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Avaliando processos de restauração utilizando redes de interação coleópteros-macrofungos

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Avaliando processos de restauração utilizando redes de interação coleópteros-macrofungos

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Encanta-me
a germinação da semente,
a mágica energética da fotossíntese,
o vai e vem do ecossistema,
a luta dos genes e das espécies.
Encanta-me ser parte da
complexa simplicidade de toda a existência.

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Resumo

A restauração ecológica visa a recuperação de ecossistemas que foram degradados, assegurando o seu restabelecimento estrutural e funcional. Porém, avaliar a funcionalidade do ecossistema ainda é um desafio, e vem sendo foco de trabalhos científicos a fim de desenvolver metodologias aplicáveis. Investigar as redes de interações ecológicas é uma forma adequada para avaliar a funcionalidade do ecossistema. As redes de interações são utilizadas na avaliação de habitats e já evidenciaram alterações na estrutura da comunidade que não foram detectadas pelas métricas tradicionais de riqueza, abundância e composição. Os macrofungos podem ser indicadores relevantes, pois realizam a decomposição e ciclagem de nutrientes e servem de alimento para diversos grupos de organismos, dentre eles os Coleoptera, que também podem utilizar a estrutura fúngica para nidificação. Este trabalho teve por finalidade construir redes tróficas formadas pela interação entre besouros fungívoros (Coleoptera) e macrofungos (Polyporales e Hymenochaetales) a fim de testar a aplicabilidade de redes ecológicas para avaliar a restauração quando comparadas às métricas tradicionais de abundância, riqueza e composição das espécies. O estudo se realizou em duas áreas sobre restauração florestal comparados às áreas de referência pareadas. A primeira área está em restauração há oito anos e a segunda há dez anos, sendo que até o momento, somente a segunda área teve sucesso na restauração da comunidade de plantas. No total, coletamos 512 macrofungos, representando 87 espécies, mas somente 181 indivíduos de 36 espécies apresentaram interações com besouros. Destes, foram obtidos 11.414 besouros de 53 espécies. Em ambas as áreas, as métricas de descritores de comunidade e também as métricas de redes não diferiram entre os tratamentos, indicando que a estrutura e também a funcionalidade das comunidades de macrofungos e besouros fungívoros está sendo recuperada nas áreas em restauração. Apesar de não haver diferença na composição de espécies, a espécie rara *Falsocis brasiliensis* e alguns exemplares da família Erotylidae somente foram encontradas em áreas de referência. Os processos de restauração diferiram qualitativamente entre as áreas, como podemos perceber através das interações realizadas. As áreas de restauração de dez anos estão mais próximas às áreas de referência, pois foram deixados troncos de madeira que serviram de substrato para os macrofungos, principalmente para o *Ganoderma australe* e suas interações, encontrado em árvores mortas da floresta de referência de ambas as áreas. Enquanto que as áreas de restauração de oito anos apresentaram pouco substrato lenhoso e baixa umidade, onde *Pycnoporus sanguineous* predominou em abundância de basidiomas e suas interações em relação à floresta de referência.

Palavras-chave: Interações Trófica, Hymenhochaetales, Polyoprales, Restauração Ecológica, Ciidae e Fungivoria.

Abstract

Ecological restoration aims to recover degraded ecosystems, ensuring both structural and functional restoration. Assessing ecosystem functionality is still a challenge, and current work is focusing on the development methods. Investigating networks of ecological interactions is a potential tool to assess ecosystem functionality. Interaction networks are used in the assessment of habitat change and have already evidenced differences in community structure that were not detected by the traditional metrics of richness, abundance and composition. Macrofungi are especially relevant indicators, due to their function in decomposition and nutrient cycling in the ecosystem, and as they serve as food source for several groups of organisms, among them the Coleoptera, which can also use the fungal structure for nesting. Here we aimed at building trophic networks formed by the interaction between fungivorous beetles (Coleoptera) and macrofungi (Polyporales and Hymenochaetales), in order to test the applicability of ecological networks for the evaluation of restoration when compared to the traditional metrics of abundance, richness and species composition through the macrofungi-beetles system. Research was conducted in two areas under forest restoration, compared to paired reference areas. The first area is under restoration process for 8 years and the second for 10 years, and in the second area the restoration success has been achieved based on plant community evaluation. During the study, we collected 512 macrofungi individuals, representing 87 species, but only 181 specimens from 36 species showed interactions with beetles. A total of 11,414 beetles from 53 species were obtained. For both areas, traditional community descriptors did not differ between treatments, nor did network metrics, indicating that the structure and also the functionality of the communities of fungivorous beetles and macrofungi are being successfully recovered in restoration areas. Although there is no difference in species composition, the rare species *Falsocis brasiliensis* and some specimens of the Erotylidae were found only in reference areas.

The processes of restoration differ qualitatively between areas, as we can perceive through the interactions. The ten year-long restoration areas are more similar to the reference areas, due to the presence of wood logs that served as substrate for the macrofungus, mainly *Ganoderma australe* and its associated beetles, occurring on dead trees found in the both reference forest areas. On the other hand, the eight year-long restoration area had less woody substrate, composed mostly of thin branches, and less humidity, where *Pycnoporus sanguineous* predominated in basidiome abundance and their interactions compared to the reference forest.

Keywords: Trophic Interactions, Hymenhochaetales, Polyoprales, Ecological Restoration, Ciidae, Fungivory.

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INTRODUÇÃO GERAL

A restauração ecológica objetiva recuperar a composição de espécies nativas de uma área degradada, assegurando o restabelecimento funcional e estrutural do ecossistema, na direção de torná-la autossustentável ecologicamente e garantir os processos de sucessão (Engel & Parrota 2003, Benayas *et al.* 2009). A avaliação sistêmica dos processos ecológicos é um objetivo crucial delimitado pela SER (2004) a fim de analisar a resiliência do ecossistema restaurado (Ruiz-Jaen &Aide 2005a).

Historicamente, grande parte dos estudos em restauração ecológica tem focado na avaliação da restauração da vegetação do ambiente em processo de restauração, baseado no princípio de que garantindo a reposição da comunidade de plantas, também o ecossistema por completo seria restaurado (hipótese *Field of dreams*; Palmer *et al.* 1997). Além disso, para avaliar o sucesso do processo de restauração, por muito tempo fez-se uso exclusivo de métricas tradicionais como índices fitossociologicos de abundânia, cobertura do dossel, diversidade e estrutura da vegetação (Young 2000; Ruiz-Jaen & Aide 2005b).

A Sociedade Internacional para a Restauração Ecológica (SER 2004) recomenda que se avalie o sucesso da restauração de maneira a incluir os processos ecológicos. Apesar do crescente esforço para tornar a avaliação cada vez mais sistêmica e funcional, Fraser *et al.* (2015) chamam atenção para a enorme lacuna na inclusão da avaliação das funções ecossistêmicas do ambiente recuperado, constatando que é preciso criar metodologias que atendam esta demanda. Assim como também relatam Kollmann *et al.* (2016) que existe um aumento, principalmente na última década, na inclusão da avaliação das funções ecossistêmicas da restauração, porém mesmo assim ainda há escassez em metodologias aplicáveis e eficientes.

Entre os tópicos utilizados para avaliar ecossistemicamente a restauração, a ciclagem de carbono e a decomposição são os mais considerados, enquanto que as interações tróficas são raramente estudadas, contemplando apenas 6% dos estudos que incluíram avaliação sistêmica publicados entre 2004 e 2013 (Kollmann *et al.* 2016). As redes de interações se tratam de uma metodologia eficiente para avaliar a restauração baseada nos serviços ecossistêmicos (Montoya *et al.* 2012; Dixon 2009).

A análise de redes de interações permite avaliar a restauração de funções ecossistêmicas quantitativamente, pois estas descrevem como as espécies em uma comunidade estão relacionadas (Pimm 1982, Ruiz-Jaen & Aide 2005a). Deste modo, o emprego das redes de interações é uma potencial ferramenta para investigar o caráter funcional de um ecossistema em recuperação ou restauração (Forup *et al.* 2008). Como também sugeriu Montoya *et al.* (2012), a estrutura das redes tróficas é sensível a alterações do ambiente e pode refletir o processo de restauração do habitat, podendo ainda ser utilizada para previsões futuras nas interações da comunidade avaliada.

A abordagem de redes em ecologia enfatiza a interação entre as espécies (Bascompte 2009), na qual cada espécie é representada por um nó, e a ligação (link) entre dois nós simboliza a interação entre duas espécies diferentes. Dessa forma, diversas métricas podem ser avaliadas, tais como: *conectância* (proporção dos possíveis links que foi efetivamente realizado, Jordano 1987); *links por espécie* (soma do número de links dividido pelo número de espécies); *robustez* (capacidade do sistema de suportar perturbações, como a perda de espécies); *especialização* (H2' nível de especialização média das espécies que interagem na rede); *assimetria da rede* (representa um balanço entre o nível inferior e superior da rede bipartida, valores negativos indicam que a rede possui mais espécies no nível inferior e valores positivos indicam mais espécies no nível superior, Blüthgen *et al.* 2007); e *equitabilidade de interações* (quantifica a distribuição das densidades de interações entre as espécies, valores baixos de equitabilidade ocorrem quando há elevada discrepância no número de interações entre espécies da rede, ou seja, quando poucas espécies concentram a maioria dos links, Tylianakis *et al.* 2007).

Análises quantitativas das métricas de redes de interações já constataram alteração da paisagem (Fortuna & Bascompte 2006, Rodriguez-Cabal *et al.* 2013), sendo uma ferramenta útil na avaliação da qualidade de um habitat (Ings *et al.* 2009). Diversos estudos já evidenciaram alterações nas métricas de conectância, especialização e robustez nas estruturas das redes de interações de polinizadores e plantas devido à perda de habitat, fragmentação e mudanças climáticas (Thébault & Fontaine 2010, Aizen *et al.* 2012, Spiesman & Inouye 2013).

O uso das redes de interação na avaliação da restauração já foi relevante nos seguintes casos: primeiro, foi possível verificar que as redes de interações polinizador-planta estavam menos conectadas em áreas restauradas em relação às áreas de referência, isso torna estas áreas mais sensíveis à perturbações (Forup & Memmott 2005); segundo, que os valores de especialização também diferiram na estrutura das redes polinizador-planta, nas áreas restauradas os visitantes florais eram mais generalistas, enquanto que em áreas de referências a rede formada era mais específica (Forup *et al.* 2008).

