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Stream fishes in a tropical agricultural landscape: Influence of environmental features at different spatial scales on multiple facets of biodiversity

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A quienes me dieron la vida y
a quien la comparte conmigo...

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Hynes (1975)

RESUMO

Contexto. Em riachos neotropicais, poucos estudos têm considerado os efeitos de variáveis ambientais em diferentes escalas espaciais sobre a ictiofauna. Além disso, estudos relacionados com a escala em sua maioria incorporam uma única faceta e um único componente da biodiversidade, proporcionando uma visão incompleta da estrutura da comunidade de peixes.

Objetivo. Determinar a contribuição relativa de características locais, de microbacia e dos padrões espaciais na explicação da variação dos componentes α e β das facetas taxonômica, funcional e filogenética de peixes de riachos.

Métodos. Foram amostrados 85 trechos de riachos (= 85 microbacias) no Alto Rio Paraná, Brasil. Diversas análises estatísticas foram utilizadas para explicar as facetas e componentes da biodiversidade em função de variáveis locais, de microbacia e espaciais.

Resultados. Para quase todas as facetas e seus componentes α e β, os fatores ambientais locais explicaram uma fração substancial da variância. As variáveis na escala de microbacia, de um modo inesperado, e a estruturação espacial, como esperado, contribuíram pouco para a variação da biodiversidade ou não foram significativas.

Conclusões. Este estudo tem implicações claras para a proteção da biodiversidade íctica regional e poderiam ser integradas na gestão de riachos de diferentes maneiras. Primeiro, os resultados destacam a importância de fatores ambientais locais para a manutenção da biodiversidade de peixes de riachos situados em paisagens agrícolas. Por conseguinte, essas características ambientais chave devem ser restauradas ou, pelo menos, preservadas. Segundo, uma vez que funções e processos ecossistêmicos exercidos pela zona ripária foram ou estão sendo perdidas, ações voltadas para a restauração das matas ciliares na rede de drenagem devem ser uma prioridade nas bacias estudadas. Terceiro, já que as espécies raras que são funcionalmente e/ou filogeneticamente ‘únicas’, possivelmente contribuíram de forma desproporcionada à dissimilaridade funcional/filogenética entre os riachos, este grupo de espécies merece atenção especial para conservação. Finalmente, os resultados destacam a importância de incorporar múltiplas facetas, e seus componentes, em avaliações da biodiversidade, já que uma faceta não pode ser usada como *proxy* para outras.

Palavras-chave: Classificação hierárquica, Restauração de riachos, Cana-de-açúcar, Pastos, Agricultura intensiva, Traços funcionais, Ecofilogenética, Bacia do Turvo-Grande, Bacia do São José dos Dourados.

ABSTRACT

Context. In Neotropical streams, very few studies have considered the effects of environmental variables at different spatial scales on fish communities. Furthermore, scale-related studies mostly include only one facet and one component of biodiversity providing an incomplete picture of fish community structure.

Objective. To determine the relative contributions of catchment and local environmental features and spatial patterns in explaining variation in the α- and β-components of taxonomic, functional and phylogenetic diversity facets of stream fish.

Methods. Fish sampling was performed in 85 stream reaches (= 85 catchments) in the Alto Rio Paraná, Brazil. Different statistical analyzes were performed to explain the facets and components of biodiversity as a function of local, catchment or spatial variables.

Results. For almost all facets and its α- and β-components, local environmental factors explained a substantial fraction of variance. Catchment variables, in an unexpected way, and spatial structuring, as expected, contributed little to the variation in the biodiversity or were not significant at all.

Conclusions. This study has clear implications for protection of regional stream fish biodiversity and would be integrated into stream management in different ways. First, the results highlight the importance of local environmental factors for maintaining stream fish biodiversity in agricultural landscapes. Therefore, these key environmental features must be restored, or at least preserved. Second, because ecosystem functions and processes provided by riparian zone were or are being lost, actions directed toward restoring riparian forest in the drainage network should be a priority in the studied basins. Third, because rare species that are functionally and/or phylogenetically 'unique' possibly contributed disproportionately to the functional/phylogenetic dissimilarity among sites this group of species deserve special attention for conservation. And finally, the results highlight the importance to incorporate multiple facets, and its components, in biodiversity assessments because one facet cannot be used as a proxy for the others.

Keywords: Hierarchical classification, Stream restoration, Sugarcane, Pasture, Intensive agriculture, Functional traits, Ecophylogenetics, Turvo-Grande basin, São José dos Dourados basin.

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GENERAL INTRODUCTION

“*We must, in fact, not divorce the stream from its valley in our thoughts at any time. If we do we lose touch with reality*.” (Hynes 1975)

Resembling the branching pattern of a tree, the lotic systems around the world occur in hierarchical networks (Lowe and Likens 2005). The finest branches of these networks are termed headwater streams (‘streams’ henceforth; Lowe and Likens 2005). Streams are characterized by strong interactions with the systems that surround them (Hynes 1975) and perhaps it is for that reason that the functions supplied by streams mirror these interactions, namely: processing of terrestrial organic matter, retention of nutrients, regulation of sediment export, maintenance of natural discharge regimes (Vannote et al 1980; Lowe and Likens 2005) and many others. Furthermore, processes and functions provided by the streams are not restricted to a local effect; rather, they are spatially extensive (Lehner et al 2011). An example of this is that some ecological processes and key ecosystems services (e.g., water provision and quality) of downstream regions depend on processes and functions that take place in the streams (Vannote et al 1980; Freeman et al 2007; Saunders et al 2002; Lowe and Likens 2005).

Despite its importance, streams and rivers around the world are being exposed to unprecedented levels of human disturbance (Saunders et al 2002; Vörösmarty et al 2010). According to Saunders et al (2002), the three primary threats to freshwater systems are: land cover disturbance, altered hydrology and non-native species introduction. Specifically, land cover changes affect fresh waters through modification of nutrient loads and decomposition, increased siltation, changes in productivity, water pollutants, and alterations in water temperature (Saunders et al 2002; Soininen et al 2015). Such alterations result in harmful effects on aquatic organisms through changes as mortality rates, reproductive success, among many others (Saunders et al 2002; Soininen et al 2015). Therefore, it is not surprising that freshwater fishes are considered as the most threatened group of vertebrates after the amphibians (Bruton 1995; Balmford and Bond 2005).

Strategies for conservation of streams, their habitats and organisms, preferably should be based on whole-catchment management, including their adjacent terrestrial areas

(Saunders et al 2002; Feld 2013). However, a dilemma for decision makers is that restoration of entire catchments is rarely feasible (Bishop et al 2009; Feld 2013) and even less in productive areas in which extensive farming practices occur (Casatti et al 2015). From the concept of hierarchical classification of streams it is possible to integrate the multiple spatial scales over which are supported the ecological processes of the streams (Frissell et al 1986; Angermeier and Winston 1998; Feld 2013). An important assumption of this framework is that the structure and dynamics of stream habitat and biological patterns are determined by the surrounding catchment (Hynes 1975; Frissell et al 1986). In other words, by considering the environmental variables in a hierarchical form, it is expected that variables measured at larger spatial scales (e.g., land cover in the catchment) influence variables measured on a smaller scales (e.g., in-stream habitat), which then in turn affect fish community structure (Hynes 1975; Frissell et al 1986; Fitzpatrick et al 2001; Wang et al 2003; Allan 2004).

Recently, there have been new research lines in the study of (meta)communities. These lines include complementary facets, as functional and phylogenetic, and the beta component of diversity. The inclusion of additional facets and the beta component of biodiversity, and their joint study, has the potential to (1) allow linking niche properties based on species traits and phylogeny to environmental and spatial variation (Peres-Neto et al 2012), (2) inform the underlying mechanisms of community assembly, mechanisms that would not be noticeable from patterns of species distributions or taxonomic facet alone (Pavoine and Bonsall 2011; Peres-Neto et al 2012; Socolar et al 2016), and (3) reveal the spatial scaling of biodiversity loss (Socolar et al 2016). In addition, for a better bioassessment of anthropogenic effects it is necessary to consider niche- and dispersal-related processes at the same time because community structure is the result of local abiotic environmental features, biotic interactions and dispersal-related effects (Heino 2013).

This thesis focuses on the relative contributions of environmental features at different spatial scales (i.e., considering the environmental features in a hierarchical form) and spatial patterns to the variation in three diversity facets of stream fish in an agricultural tropical landscape. The main objective was to assess the influences of catchment land cover, local environmental features and spatial patterns on the alfa- (Chapter 1) and beta-components (Chapter 2) of taxonomic, functional and phylogenetic diversity facets of stream fish. All chapters were prepared according the rules of Landscape Ecology journal.

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CHAPTER 1

LOCAL ENVIRONMENTAL FEATURES DETERMINE MULTIPLE FACETS OF FISH DIVERSITY IN A HEAVILY-MODIFIED TROPICAL LANDSCAPE

"...every stream is likely to be an individual and thus not really very easily classifiable."

(Hynes 1975)

Introduction

The streams are extremely heterogeneous systems at multiple spatial scales (Frissell et al 1986), and this heterogeneity is mirrored in the organization of biological communities (Heino et al 2015a). Much of the stream research has traditionally been conducted at small spatial scales (Allan 2004; Johnson et al 2007), often within stream reaches of a few hundred meters and their immediate surroundings (Allan 2004). However, it has long been recognized that local habitat and biodiversity of streams are strongly influenced by landform and land cover in the surrounding valley (Hynes 1975). This cross-scale interaction is also emphasized by hierarchy theory. Hierarchy theory predicts, for example, that biodiversity and physical variables at a small spatial scale are controlled by other variables at larger spatial scales (Allen and Starr 1982; Johnson et al 2007). This means that the stream biota occurring at a site can be seen as the product of a series of filters ranging from habitat through regional to continental (Tonn 1990; Poff 1997; Johnson et al 2007). Accordingly, each species found at a site has to pass through these filters to potentially persist at the site (Poff 1997; Johnson et al 2007).

Although researchers have increasingly adopted a catchment-scale view of streams (Allan et al 1997; Johnson et al 2007), the relative influence of local-scale versus catchment-level factors on stream biota has remained elusive (Angermeier and Winston 1998; Strayer et al 2003; Cianfrani et al 2012). Fish community structure, for example, is often considered to be responding both small-scale (e.g., reach) and large-scale (e.g. catchment) alterations in environmental characteristics (Fitzpatrick et al 2001; Strayer et al 2003), but their relative importance is subject to a debate. For instance, in temperate streams, local-scale factors (e.g., substratum composition) explained a higher amount of variation in fish community structure among sites than large-scale variables such as catchment land cover (Lammert and Allan 1999; Diana et al 2006; Johnson et al 2007). In contrast, other studies have emphasized more the importance of catchment features as drivers of stream fish community structure (e.g., Roth et al 1996).

In Neotropical streams, very few studies have considered the effects of environmental variables at different scales on fish communities. The studies that exist have found that most of the variation in fish community structure can be explained by the shared effects of catchment features and local environmental predictors (Cruz et al 2013; Bordignon et al 2015; Santos et al 2015), or even that catchment features do not play an important role in determining stream fish community structure (Casatti et al 2015; Gerhard and Verdade 2016). Hence, it is evident that unraveling the effects of small-scale versus large-scaled features as drivers of stream fish community structure should be examined more thoroughly in Neotropical streams. Furthermore, information about responses to environmental variables measured at multiple spatial scales could be used to design robust monitoring and restoration programs (Johnson et al 2007; Feld 2013; Wahl et al 2013), and therefore as a model for regional headwater stream management. This is because catchment-scale features may be manipulated to influence factors at local scale, which ultimately would influence aquatic community structure (Allan et al 1997; Wang et al 2003; Cruz et al 2013; Feld 2013). This is also in line with recent considerations on the effectiveness of restoration actions for streams, where catchment actions are more effective than interventions focused solely on in-stream habitat restoration (Palmer et al 2010).

Recently, there have been new research lines in the study of (meta)communities. These include functional and phylogenetic facets of biodiversity. Functional diversity may reflect the ability of a given community to respond effectively to environmental changes, thereby allowing the maintenance of functional capacity (Díaz et al 2007), or link changes in biological community structure driven by land modification with the consequences for ecosystem function (Luck et al 2013). In the same way, phylogenetic diversity is a proxy of the accumulated evolutionary history of a community, and therefore might be associated to either the system's ability to generate new evolutionary solutions in the face of disturbance or to persist despite those disturbances (Forest et al 2007; Faith 2008). Likewise, functional and phylogenetic facets may also provide different and complementary information about species' differences and communities' responses to disturbance because ecologically relevant information not embedded in the selected traits may still be present in the phylogeny (Helmus et al 2010; Cadotte et al 2013). From a stream biomonitoring perspective it has been proven that both functional and phylogenetic facets are sensitive to environmental disturbance (i.e., can discriminate impacted streams from preserved ones; Saito et al 2015a). Therefore, multiple and complementary facets should be contemplated in any research describing stream biodiversity and environmental assessment or biomonitoring (Heino et al 2008; Saito et al 2015a).

In addition, assessing the relative contribution of spatial structure (proxy for dispersal-related processes) to stream fish community structure may suggest guidelines for management of biodiversity in human-dominated landscapes (Bengtsson 2010; Heino 2013). For instance, when there is a low dispersal between sites and local processes determine diversity (i.e., species sorting) the management of local features and local habitat heterogeneity will be most important to maintain diversity in a site (Bengtsson 2010).

In this study, we assessed the relative contributions of catchment land cover, local environmental features and spatial structure (proxy for dispersal-related processes) in explaining variation in the α-component of taxonomic, functional and phylogenetic diversity facets of stream fish. We aimed to answer the following questions: i) Are taxonomic, functional and phylogenetic facets related with local and/or catchment environmental features? ii) Do the three facets of biodiversity respond in the same way to local and/or catchment features? And iii) Are these facets spatially structured? We hypothesized that: i) both local and catchment variables will explain variation in the three diversity facets since catchment variables would impact local features, which then would in turn influence stream communities, indicating that examining the environmental features in a hierarchical sense have high predictive power on stream fish metacommunity structure (Allan et al 1997; Diana et al 2006; Fitzpatrick et al 2001; Johnson et al 2007); ii) both functional and phylogenetic α-diversity will respond in the same way as species richness since studies relating environmental gradients to this facet suggest that the functional or phylogenetic facets are positively correlated to the taxonomic facet (Forest et al 2007; Petchey et al 2007; Faith 2008). Finally, iii) spatial structure in biodiversity among sites should be weak at best, as dispersal limitation will not be important at this spatial extent. Most stream studies have indeed found that environmental control prevails over spatial constraints within single small drainage basins (Heino et al 2015b). Furthermore, the facet of biodiversity more prone to be affected by the spatial structure should be the taxonomic as complementary facets, such as functional, distinguish stream fish communities along gradients of habitat type irrespective of spatial position (Hoeinghaus et al 2007).

