63	225.39	172.18
restoration70	forestT4637	ES	0.03	FOD	Assisted	5	107	18	0	6.96	193.34	215.09
restoration72	forestT5550.6	ES	0.03	FOD	Assisted	5	81	17	10.53	38.51	190.79	224.24
restoration78	forestT5550.6	ES	0.02	FOD	Assisted	5	17	7	0	41.56	202.12	173.35
restoration80	forestT5550.6	ES	0.03	FOD	Assisted	5	105	27	6.9	30.19	136.71	225.86
restoration83	forestT5550.6	ES	0.02	FOD	Assisted	5	37	5	16.67	39.04	236.6	186.25
restoration88	forestT5550.6	ES	0.02	FOD	Assisted	5	14	5	0	19.37	250.95	191.25
restoration89	forestT5550.6	ES	0.03	FOD	Assisted	5	40	6	0	19.27	260.67	143
restoration91	forestT5550.6	ES	0.03	FOD	Assisted	5	73	8	0	17.25	240.88	179.51
restoration93	forestT49	ES	0.02	FOD	Assisted	5	54	10	9.09	9.43	207.96	132.78
restoration97	forestT49	ES	0.15	FOD	Assisted	5	266	20	0	10.82	103.74	128.6
restoration98	forestT5550.3	ES	0.17	FOD	Assisted	5	567	42	10.64	24.75	87.68	175.15

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration163	forestT49	MG	0.18	FOD	Active	5	379	53	3.64	22.29	89.2	188.55
restoration165	forestT5550.3	MG	0.21	FOD	Active	5	191	22	18.52	23.57	45.9	163.94
restoration167	forestT3723	MG	0.76	FOD	Active	5	561	37	7.5	39.55	98.08	200.38
restoration269	forestT571	PR	0.05	FOM	Assisted	5	27	19	13.64	37.55	163.6	223.38
restoration272	forestT743	PR	0.14	FOM	Assisted	6	39	17	19.05	4.69	114.24	210.09
restoration279	forestT743	PR	0.04	FOM	Assisted	6	26	19	5	15.08	116.76	221.1
restoration281	forestT743	PR	0.04	FOM	Assisted	5	36	22	8.33	16.92	143.11	220.76
restoration284	forestT743	PR	0.25	FOM	Assisted	5	265	71	5.33	29.4	73.59	228.34
restoration287	forestT743	PR	0.13	FOM	Assisted	5	112	41	4.65	28.16	87.73	231.74
restoration290	forestT571	PR	0.05	FOM	Assisted	6	33	20	9.09	19.18	118.58	250.05
restoration293	forestT571	PR	0.07	FOM	Assisted	6	44	21	8.7	44.57	88.03	204.42
restoration296	forestT571	PR	0.15	FOM	Assisted	5	116	41	6.82	45.12	83.96	225.89
restoration298	forestT571	PR	0.02	FOM	Assisted	4	21	19	9.52	44.29	113.31	227.48
restoration304	forestT571	PR	0.15	FOM	Assisted	5	89	47	6	14.1	82.67	224.51
restoration307	forestT571	PR	0.16	FOM	Assisted	6	92	38	9.52	7.84	97.34	226.49
restoration310	forestT743	PR	0.19	FOM	Assisted	6	141	60	3.23	18.75	96.65	255.15
restoration313	forestT743	PR	0.13	FOM	Assisted	6	143	53	10.17	30.58	78.26	223.66
restoration315	forestT743	PR	0.02	FOM	Assisted	5	21	18	14.29	30.29	136.47	221.83
restoration318	forestT743	PR	0.2	FOM	Assisted	5	285	76	7.32	35.68	73.61	230.82
restoration321	forestT571	PR	0.06	FOM	Assisted	5	39	16	5.88	38.6	151.94	216.31
restoration324	forestT743	PR	0.05	FOM	Assisted	6	18	13	18.75	20.94	131.26	216.95
restoration325	forestT743	PR	0.16	FOM	Assisted	5	91	33	5.71	14.34	106.18	208.7
restoration328	forestT743	PR	0.07	FOM	Assisted	5	60	30	9.09	39.13	92.91	217.23
restoration331	forestT743	PR	0.12	FOM	Assisted	6	82	38	5	39.39	92.76	219.45