A metodologia de redes tem potencial para atender ao desafio de avaliar sistematicamente a restauração ecológica, pois é capaz de revelar o processo que a comunidade está tomando e se está se tornando sustentavelmente funcional. Como já constatado por Tylianakis *et al.* (2007), em estudos comparativos de alterações ambientais, o emprego de redes ecológicas foi importante para evidenciar alterações na estrutura da comunidade ao nível das interações entre espécies e suas funções dentro do ecossistema que não foram detectados pelas métricas tradicionais. As redes de parasitoides de abelhas e vespas se mostrou mais vulnerável nas áreas mais alteradas pelas ações antrópicas pela menor equitabilidade nas interações (Tylianakis *et al.* 2007).

Para construir redes bipartidas a fim de comparar situações ambientais distintas, usualmente são selecionados dois grupos taxonômicos que estabelecem um tipo específico de interação ecológica. As abordagens de redes tróficas quantitativas com ênfase ecológica já foram utilizadas em sistemas de interações mutualísticas como polinizador-planta (Forup *et. al*, 2008), em sistemas dispersor-planta (Pocock *et al.* 2012, Ribeiro *et al.* 2015) e também em sistemas antagonistas como hospedeiro-parasitóide (Tylianakys *et al.* 2007, Laliberté & Tylianakys 2010, Macfadyen *et al.* 2011). O uso em outros sistemas é mais escasso, como o caso da interação entre insetos e fungos (Schigel 2011).

No caso da interação de coleópteros e macrofungos, ambos exercem papéis altamente relevantes para avaliar ecossistemas florestais. Os macrofungos decompõem a celulose, a hemicelulose e a lignina da madeira, para posterior ciclagem no ecossistema. Dentre os macrofungos, aqueles capazes de decompor a madeira são denominados xilófilos, sendo os Basidiomycetes (Basidiomycota) os mais conspícuos, representando a parcela mais significativa desse grupo (Oberwinkler 1994; Gilbertson 1980).

Além importância ecológica decompositora, os fungos podem transformar estas moléculas orgânicas complexas em compostos digestivos para o consumo de outros seres, tais como insetos (Schigel 2011). Os macrofungos fazem parte da cadeia alimentar nos ecossistemas servindo de alimento para diversas espécies de artrópodes e suas fases larvais, tais como coleópteros, dípteros e lepidópteros (Lawrence 1989), A fungivoria ou micetofagia é caracterizada pelo consumo de partes do fungo: micélio, esporos ou partes do basidioma de macrofungos (Lawrence 1989). Os basidiomas de cogumelos e orelhas-de-pau são visitados por diversos insetos que se alimentam dos esporos e do tecido fúngico, e alguns ovopositam nas cavidades do himenóforo ou nas paredes de galerias que cavam, desenvolvem-se e vivem neste micro-habitat (Orledge & Reynolds 2005). Fungos e besouros são grupos altamente diversificados em seus representantes, e ambos tem suas histórias evolutivas marcadas pela gama de interações que realizam (Guevara & Dirzo 1999).

Os macrofungos de madeira, como as orelhas-de-pau (Basidiomycota, Basydiomycetes: Polyporales e Hymenochaetales) em sua maioria políporos (com himenóforo formado por tubos), são preferidos por alguns grupos específicos de besouros hospedeiros. As orelhas-de-pau ficam expostas no ambiente sobre troncos por maior tempo se comparados com cogumelos carnosos, devido à sua consistência de maior resistência (Jonsell *et al.* 2001), permitindo a especialização de algumas espécies de besouros que realizam o seu desenvolvimento e reprodução dentro da estrutura fúngica (Jonsell & Nordlander 2004). A micofagia é bastante primitiva nos hábitos alimentares em coleópteros (Gillott 1982). Entre as famílias de coleópteros mais conhecidas por hábitos de micofagia estão: Ciidae, Endomychidae, Erotylidae e Tenebrionidae (Lawrence 1973, Grimaldi & Engel 2005) (Fig. 1).

Estudos já realizados na Mata Atlântica brasileira demonstram que a interação de besouros e fungos decompositores da madeira é sensível à fragmentação de florestas (Araujo *et al.* 2015). Assim como outras espécies dependentes da madeira morta correm risco de extinção devido à degradação das florestas e diminuição da disponibilidade deste substrato nas florestas (Seibold *et al.* 2015). Características das redes de interações entre besouros e macrofungos já foram estudados por Yamashita *et al.* (2015) e Schigel (2011), no entanto, sem a finalidade de comparar condições ambientais.

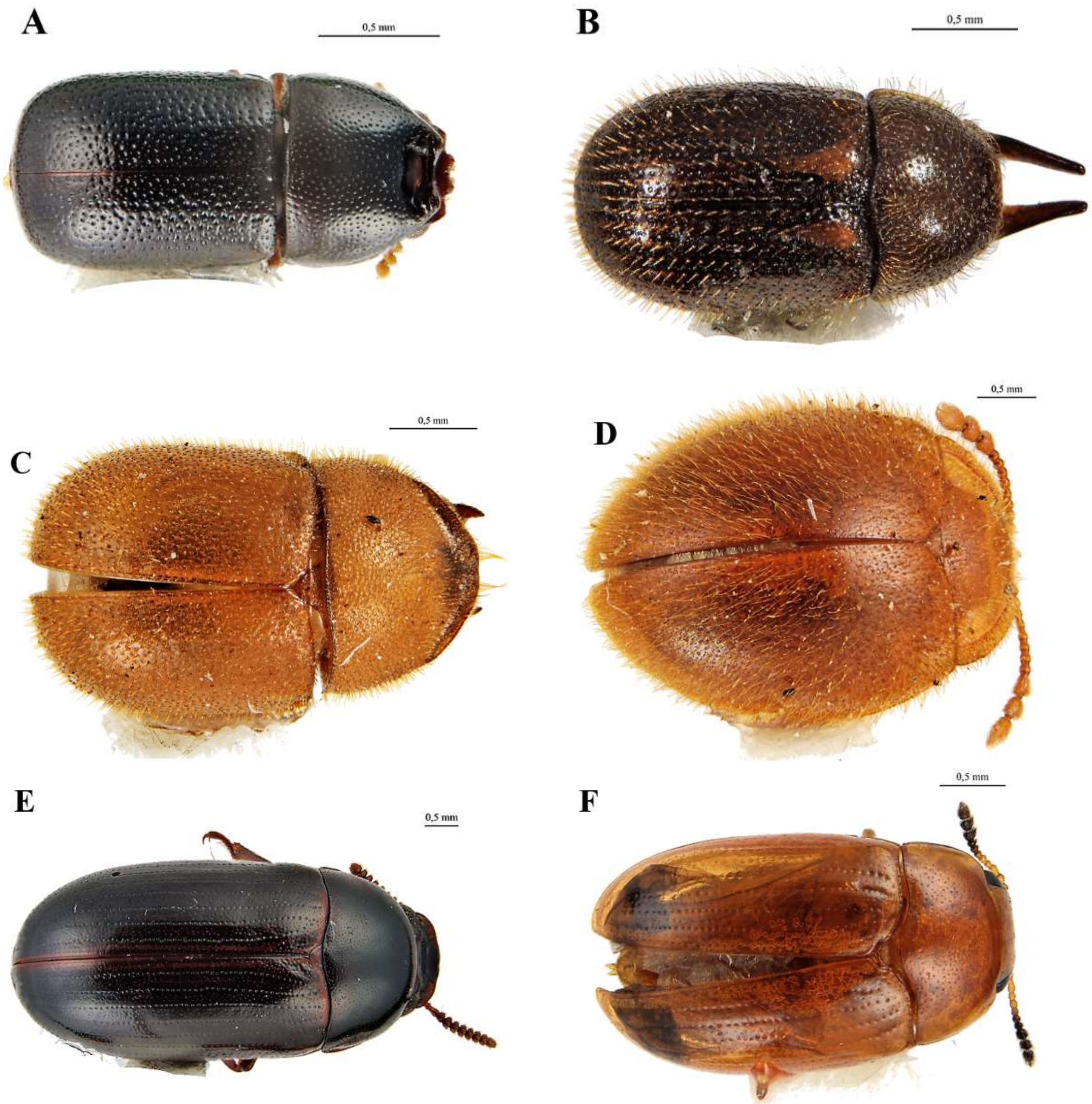

Fig. 1. Exemplo de coleópteros encontrados em macofungos nos municípios de Santa Tereza e Canela, Rio Grande do Sul, RS, Brasil. A) *Phellinocis romualdoi* (Ciidae), B) *Cis kawanabei* (Ciidae), C) *Falsocis brasiliensis* (Ciidae). D) exemplar da família Endomycethidae. E) *Neomida vitula* (Tenebrionidae), F) *Mycotretus pigmeus* (Erotylidae). * Escala no canto superior esquerdo de cada imagem.

Diante do potencial uso da metodologia de redes de interações na avaliação de projetos de restauração ecológica, este trabalho teve por finalidade comparar a área sob restauração florestal comparando-às a áreas de referência utilizando redes tróficas formadas pela interação entre besouros fungívoros (Coleoptera) e macrofungos (Polyporales e Hymenochaetales). As duas localidades selecionadas para este estudo são de mata semidecidual estacional, mas diferem no histórico da restauração. A área localizada no município de Canela teve o plantio de *Eucalyptus* sp. extraído, com o processo de restauração datando de 10 anos atrás; enquanto que a área localizada no município de Santa Tereza teve o plantio de espécies frutíferas exóticas extraído e a restauração data de 8 anos atrás (Fig. 2). Neste trabalho, comparamos as áreas em processo de restauração às áreas de referência, utilizando as interações de besouros fungivoros e macrofungos. E também, assim como em Tylianakis *et al.* (2007), testamos a aplicabilidade da metodologia de redes ecológicas na avaliação do progresso de restauração das áreas estudadas quando comparadas às métricas tradicionais de abundância, riqueza e composição das espécies, para coleópteros e fungos.