Methods

Study area

This study was carried out in the Turvo-Grande and São José dos Dourados basins, Alto Rio Paraná, northwest of São Paulo State, Brazil (Fig. 1). These two basins belong to the same biogeographical province, where the fish communities have a shared evolutionary history (Géry 1969). The region is part of the Serra Geral geological formation, characterized by having a relatively flat slope and plains of quaternary fluvial sedimentary nature (IPT 1999). The soil has a high erosive potential since it is composed of unconsolidated sand and clay sediments (Silva et al 2007). The climate is tropical and hot, with two well-defined periods: a dry season with lower rainfall and cooler temperatures between June and September, and a wet season between December and February with higher rainfall and warmer temperatures (IPT, 1999). This region was formerly covered by semi-deciduous seasonal forest (Silva et al 2007); however, the landscape has been transformed since the beginning of the last century (1900) for the development of coffee crops, followed by the establishment of cattle (Victor et al 2005), and more recently sugarcane (Rudorff et al 2010). Nowadays, the native forest is limited to less than 4% of its initial area, disseminated in small and unconnected fragments embedded in agricultural matrices (Nalon et al 2008). Like in other São Paulo state river basins (e.g., Corumbataí basin; Gerhard and Verdade 2016), the stream fish fauna of the study area is presumed to have been homogenized, probably due to habitat destruction and simplification, species introductions (Rahel 2002; Casatti et al 2009) and an extensive, dynamic and long history of land cover change (Victor et al 2005; Rudorff et al 2010).

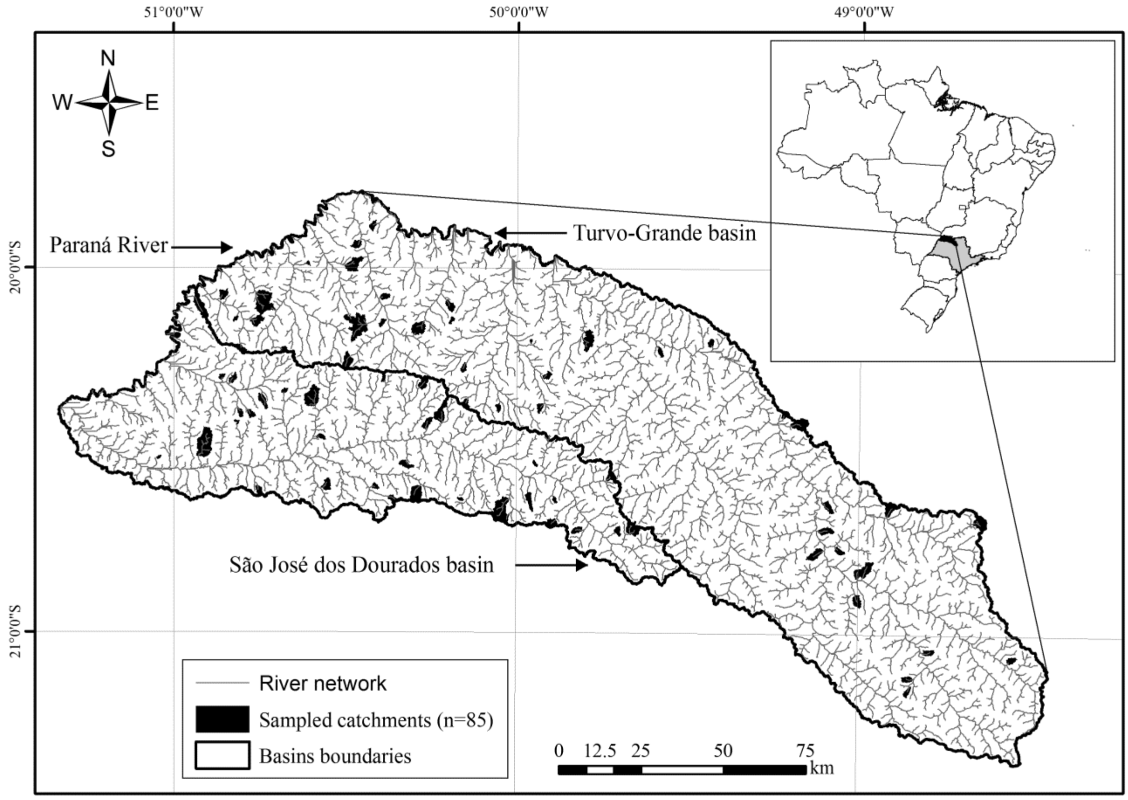


Figure 1. Sampling units (85 different catchments = 85 independent reaches) along São José dos Dourados and Turvo-Grande River basins at northwest region of São Paulo State (gray area in the country map), southeastern Brazil.

Site selection

For site selection, we performed the following procedure. First, we mapped the land cover in the São José dos Dourados and Turvo-Grande basins through the digital processing of LANDSAT-5/TM satellite images of 2011 year (221-74, 221-75 e 222-74 scenes; 30 m spatial resolution). We use 2011 data because it was the most recent year available at the time of the analysis. Four classes of land cover were defined through visual estimate using Google Earth^{TM} program: native forest, pasture, sugarcane and other land cover. As the product of processing, a thematic map with land cover information for the study area (unpublished data) was obtained. Second, using the thematic map, we conducted a catchment preselection taking into account that was listed only catchments with area between 400 and 1,400 hectares (that in the study area correspond to first-order to third-order streams according to the Strahler system, *L. Casatti personal observation*). From this preselection, 128 streams from independent catchments were filtered, considering that there was represented the environmental gradient of the region (i.e., pasture-sugarcane transition), and finally recognized in the field. After recognition in the field, evaluation of accessibility and owners consent for data collection, 85 streams were selected to compose our data set. Finally, to increase the reliability of the land cover data, we re-classified land cover in each of 85 selected catchments, but this time using orthorectified aerial photographs (‘orthophotos’) with a 1 m spatial resolution (years 2010/2011; most recent years available at the time of the analysis). Overall, eight classes of land cover were defined using orthophotos: native forest, herbaceous and shrub vegetation, pasture, sugarcane, perennial culture, reforestation, urban area and other land cover (see details in Table S2).

For the digital preparation, processing and classification of LANDSAT-5/TM satellite images and orthophotos we used ERDAS IMAGINE 9.2 and ArcGis 9.3 softwares. LANDSAT-5/TM satellite images were provided by the Instituto Nacional de Pesquisas Espaciais (INPE). Orthophotos were supplied by Empresa Paulista de Planejamento Metropolitano SA – EMPLASA (CLU Nº 060/14). For the sugarcane land cover class, the CANASAT project (sugarcane crop monitoring in Brazil; Rudorff et al 2010) provided data about area location and culture of sugarcane in São Paulo State for 2012 (most recent year available at the time of the analysis).

Fish sampling

In each of 85 selected streams, a 75 m-long reach was blocked using 5-mm-mesh stop nets according to standardized methods of fish collection for the region (see Casatti et al 2009). Forty-two of the stream reaches were sampled with an electrofishing equipment consists of a stationary generator (AC, 220V, 50–60Hz, 3.4–4.1A, 1000 W). The remaining 43 reaches were sampled using a Smith Root Model LR-24 backpack electrofishing (pulsed DC, 50-990V, 1-120Hz, 40A peak max, 400 W) with settings adjusted based on ambient conditions (i.e., with the quick set up feature activated, which automatically sets output voltage, frequency and duty cycle) and on observations of fish behavior and recovery times. In each reach, a two-pass electrofishing technique was conducted for a total of 45 minutes of standardized time. Each electrofishing pass was conducted from downstream to upstream, covering from bank to bank in order to sample all available habitats. To identify whether the observed pattern in community structure was a product of electrofishing equipment we conducted test for each of the facets of biodiversity (i.e., binary variable; 1 = stationary generator, 0 = backpack). The effect of the electrofishing equipment was only significant for species composition (taxonomic facet) but its effect was weak ($R^2_{Adj.} = 0.014$; $P = 0.002$) (Table S5).

Captured specimens were fixed in 10% formalin solution and transferred to a 70% EtOH solution. Fishes were identified to species and counted. Voucher specimens were deposited at the fish collection of the Departamento de Zoologia e Botânica da Universidade Estadual Paulista (DZSJRP 19264-19326), São José do Rio Preto, São Paulo, Brazil. Both recognition in the field and fish sampling was carried out in the dry season, between July and September 2013.

Predictor variables

Catchment scale

For each catchment (i.e., the catchment area delimited upstream from the sampled stream reach) 30 descriptors were measured (Table S1). The descriptors were related with land cover composition and heterogeneity, and they were quantified through (a) the number of classes of land cover (i.e., richness), (b) Shannon index, and (c) the relative proportion of each class of land cover (Gustafson 1998). Because riparian land cover and stream fish communities are associated (Pusey and Arthington 2003; Cruz et al 2013), we grouped the catchment descriptors in three different sets: entire catchment, drainage network and local (according to Strayer et al 2003). The entire catchment set included (1) the land cover in the whole catchment area, (2) the drainage network set comprised the land cover in a 30 m buffer zone around the river network (the minimum width established by the current Brazilian Forest Code), and (3) the local set included the land cover within a circle (150-m radius) centered on the sample site (Fig. 2; adapted from Strayer et al 2003).

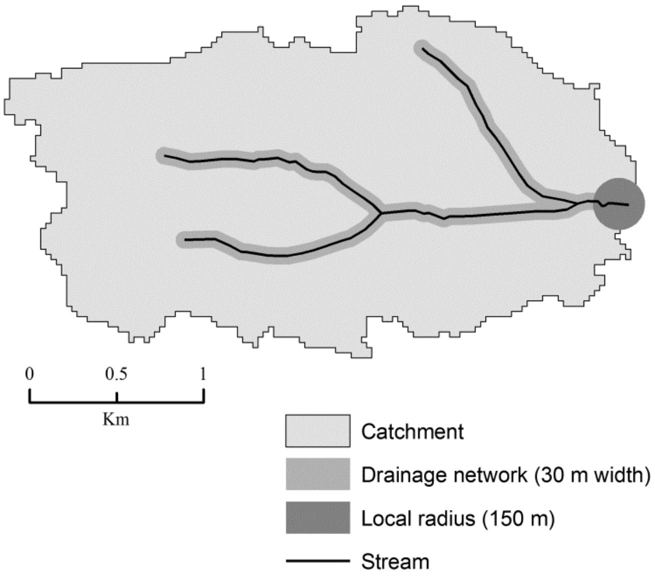


Figure 2. Schema illustrating a hypothetical catchment representing the three different sets at which land cover was assessed (adapted from Strayer et al 2003).

Local scale

Thirty-one local descriptors related to riparian physical structures, water physicochemical properties, stream morphology, habitat composition and heterogeneity were estimated at each reach (Table S1). We measured these descriptors following standardized protocols for the study area (Casatti et al 2009). These descriptors are commonly used in studies of stream fish community structure (Cruz et al 2013; Carvalho and Tejerina-Garro 2015b).

Spatial variables

We considered distance between sites as network distance (i.e., the distance between sites following the dispersal pathways dictated by the riverine dendritic network, *sensu* Brown and Swan 2010; Altermatt 2013). We used network distance because it captures spatial patterns that overland distance does not account for, and also offers better description of the spatial patterns generated by fish dispersal along a riverine dendritic network (Landeiro et al 2011; Altermatt 2013; Kärnä et al 2015). The network distance between sites was calculated using Hawth's Analysis Tool (Beyer 2004) for ArcGIS 9.3. From the network distance matrix, principal coordinates of neighbourhood matrix (PCNM) was calculated to generate spatial variables. We retained only PCNM eigenvectors with positive spatial correlation since we were mainly concerned in patterns produced by spatially contagious processes (Borcard et al 2011). For this, we used the 'PCNM' function from the PCNM package (Legendre et al 2013). The threshold value used in the PCNM analysis was the minimum distance giving connected network. All analyses were carried out in the R environment (R Development Core Team 2014).

Response variables

Taxonomic facet

For taxonomic facet, we considered species richness and species occurrence by site as response variables.

Functional traits

For each collected fish species (S = 63), information on 12 functional traits was obtained or compiled (Table S3). Seven traits were ecomorphological indexes associated with functional specializations of the fish to water flow, swimming ability and position in the water column (i.e., compression index; relative area of pectoral fin; pectoral fin aspect ratio; relative eye position; relative depth; index of ventral flattening; and fineness coefficient). Fish measurements were obtained with a digital caliper (0.01 mm resolution) and fin areas with a stereomicroscope (Zeiss® SteREO Discovery V12) and AxioVision Zeiss® image software (Ribeiro et al 2016). For specimens larger than 80 mm, fin areas were obtained by contouring the fins over graph paper (Beaumord and Petrere Jr. 1994; Ribeiro et al 2016). For details about ecological interpretations of ecomorphological indices, see Casatti and Castro (2006) and Ribeiro et al (2016).

The remaining five traits were related with trophic ecology (grouped in trophic guilds: algivores, detritivores, aquatic insectivores, terrestrial insectivores, lepidophagous, periphytivores, piscivores, and omnivores); size (categories of standard length);

preference for substrate (unconsolidated, consolidated); preference for water velocity (fast, medium, low); and adaptation to anoxic conditions (unadapted, adapted). Trophic guild was determined according to information from Zeni and Casatti (2014); size categories according to Teresa and Casatti (2012) and Casatti et al (2015); preference for substrate and water velocity according to Casatti et al (2015); and adaptation to anoxic conditions according to Chapman et al (1995), Graham (1997), Casatti et al (2009), Boswell et al (2009), Scarabotti et al (2011) and Teresa and Casatti (2012). When information about traits was not available, we analyzed at least five adult individuals of each species using fish collected in 2013 or individuals of the study area available in the fish collection of the Departamento de Zoologia e Botânica da Universidade Estadual Paulista (DZSJRP).

We use these traits because they provide important ecological information about species and have been widely used to examine the functional structure in Neotropical stream fish (Teresa and Casatti 2012; Carvalho and Tejerina-Garro 2015a,b; Dala-Corte et al 2016). Because we considered both quantitative and qualitative traits we used the mixed-variables coefficient of distance, a generalization of Gower's distance, to extract a functional distance matrix and use it in subsequent analyzes (Pavoine et al 2009). The functional distance matrix was calculated using 'ktab.list.df' and 'dist.ktab' functions of 'ade4' package (Dray and Dufour 2007) in R statistical software (R Development Core Team 2014).