restoration336	forestT571	PR	0.05	FOM	Assisted	6	15	11	15.38	49.86	149.16	200.27
restoration339	forestT806	PR	0.1	FOM	Assisted	5	71	36	5.26	47.58	96.86	227.77
restoration342	forestT571	PR	0.08	FOM	Assisted	6	55	33	8.33	18.03	114.7	230.04
restoration347	forestT743	PR	0.08	FOM	Assisted	4	129	20	13.04	21.31	115.88	194.03

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration350	forestT743	PR	0.06	FOM	Assisted	6	48	25	3.85	34.81	106.68	214.75
restoration353	forestT743	PR	0.15	FOM	Assisted	5	145	55	3.51	39.53	81.33	226.23
restoration356	forestT743	PR	0.06	FOM	Assisted	5	44	25	3.85	35.18	131.65	224.07
restoration359	forestT806	PR	0.15	FOM	Assisted	5	138	44	6.38	40.79	72.69	229.41
restoration362	forestT571	PR	0.07	FOM	Assisted	6	31	23	8	34.9	96.63	220.25
restoration365	forestT571	PR	0.08	FOM	Assisted	5	70	40	2.44	35.56	91.42	221.58
restoration369	forestT571	PR	0.28	FOM	Assisted	5	238	75	7.41	36.38	61.41	228.69
restoration371	forestT571	PR	0.04	FOM	Assisted	6	46	31	6.06	31.28	116.67	227.12
restoration374	forestT743	PR	0.06	FOM	Assisted	5	42	22	12	21.12	114.76	211.47
restoration380	forestT743	PR	0.04	FOM	Assisted	4	95	17	5.56	15.06	129.4	182.17
restoration383	forestT743	PR	0.16	FOM	Assisted	3	461	47	4.08	12.8	117.55	209.28
restoration386	forestT571	PR	0.15	FOM	Assisted	5	131	50	7.41	44.15	77.7	227.11

APPENDIX H. Information about the studied restoration sites of the Atlantic Forest, Brazil. Established stratum.

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration479	forestT3711	ES	0.44	FES	Active	5	113	18	5.26	35.2	132.71	181.44
restoration71	forestT3711	ES	0.04	FES	Assisted	5	23	9	25	20.96	214.67	177.97
restoration103	forestB5	SP	0.07	FES	Active	2	9	6	0	1.48	153.4	160.53
restoration104	forestB1	SP	0.05	FES	Active	2	10	8	20	0.74	206.49	204.18
restoration105	forestB1	SP	0.18	FES	Active	3	71	21	12.5	0.99	110.54	201.46
restoration106	forestB17	SP	0.08	FES	Active	5	45	13	7.14	1.54	177.43	201.81
restoration107	forestB1	SP	0.14	FES	Active	4	101	19	5	1.65	130.66	185.58
restoration108	forestB1	SP	0.1	FES	Active	6	84	19	9.52	0.12	132.25	200.54
restoration115	forestB13	SP	0.11	FES	Active	3	51	18	10	4.03	138.75	207.7
restoration116	forestB18	SP	0.18	FES	Active	6	73	12	25	0.6	75.63	142.65
restoration118	forestB18	SP	0.1	FES	Active	6	77	12	14.29	1.02	112.19	149.37
restoration120	forestB13	SP	0.1	FES	Active	4	91	36	14.29	0.82	79.83	204.67
restoration121	forestT3172	SP	0.29	FES	Active	12	159	21	43.24	15.3	111.11	195.76
restoration122	forestT3172	SP	0.29	FES	Active	8	160	36	26.53	16.05	80.63	213.13
restoration124	forestB9	SP	0.1	FES	Active	3	66	18	0	0.4	51.5	195.71
restoration125	forestT1631	SP	0.72	FES	Active	8	972	52	21.21	20.51	51.99	175.6
restoration126	forestB2	SP	0.05	FES	Active	5	9	7	12.5	3.38	176.56	186.39
restoration127	forestB2	SP	0.11	FES	Active	3	28	6	25	2.37	63.47	88.57