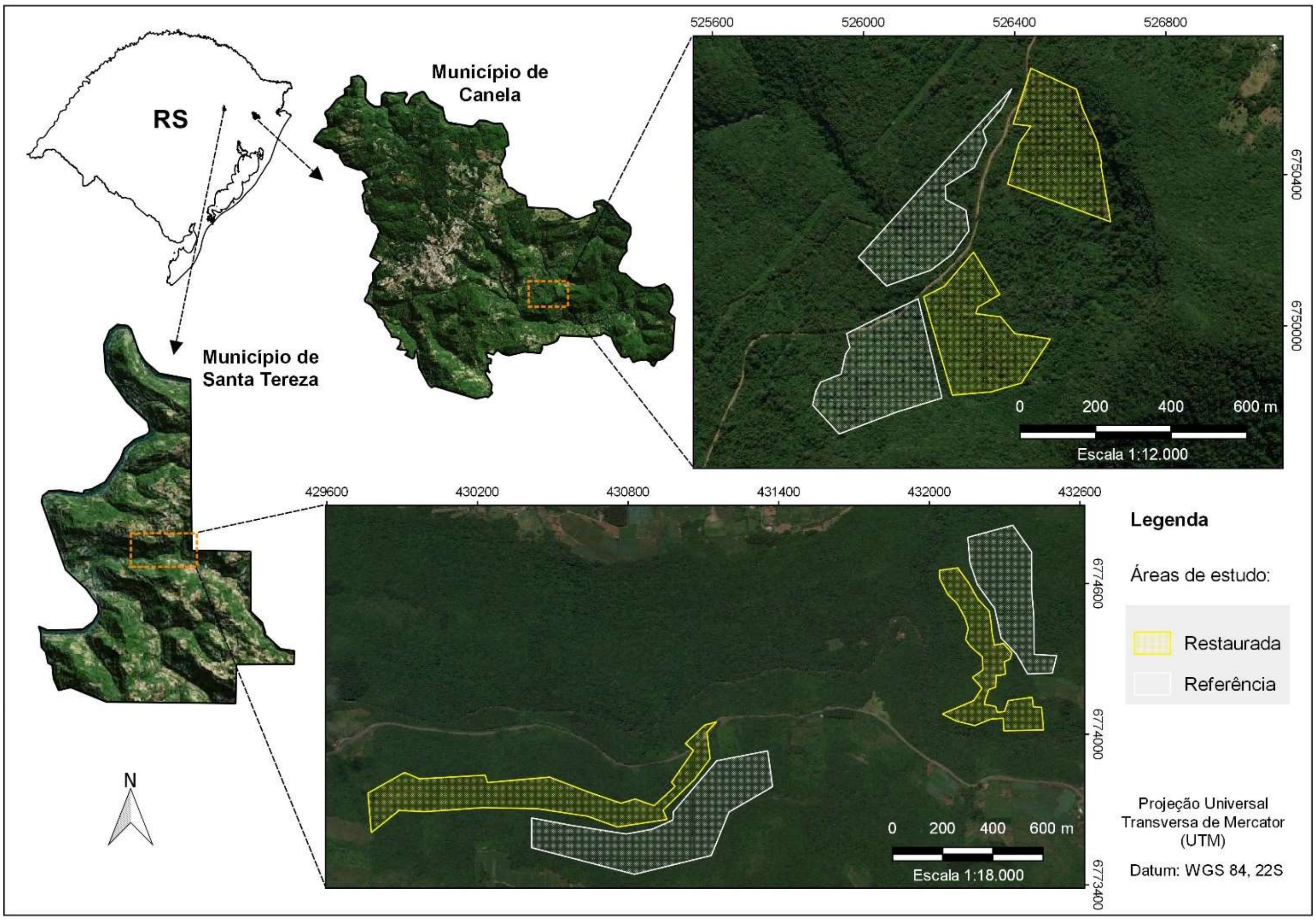

Fig 2. Localização das duas áreas de estudo no mapa do Rio Grande do Sul. A restauração de 10 anos fica no município de Canela e a de 8 anos no município de Santa Tereza. Talhões delimitados pela cor branca representam áreas de floresta de referência, e talhões delimitados pela cor amarela representam áreas em processo de restauração.

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Coleoptera-macrofungi interaction networks in an Atlantic Rainforest restoration area

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Running headline: Restoration of coleopteran-macrofungi food webs

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SUMMARY

1. Ecological restoration aims to recover degraded ecosystems, ensuring both structural and functional restoration. Assessing ecosystem functionality is still a challenge, and current studies are focusing on applicable methodologies. Investigating networks of ecological interactions is a potential tool to assess ecosystem functionality.
2. Working in two forest restoration areas in southern Brazil, we evaluated interaction networks formed by fungivorous beetles (Coleoptera) and macrofungi (Polyporales and Hymenochaetales). The restoration was done eight and ten years before this study, and still happening regarding the plant community and their functionality.
3. We test the applicability of the ecological network perspective in the evaluation of the restoration progress in the studied areas when compared to the traditional metrics of abundance, richness and species composition using macrofungi-beetle interactions as a model system.
4. Traditional community descriptors did not differ between treatments, nor did network metrics. However, some rare species such as *Falsocis brasiliensis* and some specimens of Erotylidae were found only in reference areas. The restoration processes in the both sites differ qualitatively from each other, as can be perceived in the different interactions found in each of them. The ten years site are more similar to their reference areas, due to the presence of wood logs left there, serving as substrate for the macrofungus *Ganoderma australe* and its interactors, which occurred in the reference forest as well.
5. Both the network metrics and the traditional metrics show that the restoration process is successful for both structure and functionality of the fungivorous beetle and macrofungal communities for both areas. We were able to confirm the importance of dead wood avaibility in the restoration process to allow stable macrofungi and beetle populations to get a foothold on the restoration areas. This way, restoration processes

can be sped up by offering appropriate substrates on which whole communities can depend on.

Keywords: Trophic Interactions, Hymenhochaetales, Polyoprales, Ecological Restoration, Ciidae, Fungivory.

INTRODUCTION

The goal of restoration activities is to maintain biological diversity and associated ecosystem services. However, efforts are usually focused on informing only the presence and abundance of species and not how this diversity influences ecosystem function (Cadotte 2011). Most ecological restoration studies emphasize the rebuilding of vegetation structure (Crouzilles *et al.* 2016) but there is a risk in this becoming an exclusive focus that may suppress the view of the ecosystem function (Fraser *et al.* 2015). Usually, restoration monitoring does not consider the feedback of other species groups and their interactions (Schmitz *et al.* 2010, Bardgett & Wardle 2010). To improve restoration projects there is an insistent call to include an ecosystem functions approach. Despite this, it is still necessary to design appropriate methodologies to evaluate such functions (Wortley *et al.* 2013, Fraser *et al.* 2015, Kollmann *et al.* 2016). Until now, research on restoring ecosystem functions has been directed toward nutrient cycles, productivity, water relations and geomorphological processes; trophic interactions rarely appear on surveys (Kollmann *et al.* 2016). There are no adequate standardized methods to monitor interaction functions (Kollmann *et al.* 2016), and to explore and select groups of specific organisms that can reveal new patterns and important processes in restoration (Fraser *et al.* 2015).

Assessing biotic interactions allows us to identify important species and interactions that drive the process of ecosystem restoration. Interaction networks are a promising approach to verify, beyond plant diversity, the success of restoration projects whilst also encompassing the recovery of ecosystem functions. Networks have already been used in evaluating disturbance gradients, landscape structure and restoration projects (Tylianakis 2008, 2007, Bascompet 2009, Henson *et al.* 2009, Dixon 2009, Macfadyen *et al.* 2011). Only a few studies assessed ecosystem functionality after restoration (Forup *et al.* 2008, Ribeiro da Silva *et al.* 2015) and yet their results could be used in project management and planning (Pocock *et al.* 2012, Montoya *et al.* 2012, Fraser *et al.* 2015). Ecological network can be described by various metrics (hereafter network metrics), such as connectance specialization, and interaction evenness based on multivariate analyses. On a seminal study, Tylianakis *et al.* (2007) show how networks metrics can allow detection of gradual differences in habitat modification on host-parasitoid food webs that were not through considering only univariate variables such as richness, and abundance (community descriptors).

Wood-decaying fungi have a crucial functional role in forest nutrient cycling (Gilbertson 1980, Harmon *et al.* 1986), whilst being involved in several different interactions with other species. Wood-decaying fungi can be eaten by arthropods and vertebrates, while some insects like Coleoptera, Diptera and Lepidoptera are known to actually inhabit basidiomes (Guevara *et al.* 2000, Orledge & Reynolds 2005). Macrofungi availability, specific attributes of fungi like basidiome hardness, along with microclimatic conditions such as humidity are expected to regulate beetle communities (Paviour-Smith 1960). Fungivorous beetles have bioindicator potential for evaluating the ecosystem, as part of the network of interactions. Araujo *et al.* (2015) have shown that landscape fragmentation affected the fungivorous beetle community by reducing macrofungi and dead wood availability. Additionally, for colonizing new areas, decaying wood fungi diversity depends on the nearby pool of species and coarse woody debris available or made available in the potential area (Edman *et al.* 2004). Thus, macrofungi-beetle interactions have the capacity to reflect environmental disturbances and can become a promising approach to access ecosystem function in areas under restoration.

Aiming to assess the effect of ecological restoration on species interactions, we present a study on the use of macrofungi-beetle networks in a restoration context. We compared network metrics (connectance, links per species, interaction evenness, robustness and web asymmetry) and community descriptors (macrofungi and beetle species richness, abundance and composition) between treatments. We sampled sites under restoration and subtropical forest reference sites on two sites and constructed quantitative networks for either treatment. Because network metrics describe communities in more detail by dealing with interactions explicitly, and not only with its component species, we expected network metrics to capture differences in macrofungi-beetles association between treatments better than standard community descriptors (as found by Tylianakis *et al.* 2007).

MATERIALS AND METHODS

Study Region

This study was conducted in Canela (29º22'45"S and 50º43'47"W) and Santa Tereza municipalities (29º09'29"S and 51º41'49"W), Rio Grande do Sul state, Brazil. Both areas had semidecidual seasonal forest and *Cfa* climate according to the Köppen-Geiger classification (Pell *et al.* 2007), with average precipitation of 1538 mm, well distributed throughout the year, average temperature of the hottest month at 20.5ºC and of the coldest month colder than 12ºC. Restoration activities in Canela sites employed planting native species in 2006, after the removal of an eucalyptus plantation (Boeni 2015), hereafter ten years sites. Cutting the trees did not involve removing tree stumps and they provide a woody substrate for fungi in this area. In Santa Tereza, however, this woody substrate was removed after cutting the exotic fruit tree plantation, and restoration beginning in 2008 by planting native species (Andreis *et al.* 2005), herafter eight years sites. Because of this woody substrate distinction between restoration areas, we maintain analysis separate for each area, comparing reference sites to those under restoration.