Phylogenetic hypothesis

For all collected fish species (*S* = 63), we constructed a composite phylogenetic hypothesis (Fig. S1) based in the following studies: Montoya-Burgos (2003), Genner et al (2007), Near et al (2012), Betancur-R et al (2013), Chen et al (2013), Mariguela et al (2013) and Sullivan et al (2013). The phylogeny was built manually using Mesquite software v.2.75 (Maddison and Maddison 2011). Because there is no general consensus on the timing of divergence among the major actinopterygian and teleostean lineages (Near et al 2012), the phylogenetic distance between species was estimated using the 'bladj' utility in Phylocom software (Webb et al 2011). Even if only some nodes are dated, the resulting phylogenetic distances can be a marked improvement on simply using the number of intervening nodes as a phylogenetic distance (Webb et al 2011). A phylogenetic distance matrix was then extracted from the composite phylogeny to use in further analysis. The phylogenetic distance matrix was calculated using the 'cophenetic' function in R statistical software (R Development Core Team 2014).

Functional and phylogenetic diversity indexes

We used metrics based on functional and phylogenetic distances among species because they provide the same mathematical basis for comparing both facets (Swenson 2014; but see Maire et al (2015) for potential drawbacks of assessing functional diversity using distance measurements). Specifically, we used the standardized effect size of mean pairwise distance (i.e., NRI) and standardized effect size of the mean nearest taxon distance (i.e., NTI; Webb 2000). We used the standardized effect size of each metric because the observed phylogenetic and functional metrics could be correlated with the species richness of the community, creating severe problems to identify which additional information is actually being gained using phylogenetic and functional facets (Swenson 2014). The NRI and NTI metrics represent the average phylogenetic/functional difference between taxa in a community (Tucker et al 2016) indicating functional/phylogenetic clustering when greater than zero or functional/phylogenetic overdispersion when values are lower than zero (Webb et al 2002). Likewise, NRI is often considered to be a "basal" metric of diversity being sensitive to dendrogram-wide patterns of clustering or evenness (Swenson 2014; Geheber and Geheber 2016). Conversely, NTI is considered a "terminal" relatedness measure being more sensitive to variations towards the tips of the dendrogram (Webb 2000, Webb et al 2002). For these reasons, contrasting the results is useful for both types of metrics (Swenson 2014).

To calculate standardized effect size, we used the independent swap null model with a mean value obtained from 999 randomly generated communities. This null model preserves row and column totals of the original matrix, i.e., maintains the observed species richness and occurrence frequency in the null communities (Gotelli and

Entsminger 2001). We established our species pool as all fish species (*S* = 63) found in the 85 stream reaches because (i) we assume that species sampled in each site were not dispersal limited, thus it was feasible that all species had similar potential to occur in each site (Geheber and Geheber 2016) and (ii) stream reaches are located in the same biogeographical province (Géry 1969). All functional and phylogenetic metrics were calculated using incidence-based community data. Functional and phylogenetic metrics were estimated using 'ses.mpd' and 'ses.mntd' functions of 'picante' package (Kembel et al 2010) in R statistical software (R Development Core Team 2014).

Analytical methods

Exploratory data analysis (box-plot and quantile-quantile plots) was used to assess predictor variables normality and the presence of outliers (See Fig. S2 for a schematic representation of the analysis procedure). We transformed non-normal predictor variables to make the frequencies of distributions as symmetric as possible, linearize the relationships, as well as to reduce the effect of outliers (Legendre and Legendre 2012; Table S1). The logit transformation was applied to the variables of proportion (Warton and Hui 2011). For variables in other units, square root or $\log_e$ (X) transformations were used. The square-root transformation is the least severe to normalize data, whereas logarithmic is appropriate for data that depart broadly from a normal distribution (Legendre and Legendre 2012). Subsequently, predictor variables were standardized to zero mean and unit variance since these were measured in different units.

To reduce the initial number of predictor variables and strong linear dependencies among them, we used two approaches (Fig. S2). First, since strong collinearity can affect the ability to correctly estimate the regression parameters (Legendre and Legendre 2012) we discard those predictor variables, assessed separately within each scale, with Spearman correlation ≥ 0.7 (Dormann et al 2013). Second, we performed a forward selection procedure (sensu Blanchet et al 2008; Table S5). To prevent the inflation of Type I error in forward selection procedure, a global test needs to be done prior to any variable selection (Blanchet et al 2008). Therefore, we carried out three global tests (999 permutations each): one with the catchment-scale variables, another with the local-scale variables and last one with the PCNM eigenvectors with positive spatial correlation. We also used two stopping criteria in the forward selection procedure: i) the corrected alpha level of rejection of null hypothesis (i.e., only if the global test was significant, the corresponding set was used to continue with forward selection procedure) and ii) the adjusted R^2 statistic (R^2adj) of the global test (Blanchet et al 2008).

To identify the influence of local-scale, catchment-scale and spatial variables retained by the forward selection procedure on taxonomic facet (species occurrence by site) partial redundancy analysis (p-RDA) was performed (Fig. S2). The p-RDA allowed the variance partitioning of response variable into fractions explained by each set of explanatory variables (Legendre and Legendre 2012). We used permutation procedures (10,000 permutations; $P < 0.05$) to test the partial contribution of each predictor variables set and to test the significance of environmental variables assessed individually.

Finally, we performed a series of multiple regression analysis to explain the taxonomic (species richness), functional and phylogenetic facets of biodiversity as a function of local, catchment or spatial variables retained by the forward selection procedure (Fig. S2). Additionally, to use the beta coefficients to interpret multiple regression, we considered the structure and commonality coefficients to gain a broader and fuller perspective on the contributions that predictor variables made to the regression equation (Nathans et al 2012); this was done through the commonality analysis. Commonality analysis decomposes the variance of R^2 into *unique* and *common* effects of predictors (Ray-Mukherjee et al 2014). Unique effects (U) represent the amount of variance in the response variable that is uniquely accounted for by a single predictor variable. Common effects (C) represent the amount of variance in the response variable that can be jointly explained by two or more predictors together. Total (Total = U + C) represents the total contribution of a predictor to the response variable irrespective of collinearity with other variables (Prunier et al 2015). In addition, by using commonality analysis was possible to identify those predictor variables with suppression effect (i.e., variables that indirectly enhances the prediction, by improving the prediction of others, Nathans et al 2012; Ray-Mukherjee et al 2014).

For forward selection procedure we used the ‘forward.sel’ and ‘rda’ functions of ‘packfor’ (Blanchet et al 2008) and ‘vegan’ (Oksanen et al 2015) packages respectively; ‘lm’ function for multiple regression analysis; and ‘regr’ function of ‘yhat’ package for calculate structure and commonality coefficients (Nimon et al 2008). All analyses were carried out in R (R Development Core Team 2014).

Results

Overall, 63 fish species belonging to 18 families and six orders were sampled in the 85 stream reaches (Table S4). In general, local-scale environmental variables explained taxonomic, functional and phylogenetic facets the best (Tables 1 and 2). Catchment-scale variables accounted only for variation in the phylogenetic NTI metric, whereas spatial variables were only related with taxonomic facet (species occurrence by site), but its effect was weak (Tables 1 and 2).

For taxonomic facet (species occurrence by site), 18% of variability was accounted by the predictor variables ($R^2_{Adj.} = 0.18$, $P = 0.001$). Explained variation was partitioned between the explained fractions as follows: pure local 10% ($P = 0.001$), pure catchment <1% ($P = 0.164$), pure spatial 4% ($P = 0.001$), and shared environmental and spatial location <1% (fraction not testable). Local environmental variables that contributed most to the variation in species occurrence by site were mean depth and mean water velocity (Table 2).

For taxonomic facet (species richness), the local-scale variables accounted for 33% of the variation ($P < 0.001$; Table 1). The squared structure coefficients (r^2_s) showed that mean depth, standard deviation of width and proportion of pools were able to account for 33%, 32% and 25% of the regression effect given by the R^2, respectively. Mean depth was thus the predictor variable that had the higher *unique* effect (10%) to predict variation in species richness (Table 1). It should be noted that although the proportion of large roots in contact with water has large beta coefficient and higher *unique* effect, its *common* (C = -0.046) and *total* (0.065) effects indicate that this variable aids other predictors to better predict the regression, although the variable itself is weakly related to the species richness than the other predictor variables (i.e., a great part of its variance is shared with another predictor and not with the response variable and, hence, it does not directly affect R^2; for details see Ray-Mukherjee et al 2014).

Standardized effect size of "basal" metrics (i.e. fNRI and pNRI) also was only influenced by local scale variables; which accounted for ≥19% of the variation in the dependent variable (Table 1). Functional NRI was affected by proportion of unconsolidated substrate, mean water velocity and mean depth (R^2_{Adj} = 0.297; Table 1); with squared structure coefficients (r^2_s) indicating that these variables were able to account for 65%, 35% and 17% of the regression effect given by the R^2, respectively (Table 1). The proportion of unconsolidated substrate had the higher *unique* effect (16%) to predict variance in fNRI (Table 1). The β coefficients of fNRI multiple regression indicated that increases in the proportion of unconsolidated substrate and mean depth led to a functional clustering of stream fish communities (*β coefficient* = 0.454; *β coefficient* = 0.242), whereas the increase in mean water velocity led to a functional overdispersion (*β coefficient* = -0.280; Table 1).

On the other hand, pNRI was significantly affected by mean depth and proportion of grasses (R^2_{Adj} = 0.192; Table 1). Squared structure coefficients (r^2_s) indicated that mean depth and proportion of grasses were able to account for 43% and 30% of the regression effect given by the R^2, respectively. Mean depth thus had the higher *unique* effect (10%) to predict variance in pNRI (Table 1). The β coefficients of pNRI multiple regression indicated that increase in mean depth led to a phylogenetic clustering of stream fish communities (*β coefficient* = 0.385), whereas that higher proportion of grass led to a phylogenetic overdispersion (*β coefficient* = -0.288; Table 1). The phylogenetic NTI (pNTI) was the only metric influenced by a catchment-scale variable. Specifically, catchment land cover diversity accounted for 7% of the variation in the pNTI and its *unique* effect was 6% (Table 1). The *β* coefficients of pNTI multiple regression indicated that high catchment land cover heterogeneity led to a phylogenetic overdispersion towards the tips of the phylogeny (β *coefficient* = -0.263; Table 1).

Commonality analysis identified the proportion of leaf litter as a suppressor variable of the phylogenetic NRI regression, since its *unique* effect (U = 0.065) is offset by its *common* effect (C = -0.064; Table S6). The same was observed for the catchment land cover richness variable in the phylogenetic NTI regression (U = 0.094; C = -0.094; Table S6). For this motive, these variables were omitted from the multiple regression analysis of phylogenetic NRI and NTI, respectively.

Table 1. Multiple regression and commonality analysis predicting the three facets of stream fish diversity by forward selected environmental variables. This table includes P-value (*P*), multiple R^2, adjusted R^2 ($R^2_{Adj.}$), beta coefficients (β), standard error of beta coefficients (SE), t-value (t), structure coefficients (r_s), squared structure coefficient (r^2_s), each predictor's total unique (U), total common (C), and total variance (Total) in the regression equation.

Facet	Effects	β	SE	*t*	*P*	r_s	r^2_s	Commonality analysis*		
								U	C	Total
Species richness	(Intercept)	9.024	0.341	26.481	< 0.001	-	-	-	-	-
($P < 0.001$; $R^2 = 0.362$; $R^2_{Adj.} = 0.330$)	dep	1.236	0.349	3.542	0.001	0.577	0.333	0.100	0.021	0.121
	widSD	0.959	0.362	2.648	0.010	0.562	0.316	0.056	0.058	0.114
	Lro	-1.336	0.358	-3.730	< 0.001	-0.423	0.179	0.111	-0.046	0.065
	pool	0.993	0.382	2.603	0.011	0.497	0.247	0.054	0.035	0.089
Functional NRI	(Intercept)	0.324	0.101	3.196	0.002	-	-	-	-	-
($P < 0.001$; $R^2 = 0.322$; $R^2_{Adj.} = 0.297$)	usu	0.454	0.104	4.379	< 0.001	0.806	0.650	0.161	0.049	0.209
	vel	-0.280	0.104	-2.699	0.008	-0.592	0.351	0.061	0.052	0.113
	dep	0.242	0.102	2.377	0.020	0.413	0.170	0.047	0.008	0.055
Phylogenetic NRI	(Intercept)	0.185	0.109	1.691	0.095	-	-	-	-	-
($P < 0.001$; $R^2 = 0.220$; $R^2_{Adj.} = 0.192$)	phi	0.160	0.141	1.134	0.260	0.722	0.521	0.012	0.102	0.115
	dep	0.385	0.121	3.191	0.002	0.658	0.433	0.098	-0.003	0.095
	gra	-0.288	0.142	-2.024	0.046	-0.551	0.304	0.039	0.028	0.067
Phylogenetic NTI	(Intercept)	-0.022	0.106	-0.208	0.836	-	-	-	-	-

Facet	Effects	β	SE	*t*	*P*	r_s	r^2_s	Commonality analysis*		
								U	C	Total
(*P* = 0.027; R^2 = 0.107; $R^2_{Adj.}$ = 0.073)	cat_H	-0.263	0.109	-2.409	0.018	-0.851	0.725	0.064	0.013	0.077
	Lfor	0.154	0.107	1.441	0.153	0.494	0.244	0.023	0.003	0.026
	Npas	-0.082	0.109	-0.751	0.455	-0.400	0.160	0.006	0.011	0.017

*Unique effects (U) represent the amount of variance in the response variable that is uniquely accounted for by a single predictor variable. Common effects (C) represent the amount of variance in the response variable that can be jointly explained by two or more predictors together. Total (Total = U + C) represents the total contribution of a predictor to the response variable irrespective of collinearity with other variables (Prunier et al 2015).

Table 2. Predictor variables significantly related to taxonomic facet (species occurrence by site). Test based on 10,000 permutations. In bold P values < 0.05.

	Variance	F	*P*
Mean depth	0.21	4.08	**0.001**
Mean water velocity	0.21	4.01	**0.001**
Shrubs	0.13	2.59	**0.001**
Standard deviation of width	0.12	2.34	**0.001**
Total dissolved solids	0.11	2.22	**0.003**
Water temperature	0.11	2.13	**0.004**
Grasses	0.10	1.86	**0.011**
Mean width	0.08	1.63	**0.027**
pH	0.09	1.72	**0.028**
Large roots	0.08	1.55	**0.043**
Native forest in the drainage network	0.08	1.54	0.048
PCNM2	0.12	2.36	**0.001**
PCNM1	0.05	0.94	0.51
PCNM7	0.10	2.02	**0.003**
PCNM6	0.09	1.68	**0.021**
PCNM17	0.07	1.27	0.177
PCNM5	0.08	1.54	0.047

Discussion

We found that, for almost all biodiversity facets, local environmental factors explained a substantial fraction of variance, whereas catchment variables and spatial structuring contributed little to the variation in the biodiversity or were not significant at all. These findings are partially consistent with our first hypothesis that environmental features measured at different spatial scales will have high predictive power on the three facets evaluated, but rather, our results point out to the importance of the local scale environmental features for fish communities in streams embedded in highly impacted landscapes.