restoration128	forestB5	SP	0.12	FES	Active	1	28	11	0	5.34	114.38	195.24
restoration133	forestB2	SP	0.05	FES	Active	5	8	4	0	11.93	234.14	161.75
restoration134	forestT714	SP	0.09	FES	Active	46	87	24	20	44	114.81	215.53
restoration135	forestB9	SP	0.07	FES	Active	3	12	8	11.11	2.19	99.91	157.46
restoration136	forestB13	SP	0.07	FES	Active	3	15	7	0	2.49	209.92	180.95
restoration137	forestB16	SP	0.16	FES	Active	1	32	13	13.33	1.13	65.05	181.66

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration138	forestB16	SP	0.32	FES	Active	4	144	27	18.18	1.16	82.54	200.91
restoration139	forestB12	SP	0.1	FES	Active	6	113	22	8.33	1.25	108.17	203.25
restoration140	forestT1505	SP	0.54	FES	Active	55	468	75	18.48	19.5	84.06	220.51
restoration141	forestB3	SP	0.07	FES	Active	2	37	16	11.11	0.92	146.6	195.44
restoration143	forestB3	SP	0.1	FES	Active	5	84	29	14.71	1.09	92.41	210.54
restoration146	forestT1484	SP	0.09	FES	Active	11	82	47	9.62	4.74	79.48	211.81
restoration147	forestT1484	SP	0.09	FES	Active	13	128	16	15.79	4.74	100.3	194.85
restoration149	forestB5	SP	0.06	FES	Active	2	19	10	23.08	2.88	131.48	187.18
restoration150	forestB9	SP	0.06	FES	Active	4	22	6	14.29	3.1	83.51	143.52
restoration152	forestB9	SP	0.05	FES	Active	3	7	4	20	1.91	224.98	162.02
restoration156	forestB5	SP	0.04	FES	Active	1	5	3	0	2.74	239.22	136.11
restoration169	forestT1477	SP	0.75	FES	Active	23	570	60	34.78	20.19	65.68	221.36
restoration170	forestT5994	SP	0.27	FES	Active	5	212	11	0	7.57	63.48	174.42
restoration171	forestT5994	SP	0.27	FES	Active	5	108	17	5.56	7.57	103.61	188.59
restoration172	forestT5994	SP	0.27	FES	Active	5	140	14	6.67	7.57	43.49	155.62
restoration173	forestT5994	SP	0.27	FES	Assisted	5	58	10	16.67	7.57	102.41	162.84
restoration174	forestT5994	SP	0.27	FES	Assisted	5	38	9	18.18	7.57	91.07	116.42
restoration180	forestB9	SP	0.04	FES	Active	2	7	7	12.5	1.92	148.05	191.57
restoration181	forestB10	SP	0.06	FES	Active	4	18	9	10	6.08	180.27	195.23
restoration215	forestB16	SP	0.18	FES	Active	3	67	15	16.67	2.97	158.66	204.72
restoration216	forestB9	SP	0.04	FES	Active	1	3	2	0	6.75	237.16	105.4
restoration221	forestB15	SP	0.49	FES	Active	5	109	21	19.23	2.35	94.89	203.35
restoration222	forestB2	SP	0.07	FES	Active	3	36	15	0	3.57	67.92	199.52
restoration223	forestB10	SP	0.04	FES	Active	5	12	5	0	4.99	159.5	161.03
restoration225	forestB2	SP	0.1	FES	Active	4	79	24	14.29	0.95	87.28	208
restoration226	forestB13	SP	0.18	FES	Active	2	93	22	21.43	4.12	79.82	205.13
restoration227	forestB5	SP	0.04	FES	Active	4	4	4	20	1.54	171.86	164.76

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration229	forestB11	SP	0.02	FES	Active	3	3	2	0	21.3	146.94	65.31
restoration230	forestB11	SP	0.15	FES	Active	3	47	25	10.71	22.17	83.38	200.33
restoration233	forestB11	SP	0.12	FES	Active	4	26	9	10	20.83	63.24	157.21