Rosenfield & Müller (2018) conducted plant surveys on the same study sites as ours. They concluded vegetation structure in sites under restoration is still different from reference sites, despite this they showed that ecosystems functions may happen even before the full recovery of aboveground vegetation structure. An overview of site characteristics regarding location, restoration and vegetation comparisons (Rosenfield & Müller, 2018) is presented in Table 3.

Sampling design

Field work was conducted from August 2015 to May 2016. We made six field trips to eight years site and five field trips to ten years site. Each field trip sampling was composed of two transects on each treatment: two in sites under restoration and two in reference sites Transects were determined a priori and four of them randomized per field trip to avoid sampling the same transect in consecutive field trips. Transects had 50m x 10m each and were at least 50m apart. Overall, we sampled 24 transects in eight years site, 12 for each treatment (once during winter and spring, and twice during fall and summer); and 18 transects in ten years sites, 9 for each treatment (once during winter, spring and fall, but twice during summer). Field trips had to be irregular in time since we relied on factors such as accessibility to the area (due to weather conditions).

Basidiome sampling, Coleoptera rearing and identification

All basidiomes of the orders Polyporales and Hymenochaetales detected within the limits of each transect were sampled. Basidiomes found in the same piece of tree trunk were considered as the same individual, due to the high probability of being genetically identical. In cases where we found more than 10 basidiomes of the same species in the same trunk, we collected three for each ten of them found. We photographed all basidiomes *in situ* for identification. In the laboratory, we captured visible beetles and stored them in eppendorf tubes with ethanol 80%. We then placed basidiomes separately in containers to help keep the insects inside and allow any beetle eggs to eventually hatch. One basidiome of each fungi species was dried up for identification purposes. All containers were monthly checked for beetles. At the end of three months, basidiomes were dissected to capture any live adult beetles still inside them. There are divergent opinions on how many insect records are necessary to consider a fungus species as a host (Lawrence 1973, Orledge & Reynolds 2005). In our study, to exclude the possibility of false or eventual interactions, only interactions with two or more individuals of a beetle species present in a fungi species were considered.

Macrofungi were identified with proper taxonomic keys (Ryvarden & Johansen 1980, Núnez & Ryvarden 2000, 2001, Westphalen *&* Silveira 2013) and online databases (Index Fungorum 2017, Mycobank 2017). Specimen samples were deposited in the ICN Herbarium (Universidade Federal do Rio Grande do Sul, Brazil). Beetles were identified by visiting the Entomological Collection in Laboratório de Sistemática e Biologia de Coleoptera (CELC), housed at the Universidade Federal de Viçosa (UFV, Viçosa, MG, Brazil) (curator: C. Lopes-Andrade) and checking appropriate literature (Lawrence 1967, 1971, Gumier-Costa *et al.* 2003, Lopes-Andrade & Lawrence 2005, 2011, Lopes-Andrade 2008, Antunes-Carvalho *et al.* 2012, Oliveira *et al.* 2013, Oliveira & Lopes-Andrade 2013, Pecci-Maddalena & Lopes-Andrade 2017). Voucher specimens of the adult beetles were deposited at the abovementioned collection.

Data Analysis

Analyses were performed separately between the two sites because of the different starting conditions in each restoration process (Table 3). We constructed a network for the macrofungi-beetle community per treatment for comparative purposes. We used records obtained from each transect to compare treatments (restoration vs. reference) using standard community descriptor parameters and also network metrics (see below). For the network metrics, samples with less than three macrofungi or beetle species (following Osorio *et al.* 2015) were pooled with the other transect of the same treatment and same field trip (Morris *et al.* 2015). Pooled transect data are heretofore called a transect unit, which was used for both network metrics and community descriptors. Statistical analyses were performed using R statistical software (R Development Core Team 2015).

Community Descriptors

Community descriptors evaluated for each transect unit were species richness, abundance, interaction rate and composition. We calculated the interaction rate based on the proportion of sampled macrofungi that actually interacted with any species of beetle. We used generalized linear models (GLM) to compare the first three variables between treatments, with transects repetitions. Models were designed with each community descriptor as a response variable and treatment as a predictor variable; then we chose the simplest model to describe our data. We assumed Poisson errors for counts and binomial errors for proportions (Crawley 2007). To compare species composition of the macrofungi and beetle communities between treatments, we performed permutation MANOVAs with the *vegan* R package using 9999 permutations with the Bray-Curtis dissimilarity index. To evaluate sampling effort we estimated species richness (and confidence intervals) for the whole beetle community using the abundance-based index Chao 1, using the *specpool* function of the *vegan* R package (Oksanen *et al.* 2015).

Network metrics

Each transect unit originated a network; we calculated network metrics to compare treatments for both sites. Network metrics evaluated were: connectance (proportion of realized links relative to possible links); links per species (average realized links for each species); H^{2}*'* (average level of specialization in the network) (Bersier *et al.* 2002, Blüthgen *et al.* 2006); robustness (a measure of the secondary extinctions for one trophic level of the network caused by simulated extinctions on the other level); web asymmetry (balance between number of species in the two trophic levels, positive values indicate more higher-trophic level species, negative more lower-trophic level species, Blüthgen *et al.* 2007); and interaction evenness (uniformity of the species interactions in the network, based on Shannon evenness). These analyses were performed with the *bipartite* v.2.02 package (Dormann *et al.* 2008).

A GLM was performed for each network metric as the response variable and treatment as the predictor variable. Since network size (macrofungi richness + beetle richness) can affect at least some of the metrics (Dormann *et al.* 2009), we also included this variable in the models, with our maximum models containing it as a covariable. We assumed normally distributed errors for all metrics, except for connectance to which we used binomial errors (since it is a proportion).

To assess species level effects in our networks, we cathegorized species within each network as generalist-core (those with the most interactions) or peripheral-core (those with fewer interactions), based on Dáttilo *et al.* 2013. We used the Generalist Core measurement as $G_C = (K_i - K_{mean})/\sigma_k$, where K_i is the mean number of links for a given macrofungus/beetle species; K_{mean} is the mean number of links for all macrofungi/beetles species in the network and σ_k is the standard deviation of the number of links for macrofungus/beetle species. Species with $G_C > 1$ were considered generalists, and those with $G_C < 1$ were considered peripheral.

This enabled us to evaluate the change in the generalist core position of each species under different treatments.

RESULTS

We collected a total 512 basidiomes of 87 fungi species in both sites. Only 181 (35.4%) basidiomes presented interactions with beetles (Table 1). We obtained 11,414 beetles of 53 species. (Table S2.1 and Table S2.2, Supporting Information).

Beetle communities sampled in reference sites for ten years site corresponded to 61% of the estimated species pool (Chao1= 57.57 species, SE= 14.22) and for sites under restoration 67% of the estimated species pool (Chao1= 70.51 species, SE= 13.22). For Santa Tereza, sampled coleopterans represented 76% of the estimated richness (Chao1 = 61.66 species, SE= 8.25) for reference sites, and 49% in sites under restoration (Chao1 =80.92 species, SE= 23.41). For the macrofungi community, in ten years site, reference sites had 46% of the estimated species pool (Chao1= 78.67 species, SE= 25.48) and sites under restoration had 67% (Chao1= 48.00 species, SE= 10.07). For eight years site, the macrofungi sampled represented 51% of the estimated number (Chao1= 82.92 species, SE= 23.41) for the reference sites, and 64% for sites under restoration (Chao1= 52.92 species, SE= 12.42).

Community Structure

Species richness and abundance of Polyporales and Hymenochaetales macrofungi did not differ between treatments in ten years site (Table 2). The same happened for coleopteran species richness and abundance between treatments in eight years site (Table 2). Interaction rates did not differ between treatments either for ten years site ($F_{1,16}$= 1.01; p= 0.33) or eight years sites ($F_{1,22}$=0.12; p=0.73). Coleopteran community composition did not differ between treatments either for ten years site ($F_{1,16}$= 1.39; p=0.12) or for the eight years sites ($F_{1,22}$=1.36;

p= 0.13). The same occurred for the fungi composition, with no differences between treatments in either area (ten years site, $F_{1,16}$= 1.48; p=0.13; eight years site, $F_{1,22}$= 1.38; p= 0.16).

Network Structure

Evaluating the validated interactions, we excluded 68 unique interactions to avoid false positives. Network metrics results were very similar between reference sites and those under restoration (Table 2). Network metrics were affected only by network size in the models, not by treatment. Network size appears as significantly explaining robustness (of the higher trophic level), links per species and web asymmetry metrics (Table 2). Species of beetle considered generalists changed between treatments (Figs. 1 and 2). However, for macrofungi, *Fuscoporia gilva* was classified as a generalist in all networks. *Ganoderma australe* was a generalist species of macrofungi in ten years site networks, for both treatments (Fig. 1), while in eight years site, *Trametes villosa* and *Trametes membranaceae* were the generalist species (Fig. 2).

F. gilva was the main macrofungus host in network's for both treatments and sites. It was also the species with highest number of basidiomes sampled (Table 1). It was found in 84% of transects and represented about 25% of all basidiomes (101 individuals); furthermore, 66 of these individuals interacted with beetles (Fig. 1, Fig. 2). These interactions represent 46.4% (188) of the total, with 29 species of beetles present in these basidiomes; 24 species in ten years site (16 in reference sites and 20 in sites under restoration) and 24 species in eight years site (19 in reference sites and 15 in sites under restoration).

G. australe was not only generalist, but also the dominant host in number of interactions in reference sites from both ten years site (1427 interactions, Fig. 1a), and eight years site (1678, Fig. 2a). However, sites under restoration had for example the genus *Trametes* (Porypolares: Polyporaceae) dominating, with two species: *T. membranacea* (613 interactions) and *T.villosa* (528) (Fig. 1b), also generalists, as above. In Santa Tereza, sites under restoration had *Pycnoporus sanguineous* with the highest interaction abundance (3320) (Fig. 2b). These species-level changes, however, did not appear to affect network metrics (Table 2).

DISCUSSION

Differently from what we expected based on Tylianakis *et al.* (2007), in this case, networks metrics did not reveal overall differences between sites under restoration and their references better than community descriptors did. Yet, network metrics evaluated here can also be interpreted as indicating a recovery of the restored areas: interactions between macrofungi and beetles seem to have been reestablished in sites under restoration. This is also an indication that forest environmental conditions have recovered in the first place, since these organisms are known to be dependent on them (Araujo *et al.* 2015). Corroborating with Rosenfield & Müller, 2018 the ecossystems functions apper to have recovered earlier in relation to vegetations parameters, the macrofungi beetles ecosystem function appers to recovered in the same way. For the latter, it could be due to higher canopy openness in areas under restoration (Schüler *et* al. 2016) which can increase saproxylic beetles richness (Widerberg et al. 2012).