In general, studies addressing the importance of scale-related factors for stream fish have reported that both local and catchment scale features influence the community structure. However, these studies also emphasize that local habitat variables are more important in explaining variance in community structure (Lammert and Allan 1999; Wang et al 2003; Diana et al 2006 but see Fitzpatrick et al 2001). Influences of local-scale environmental factors on the structure of stream fish communities have been recognized comprehensively. For instance, variation in taxonomic and/or functional stream fish facets has been associated with the addition of deeper areas (Sheldon 1968; Schlosser 1982; Carvalho and Tejerina-Garro 2015b), widespread propagation of marginal vegetation as grasses (mostly *Brachiaria* spp.; Casatti et al 2009; Casatti et al 2015), substrate categories (Casatti et al 2015), increased extent and volume of pool habitats (Schlosser, 1982) and stream width (Angermeier and Karr 1983; Lammert and Allan 1999). Our results are consistent with these previous findings. In particular, variables such as mean depth, mean and standard deviation of width and mean water velocity were shown to be important predictors of the three facets suggesting that species' niche differences, in terms of environmental characteristics related with stream morphology, contribute to the variability in stream fish community structure at the spatial scale evaluated by us (Heino and Mykrä 2008). This outcome is also in accordance with species sorting, the typical mechanism structuring stream communities (Heino and Mykrä 2008; Carvalho and Tejerina-Garro 2015; but see Saito et al 2015b).

As noted by Allan et al (1997), contrasting results regarding the importance of environmental variables at different scales would be a consequence of the study design or indicate that mechanisms operating at local and catchment scales are in fact different and uncorrelated. Considering that only one set of local variables was obtained in each catchment, we assumed that our sampling design was not implicitly biased to detecting local-scale effects and, therefore, local and catchment influences would have been in fact distinct. Among the possible reasons for the stronger control of local-scale variables on the aquatic community structure are: firstly, in agricultural areas, the past (i.e., decades ago) land cover both in the catchment and in the riparian zone is a better predictor of present-day taxonomic facet of stream biota than the current land cover (Harding et al 1998; Surasinghe and Baldwin 2014). This would be related to that stream fish communities already overpass the threshold of response to catchment modification (i.e., initial exposure to a disturbance may selectively filter those species which are most sensitive to it), suggesting that post-threshold fish communities display a weak response to agricultural intensification (Balmford 1996; Fitzpatrick et al 2001; Balmford and Bond 2005). Secondly, catchment variables simply displayed little variability (e.g., homogeneous landscape) to overwhelm the influence of local environmental variables (Heino et al 2007; Casatti et al 2015). The second explanation is plausible since, of the eight land cover classes, two were highly dominant (≈ 70%) in our study area: sugarcane (mean proportion = 0.31) and pasture (mean proportion = 0.39). From the above, it is possible to assert that the local-scale environmental features become even more important for stream fish biodiversity could be a common pattern in heavily-modified tropical landscapes (Casatti et al 2015; Gerhard and Verdade 2016; but see Wang et al 2003 for opposite conclusion for temperate streams).

We also found that different local-scale variables were important in accounting for variation in the three diversity facets, and the effects of common environmental variables could be different in function of the diversity facets analyzed. Although these results could be partially incompatible to our second hypothesis (i.e., that both functional and phylogenetic facets will respond to environmental factors similarly to species richness), the differentiated effects of local environmental features highlight the importance of addressing different facets of biodiversity once each point out different patterns in the structure of stream fish communities. For example, by considering only the taxonomic facet, we may underestimate the importance of some environmental variables affecting complementary facets (i.e., water velocity and substrate type for functional diversity and proportion of grasses for phylogenetic diversity). In the same way, by assessing only the taxonomic facet, we may concluded that the increase in mean depth follows the increase in the species number; however, from functional and phylogenetic information, it is possible to state that the increase in species richness, mediated by the increase in mean depth, is given from addition of functional and phylogenetically similar species (i.e., functional and phylogenetic clustering). Likewise, through complementary facets of biodiversity, we could identify environmental variables that are responsible for the functional and/or phylogenetic overdispersion, such as water velocity and proportion of grasses respectively. According to Lyashevska and Farnsworth (2012), using only species richness, the most commonly used measure to describe biodiversity, may result in the loss of a significant portion of the information (≈ 89%) being therefore a poor substitute of other diversity facets.

In general, we found no effects of the network distance between sites on the facets of biodiversity. In a certain way, this is not remarkable, since the environmental control prevails over spatial constraints within single small drainage basins (Mykrä et al 2007; Heino and Mykrä 2008; Heino et al 2015b). According to Heino and Mykrä (2008), among the possible reasons for absence of spatial structure in stream communities is that, given enough time, stream biota can disperse readily between sites. Another possibility – that does not exclude the first - is that the fish fauna has already gone through a homogenization process in the study area, through extensive introductions of non-native species (e.g., *Poecilia reticulata*), habitat modification and extirpation of native species, generating fish communities probably dominated by mobile and widespread habitat generalist species (McKinney and Lockwood 1999; Devictor et al 2008), and phylogenetically closely-related species. It is also known that the importance of spatial processes (e.g., colonization history or mass effects) is less expected to occur when the regional species pool is small, or it has been decimated, and the condition of disturbance is considerable (Chase 2003; Goldenberg Vilar et al 2014).

Restoration and conservation of stream fish in human-altered landscapes

Although one critical factor for the success of stream restoration is the spatial scale of intervention (Lake et al 2007), habitat restoration projects are implemented without an understanding of the spatial scale necessary for measurable positive ecological effects (Alexander and Allan 2007; Sheldon et al 2012). In fact, many river restoration projects have focused on improving local environmental features to increase biodiversity, but ignoring larger scale effects at the same time (Alexander and Allan 2007). These scale-related effects remain an important and poorly understood question and might be one of the reasons for why a part of restoration projects have provided little evidence of ecological success (Alexander and Allan 2007). One traditional decision for restoring the ecological integrity of streams is the re-establishment of riparian vegetation (Harding et al 1998; Sheldon et al 2012) since it has been demonstrated that it can regulate water temperature, diminish sediment inputs, stabilize stream banks (Osborne and Kovacic 1993), provide large wood debris to stream channels in tropical agricultural landscapes (Paula et al 2013) and maintain the biotic integrity of fish communities in agricultural streams (Fitzpatrick et al 2001).

Our results indicated that riparian vegetation, measured as a 30 m buffer zone around the river network – the minimum width established by the current Brazilian Forest Code – had little or no influence on the three biodiversity facets. This does not mean that riparian vegetation is not important for fish (for a comprehensive review see Pusey and Arthington 2003). Rather, since in our study area the riparian vegetation structure has been depleted over decades (Silva et al 2007), a weak buffering effect on biodiversity could indicate that ecosystem functions and processes mediated by this structure was or is being lost. Indeed, in the 85 studied catchments only, on average, 21% of the buffer zone along drainage network corresponds to areas occupied by forests, whereas 60% is covered by herbaceous and shrub vegetation and 12% by pasture for livestock (unpublished data). According to Fitzpatrick et al (2001), in agricultural landscapes even minor alterations of stream network buffer (e.g., 10% agriculture within a 50-m buffer) may have harmful effects on fish fauna. Consequently, actions directed toward restoring riparian forest in the drainage network should be a priority in the studied basins, as previously suggested in other studies (e.g., Casatti et al 2012; Casatti et al 2015). Moreover, riparian forest restoration would bring benefits not only for the stream's habitats and organisms but could also have positive impacts on terrestrial organisms through improving connectivity between habitat patches (Noss and Harris 1986).

On the other hand, our results suggest that in highly altered tropical streams actions even on a local-scale could produce effects on the three facets of biodiversity. Although it is an interesting finding, we must recognize that stream restoration is a challenge to be faced by ecologists. Mostly because it is recognized that substantial improvements in the ecological integrity of streams are more likely to be accomplished with large-scale actions (Lake et al 2007; Palmer et al 2010; Wahl et al 2013), once multiple factors controlled by larger spatial scales influence stream biodiversity (e.g., water quality, disturbance regime, regional species pools, differences in species dispersal capacity, degraded hydrological regimes; Palmer et al 2010 and references therein). By contrast, restoration actions at larger spatial scales can be unfeasible either due to the scarcity of financial resources or conflicts of interest among parties (Lake et al 2007). In agricultural areas, large scale restoration is even more difficult to be achieved since the crop fields and pastures will hardly be replaced by forests (Casatti et al 2015).

Finally, it should also be noted that (i) responses of the biodiversity facets to each local environmental variable must be better assessed because changes in one environmental feature could generate dissimilar effects between the facets, and (ii) the same spatial scale may not be important for every catchment or reach in the same way and, therefore, it will not be transferable between sites (Sheldon et al 2012). For this reason, any restoration actions based on our findings would need to be correctly monitored (Palmer et al 2010; Sheldon et al 2012), mainly considering that sustained and intensive agricultural practices may severely alter stream biota, and the influence of this disturbance may be long lasting (Harding et al 1998).

In conclusion, our results indicated that local environmental factors are the most important predictors of taxonomic, functional and phylogenetic facets of stream fish communities in a heavily-modified tropical landscape. Moreover, that catchment features and spatial structuring contributed little to the variation in the biodiversity or were not significant at all. Our results also suggest that restoration actions on a local-scale could produce effects on the three facets of biodiversity.

Supplementary material

Tables

Table S1. Predictor variables measured in the 85 sampling sites, Turvo-Grande and São José dos Dourados River basins at the northwest region of São Paulo State, southeastern Brazil.

Category	Variable	Unit	Transformation	Code
	Catchment-scale variables			
Entire catchment	Number of classes of land cover	-	square root	cat_S
	Shannon index	-	-	cat_H
	Native forest	proportion	logit	Cfor
	Herbaceous and shrub vegetation	proportion	logit	Cher
	Pasture	proportion	logit	Cpas
	Sugarcane	proportion	logit	Csug
	Perennial culture	proportion	logit	Cper
	Reforestation	proportion	logit	Cref
	Urban area	proportion	logit	Curb
	Other land cover	proportion	logit	Coth
Drainage network	Number of classes of land cover	-	square root	net_S
	Shannon index	-	-	net_H
	Native forest	proportion	logit	Nfor

Category	Variable	Unit	Transformation	Code
	Herbaceous and shrub vegetation	proportion	logit	Nher
	Pasture	proportion	logit	Npas
	Sugarcane	proportion	logit	Nsug
	Perennial culture	proportion	logit	Nper
	Reforestation	proportion	logit	Nref
	Urban area	proportion	logit	Nurb
	Other land cover	proportion	logit	Noth
Local land cover	Number of classes of land cover	-	square root	loc_S
	Shannon index	-	-	loc_H
	Native forest	proportion	logit	Lfor
	Herbaceous and shrub vegetation	proportion	logit	Lher
	Pasture	proportion	logit	Lpas
	Sugarcane	proportion	logit	Lsug
	Perennial culture	proportion	logit	Lper
	Reforestation	proportion	logit	Lref
	Urban area	proportion	logit	Lurb
	Other land cover	proportion	logit	Loth
	Local-scale variables			
Stream physical habitat condition	Physical Habitat Index*	absolute value	square root	phi

Category	Variable	Unit	Transformation	Code
Mesohabitats	Pool	proportion	logit	pool
	Riffle	proportion	logit	rif
	Run	proportion	logit	run
	Mesohabitats richness	-	log	mes_S
	Mesohabitats heterogeneity	-	-	mes_H
Physicochemical descriptors	pH	-	-	pH
	Conductivity	µs	square root	con
	Total dissolved solids	g/L	square root	TDS
	Water temperature	°C	square root	tem
Substratum	Unconsolidated substrate: clay, silt and sand	proportion	logit	usu
	Consolidated substrate: gravel, rock, boulder and bedrock	proportion	logit	csu
In-stream cover	Leaf litter	proportion	logit	lit
	Small and large woody debris	proportion	logit	woo
	In-stream cover richness	-	square root	sub_S
	In-stream cover heterogeneity	-	-	sub_H
Stream morphology	Mean width	m	square root	wid
	Standard deviation of width	-	-	widSD
	Mean depth	m	square root	dep
	Standard deviation of depth	-	-	depSD

Category	Variable	Unit	Transformation	Code
	Mean water velocity	m/s	square root	vel
	Standard deviation of water velocity	-	-	velSD
Marginal vegetation	Bryophytes and pteridophytes	proportion	logit	bry
	Fine roots	proportion	logit	Fro
	Large roots	proportion	logit	Lro
	Grasses (mostly *Brachiaria* spp.)	proportion	logit	gra
	Shrubs	proportion	logit	shr
	Exposed streambank	proportion	logit	exb
	Aquatic macrophytes	proportion	logit	mac
	Ecotone richness	-	log	eco_S
	Ecotone heterogeneity	-	-	eco_H
	Spatial variables			
Network distance	PCNM eigenvectors with positive spatial correlation	-	-	-

* As adapted for study area by Casatti et al (2006).

Table S2. Description of land cover classes.

Land cover class	**Description**
Native forest	Areas occupied by the different native forest found in the study area (i.e., Savanna and Semi-deciduous seasonal forest).
Herbaceous and shrub vegetation	Areas occupied by herbaceous and shrub vegetation, which also included species of cattail (*Typha* spp.).
Pasture	Areas used for intensive and extensive livestock, also including areas covered by native grasses but to a lesser extent.
Sugarcane	Areas covered with sugarcane culture (*Saccharum* spp.) or that showed evidences of being used for this culture.
Perennial culture	Areas covered with perennial cultures (e.g., *Citrus* spp., *Hevea* spp., *Coffea* spp.).
Reforestation	Included planted forests and restored areas with *Eucalyptus* spp. or *Pinus* spp..
Urban area	Include towns and villages.
Other land cover	It groups rural installations, temporary cultures, highways and exposed soil.

Table S3. Traits used for the description of fish species. Trait type codes: Nominal (N); Quantitative (Q); Ordinal (O).