restoration234	forestB11	SP	0.04	FES	Active	2	6	5	0	23.28	149.58	151.32
restoration238	forestB11	SP	0.03	FES	Active	3	3	2	50	18.77	237.16	105.4
restoration241	forestB11	SP	0.32	FES	Active	4	110	23	4.17	23.37	74.81	188.14
restoration245	forestB11	SP	0.16	FES	Active	4	53	15	0	34.49	77.5	178.46
restoration248	forestB11	SP	0.05	FES	Active	4	11	6	0	33.31	80.93	139.1
restoration250	forestB11	SP	0.28	FES	Active	4	76	18	5.26	34.96	77.31	186.18
restoration252	forestB11	SP	0.12	FES	Active	4	30	16	5.88	33.57	81.14	197.37
restoration254	forestB11	SP	0.06	FES	Active	4	43	18	10	34.22	96.09	193.87
restoration255	forestB11	SP	0.03	FES	Active	2	2	2	33.33	34.95	247.47	123.73
restoration261	forestB8	SP	0.07	FES	Active	1	18	6	14.29	12.89	148.12	166.55
restoration263	forestB4	SP	0.04	FES	Active	4	3	2	0	1.28	231.57	102.92
restoration265	forestB11	SP	0.13	FES	Active	4	48	13	18.75	0.83	106.71	193.31
restoration266	forestB16	SP	0.1	FES	Active	6	93	17	15	2.07	151.2	200.47
restoration389	forestT1631	SP	1	FES	Active	12	763	42	22.22	24.55	83.41	202.47
restoration391	forestT3593	SP	0.18	FES	Active	3	94	20	16.67	33.66	64.16	182.33
restoration392	forestT1350	SP	0.11	FES	Active	2	35	19	5	25.93	76.88	198.79
restoration393	forestT3593	SP	0.07	FES	Active	2	37	15	16.67	28.9	148.04	209.97
restoration394	forestT3172	SP	0.12	FES	Active	94	172	23	4.17	7.39	147.39	178.81
restoration395	forestT1477	SP	0.09	FES	Active	10	96	43	15.69	0.25	86.19	213.01
restoration396	forestT1477	SP	0.09	FES	Active	12	60	22	15.38	1.09	109.37	199.76
restoration397	forestT1477	SP	0.09	FES	Active	14	54	31	6.06	1.22	113.75	204.98
restoration398	forestT1618	SP	0.09	FES	Active	15	122	27	15.62	12.45	82.56	201.42
restoration491	forestB2	SP	0.08	FES	Active	2	18	8	0	3.49	179.23	181.99

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration495	forestB4	SP	0.1	FES	Active	3	90	25	3.85	1.38	68.08	193.88
restoration497	forestB17	SP	0.1	FES	Active	8	126	36	20	1.46	102.07	210.03
restoration498	forestB6	SP	0.1	FES	Active	7	95	21	4.55	1.04	124.5	190.47
restoration499	forestB11	SP	0.14	FES	Active	4	70	17	15	1.3	134.26	197.56
restoration500	forestB10	SP	0.1	FES	Active	6	79	22	12	1.58	143.91	203.59
restoration502	forestB13	SP	0.14	FES	Active	4	30	15	11.76	2.68	98.3	190.47
restoration503	forestB13	SP	0.18	FES	Active	4	61	21	12.5	3.26	84.48	201.87
restoration504	forestB2	SP	0.08	FES	Active	2	18	6	0	2.38	213.89	164.75
restoration505	forestB13	SP	0.04	FES	Active	3	8	4	0	5.14	167.56	144.45
restoration507	forestB14	SP	0.1	FES	Active	6	72	24	20	0.54	97.61	199.08
restoration508	forestB9	SP	0.06	FES	Active	1	9	7	22.22	2.53	152.39	182.14
restoration509	forestB9	SP	0.08	FES	Active	1	18	13	13.33	2.55	103.29	191.42
restoration510	forestB13	SP	0.2	FES	Active	3	65	20	9.09	2.53	60.58	195.21
restoration514	forestB13	SP	0.2	FES	Active	4	58	22	12	1.7	74.89	201.21