Even though network metrics did not reveal differences between treatments, this is not due to low sampling or low interaction rates. Our interaction rate of 36% had a similar value to what Graf *et al.* (2011) found (40.4%) in a fungus-beetle study developed in a nearby region in southern Brazil. Also, a species richness value well below the estimated community species pool is a common aspect for fungus sampling in ecological research, which usually requires huge sampling efforts to reach a stable collector curve (Straatsma *et al.* 2001). On the other hand, variability in network size may have affected general patterns in network metrics. Network metrics robustness, links per species and web asymmetry were significantly affected by network size (Table 2). Although we attempted to have an experimental design and sampling procedure able to capture minimum sample sizes, such outcomes are somewhat inherent to observational studies.

The macrofungus-beetle networks had high values of specialization (Table 1), because the majority of beetle species interact with only one or a few species of macrofungi. The low values for connectance (Table 1) also show beetle community as not being very generalist. Network structure is often given by a few species with many links and several species establishing few links (Bascompte *et al.* 2003, Jordano *et al.* 2003). This pattern was found here for the lower trophic level (macrofungi), where there are some species with many interactions. However, in the upper trophic level (beetles), few species were found on more than one fungus species, and this might be occurring as a result of species in this guild specifically avoiding interspecific competition.

A suggested mechanism for avoiding competition, for example, would be that ciid beetles have the ability to identify specific volatile substances released by its host to locate it (Guevara *et al.* 2000, Lawrence 1973). These beetles live inside the basidiome and depend on it for food and shelter, which is in contrast with facultative fungi-feeders or mycetophages that might not be in direct competition with them. For example, Nitidulidae, Ptilidae, and Nanosellinae feed exclusively outside the basidiome surface (Pavior-Smith 1960), while ciids dig tunnels (Lopes-Andrade & Lawrence 2005, Lawrence 1973). The ability some beetles present, of feeding and housing themselves in different macrofungi species, depends on the habits and specific morphology of fungivorous coleopteran groups (Graf-Peters *et al.* 2011).

Although the most abundant fungus, *F. gilva*, occurred both in reference and sites under restoration, and was the generalist species for all networks, two species hosted at *F. gilva* were exclusive from reference sites, *Xylographus* sp. A and *Falsocis brasiliensis*. It might be the case where some specific resource condition is required for these species to occur (e.g.

Thorn *et al.* 2015, Franc *et al.* 2007), one that only reference sites could provide as yet in the restoration process. *F. brasiliensis* is known as a rare ciid beetle, and species of *Falsocis* are presently restricted to well-preserved forests of the Neotropical region (Araujo & Lopes-Andrade 2016). Additionally, Erotylidae species, reported to be a family of fungivorous beetles sensitive to environmental disturbance (Franc 2001), were found only in reference forests and probably will colonize sites under restoration on the future, as the forest keeps recovering.

The two sampled sites appear to have different restoration paths: species found on each one of them and the way they interact differ although slightly between the two areas. For example, *G. australe* can generally be found inside the forest, and is a large fungus that can accommodate a large number of beetles in its basidiome. Interactions involving this species were quite common for both reference areas in both sites. At the ten years site, however, *G. australe* was the generalist species for both treatments. This may have happened because in such site areas under restoration had the cutted tree stumps left there (Table 3), serving as substrates for macrofungi. In a similar situation, Seibold *et al.* (2015) worked with European saproxylic beetles predicting species that depend on large diameter wood had a higher risk of extinction, due to forest degradation and loss of old-growth sites with available dead wood .

P. sanguineous was another important host, a species associated with open areas, such as canopy openings, which suggests adaptation to less humid environments or higher temperatures (Lodge & Cantrell 1995, Gibertoni *et al.* 2007). The interactions between *P. sanguineous* and beetles were abundant in the eight years site under restoration but had a single occurence in ten years site. This corroborates findings by Schüler *et al.* (2016) in the same study areas, concluding canopy openness of the plant community of sites under restoration are still different from the reference in eight years site (Table 3). Although capony openness, species richness and regenerating individual density were different in the restoration areas, these factors were beneficial for the restoration of the interactions, since the canopy opening can be relatively positive for the biodiversity of saproxylic beetles (Widerberg *et al.* 2012). However, by using an interaction network approach we were able to detect differences regarding the occurrence of rare beetle species (and their interactions) and possible drivers of dominant host presence that would have a direct effect on their interactions and, consequently, in ecosystem functioning.

In our study, network structure appeared to recover due to macrofungal ability to spread out from adjacent reference sites to the new areas (or remain in them, when tree stumps were left). The most abundant coleopteran species were also able to colonize sites under restoration, supposedly following their host fungi. Forup *et al.* (2008) found that common insects were able to colonize areas under restoration easily where the host plant was present. Thus, ecosystem function in terms of species interactions seems to have recovered due to restoration actions. It is already known that substrate availability controls wood-decaying fungi colonization in areas under restoration (Edman *et al.* 2004). Moreover, Komonen (2003) pointed out the importance of macrofungic basidiomes in to insect biodiversity in a boreal forest, reaffirming the importance of dead wood availability to allow stable beetle population establishment and maintenance. This way, for Coleoptera-macrofungi interactions, the restoration process can be sped up by offering an appropriate substrate in sites under restoration.

CONCLUSIONS

The macrofungi community and their associated fungivorous beetles appear to have achieved a considerable degree of recovery over the eight and ten years under restoration. All community descriptors evaluated show that sites under restoration were quite similar to the adopted reference sites. This suggests macrofungi can colonize the new habitat offered by the restoration process with relative ease, and that fungivorous beetles also follow suit. Therefore, judging by community descriptors, the restoration process is successfully recovering for macrofungi and beetles community at the studied sites. Unlike what we expected, network metrics did not point to conspicuous differences in comparison to community descriptors, as in Tylianakis *et al.* (2007), but that may occur because restoration was already advanced regarding Coleoptera-macrofungi interactions for both areas. For future research, studies considering the restoration process from the beginning might allow capturing changes in community characteristics and specifically how networks reassemble. Nevertheless, we could identify slight differences through a deeper evaluation of indicator interactions which suggest that the process of restoration is still undergoing. During the restoration process, in a long-term perspective, slight differences can be magnified and become a problem. Therefore, once identified, these differences could be the aim of restoration management actions. Moreover, we left the suggestion that restoration of fungus-bettle communities and networks in forests can be sped up by offering appropriate substrates (wood, here in the form of tree stumps) in sites under restoration. Our research can also serve to stress the importance of investigating more than one set of organisms in assessing the restoration process, so as to gather a better understanding of the different "points of view". In addition, this also highlights the importance of using ecosystem functions as recommended by Kollmann *et al.* (2016), such as interactions, to understand the paths which restoration might be taking.

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TABELAS

Table 1. Community parameters and selected network metrics for the whole macrofungi-fungivorous beetle network and for each area separately. The most abundant species for macrofungi and beetles are shown separately to highlight their predominance in the community. For more details see text.

	Overall Community	**Ten years site**			**Eight years site**		
		Reference	*Under Restoration*	**Total**	*Reference*	*Under Restoration*	**Total**
Number of sites	**22**	5	5	**10**	6	6	**12**
Communities Descriptors							
Basidiome species richness	**87**	36	32	**53**	42	34	**58**
Species of macrofungi with interactions	**36**	13	14	**23**	13	14	**21**
Beetle species richness	**53**	28	35	**39**	39	33	**46**
Number of macrofungi-beetle interactions	**405**	88	120	**208**	121	76	**197**
Basidiome abundance	**512**	106	132	**238**	149	125	**274**
Abudance of interacting basidiomes	**181**	38	49	**87**	53	41	**94**
Fuscoporia gilva abundance	**101**	26	33	**59**	29	13	**42**
Beetle abundance	**11414**	1838	1812	**3650**	3698	4066	**7764**
Ceracis cornifer abundance	**3438**	0	0	**0**	291	3147	**3438**
Interaction rate	**35.35%**	35.85%	37.12%	**36.55%**	35.57%	32.80%	**34.31%**
Network metrics							
H2'	**0.84**	0.89	0.81	**0.81**	0.92	0.87	**0.86**
Robusteness (higher level)	**0.63**	0.57	0.56	**0.61**	0.6	0.58	**0.63**
Connectance	**0.07**	0.11	0.11	**0.08**	0.12	0.11	**0.09**
Interaction evenness	**0.37**	0.35	0.44	**0.43**	0.39	0.2	**0.33**
Links per species	**1.44**	1.17	1.04	**1.33**	1.17	1.04	**1.33**
Web asymmetry	**0.19**	0.37	0.44	**0.26**	0.5	0.4	**0.37**

Table 2. Effects of treatment (restoration) on the dependent variables (taxonomic community descriptors or network metrics) under general linear models (for details, see text). Network size was included in the models for network metrics.