Traits	Statistical type	Attributes
Compression index (CI)	Q	MBD/MBW
Relative area of pectoral fin (RAPF)	Q	PFA/BA
Pectoral fin aspect ratio (PFAR)	Q	LPF/WPF
Relative eye position (REP)	Q	DEM/HD
Relative depth (RD)	Q	MBD/SL
Index of ventral flattening (IVF)	Q	MMD/MBD
Fineness coefficient (FC)	Q	$\frac{SL}{\sqrt{\mathrm{MBD\ x\ MBW}}}$
Trophic guild	O	1 = Algivores; 2 = Detritivores; 3 = Aquatic insectivores; 4 = Terrestrial insectivores; 5 = Lepidophagous; 6 = Periphytivores; 7 = Piscivores; 8 = Omnivores
Size	O	1 = 1 - 50 mm standard length (SL); 2 = 51-100mm SL; 3 = > 101 mm SL
Preference for substrate	N	0 = Unconsolidated; 1 = Consolidated
Preference for water velocity	O	0 = Low; 1 = Medium; 2 = Fast
Adaptation to anoxic conditions	N	0 = No; 1 = Yes

Codes for morphological measurements: BA: body area; DEM: depth of the eye midline; HD: head depth; LPF: maximum length of pectoral fin; MBD: maximum body depth; MBW: maximum body width; MMD: maximum midline depth; PFA: pectoral fin area; SL: standard length; WPF: maximum width of pectoral fin.

Table S4. The 63 fish species collected in the 85 stream reaches

Order and families, species and authors	Codes
Characiformes	
Parodontidae	
Apareiodon affinis (Steindachner 1879)	Apaaff
Apareiodon piracicabae (Eigenmann 1907)	Apapir
Parodon nasus Kner 1859	Parnas
Curimatidae	
Cyphocharax vanderi (Britski 1980)	Cypvan
Steindachnerina insculpta (Fernández-Yépez 1948)	Steins
Anostomidae	
Leporinus friderici (Bloch 1794)	Lepfri
Leporinus lacustris Amaral Campos 1945	Leplac
Crenuchidae	
Characidium gomesi Travassos 1956	Chagom
Characidium zebra Eigenmann 1909	Chazeb
Characidae	
Astyanax altiparanae Garutti & Britski 2000	Astalt
Astyanax fasciatus (Cuvier 1819)	Astfas
Astyanax paranae Eigenmann 1914	Astpar
Astyanax schubarti Britski 1964	Astsch
Bryconamericus stramineus Eigenmann 1908	Brystr
Hasemania sp.	Hassp
Hemigrammus marginatus Ellis 1911	Hemmar
Hyphessobrycon anisitsi (Eigenmann 1907)	Hypani
Hyphessobrycon eques (Steindachner 1882)	Hypequ
Knodus moenkhausii (Eigenmann & Kennedy 1903)	Knomoe
Moenkhausia sanctaefilomenae (Steindachner 1907)	Moesan
Oligosarcus pintoi Amaral Campos 1945	Olipin
Piabina argentea Reinhardt 1867	Piaarg
Planaltina britskii Menezes, Weitzman & Burns 2003	Plabri
Roeboides descalvadensis Fowler 1932	Roedes
Serrapinnus heterodon (Eigenmann 1915)	Serhet

Order and families, species and authors	Codes
Serrapinnus notomelas (Eigenmann 1915)	Sernot
Acestrorhynchidae	
Acestrorhynchus lacustris (Lütken 1875)	Acelac
Erythrinidae	
Erythrinus erythrinus (Bloch & Schneider 1801)	Eryery
Hoplias malabaricus (Bloch 1794)	Hopmal
Lebiasinidae	
Pyrrhulina australis Eigenmann & Kennedy 1903	Pyraus
Siluriformes	
Callichthyidae	
Aspidoras fuscoguttatus Nijssen & Isbrücker 1976	Aspfus
Callichthys callichthys (Linnaeus 1758)	Calcal
Corydoras aeneus (Gill 1858)	Coraen
Hoplosternum littorale (Hancock 1828)	Hoplit
Lepthoplosternum pectorale (Boulenger 1895)	Leppec
Megalechis thoracata (Valenciennes 1840)	Megtho
Loricariidae	
Hisonotus francirochai (Ihering 1928)	Hisfra
Hypostomus ancistroides (Ihering 1911)	Hypanc
Hypostomus cf. *nigromaculatus* (Schubart 1964)	Hypnig
Pterygoplichthys ambrosettii (Holmberg 1893)	Pteamb
Pseudopimelodidae	
Pseudopimelodus mangurus (Valenciennes 1835)	Pseman
Pseudopimelodus pulcher (Boulenger 1887)	Psepul
Heptapteridae	
Cetopsorhamdia iheringi Schubart & Gomes 1959	Cetihe
Imparfinis cf. *schubarti* (Gomes, 1956)	Impsch
Pimelodella cf. *avanhandavae* Eigenmann 1917	Pimava
Rhamdia quelen (Quoy & Gaimard 1824)	Rhaque
Gymnotiformes	
Gymnotidae	
Gymnotus inaequilabiatus (Valenciennes 1839)	Gymina

Order and families, species and authors	Codes
Gymnotus paraguensis Albert & Crampton 2003	Gympar
Gymnotus cf. *sylvius* Albert & Fernandes-Matioli 1999	Gymsyl
Sternopygidae	
Eigenmannia trilineata López & Castello 1966	Eigtri
Cyprinodontiformes	
Rivulidae	
Melanorivulus pictus (Costa 1989)	Melpic
Poeciliidae	
Phalloceros harpagos Lucinda 2008	Phahar
Poecilia reticulata Peters 1859	Poeret
Xiphophorus maculatus (Günther 1866)	Xipmac
Synbranchiformes	
Synbranchidae	
Synbranchus marmoratus Bloch 1795	Synmar
Perciformes	
Cichlidae	
Cichlasoma paranaense Kullander 1983	Cicpar
Crenicichla britskii Kullander 1982	Crebri
Crenicichla haroldoi Luengo & Britski 1974	Crehar
Crenicichla semifasciata (Heckel 1840)	Cresem
Geophagus brasiliensis (Quoy & Gaimard 1824)	Geobra
Laetacara araguaiae Ottoni & Costa 2009	Laeara
Oreochromis niloticus (Linnaeus 1758)	Orenil
Satanoperca pappaterra (Heckel 1840)	Satpap

Table S5. Results of forward selection procedure for each facet of biodiversity and each set of predictor variables (i.e., local, catchment, spatial, method). For variables codes, see Table S1. In bold *P* values < 0.05.

Facet	Predictor variables	Global model		Selected variables
		R^2_{Adj}	*P*	
Species richness	Local	0.318	**0.001**	dep, widSD, Lro, pool
	Catchment	0.094	0.185	
	Spatial	-0.095	0.865	
	Method	-0.012	0.913	
Species composition	Local	0.134	**0.000**	dep, vel, shr, widSD, TDS, tem, gra, wid, pH, Lro
	Catchment	0.043	**0.025**	Nfor
	Spatial	0.062	**0.000**	V2, V1, V7, V6, V17, V5
	Method	0.014	**0.002**	
Functional NRI	Local	0.265	**0.003**	usu, vel, dep
	Catchment	0.152	0.072	
	Spatial	0.037	0.282	
	Method	0.017	0.117	
Functional NTI	Local	-0.009	0.514	
	Catchment	0.074	0.254	
	Spatial	0.029	0.383	
	Method	-0.012	0.921	
Phylogenetic NRI	Local	**0.233**	**0.006**	phi, dep, lit, gra
	Catchment	-0.068	0.724	
	Spatial	0.107	0.108	
	Method	-0.006	0.482	
Phylogenetic NTI	Local	0.059	0.231	
	Catchment	**0.194**	**0.038**	cat_H, cat_S, Lfor, Npas
	Spatial	-0.013	0.548	
	Method	0.020	0.112	

Table S6. Multiple regression and commonality analysis identified the proportion of leaf litter and the catchment land cover richness as suppressor variables of the phylogenetic NRI and phylogenetic NTI multiple regression. This table includes beta coefficients (β), standard error of beta coefficients (SE), t-value (*t*), P-value (*P*), structure coefficients (r_s), squared structure coefficient (r^2_s), each predictor's total unique (U), total common (C), and total variance (Total) in the regression equation.

Facet	Effects	β	SE	*t*	*P*	r_s	r^2_s	Commonality analysis*		
								U	C	Total
Phylogenetic NRI	(Intercept)	0.185	0.106	1.755	0.083					
	phi	0.292	0.144	2.027	0.046	0.635	0.403	0.037	0.078	0.115
	dep	0.417	0.117	3.573	0.001	0.579	0.335	0.114	-0.019	0.095
	lit	-0.349	0.130	-2.687	0.009	0.034	0.001	0.065	-0.064	0.000
	gra	-0.379	0.141	-2.686	0.009	-0.485	0.235	0.065	0.002	0.067
Phylogenetic NTI	(Intercept)	-0.022	0.101	-0.219	0.827					
	cat_H	-0.482	0.126	-3.830	< 0.001	-0.620	0.384	0.147	-0.069	0.077
	cat_S	0.433	0.141	3.074	0.003	0.020	0.000	0.094	-0.094	0.000
	Lfor	0.228	0.105	2.180	0.032	0.360	0.129	0.047	-0.021	0.026
	Npas	-0.230	0.114	-2.012	0.048	-0.291	0.085	0.040	-0.023	0.017

*Unique effects (U) represent the amount of variance in the response variable that is uniquely accounted for by a single predictor variable. Common effects (C) represent the amount of variance in the response variable that can be jointly explained by two or more predictors together. Total (Total = U + C) represents the total contribution of a predictor to the response variable irrespective of collinearity with other variables (Prunier et al 2015).

Figures

Figure S1. Composite phylogeny for 63 stream fish species. For species codes, see Table S4.

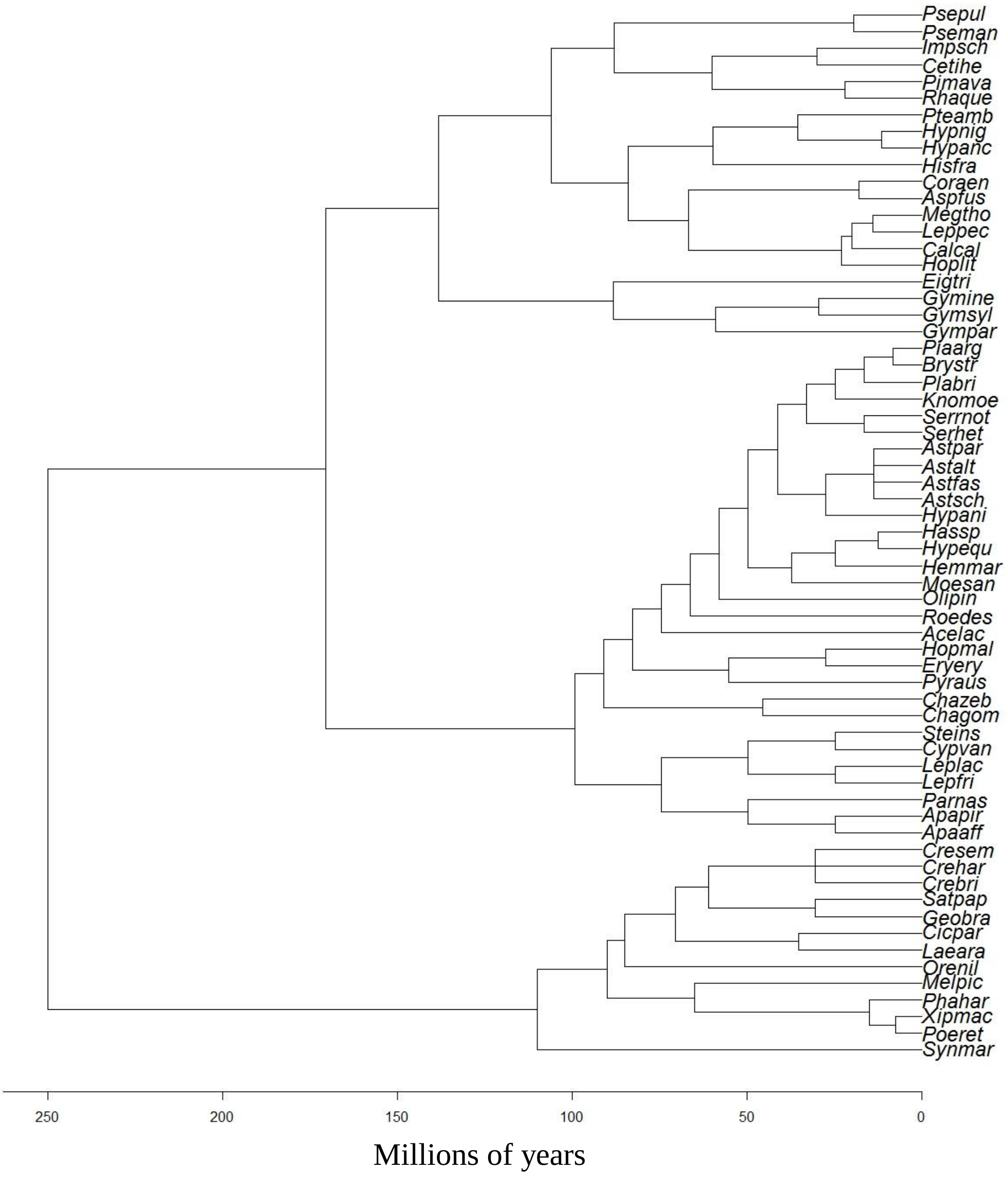
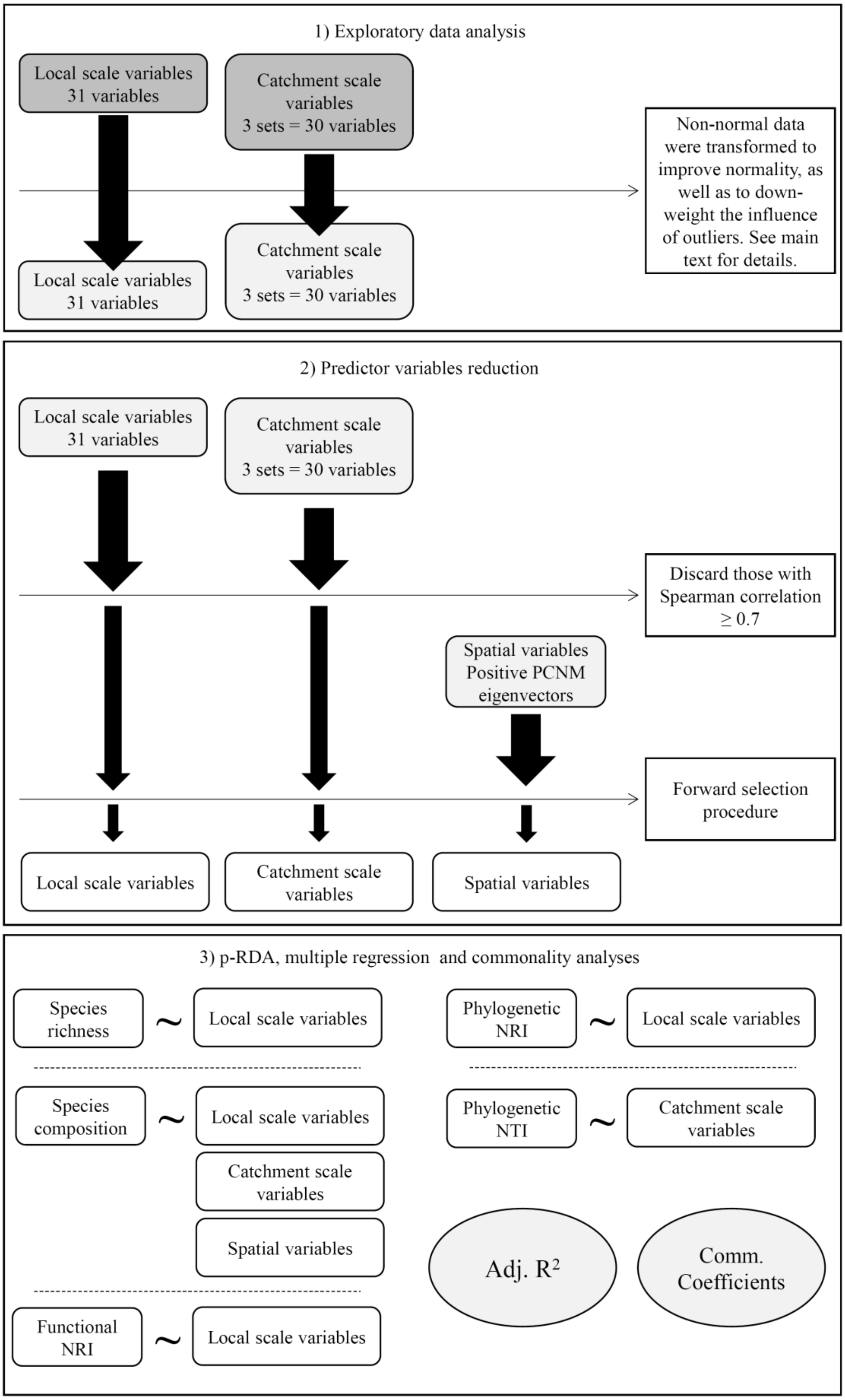