restoration515	forestB8	SP	0.11	FES	Active	3	43	20	4.76	3.7	85.15	204.83
restoration516	forestB9	SP	0.05	FES	Active	2	10	7	22.22	13.76	155.28	165.14
restoration517	forestB5	SP	0.11	FES	Active	5	38	16	15.79	3.75	117.65	208.08
restoration518	forestB2	SP	0.05	FES	Active	2	6	4	0	0.87	235.15	160.04
restoration519	forestB5	SP	0.16	FES	Active	3	29	8	0	2.56	119.07	165.96
restoration521	forestB8	SP	0.1	FES	Active	1	13	8	20	2.76	141.83	175.58
restoration522	forestB16	SP	0.07	FES	Active	4	22	6	14.29	0.49	226.61	180.08
restoration523	forestB13	SP	0.04	FES	Active	1	6	4	0	2.76	87.7	119.73
restoration524	forestB13	SP	0.02	FES	Active	2	2	2	0	0.92	231.57	115.79
restoration525	forestB5	SP	0.02	FES	Active	2	5	5	16.67	2.58	195.8	178.02
restoration526	forestB5	SP	0.04	FES	Active	3	7	3	0	2.1	105.85	108.13
restoration527	forestB2	SP	0.07	FES	Active	2	17	10	9.09	1.4	161.03	200.81
restoration528	forestB9	SP	0.02	FES	Active	2	9	8	0	14.64	166.26	186.41

ID	Reference ecosystem	State	Effort (ha)	Vegetation type	Restoration method	Age (years)	Abundance	Richness	Exotic species percentage	Distance to Reference Ecosystem	MNTD	MPD
restoration529	forestB8	SP	0.05	FES	Active	1	5	5	0	3.32	148.54	165.14
restoration530	forestB8	SP	0.06	FES	Active	3	6	2	33.33	3.5	247.47	123.73
restoration532	forestB13	SP	0.07	FES	Active	3	14	10	0	3.76	138.91	203.21
restoration566	forestT714	SP	0.09	FES	Active	29	84	16	5.88	37.43	195.6	191.76
restoration568	forestB15	SP	0.1	FES	Active	5	140	25	10.71	0.9	156.45	181.87
restoration109	forestT3723	BA	0.08	FOD	Active	1	9	6	0	33.88	202.84	194.46
restoration110	forestT3723	BA	0.06	FOD	Active	1	6	6	0	31.39	206.25	201.83
restoration112	forestT3723	BA	0.07	FOD	Active	1	11	8	11.11	30.72	179.49	206.29
restoration114	forestT3723	BA	0.19	FOD	Active	1	19	12	14.29	30.25	176.78	216.06
restoration189	forestT4573	BA	0.05	FOD	Assisted	5	7	5	28.57	17.52	202.67	180.45
restoration190	forestT3723	BA	0.02	FOD	Assisted	5	4	2	0	17.52	237.16	118.58
restoration192	forestT3723	BA	0.03	FOD	Assisted	5	10	5	28.57	32.16	129.13	147.77
restoration193	forestT3723	BA	0.02	FOD	Assisted	5	11	5	0	33.93	241.35	179.77
restoration194	forestT3723	BA	0.03	FOD	Assisted	5	5	3	25	31.08	176.36	126.12
restoration196	forestT3723	BA	0.07	FOD	Assisted	5	21	5	28.57	33	240.51	159.01
restoration197	forestT3723	BA	0.09	FOD	Assisted	5	33	7	12.5	32.1	226.48	178.01
restoration198	forestT3723	BA	0.02	FOD	Assisted	5	2	2	33.33	29.74	271.82	135.91
restoration208	forestT49	BA	0.05	FOD	Assisted	5	27	14	12.5	9.43	119.7	192.33
restoration209	forestT49	BA	0.03	FOD	Assisted	5	3	3	40	9.8	238.48	161.98
restoration212	forestT49	BA	0.08	FOD	Assisted	5	23	14	12.5	8.84	199.11	215.99
restoration213	forestT49	BA	0.04	FOD	Assisted	5	22	6	14.29	21.25	240.01	196.37
restoration214	forestT3723	BA	0.04	FOD	Active	1	5	3	0	47.93	124.9	121.85