	Ten years site			**Eight years site**		
Dependent variable	*Minimum model*	*Statistic*	*P*	*Minimum model*	*Statistic*	*P*
Community descriptors						
Macrofungi abundance	Treatment	$F_9 = 1.94$	0.20	Treatment	$F_{11} = 0.42$	0.53
Macrofungi species richness	Treatment	$F_9 = 0.01$	0.91	Treatment	$F_{11} = 0.74$	0.41
Coleoptera abundance	Treatment	$F_9 = 1.24$	0.30	Treatment	$F_{11} = 0.26$	0.62
Coleoptera species richness	Treatment	$F_9 = 1.45$	0.26	Treatment	$F_{11} = 0.005$	0.95
Interaction Rate	Treatment	$F_9 = 0.33$	0.58	Treatment	$F_{11} = 0.10$	0.75
Network metrics						
H2'	Treatment	$\chi^2_9 = 1.25$	0.88	Treatment	$\chi^2_{11} = 0.298$	0.88
Robustness (high level)	**Network Size**	$\boldsymbol{\chi^2_9 = 0.050}$	**<0.001**	**Network Size**	$\boldsymbol{\chi^2_{11} = 0.09}$	**<0.001**
Connectance	Treatment	$\chi^2_9 = 0.015$	0.48	Treatment	$\chi^2_{11} = 0.02$	0.11
Interaction evenness	Treatment	$\chi^2_9 = 0.050$	0.91	Treatment	$\chi^2_{11} = 0.31$	0.28
Links per species	**Network Size**	$\boldsymbol{\chi^2_9 = 0.407}$	**<0.001**	**Network Size**	$\boldsymbol{\chi^2_{11} = 0.36}$	**<0.001**
Web asymmetry	**Network Size**	$\boldsymbol{\chi^2_9 = 0.407}$	**<0.001**	**Network Size**	$\boldsymbol{\chi^2_{11} = 0.58}$	**<0.001**

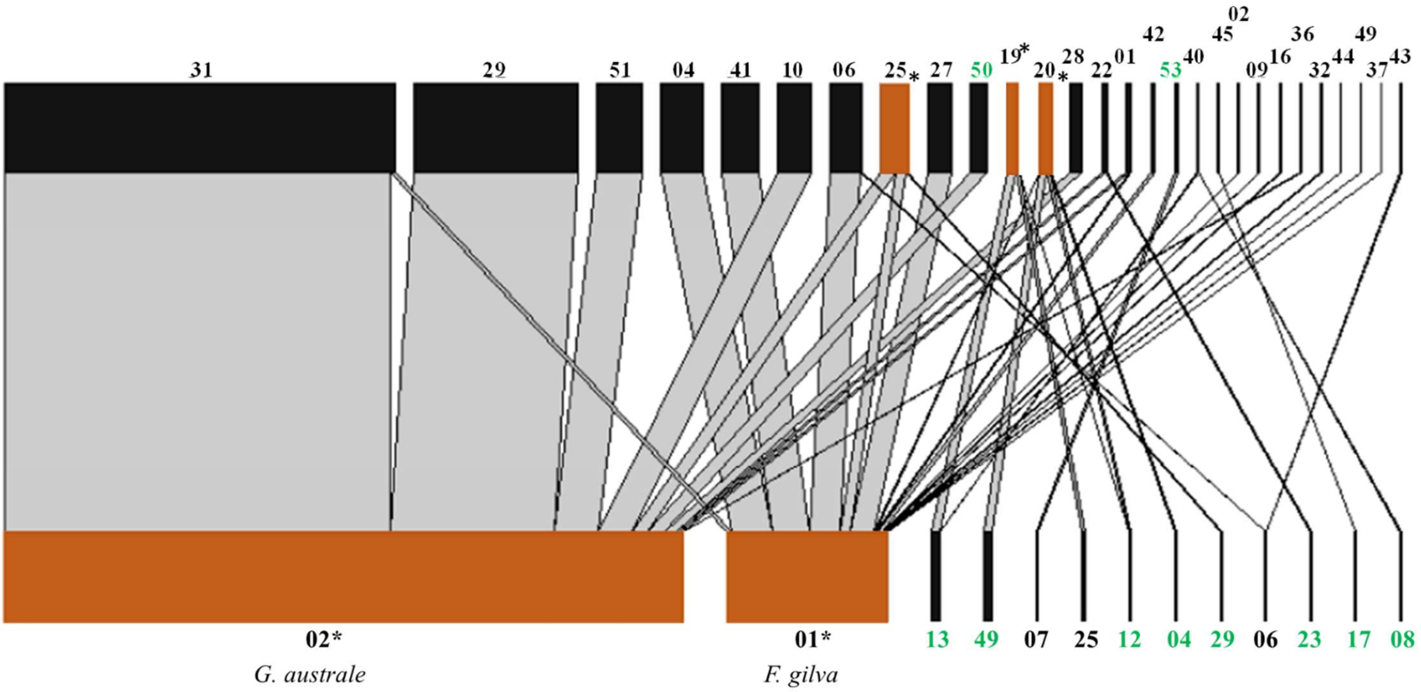
Table 3. Chacarcteristics overview of the two sampled sites. * indicates results from Rosenfield & Müller 2018.

Characteristic	Ten years site	Eight years site
Location	Canela, Rio Grande do Sul, Brazil	Santa Tereza, Rio Grande do Sul, Brazil
Coordinates	29º22'45"S and 50º43'47"W	29º09'29"S and 51º41'49"W
Year of restoration implementation	2006	2008
Previous land-use (reference)	Eucalyptus plantation (Boeni 2015)	Exotic fruit plantation (Andreis *et al.* 2005)
Particularity of restoration	Tree trunks and stumps left	Tree stumps removed
Plant species richness*	Differ between reference and restoration	Differ between reference and restoration
Multifunctionality *	Differ between reference and restoration	Differ between reference and restoration

FIGURES

Figure 1.

a) Reference sites



b) Sites under restoration

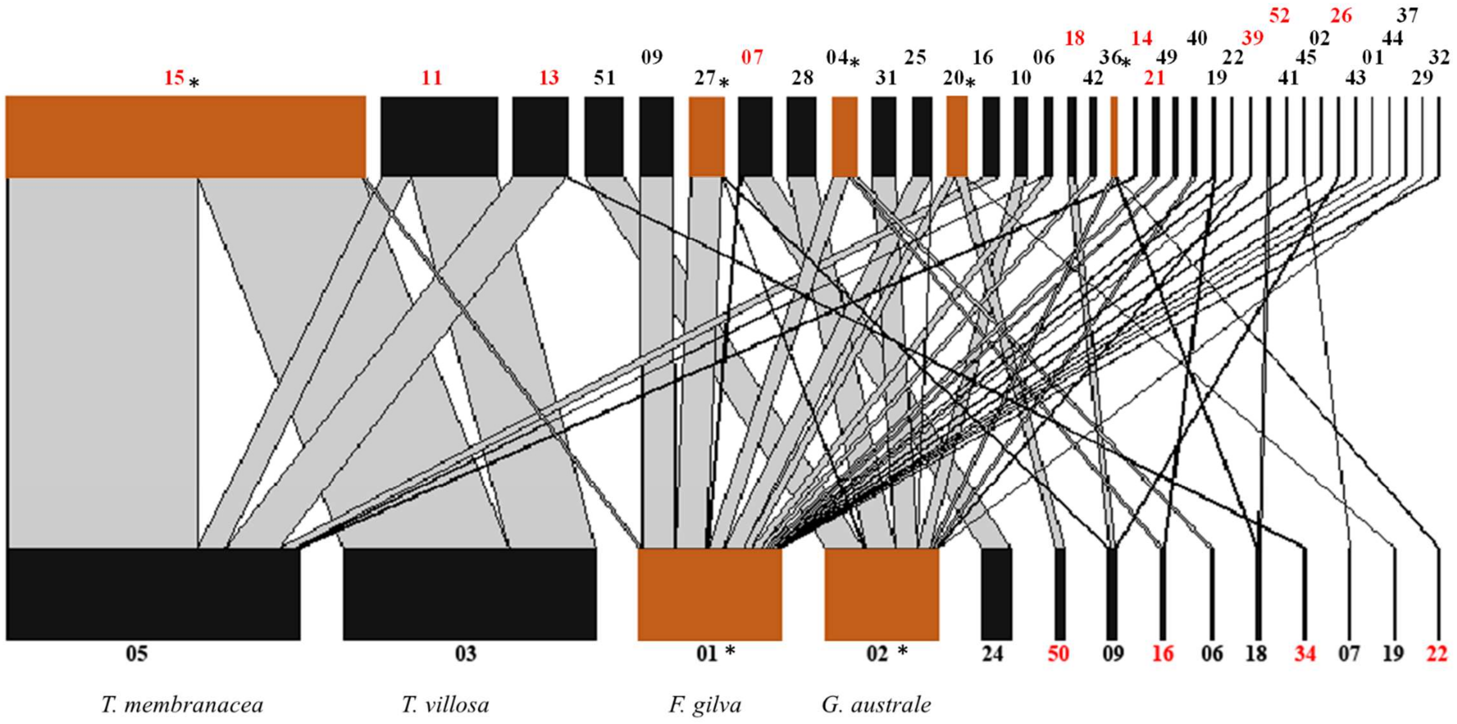
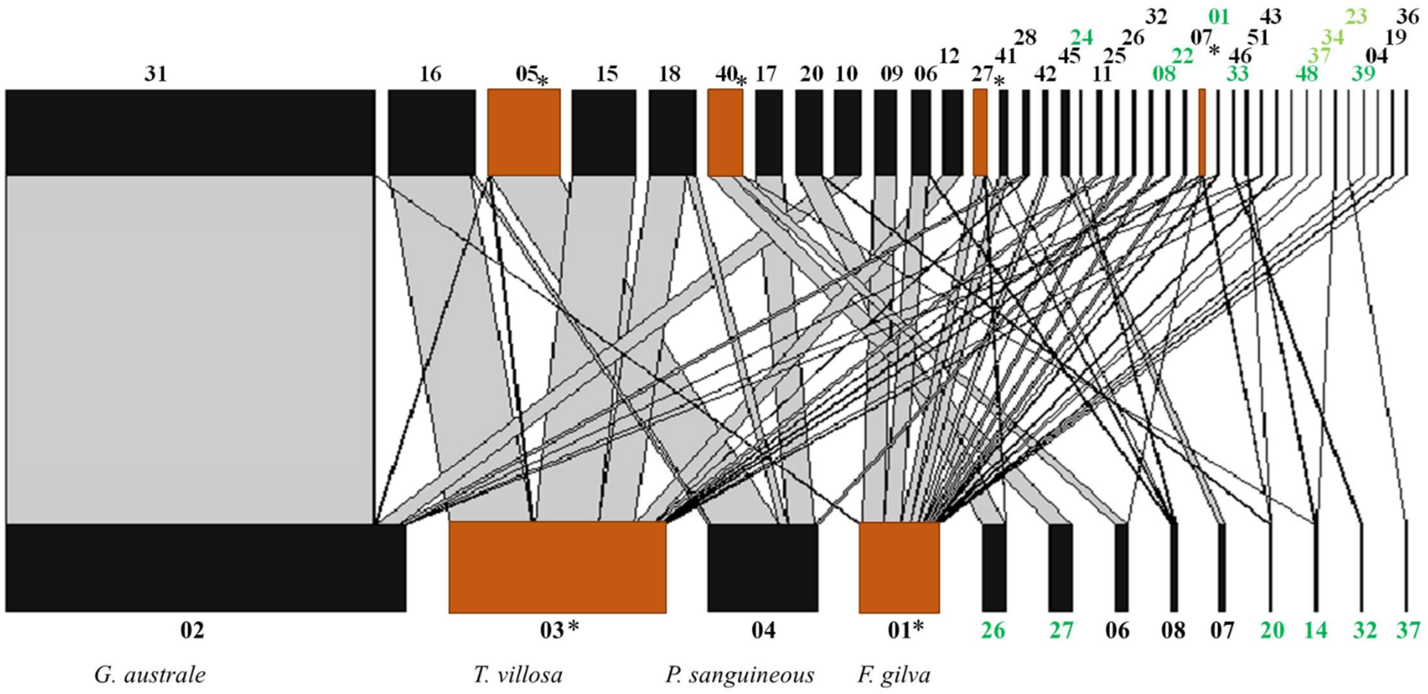