Figure S2. Schematic representation of the analysis procedure.



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CHAPTER 2

ASSESSMENT OF MULTIPLE FACETS OF DIVERSITY SUGGEST DIFFERENT PROCESSES GOVERNING STREAM FISH β-DIVERSITY IN A TROPICAL AGROECOSYSTEM

"*…we may expand Hynes' paradigm and state that the valley rules the stream, while the riparian buffer rules the in-stream biology.*" (Feld 2013)

Introduction

Species diversity can be decomposed into gamma, alpha and beta components (Whittaker 1960). Of these components, β-diversity represents the variation in species composition among sampling units within a given area (Anderson et al 2006; Soininen 2010). Recognizing that diversity assessments have often centered solely on patterns of α-diversity neglect other important components of diversity, recent ecological research has focused on β-diversity patterns (Anderson et al 2011; Swenson et al 2012; Heino et al 2015a) even in understudied environments such as streams (Heino et al 2013; Larsen and Ormerod 2014; Hawkins et al 2015). In general, β-diversity has frequently been analyzed using lists and abundances of species following a species diversity-centric approach (*sensu* Swenson et al 2012). In this approach, all species are treated as functionally equivalent (Swenson et al 2011) or considered evolutionarily independent (Swenson et al 2012).

Facets of biodiversity alternative to taxonomic facet, such as phylogenetic and functional ones, have the capacity to considerably improve our understanding of the mechanisms underlying biodiversity patterns and community assembly (Webb et al 2002; Petchey and Gaston 2006; Swenson et al 2012). For instance, considering two sampled communities, it is possible to find complete turnover in species composition but none or little turnover in functional composition (Swenson et al 2012). A species diversity-centric approach may attribute such turnover to dispersal limitation and stochasticity (Swenson et al 2012) while analyses including functional and phylogenetic data would more clearly recognize dispersal limitation and ecological determinism governing community structure (Swenson et al 2012; Wang et al 2013). However, there has been a lot of discussion about the existence of assembly rules structuring communities (Weiher and Keddy 1999) being useful include methods, as null models, to compare if observed patterns are more or less similar than expected by chance, providing evidence for certain community assembly mechanisms (Chase 2010; Tucker et al 2016). Another important reason to include multiple facets in the study of communities is that changes in the taxonomic facet typically cannot be used to predict changes in another and vice versa (Higgins 2010; Tobias and Monika 2011; Villéger et al 2014). In the same vein, though phylogenetically dissimilar species are expected to also have dissimilar functional traits (Winter et al 2013; Roa-Fuentes et al 2015a), phylogenetic diversity not always can be considered as a proxy of functional diversity (Winter et al 2013). After recognizing these potential limitations ecologists are increasingly attempting to quantify the phylogenetic and functional dissimilarity between communities (Swenson et al 2012; Wang et al 2013).

In agricultural areas, consequences of land use alterations for β-diversity and all of its facets – taxonomic, functional and phylogenetic – are largely unknown, especially in the tropics (Karp et al 2012; but see Fugère et al 2016; Siqueira et al 2015). It can be expected that only species with a distinct set of physical, life-history and other functional traits survive in intensively used agriculture landscapes (Tscharntke et al 2008; Karp et al 2012; Casatti et al 2015). For instance, it has been found that intensive land-use practices may select for species with high dispersal abilities and, consequently, a continuing agricultural intensification may allow a characteristic suite of good dispersers to spread over large distances, thereby decreasing β-diversity (Vellend et al 2007; Ekroos et al 2010). This suggests that taxonomic, functional and phylogenetic β-diversity may decline in response to physical alterations, which are a product of agricultural intensification and other disturbances caused by humans (Baiser and Lockwood 2011; Karp et al 2012; Gutiérrez-Cánovas et al 2013; Sonnier et al 2014; Villéger et al 2014).

There is no general consensus that β-diversity always declines with environmental disturbance (Socolar et al 2016; Siqueira et al 2015). Among the possible explanations for different patterns are that the disturbance effects are scale-dependent (i.e., β-diversity declines most when evaluated at larger scales; Karp et al 2012) and that the disturbance-β-diversity relationship is dependent on which external environmental gradient is selected and which part of that gradient is surveyed (Tuomisto 2010; Siqueira et al 2015). Another reason is that under disturbance conditions higher values of β-diversity are related with increased occurrence of rare but tolerant taxa, and decreased occupancies of some relatively common but sensitive species (Hawkins et al 2015). This indicates that the effects of anthropogenic disturbance on community composition could be variable and possibly dependent on at least three aspects: (1)

initial ecological conditions; (2) the magnitude, type and uniformity of environmental disturbance taking place in the study area; and (3) the vulnerability of individual taxa (Hawkins et al 2015).

Tropical landscapes are threatened by various land uses related to the production of goods for humans. For example, the recent boom of ethanol production has attracted international attention to the environmental impacts of land conversion into sugarcane monocultures (Goldemberg et al 2008; Martinelli and Filoso 2008; Scharlemann and Laurance 2008; Fischer et al 2009). Major areas of concern include deforestation and threats to biodiversity, environmental pollution and competition with food crops (Martinelli and Filoso 2008; Scharlemann and Laurance 2008; Fischer et al 2009). Nowadays, Brazil is the largest producer of sugarcane in the world (FAOSTAT 2016) with an estimate of 658.7 million tons in the 2015/16 period (Conab 2015). In Brazil, the increase in ethanol demand has led to an increase in the planted area with sugarcane; therefore, key ecosystems such as riparian forests have been highly affected to give way to cropping areas (Martinelli & Filoso 2008). Since headwater streams, the in-stream habitat and the organisms that inhabit them, are inextricably linked to riparian forests and processes occurring at the catchment scale (Pusey and Arthington 2003; Allan 2004; Sweeney et al 2004), stream fish may be severely affected by the expansion of sugarcane plantations (Arthington et al 1997; Santos et al 2015; but see Schiesari and Corrêa 2016).

The present study provides an analysis of stream fish β-diversity for three different facets (i.e., taxonomic, phylogenetic and functional) in an intensively cultivated tropical region. Specifically, we focused on a transition from pasture to sugarcane to answer the following questions: (i) Is the taxonomic, phylogenetic and functional β-diversity between sampling units higher or lower than expected by chance (i.e., whether fish community β-diversity is stochastic or deterministic)? (ii) The taxonomic, phylogenetic and functional similarity between sites decreases or decays as the environmental and/or spatial distance increases? Namely, is there significant environmental and/or spatial distance decay in taxonomic, phylogenetic and functional similarity? And (iii) if there is environmental distance decay, do environmental features measured at different spatial scales (i.e., stream reach and catchment-scales) have the same relative influence on observed β-diversity?

We hypothesized that: (i) observed patterns of taxonomic, functional and phylogenetic β-diversity will be non-random, thus supporting a deterministic model of stream fish community assembly in agricultural areas; (ii) since our study area has a history of anthropogenic disturbance longer than 100 years (Victor et al 2005), which leads to a high functional redundancy (for α-diversity; see Casatti et al 2015) and presumably taxonomic homogenization, fish β-diversity probably will be lower than expected by chance, indicating taxonomic, functional and phylogenetic homogenization; and (iii) once complete homogenization is unlikely, environmental features will drive the distance decay in the three β-diversity facets, rather than spatial distance within a drainage basin (Heino et al 2015b). Also both local and catchment variables should explain β-diversity because catchment variables would impact local variables, which would in turn influence stream fish communities (Allan et al 1997; Diana et al 2006).

Methods

Study area

We sampled 43 stream reaches located in the Turvo-Grande and São José dos Dourados basins, northwest region of São Paulo State, southeastern Brazil (Figure 1). These two basins belong to the same biogeographical province, where the fish communities have a shared evolutionary history (Géry 1969). The study area is located in the Serra Geral geological formation, presenting a relatively flat slope and plains of quaternary fluvial sedimentary nature (IPT 1999). The soil has a high erosive potential since it is composed of unconsolidated sand and clay sediments (Silva et al 2007). The climate is tropical and hot, with two well-defined periods: a dry season with lower rainfall and cooler temperatures between June and September, and a wet season between December and February with higher rainfall and hotter temperatures (IPT 1999). Initially, this region was covered by semi-deciduous seasonal forest (Silva et al 2007); but, the landscape has been fragmented since the beginning of the last century (1900) for the development of coffee crops, followed by the establishment of cattle (Victor et al 2005), and more recently by sugar cane plantations (Rudorff et al 2010). Nowadays, the native vegetation is restricted to less than 4% of its original area, distributed in small and unconnected fragments embedded in agricultural matrices (Nalon et al 2008) or limited to riparian areas (Silva et al 2007). Like in other São Paulo state river basins (e.g., Corumbataí basin; Gerhard and Verdade 2016), the stream fish fauna of the study area is presumed to have been homogenized due to species introductions (Rahel 2002; Casatti et al 2009) and habitat destruction and simplification led by an extensive, dynamic and long history of land cover change (Victor et al 2005; Silva et al 2007; Rudorff et al 2010).

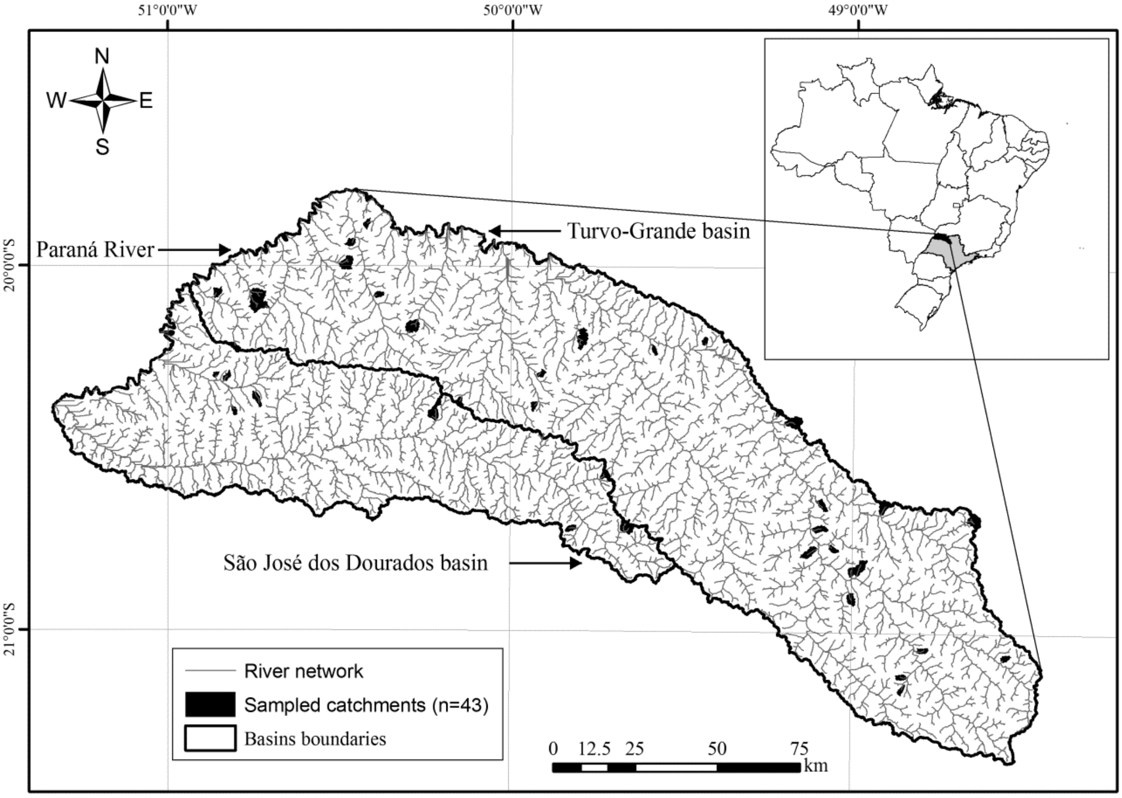


Figure 1. Sampling units (43 different catchments = 43 independent reaches) along São José dos Dourados and Turvo-Grande River basins at northwest region of São Paulo State (gray area in the country map), southeastern Brazil. Some catchments were neighbors therefore it is not possible to differentiate on the map.