restoration535	forestT3723	BA	0.02	FOD	Assisted	5	14	4	20	47.67	238.5	142.41
restoration538	forestT3723	BA	0.12	FOD	Assisted	5	32	10	9.09	39.55	190.98	166.33
restoration545	forestT3723	BA	0.04	FOD	Assisted	5	14	5	16.67	19.73	191.72	163.54
restoration555	forestT3723	BA	0.02	FOD	Active	5	7	6	0	14.88	240.58	203.63

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restoration557	forestT3723	BA	0.02	FOD	Assisted	5	3	3	0	46.02	227.42	166.41
restoration558	forestT3723	BA	0.25	FOD	Assisted	5	80	20	9.09	32.76	114.94	206.39
restoration560	forestT3723	BA	0.26	FOD	Assisted	5	64	18	0	32.26	117.53	194.04
restoration562	forestT3723	BA	0.09	FOD	Assisted	5	18	11	8.33	30.29	159.9	201.09
restoration564	forestT3723	BA	0.03	FOD	Active	5	4	2	0	44.85	237.16	118.58
restoration57	forestT4637	BA	0.07	FOD	Assisted	5	33	8	20	7.57	220.34	159.73
restoration101	forestT49	ES	0.81	FOD	Active	5	248	36	12.2	19.62	79.75	186.93
restoration28	forestT4636	ES	0.03	FOD	Assisted	5	40	5	16.67	2.45	251.19	133.1
restoration31	forestT4636	ES	0.03	FOD	Assisted	5	2	2	50	2.78	271.82	135.91
restoration32	forestT4636	ES	0.04	FOD	Assisted	5	11	5	28.57	9.5	234.32	181.3
restoration33	forestT4636	ES	0.05	FOD	Assisted	5	18	3	25	12.79	249.46	168.54
restoration34	forestT4636	ES	0.02	FOD	Assisted	5	3	2	50	12.56	271.82	120.81
restoration36	forestT4636	ES	0.05	FOD	Assisted	5	5	3	40	11.11	257.96	149.45
restoration37	forestT4636	ES	0.02	FOD	Assisted	5	15	3	40	11.49	265.33	112.91
restoration38	forestT4636	ES	0.02	FOD	Assisted	5	3	2	0	11.49	237.16	105.4
restoration40	forestT4636	ES	0.02	FOD	Assisted	5	11	6	14.29	12.32	251.86	190.89
restoration404	forestT5550.3	ES	0.03	FOD	Assisted	5	10	4	20	26.38	238.39	162.32
restoration405	forestT5550.3	ES	0.02	FOD	Assisted	5	11	5	16.67	24.75	248.38	182.57
restoration409	forestT49	ES	0.02	FOD	Assisted	5	3	2	0	26.73	237.16	105.4
restoration41	forestT4636	ES	0.04	FOD	Assisted	5	16	8	20	7.95	185.5	208.52
restoration410	forestT49	ES	0.02	FOD	Assisted	5	9	6	14.29	9.03	208.11	191.95
restoration411	forestT49	ES	0.02	FOD	Assisted	5	2	2	0	10.48	271.82	135.91
restoration419	forestT49	ES	0.03	FOD	Assisted	5	7	4	20	20.97	233.3	144.45
restoration42	forestT4636	ES	0.05	FOD	Assisted	5	18	4	20	6.16	254.8	151.48
restoration420	forestT49	ES	0.02	FOD	Assisted	5	2	2	33.33	23.49	271.82	135.91
restoration424	forestT49	ES	0.02	FOD	Assisted	5	10	3	0	23.61	259.65	155.71
restoration428	forestT5550.3	ES	0.03	FOD	Assisted	5	13	5	16.67	24.75	238.99	185.88

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restoration44	forestT4636	ES	0.03	FOD	Assisted	5	8	3	40	14.02	265.67	143.38
restoration442	forestT49	ES	0.1	FOD	Assisted	5	24	6	0	25.94	203.66	196.25
restoration443	forestT49	ES	0.04	FOD	Assisted	5	14	8	0	24.11	181.45	190.24
restoration444	forestT49	ES	0.03	FOD	Assisted	5	5	3	0	19.62	148.05	114.99