Figure 2.

a) Reference sites



b) Sites under restoration

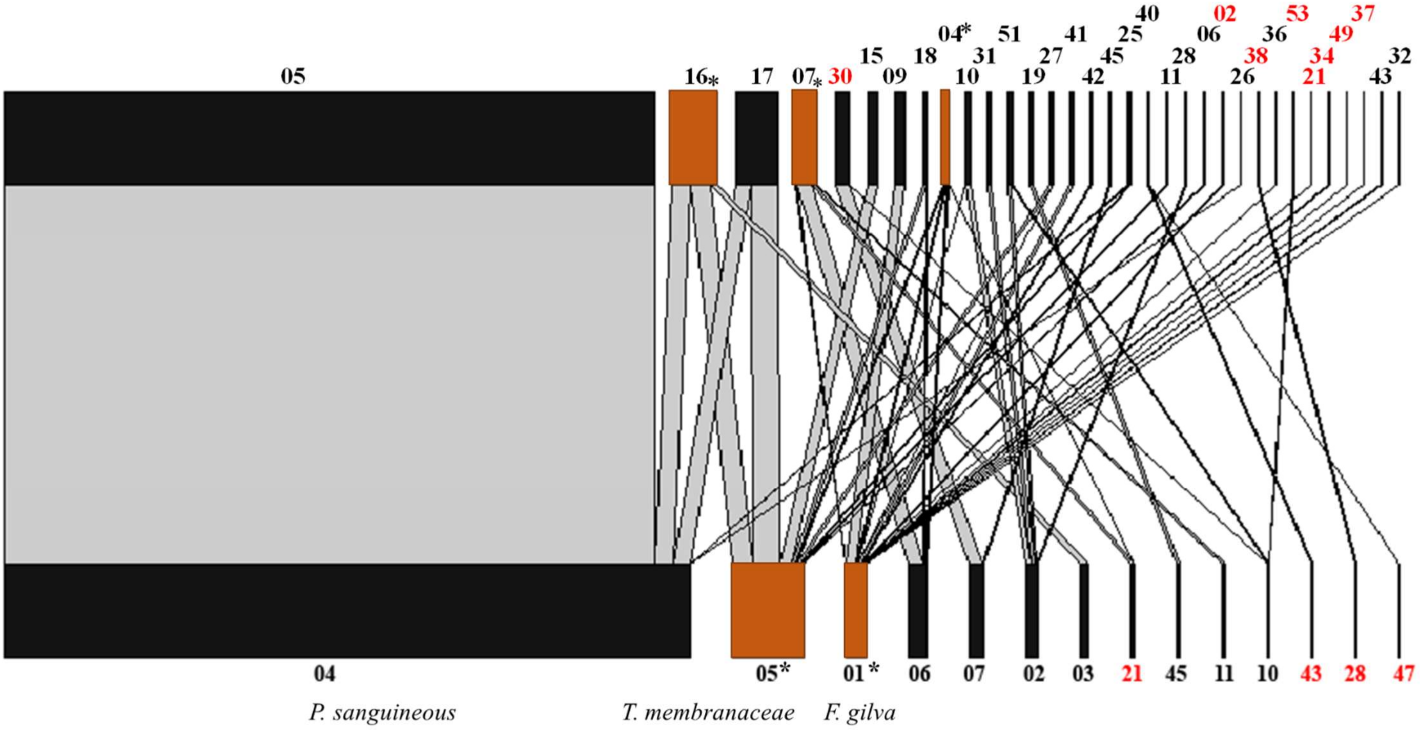


Figure 1. Macrofungi-beetle bipartite networks for a) reference sites and b) sites under restoration in ten years site on Canela, Rio Grande do Sul state, Brazil. Data were pooled from all sites belonging to each treatment. For clarity, in larger webs, beetle abundance was equal to the number of interactions associated with it. The color of species codes indicates beetles and macrofungi that occurred only in reference sites (green), only in under restoration sites (red), or in both (black); species codes are given in Tables S1.1 and S1.2. Rectangle height is proportional to the number of interactions of each species. Asterisks (*) and color rectangles denote species that were considered generalists.

Figure 2. Macrofungi-beetle bipartite networks for a) reference sites and b) sites under restoration of eight years site on Santa Tereza Rio Grande do Sul state, Brazil. Data were pooled from all sites belonging to each treatment. For clarity, in larger webs, beetle abundance was equal to the number of interactions associated with it. The color of species codes indicates beetles and macrofungi that occurred only in reference sites (green), only in under restoration sites (red), or in both (black); species codes are given in Tables S1.1 and S1.2. Rectangle height is proportional to the number of interactions of each species. Asterisks (*) and color rectangles denote species that were considered generalists.

SUPPORTING INFORMATION

S1 – Species Lists

Table S1.1 Host species sampled and their abundances in reference and under restoration sites.

Code	**Fungus species**	**Ten years site**			**Eight years site**			**Grand Total**
		Reference	Under Restoration	**Total**	Reference	Under Restoration	**Total**	
01	*Fuscoporia gilva (Schwein.) T. Wagner & M. Fisch.*	26	33	**59**	29	13	**42**	**101**
02	*Ganoderma australe* (Fr.) Pat.	12	17	**29**	4	6	**10**	**39**
03	*Trametes villosa* (Sw.) Kreisel	3	6	**9**	20	5	**25**	**34**
04	*Pycnoporus sanguineous* (L.) Murrill	1	0	**1**	3	14	**17**	**18**
05	*Trametes membranacea* (Sw.) Kreisel	3	10	**13**	3	3	**6**	**19**
06	*Funalia rígida* (Berk. & Mont.) Peck, Bull.	5	2	**7**	9	18	**27**	**34**
07	*Cymatoderma caperatum (Berk. & Mont.) D.A. Reid*	10	2	**12**	19	18	**37**	**49**
08	*Polyporus dictyopus* Mont.	2	0	**2**	6	5	**11**	**13**
09	*Trametes sp. C*	1	2	**3**	0	0	**0**	**3**
10	*Cymatoderma dendriticum* (Pers.) D.A. Reid, Kew	1	1	**2**	3	6	**9**	**11**
11	*Polyporus virgatus* Berk. & M.A. Curtis	1	2	**3**	5	2	**7**	**10**
12	*Rigidoporus sp. A*	2	0	**2**	0	0	**0**	**2**
13	*Steccherinumsp. B*	6	0	**6**	3	1	**4**	**10**
14	Polyporales sp. 1	0	0	**0**	1	0	**1**	**1**
15	Polyporales sp. 2	1	0	**1**	0	0	**0**	**1**
16	Polyporales sp. 3	0	1	**1**	0	0	**0**	**1**
17	*Favolus tenuiculu* P. Beauv	3	0	**3**	4	3	**7**	**10**
18	*Laetiporus sulphureus* (Bull.) Murrill	2	3	**5**	0	0	**0**	**5**
19	*Lentinus citrinus* Walleyn & Rammeloo	2	25	**27**	0	0	**0**	**27**
20	*Perenniporia sp. A*	0	0	**0**	1	0	**1**	**1**

Code	Fungus species	Ten years site			Eight years site			Grand Total
		Reference	Under Restoration	**Total**	Reference	Under Restoration	**Total**	
21	*Trametes sp. B*	0	0	**0**	0	1	**1**	**1**
22	*Trametes sp. A*	0	1	**1**	0	2	**2**	**3**
23	Polyporales sp. 4	1	0	**1**	0	0	**0**	**1**
24	*Abundisporus subflexibilis* (Berk. & Curtis) Parm.	1	4	**5**	1	0	**1**	**6**
25	Polyporales sp. 5	4	1	**5**	1	0	**1**	**6**
26	Polyporales sp. 6	0	0	**0**	1	0	**1**	**1**
27	Polyporales sp. 7	0	0	**0**	2	0	**2**	**2**
28	*Polyporus sp. C*	0	0	**0**	0	1	**1**	**1**
29	Polyporales sp. 8	1	0	**1**	0	0	**0**	**1**
30	Polyporales sp. 9	1	0	**1**	0	0	**0**	**1**
31	Polyporales sp. 10	0	0	**0**	1	0	**1**	**1**
32	Polyporales sp. 11	0	0	**0**	1	0	**1**	**1**
33	Polyporales sp. 12	0	1	**1**	0	0	**0**	**1**
34	*Trametes cubensis* (Mont.) Sacc	0	1	**1**	0	0	**0**	**1**
35	Polyporales sp. 13	1	0	**1**	0	0	**0**	**1**
36	Polyporales sp. 14	0	1	**1**	0	0	**0**	**1**
37	Polyporales sp. 15	0	0	**0**	1	0	**1**	**1**
38	Polyporales sp. 16	0	0	**0**	0	1	**1**	**1**
39	Polyporales sp. 17	0	0	**0**	1	0	**1**	**1**
40	Polyporales sp. 18	1	0	**1**	0	0	**0**	**1**
41	Polyporales sp. 19	1	0	**1**	0	0	**0**	**1**
42	*Antrodiella sp. A*	1	0	**1**	0	0	**0**	**1**
43	*Fomitiporia maxoni* Murrill	0	0	**0**	0	2	**2**	**2**
44	*Fuscocerrena portoricensis* (Spreng. ex Fr.) Ryvarden	0	2	**2**	1	1	**2**	**4**
45	*Gloeoporus dichorus* (Fr.) Bres.	0	0	**0**	3	1	**4**	**4**
46	Polyporales sp. 20	2	2	**4**	0	0	**0**	**4**
47	*Perenniporia sp. B*	0	0	**0**	0	1	**1**	**1**
48	*Polyporus varius* (Pers.) Fr.	1	2	**3**	4	5	**9**	**12**

S1 – Species Lists

Table S1.2 Fungivorous beetle species, with their abundances in reference sites and sites under restoration with code(s) for hosts which they were associated. See Table S2.2 for host codes.