Site selection and land cover characterization

For site selection, we performed the following procedure. First, we mapped the land cover in the São José dos Dourados and Turvo-Grande basins through the digital processing of LANDSAT-5/TM satellite images of 2004, 2005, 2007 and 2011 years (221-74, 221-75 e 222-74 scenes; 30 m spatial resolution). Four classes of land cover were defined through visual estimate using Google Earth^{TM} program: native forest, pasture, sugarcane and other land cover. As the product of processing, thematic maps with land cover information for the study area (unpublished data) were obtained. Second, using the thematic maps, we conducted a catchment preselection taking into account that was represented a transition from pasture to sugarcane (2004-2011) and that was listed only catchments with area between 400 and 1,400 hectares (that in the study area correspond to first-order to third-order streams according to the Strahler system, *L. Casatti personal observation*). From this preselection, 128 different catchments were filtered and finally recognized in the field. Previous evaluation of accessibility and owners' consent for data collection, 43 streams reaches from independent catchments were selected to compose our data set. Finally, to increase the reliability of the land cover data, we re-classified land cover in each of 43 selected catchments, but this time using orthorectified aerial photographs ('orthophotos') with a 1 m spatial resolution (years 2010/2011). Overall, eight classes of land cover were defined using orthophotos (For details see Table S1), but as we are interested mainly in the pasture-sugarcane transition and forest influence, we grouped them into four broad classes: native forest, pasture, sugarcane and other land cover.

For the digital preparation, processing and classification of LANDSAT-5/TM satellite images and orthophotos, we used ERDAS IMAGINE 9.2 and ArcGis 9.3 softwares. LANDSAT-5/TM satellite images were provided by the Instituto Nacional de Pesquisas Espaciais (INPE). Orthophotos were supplied by Empresa Paulista de Planejamento Metropolitano SA – EMPLASA (CLU Nº 060/14). For the sugarcane land cover class, the CANASAT project (sugarcane crop monitoring in Brazil; Rudorff et al 2010) provided data about area location and culture of sugarcane in São Paulo State for 2012 (most recent year available at the time of the analysis).

Fish sampling

In each stream of 43 selected streams, a 75 m-long reach was blocked using 5-mm-mesh stop nets according to standardized methods of fish collection for the region (see Casatti et al 2009). The stream reaches were sampled using a Smith Root Model LR-24 backpack electrofishing (pulsed DC, 50-990V, 1-120Hz, 40A peak max, 400 W) with settings adjusted based on ambient conditions (i.e., with the quick set up feature activated, which automatically sets output voltage, frequency and duty cycle) and on observations of fish behavior and recovery times. A two-pass electrofishing technique was conducted for a total of 45 minutes of standardized time in each reach. Each electrofishing pass was conducted from downstream to upstream, covering from bank to bank in order to sample all available habitats. Captured specimens were fixed in 10% formalin solution and transferred to a 70% EtOH solution. Fishes were identified to species and counted. Voucher specimens were deposited at the fish collection of the Departamento de Zoologia e Botânica da Universidade Estadual Paulista (DZSJRP 19264 - 19326), São José do Rio Preto, São Paulo, Brazil. Both recognition in the field and fish sampling were carried out in the dry season between July and September 2013.

Predictor variables

Local-scale features

Ten local scale variables related to in-stream features, riparian physical structures, water physicochemical properties, stream morphology, habitat composition and heterogeneity were estimated at each reach (Table S2). We measured these variables following standardized protocols for the study area (Casatti et al 2006; Casatti et al 2009). These variables are commonly used in studies of stream fish community structure (Cruz et al 2013; Carvalho and Tejerina-Garro 2015b).

Catchment-scale features and landscape dynamic indicators

For each catchment (i.e., the catchment area delimited upstream from the sampled stream reach), six variables were measured (Table S2). Four were the proportions of native forest, pasture, sugarcane and other land cover in the whole catchment area, as defined by the orthophotos processing (years 2010/2011). The remaining two variables were landscape dynamic indicators that represented the history of changes in land cover between the years 2004-2011. We chose this period, as it comprises the steep increase in the area used for cultivation of sugarcane in São Paulo State (Rudorff et al 2010). Specifically, we estimated the mean annual forest change rate (q) and forest change curvature profile (FCCP). The q index measures annual forest change rate on catchments using the annual rate of forest change equation (FAO 1995). Positive values represent forest increment and negative values represent forest loss over 2004-2011 period (Ferraz et al 2009, 2014). The FCCP index represents the maximum deviation of the forest change curve in relation to the linear model linking initial (2004) and final (2011) forest amount over time (Ferraz et al 2014). Positive deviations represent forest change concentrated in early years, while negative deviations represent forest change concentrated in recent years (Ferraz et al 2014). Small deviations represent scattered changes in patterns over time (Ferraz et al 2014). Landscape dynamic indicators were calculated using Land-Use Change Analysis Tools, an ArcGIS extension (Ferraz et al. 2012).

Spatial variables

We considered distance between sites as network distance (i.e., the distance between sites following the dispersal pathways dictated by the riverine dendritic network, *sensu* Brown and Swan 2010; Altermatt 2013). We used network distance because, for aquatic organisms, it captures spatial patterns that overland distance does not account for, and also may offer better description of the spatial patterns generated by fish dispersal along a riverine dendritic network (Landeiro et al 2011; Altermatt 2013; Kärnä et al 2015). The network distance between sites was calculated using Hawth's Analysis Tool (Beyer 2004) for ArcGIS 9.3.

Response variables

Functional traits

For each collected fish species, information on 12 functional traits was obtained or compiled (Table S3). Seven traits were ecomorphological indexes linked with functional specializations of the fish to water flow, position in the water column and swimming ability (i.e., compression index; relative area of pectoral fin; pectoral fin aspect ratio; relative eye position; relative depth; index of ventral flattening; and fineness coefficient). Distance measurements were taken with a digital caliper (0.01 mm precision) and fin areas with a Zeiss® SteREO Discovery V12 stereomicroscope and AxioVision Zeiss® image software. For specimens larger than 80 mm, fin areas were obtained by contouring the fins over graph paper due to the view limitation of the optic equipment field (Casatti et al 2015). For details about ecological interpretations of ecomorphological indices, see Casatti and Castro (2006) and Casatti et al (2015).

The remaining five traits were related with trophic ecology (grouped in trophic guilds: algivores, detritivores, aquatic insectivores, terrestrial insectivores, lepidophagous, periphytivores, piscivores, and omnivores); size (categories of standard length); preference for substrate (unconsolidated, consolidated); preference for water velocity (fast, medium, low); and adaptation to anoxic conditions (unadapted, adapted). Trophic guild was determined according to information from Zeni and Casatti (2014); size categories according to Teresa and Casatti (2012) and Casatti et al (2015); preference for substrate and water velocity according to Casatti et al (2015); and adaptation to anoxic conditions according to Chapman et al (1995), Graham (1997), Casatti et al (2009), Boswell et al (2009), Scarabotti et al (2011) and Teresa and Casatti (2012). When information about traits was not available, we analyzed at least five adult individuals of each species using fish collected in 2013 or individuals of the study area available in the fish collection of the Departamento de Zoologia e Botânica da Universidade Estadual Paulista (DZSJRP).

We used these traits because they provide important ecological information about species and have been widely used to examine the functional structure in Neotropical stream fish communities (Teresa & Casatti 2012; Carvalho and Tejerina-Garro 2015 a, b; Bordignon et al 2015). Because we considered both quantitative and qualitative traits we used the mixed-variables coefficient of distance, a generalization of Gower's distance, to extract a functional distance matrix and use it in subsequent analyzes (Pavoine et al 2009). The functional distance matrix was calculated using 'ktab.list.df' and 'dist.ktab' functions of 'ade4' package (Dray and Dufour 2007) in R statistical software (R Development Core Team 2014).

Phylogenetic hypothesis

Using all 63 fish species collected in 2013 (i.e., including species collected in other 42 different catchments localized in the same basins, for details see Chapter 1) we built a composite phylogeny (Fig. S1). For this, we considered the following studies: Montoya-Burgos (2003), Genner et al (2007), Near et al (2012), Betancur-R et al (2013), Chen et al (2013), Mariguela et al (2013) and Sullivan et al (2013). The phylogeny was built manually using Mesquite 2.75 (Maddison and Maddison 2011). Because there is no broad agreement on the timing of diversification among the major actinopterygian and teleostean lineages (Near et al 2012), we estimated the phylogenetic distance between species using the 'bladj' utility in Phylocom software (Webb et al 2011). Even if a few nodes are dated, the resulting phylogenetic distances can be a clear enhancement on simply using the number of intervening nodes as a phylogenetic distance (Webb et al 2011). A phylogenetic distance matrix was then calculated from the composite phylogeny using the 'cophenetic' function in R statistical software (R Development Core Team 2014) and used in further analysis.

Quantifying β-diversity

Taxonomic β-diversity and null modeling

We estimated taxonomic β-diversity using a null-modeling approach and a modified Raup-Crick metric (Raup and Crick 1979) following Chase et al (2011) for incidence data ($\beta_{RC\text{-}in}$) and Püttker et al (2015) for abundance data (square-root-transformed, $\beta_{RC\text{-}ab}$). The β_{RC} metric with a null-model approach has the advantage that it is independent of α-diversity (i.e. local species richness; Chase et al 2011). Therefore, it allows discriminating whether variation in the measured dissimilarity among communities results from differences in the compositional variation among local communities and not due to difference in local species richness among localities (Chase et al 2011). Furthermore, the null-modeling approach measures the deviation from the null expectation that pairwise community dissimilarity is stochastic (i.e., mainly influenced by random extinction and ecological drift; Raup and Crick 1979; Chase et al 2011; Püttker et al 2015), allowing to assess the importance of deterministic (niche-based) and stochastic (neutral) processes in community assembly (Chase et al 2011; Püttker et al 2015; but see Tucker et al 2016).

The original β_{RC} metric was modified by Chase et al (2011) by re-scaling it to vary from -1 to 1. Values of 0 represent no difference in the observed (dis)similarity from the null expectation; values of 1 indicate observed dissimilarity higher than the expected by null expectation (i.e., communities completely more different from each other than expected by chance), and vice versa for a value of -1 (i.e., communities completely less different [more similar] than expected by chance; Chase et al 2011). In terms of processes and mechanisms controlling community assembly, mean β_{RC} values among sampling sites are close to 0 when community assembly is highly stochastic and dispersal is high among communities, and will draw near -1 when deterministic environmental filters shared across sampling sites create highly similar communities (Chase 2010; Chase et al 2011). Otherwise, mean β_{RC} values will be closer to 1 if deterministic environmental filters favor dissimilar species compositions; e.g., if there are strong biotic structuring forces generating very dissimilar communities on contiguous sites or if dispersal among sites is very low, leading to dispersal limitation (Chase et al 2011).

For $\beta_{RC\text{-}in}$, we defined the regional species pool as all fish species that can possibly colonize the study sites within a reasonable time period (Chase et al 2011; Püttker et al 2015) thus assuming that species sampled in each site were not dispersal limited (Geheber and Geheber 2016). Namely, our regional species pool was all 63 fish species collected in 2013 (i.e., including fish species collected in other 42 different sites localized in the same basins, for details see Chapter 1). For $\beta_{RC\text{-}ab}$ the pool of individuals, instead of species, was used to delimit the regional pool and draw randomly individuals instead of species from the pool (see Püttker et al 2015 for details). For $\beta_{RC\text{-}in}$ calculation, we weighted species by frequency of occupancy as recommended by Chase et al (2011). For calculation of $\beta_{RC\text{-}in}$ and $\beta_{RC\text{-}ab}$, we used the R-scripts provided in Chase et al (2011) and Püttker et al (2015), respectively, with 10,000 random samples without reposition.

Functional and phylogenetic β-diversity and null modeling

To estimate the functional and phylogenetic β-diversity, we used distance metrics based on pairwise and nearest neighbor distances coupled with a null-modeling approach. We used distance metrics since they can be applied for phylogenetic and functional data (Swenson 2014). For the pairwise measure, we used the extension of the alpha diversity metric (i.e., MPD) to beta diversity (i.e., βMPD hereafter) (Webb et al 2011). For the nearest neighbor measure, we used the extension of the alpha diversity metric (i.e., MNTD) to beta diversity (i.e., βMNTD hereafter) (Webb et al 2011). Specifically, βMPD examines the overall similarity or dissimilarity between two samples or communities, while βMNTD quantifies whether the closest relative of each species or individual in one community to the next is distantly or closely related (Swenson 2014). The βMPD measure is often considered to be a "basal" metric of diversity (Swenson 2014) and βMNTD is considered a terminal relatedness measure being more sensitive to variations towards the tips of the dendrogram (Webb 2000). For these reasons, βMPD and βMNTD measures are complementary and may be employed to discriminate patterns in β-diversity (Swenson 2011).

Since we were interested in determining whether the functional and/or phylogenetic β-diversity was higher or lower than expected by chance, we performed null modelling analyses. Since we were using abundance data (see explanation below), we considered randomizations that fixed the entire community data matrix while randomizing the phylogenetic and functional information (Swenson 2014). Specifically, we randomized 1,000 times the names of taxa in the functional distance matrix and phylogenetic tree respectively. With this randomization procedure, the abundance of species within and across communities, the occupancy rates of species across communities, the species alpha and beta diversity are all fixed and the observed dispersal limitation of species is conserved (Swenson et al 2011; Swenson 2014). After each randomization, the functional and phylogenetic β-diversity was calculated across the entire agricultural gradient. These values were used to generate the null distribution. For each metric (i.e., βMPD and βMNTD) of functional and phylogenetic β-diversity, we calculated a standardized effect size as follows:

standardized effect size = (obsMetric − rndMetric)/sd.rndMetric where obsMetric is the observed value of β-diversity index, rndMetric the mean of the null distribution and sd.rnd the standard deviation of the null distribution (Gotelli and Graves 1996). Positive values indicate a higher than expected functional and phylogenetic β-diversity, meaning that each community generally contains distantly functional and/or distantly related species or individuals (Swenson et al 2011; Swenson 2014; González-Caro et al 2014). Negative values indicate a lower than expected functional and phylogenetic β-diversity, meaning that variation between the two communities occurs between closely functional and/or closely related species or individuals (Swenson et al 2011; Swenson 2014; González-Caro et al 2014). Non-random standardized effect size values could be produced by functionally and phylogenetic non-random variation of species along the gradient and/or functional and phylogenetic shifting directionally along the environmental gradient (Swenson et al 2011).