restoration445	forestT49	ES	0.02	FOD	Assisted	5	6	4	20	19.62	250.43	188.41
restoration451	forestT49	ES	0.02	FOD	Assisted	5	2	2	0	20.64	237.16	118.58
restoration455	forestT49	ES	0.04	FOD	Assisted	5	5	2	33.33	16.22	271.82	86.98
restoration456	forestT49	ES	0.16	FOD	Assisted	5	28	8	20	14.99	215.58	185.8
restoration458	forestT49	ES	0.17	FOD	Assisted	5	32	7	22.22	15.39	200.88	181.5
restoration46	forestT4636	ES	0.07	FOD	Assisted	5	41	12	20	12.03	219.46	209.52
restoration461	forestT49	ES	0.02	FOD	Assisted	5	7	5	0	10.14	167.97	169.35
restoration464	forestT49	ES	0.03	FOD	Assisted	5	10	4	20	13.93	136.37	152.05
restoration468	forestT5550.3	ES	0.04	FOD	Assisted	5	14	2	50	19.66	231.57	56.71
restoration470	forestT5550.3	ES	0.03	FOD	Assisted	5	6	5	0	22.75	170.27	177.05
restoration472	forestT5550.3	ES	0.04	FOD	Assisted	5	12	6	0	14.24	142.59	163.73
restoration473	forestT5550.3	ES	0.04	FOD	Assisted	5	10	3	40	14.8	106.24	101.29
restoration475	forestT49	ES	0.02	FOD	Assisted	5	11	3	25	24.06	240.31	80.21
restoration489	forestT10	ES	0.12	FOD	Assisted	5	56	11	15.38	26.9	210.39	200.1
restoration49	forestT4637	ES	0.02	FOD	Assisted	5	20	4	33.33	2.35	251.31	122.82
restoration50	forestT4637	ES	0.05	FOD	Assisted	5	35	2	60	2.5	271.82	135.8
restoration63	forestT4637	ES	0.09	FOD	Assisted	5	58	7	36.36	23.61	233.17	186.53
restoration64	forestT4637	ES	0.02	FOD	Assisted	5	3	2	0	10.95	271.82	120.81
restoration66	forestT4637	ES	0.02	FOD	Assisted	5	18	7	12.5	9.5	205.49	191.78
restoration67	forestT4637	ES	0.03	FOD	Assisted	5	5	4	33.33	7.4	128.84	144.62
restoration69	forestT4637	ES	0.02	FOD	Assisted	5	4	2	33.33	11.63	247.47	123.73
restoration70	forestT4637	ES	0.03	FOD	Assisted	5	10	6	14.29	6.96	244.62	198.48

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restoration72	forestT5550.6	ES	0.03	FOD	Assisted	5	8	5	28.57	38.51	242.48	195.69
restoration78	forestT5550.6	ES	0.02	FOD	Assisted	5	2	2	0	41.56	247.47	123.73
restoration80	forestT5550.6	ES	0.03	FOD	Assisted	5	20	7	22.22	30.19	197.11	131.66
restoration83	forestT5550.6	ES	0.02	FOD	Assisted	5	6	3	25	39.04	240.4	158.26
restoration88	forestT5550.6	ES	0.02	FOD	Assisted	5	4	4	0	19.37	207.16	181.2
restoration89	forestT5550.6	ES	0.02	FOD	Assisted	5	7	3	0	19.27	257.91	163.44
restoration91	forestT5550.6	ES	0.03	FOD	Assisted	5	11	6	14.29	17.25	220.99	201.46
restoration93	forestT49	ES	0.02	FOD	Assisted	5	16	5	16.67	9.43	222.08	121.53
restoration97	forestT49	ES	0.24	FOD	Assisted	5	127	16	5.88	10.82	195.68	93.54
restoration98	forestT5550.3	ES	0.28	FOD	Assisted	5	121	16	15.79	24.75	106.77	182.3
restoration163	forestT49	MG	0.17	FOD	Active	5	62	23	8	22.29	118.57	197.09
restoration165	forestT5550.3	MG	0.2	FOD	Active	5	46	18	14.29	23.57	117.45	188.14
restoration167	forestT3723	MG	0.42	FOD	Active	5	107	27	3.57	39.55	104.06	195.08
restoration269	forestT571	PR	0.02	FOM	Assisted	5	5	5	0	37.55	225.19	190.79