Code	Family	Coleoptera Species	Host Macrofungi Code	Beetle abundance						Grand Total
				Ten years site			Eight years site			
				Ref.	*Rest.*	***Total***	*Ref.*	*Rest.*	***Total***	
01	Anthicidae	Anthicidae sp. A	01, 02	10	1	**11**	6	0	**6**	**17**
02	Carabidae	*Bembidion* sp. A	01, 19, 44	2	2	**4**	0	4	**4**	**8**
03	Cerylonidae	Cerylonidae sp. A	1	0	2	**2**	0	0	**0**	**2**
04	Ciidae	*Ceracis bicornis* (Mellié)	01, 04, 05, 06, 16, 21	87	51	**138**	1	22	**23**	**161**
05	Ciidae	*Ceracis conifer* (Mellié)	02, 03, 04, 05	0	0	**0**	291	3148	**3439**	**3439**
06	Ciidae	*Ceracis limai* (Lopes-Andrade)	01, 02, 05, 06, 08, 09	65	21	**86**	82	5	**87**	**173**
07	Ciidae	*Ceracis* sp. C (aff. *variabilis*)	01, 03, 06, 11,20, 21, 24, 25, 38	0	66	**66**	12	107	**119**	**185**
08	Ciidae	*Ceracis* sp. D	3	0	0	**0**	12	0	**12**	**12**
09	Ciidae	*Cis kawanabei* (Lopes-Andrade)	01, 05	2	71	**73**	93	50	**143**	**216**
10	Ciidae	*Cis pubescens* (Friedenreich)	01, 02, 12	73	22	**95**	103	21	**124**	**219**
11	Ciidae	*Cis* sp. A (gr.*vitulus*)	03, 05	0	242	**242**	21	8	**29**	**271**

Code	**Family**	**Coleoptera Species**	**Host Macrofungi Code**	**Beetle abundance**						**Grand Total**
				Ten years site			**Eight years site**			
				Ref.	*Rest.*	***Total***	*Ref.*	*Rest.*	***Total***	
12	Ciidae	*Cis* cf. *pallidus* (Mellié)	03, 05	0	0	**0**	74	1	**75**	**75**
13	Ciidae	*Cis* sp. E (gr.*tricornis*)	5	0	115	**115**	0	0	**0**	**115**
14	Ciidae	*Cis* sp. F (gr.*tricornis*)	5	0	9	**9**	0	0	**0**	**9**
15	Ciidae	*Cis* sp. G (gr.*tricornis*)	01, 03, 05	0	750	**750**	268	54	**322**	**1072**
16	Ciidae	*Cis* sp. H (gr.*bilamellatus*)	01, 03, 04, 05	2	34	**36**	381	202	**583**	**619**
17	Ciidae	*Cis* sp. I (gr.*bilamellatus*)	03, 04, 05	0	0	**0**	112	210	**322**	**322**
18	Ciidae	*Cis* sp. J (gr.*comptus*)	01, 03, 04, 05, 06, 09	0	12	**12**	187	23	**210**	**222**
19	Ciidae	*Cis* sp. N (gr. *taurus*)	01, 12,13,16, 25, 45	26	5	**31**	1	16	**17**	**48**
20	Ciidae	*Cis*sp. O (gr. *taurus*)	01, 04, 12,19, 20, 26, 40,48, 49, 50	27	40	**67**	107	1	**108**	**175**
21	Ciidae	*Cis* sp. P (gp. *taurus*)	1	0	8	**8**	0	2	**2**	**10**
22	Ciidae	*Cis* sp. Q (gr. *taurus*)	01, 02, 06, 23	12	5	**17**	13	0	**13**	**30**
23	Ciidae	*Cis* sp. T (gr. *taurus*)	01, 37	0	1	**1**	2	0	**2**	**3**
24	Ciidae	*Falsocis brasiliensis (*Lopes-Andrade)	01, 08	0	0	**0**	22	0	**22**	**22**
25	Ciidae	Gen. A sp. A	01, 02, 03, 04, 05, 29, 36	58	41	**99**	16	9	**25**	**124**
26	Ciidae	*Grossicis diadematus* (Mellié)	01, 03, 04, 09	0	2	**2**	15	3	**18**	**20**

Code	**Family**	**Coleoptera Species**	**Host Macrofungi Code**	**Beetle abundance**						**Grand Total**
				Ten years site			**Eight years site**			
				Ref.	*Rest.*	***Total***	*Ref.*	*Rest.*	***Total***	
27	Ciidae	*Phellinocis romualdoi* (Lopes-Andrade & Lawerence)	01, 02, 05, 08, 09, 26	51	70	**121**	43	16	**59**	**180**
28	Ciidae	*Porculus vionoi*	01, 02, 03, 05, 16	26	62	**88**	29	8	**37**	**125**
29	Ciidae	*Scolytocis fritzplaumanni* (Lopes-Andrade)	01, 02	343	1	**344**	0	0	**0**	**344**
30	Ciidae	*Strigocis* sp. A	01, 07,10, 11	0	0	**0**	0	72	**72**	**72**
31	Ciidae	*Xylographus* sp. A	01, 02	821	48	**869**	1543	19	**1562**	**2431**
32	Ciidae	*Xylographus* sp. B	1	2	1	**3**	13	1	**14**	**17**
33	Endomychidae	Endomychidae sp. A	01, 32	0	0	**0**	5	0	**5**	**5**
34	Histeridae	*Aeletes* sp. A	1	0	0	**0**	2	0	**2**	**2**
35	Histeridae	Histeridae sp. A	01, 02, 15	1	1	**2**	0	2	**2**	**4**
36	Lateridae	Lateridae sp. A	01, 02, 03, 13, 15, 18	4	10	**14**	1	4	**5**	**19**
37	Melandryidae	*Orchesia* cf. *brasiliensis* (Champion)	01,	1	1	**2**	3	1	**4**	**6**
38	Nitidulidae	*Hebascus* sp. A	01, 28	0	0	**0**	0	3	**3**	**3**
39	Nitidulidae	Nitidulidae sp. A	01, 02	0	5	**5**	2	0	**2**	**7**
40	Ptiliidae	*Throscoptilium* cf. *duryi* (Barber)	01, 02, 04, 06, 08, 13, 14, 21, 27, 43, 47	5	7	**12**	142	11	**153**	**165**
41	Ptinidae	Ptinidae sp. A	01, 08, 11	77	4	**81**	37	13	**50**	**131**

Code	Family	Coleoptera Species	Host Macrofungi Code	Beetle abundance						Grand Total
				Ten years site			Eight years site			
				Ref.	*Rest.*	***Total***	*Ref.*	*Rest.*	***Total***	
42	Ptinidae	Ptinidae sp. B	01, 09	10	13	**23**	24	10	**34**	**57**
43	Ptinidae	Ptinidae sp. C	01, 06, 22	1	2	**3**	4	2	**6**	**9**
44	Scarabaeidae	Aphodiinae sp. A	01,	1	1	**2**	0	0	**0**	**2**
45	Staphilynidae	Aleocharinae sp. A	01, 05, 07,17	3	2	**5**	24	9	**33**	**38**
46	Staphilynidae	Aleocharinae sp. C	01, 14, 20, 51	0	1	**1**	4	1	**5**	**6**
47	Staphilynidae	Aleocharinae sp. D	01, 14	0	0	**0**	2	0	**2**	**2**
48	Staphilynidae	Aleocharinae sp. F	01, 03, 30	1	0	**1**	3	0	**3**	**4**
49	Tenebrionidae	*Neomida divergicornis* Triplehorn	01	1	7	**8**	0	1	**1**	**9**
50	Tenebrionidae	*Neomida luteonotata* (Pic)	02	36	0	**36**	0	0	**0**	**36**
51	Tenebrionidae	*Neomida vitula* (Chevrolat)	02, 03, 10	95	82	**177**	4	17	**21**	**198**
52	Tenebrionidae	*Platydema* sp. A	18	0	5	**5**	0	0	**0**	**5**
53	Tenebrionidae	*Rhipidandrus* sp. A	07,10	6	0	**6**	0	3	**3**	**9**
			Number of species	**28**	**35**	**44**	**39**	**33**	**46**	**53**
			Number of individuals	**1838**	**1812**	**3650**	**3698**	**4066**	**7764**	**11414**

CONSIDERAÇÕES FINAIS

As redes de interações macrofungo-besouros fungívoros refletiram as condições encontradas nas áreas de referência e de restauração e podem ser utilizadas para avaliar sistematicamente os processos de restauração. Nas áreas de Canela e Santa Tereza, as métricas tradicionais de avaliação de comunidade mostraram que a comunidade de macrofungos Polyorales e Hymenochaetales e a comunidade de besouros fungívoros estão sendo recuperadas durante o processo de restauração, assim como as métricas de redes mostraram que as interações estão sendo recuperadas também.

Diferentemente do que esperávamos, as métricas de redes não acrescentaram informações que as métricas tradicionais não pudessem evidenciar (conforme esperado por Tylianakis *et al.*, 2007). Isso pode ser devido ao estágio de restauração já estar avançado para ambas as áreas, e neste caso uma solução seria um contraste de tempo de restauração maior para capturar estes aspectos, além de adicionar mais áreas de restauração para comparação, pois estas são escassas e costumam ser por demais distintas entre si para permitir funcionarem como réplicas adequadas.

Apesar disso, esta análise conjunta da diversidade da biota e das redes formadas fornece pistas sobre como o processo de restauração está qualitativamente, através da seleção de algumas espécies-chave. Algumas espécies raras só foram encontradas em áreas de referência com florestas antigas e bem conservadas, como o besouro *Falsocis brasiliensis* e representantes da família Erotylidae. Além deste, o fungo *Pycnoporus sanguineous* só está presente em condições de baixa umidade, associadas às áreas de restauração. Estes indicadores biológicos de condições e recursos específicos devem ser levados em consideração, integrando a prática da restauração entre os níveis organismal, populacional e de comunidades.

Nossa pesquisa reafirma a importância de investigar mais de um grupo de organismos na avaliação do processo de restauração, com o objetivo de melhor entender este processo por diferentes “pontos de vista” organismais. A complementaridade entre diferentes táxons e guildas tróficas representa uma arma ainda pouco utilizada pela ecologia da restauração. Esperamos que este trabalho sirva, ainda, para destacar a importância do uso das funções do ecossistema para entender o caminho que a restauração está tomando em cada sítio restaurado, sendo as interações ecológicas formas costumeiramente práticas e interessantes de levar a cabo essa avaliação.

Referência.

Tylianakis, J.M., Tscharntke, T. & Lewis, O.T. (2007) Habitat modification alters the structure of tropical host – parasitoid food webs. *Nature*, **445**, 202–205.