restoration272	forestT743	PR	0.08	FOM	Assisted	6	20	6	0	4.69	162.02	171.33
restoration279	forestT743	PR	0.03	FOM	Assisted	6	13	2	0	15.08	247.47	117.14
restoration281	forestT743	PR	0.04	FOM	Assisted	5	39	7	0	16.92	216.63	132.75
restoration284	forestT743	PR	0.23	FOM	Assisted	5	178	25	3.85	29.4	73.83	151.13
restoration287	forestT743	PR	0.12	FOM	Assisted	5	95	21	0	28.16	72.17	178.02
restoration290	forestT571	PR	0.04	FOM	Assisted	6	9	4	0	19.18	125.02	139.22
restoration293	forestT571	PR	0.05	FOM	Assisted	6	21	7	12.5	44.57	201.2	148.56
restoration296	forestT571	PR	0.1	FOM	Assisted	5	44	6	0	45.12	209.14	129.03
restoration298	forestT571	PR	0.02	FOM	Assisted	4	7	3	0	44.29	218.34	130.31
restoration304	forestT571	PR	0.09	FOM	Assisted	5	23	7	0	14.1	219.98	152.34
restoration307	forestT571	PR	0.1	FOM	Assisted	6	41	13	0	7.84	74.31	136.91
restoration310	forestT743	PR	0.11	FOM	Assisted	6	41	10	0	18.75	124.11	150.35
restoration313	forestT743	PR	0.11	FOM	Assisted	6	73	12	7.69	30.58	186.16	150.93

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restoration315	forestT743	PR	0.02	FOM	Assisted	5	6	3	0	30.29	234.22	145.93
restoration318	forestT743	PR	0.11	FOM	Assisted	5	50	16	5.88	35.68	64.37	124.02
restoration321	forestT571	PR	0.04	FOM	Assisted	5	17	6	0	38.6	141.57	147.72
restoration324	forestT743	PR	0.03	FOM	Assisted	6	5	2	0	20.94	247.47	118.78
restoration325	forestT743	PR	0.11	FOM	Assisted	5	23	5	28.57	14.34	115.31	65.88
restoration328	forestT743	PR	0.06	FOM	Assisted	5	32	10	9.09	39.13	198.82	193.18
restoration331	forestT743	PR	0.07	FOM	Assisted	6	39	12	0	39.39	155.29	198.14
restoration336	forestT571	PR	0.04	FOM	Assisted	6	17	5	0	49.86	229.31	171.75
restoration339	forestT806	PR	0.07	FOM	Assisted	5	19	6	0	47.58	243.37	141.34
restoration342	forestT571	PR	0.08	FOM	Assisted	6	24	6	0	18.03	239.12	158.2
restoration347	forestT743	PR	0.02	FOM	Assisted	4	4	3	0	21.31	99.38	95.39
restoration350	forestT743	PR	0.06	FOM	Assisted	6	33	7	0	34.81	66.93	68.28
restoration353	forestT743	PR	0.12	FOM	Assisted	5	106	17	0	39.53	128.45	189.55
restoration356	forestT743	PR	0.03	FOM	Assisted	5	18	7	0	35.18	156.77	179.75
restoration359	forestT806	PR	0.15	FOM	Assisted	5	93	17	5.56	40.79	177.66	164.92
restoration362	forestT571	PR	0.05	FOM	Assisted	6	32	8	0	34.9	159.96	170.22
restoration365	forestT571	PR	0.07	FOM	Assisted	5	24	10	9.09	35.56	74.81	97.66
restoration369	forestT571	PR	0.15	FOM	Assisted	5	77	17	5.56	36.38	67.94	133.7
restoration371	forestT571	PR	0.03	FOM	Assisted	6	4	4	0	31.28	160.5	157.49
restoration374	forestT743	PR	0.02	FOM	Assisted	5	5	4	0	21.12	126.97	146.63
restoration380	forestT743	PR	0.04	FOM	Assisted	4	12	4	0	15.06	178.08	121.36
restoration383	forestT743	PR	0.07	FOM	Assisted	3	12	5	0	12.8	142.52	114.63
restoration386	forestT571	PR	0.14	FOM	Assisted	5	55	10	0	44.15	94.64	149.67