As for the taxonomic facet, functional and phylogenetic β-diversity metrics were calculated both based on the incidence and abundance-weighted versions. Although it is more common to use the incidence of species for β-diversity studies, the variation of the abundance distribution across communities brings important ecological information for analyses of community structure (Anderson et al 2011; Swenson 2014). Furthermore, β-diversity null modeling based on abundance data are more robust than that based on incidence to changes in certain processes (e.g., changes in assembly mechanism through time; Tucker et al 2016). Abundance data were square-root-transformed since normalized abundances reflect the role of each species in the ecosystem better than the raw data (Legendre and Legendre 2012) and allows rare species to contribute more to the overall (dis)similarity (Márquez and Kolasa 2013). When calculated βMNTD we maintained conspecific species shared between two communities (Swenson 2014). Functional and phylogenetic β-diversity metrics were estimated using ‘comdist’ and ‘comdistnt’ functions of ‘picante’ package (Kembel et al 2010) and null models were prepared according Swenson (2014). Both procedures were conducted using R statistical software (R Development Core Team 2014).

Analytical methods

Exploratory data analysis (box-plot and quantile-quantile plots) was used to assess predictor variables normality and the presence of outliers (See Fig. S2 for a schematic representation of the analysis procedure). We transformed non-normal predictor variables to make the frequencies of distributions as symmetric as possible, linearize the relationships, as well as to reduce the influence of outliers (Legendre and Legendre 2012; Table S2). The logit transformation was applied to the variables of proportion (Warton and Hui 2011). For variables in other units, square root transformation was used. Since strong collinearity can affect the ability to correctly estimate the regression parameters (Legendre and Legendre 2012), we checked strong linear dependencies among predictor variables, assessed separately within each scale, using the threshold Spearman's correlation (rho) ≥ 0.7 (Dormann et al. 2013). Since all values displayed rho < 0.7, all predictor variables were kept in the statistical analyses. Subsequently, predictor variables were standardized to zero mean and unit variance to be used in the successive analyzes.

For each β-diversity metric, we calculated the mean pairwise dissimilarity between each site and all other sites (Tobias and Monika 2011; Wang et al 2013). To verify whether the mean value of each β-diversity metric among sites was significantly different from expected value of zero for random data, we performed a series of one sample *t-test* ($P < 0.05$; Wang et al 2013). To examine variation in β-diversity for the three facets we used a distance-based approach (Tuomisto and Ruokolainen, 2006), where β-diversity was related to environmental and spatial distances among sampled communities. Environmental distance was measured as Euclidean distance using a subset of environmental variables best correlated (Pearson's correlation) with community β-diversity (Clarke and Ainsworth 1993) and selected with 'bioenv' function of 'vegan' package (Oksanen et al 2015). The subsets of environmental variables that had the maximum correlation with community β-diversity are listed in Table S4. The β-diversity metrics were regressed against environmental or stream network distances using a Gaussian generalized linear model (Wang et al 2013). To determine the significance in variation in β-diversity related to environmental and spatial distances, we used Mantel and partial Mantel tests (Pearson's correlation) with 10,000 permutations (Legendre and Legendre 2012). We used partial Mantel tests to compare the ability of environmental and spatial distances to explain the community β-diversity after accounting for each one (Legendre and Legendre 2012).

To determine the relative contributions of local-scale, catchment-scale and stream network distance on fish community β-diversity, we used the multiple regression on matrices (MRM) approach (Pearson's correlation with 10,000 permutations; Legendre et al 1994). To reduce the influence of spurious relationships between predictor variables (i.e., local-scale, catchment-scale and network distance), first we ran the MRM analysis, then removed the nonsignificant predictor variables, and lastly re-ran the MRM analysis (Martiny et al 2011). When the number of predictor variables was ≥ 2 we partitioned the variances of β-diversity metrics using commonality analysis (Prunier et al 2015). Commonality analysis allowed the partition of the coefficient of determination (R^2) into (i) the effects uniquely (*Unique*) explained by each predictor or predictor subset and (ii) the effects commonly (*Common*) explained by all possible combinations of predictors or predictor subsets (Sorice and Conner 2010; Ray-Mukherjee et al 2014). We also used beta, commonality and structure coefficients to gain a broader and fuller perspective on the contributions that each predictor variable made to the community β-diversity (Nathans et al 2012). As for the Mantel and partial Mantel tests, MRM and commonality analyses we only considered for the subset of environmental variables that had the maximum Pearson's correlation with community β-diversity (Table S4). For MRM analysis and estimations of beta coefficients we used 'MRM' function in 'ecodist' package (Goslee and Urban 2007); and for commonality analysis and structure coefficients we used 'regr' function of 'yhat' package (Nimon et al 2008). All the analyses were performed in R statistical software (R Development Core Team 2014).

Results

Overall, 51 fish species belonging to 17 families and six orders were sampled in the 43 stream reaches (Table S5). In seven of the 10 metrics analyzed, mean β-diversity values among sites were significantly different from the expected value of zero ($P < 0.05$; Fig.

2, Table S6). Of these, six metrics exhibited mean values greater than zero, indicating that fish communities were different from each other than expected by chance (Fig. 2). In contrast, taxonomic ses.β.RC$_{in}$ displayed mean values lower than zero, indicating communities more similar than expected by chance (Fig. 2). Mean values of phylogenetic ses.β.MPD$_{in}$, ses.β.MPD$_{ab}$ and ses.β.MNTD$_{ab}$ were not different from expected by chance (Fig. 2).

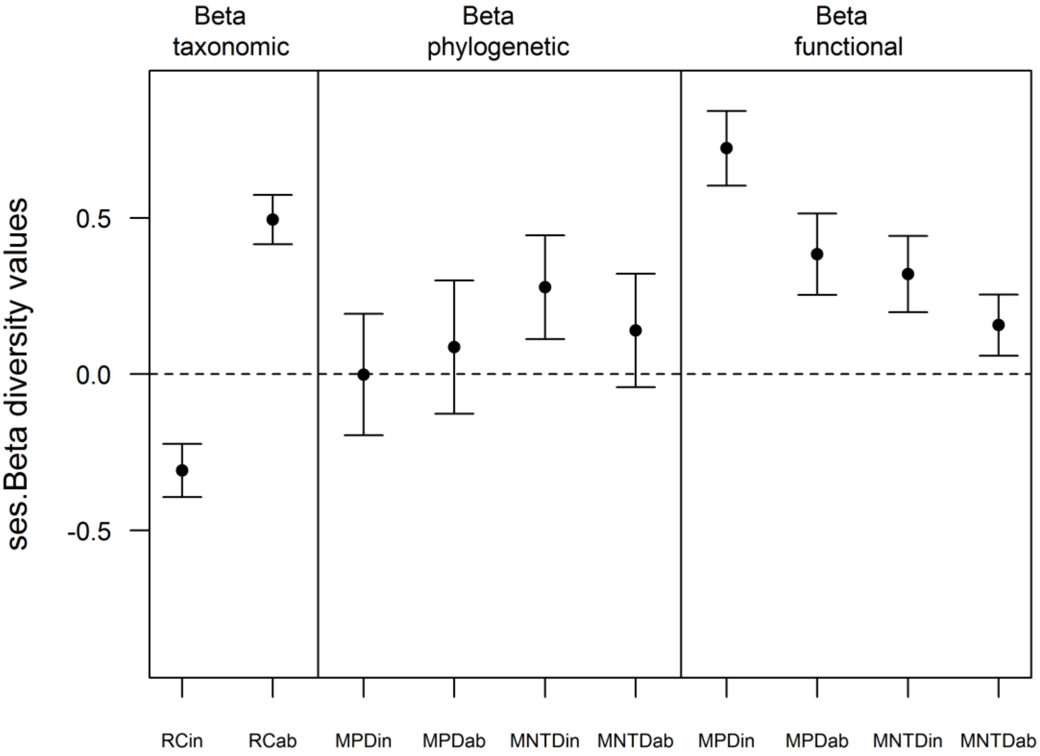


Figure 2. Mean values among sites of standardized effect sizes of each taxonomic, phylogenetic and functional β-diversity metrics and their 95% confidence intervals. Significant differences from expected value of zero for random data were assessed through a series of one sample *t-test* (*P* < 0.05; Table S6). RC = Raup-Crick; MPD = mean pairwise distance; MNTD = mean nearest taxon distance; subscripts ‘in’ and ‘ab’ denote metrics based on incidence or abundance, respectively.

Plots of pairwise β-diversity versus environmental distance indicated that there was a significant distance-decay relationship for all standardized effect size of the β-diversity metrics (Fig. S3, Table 1). Besides, after controlling for stream network distance, all standardized effect sizes of β-diversity metrics remained significantly correlated with environmental distance (partial Mantel test, r=0.155-0.379, *P*<0.05; Table 1). On the other hand, plots of distance-decay relationships between pairwise β-diversity and stream network distance were only significant for taxonomic ses.β.RC and functional ses.β.MNTD, for both abundance and incidence based metrics (Fig. S4, Table 1). Nevertheless, after controlling for environmental distance, stream network distance was only correlated significantly with ses.β.MNTD$_{in}$ (partial Mantel test, ρ=0.110, *P*<0.05; Table 1).

Table 1. Mantel and partial Mantel tests for the correlation between standardized effect size of β-diversity metrics and the predictor distances (environmental and network) using Pearson's correlation (ρ) with 10,000 permutations. In bold significant values: *** *P* < 0.001; ** *P* < 0.01; * *P* < 0.05.

β-diversity facet	Effect of environment	Effect of network	Effect of environment controlling for network	Effect of network controlling for environment
Taxonomic				
ses.β.RC$_{in}$	**0.384*** **	**0.153***	**0.363*** **	0.077
ses.β.RC$_{ab}$	**0.398*** **	**0.139** **	**0.379*** **	0.046
Phylogenetic				
ses.β.MPD$_{in}$	**0.249***	0.071	**0.239***	0.007
ses.β.MPD$_{ab}$	**0.253** **	0.122	**0.234***	0.075
ses.β.MNTD$_{in}$	**0.272*** **	-0.040	**0.286*** **	-0.102
ses.β.MNTD$_{ab}$	**0.265*** **	-0.052	**0.274*** **	-0.089
Functional				
ses.β.MPD$_{in}$	**0.165***	0.076	**0.155***	0.051
ses.β.MPD$_{ab}$	**0.257** **	0.011	**0.256** **	-0.009
ses.β.MNTD$_{in}$	**0.200** **	**0.139***	**0.181** **	**0.110***
ses.β.MNTD$_{ab}$	**0.268*** **	**0.090***	**0.263*** **	0.070

According to the MRM and commonality analyses, only local- and catchment-scale features explained the variation in community β-diversity; however, environmental-β-diversity relationship was mostly weak ($R^2 \leq 0.15$; $P < 0.05$; Fig. 3; Table S7). For all β-diversity metrics, pure local-scale features explained most of variance ($R^2 = 0.04$-0.10; $P < 0.05$) and presented the largest partial regression coefficients (b = 0.165-0.364, $P < 0.05$; Table S7). Moreover, pure catchment and landscape dynamical features were only significant for taxonomic ses.β.RC_{in} and phylogenetic ses.β.$MNTD_{in}$ (R^2 = 0.014 and 0.044; $P < 0.05$; Fig. 3; Table S7) and displayed smaller partial regression coefficients (β = 0.116-0.170, $P < 0.05$; Table S7). In both cases, shared variance was $R^2 \leq 0.01$ (Fig. 3; Table S7).

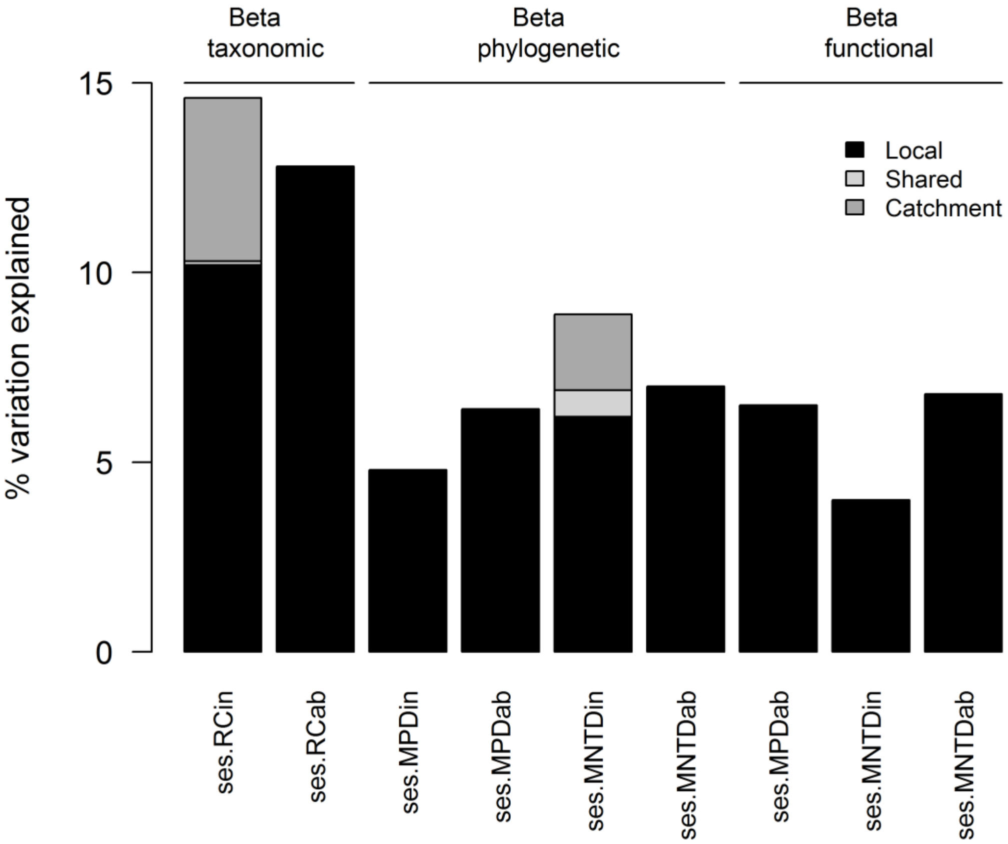


Figure 3. Explained variation in β-diversity metrics partitioned by MRM and associated commonality analysis into pure local, shared and pure catchment components. RC = Raup-Crick; MPD = mean pairwise distance; MNTD = mean nearest taxon distance; subscripts ‘in’ and ‘ab’ denote metrics based on incidence or abundance, respectively. Note that are the standardized effect size measures.

Discussion

In the present study, we analyzed β-diversity for three different facets (i.e., taxonomic, phylogenetic and functional) in an intensively cultivated tropical region, focusing on an agricultural transition from pasture to sugarcane. In general, we found that, for almost all β-diversity metrics (70%), mean values among sites were significantly different than expected by chance, indicating the prevalence of deterministic processes structuring stream fish β-diversity in agricultural landscapes (Chase et al 2011; Hawkins et al 2015; Püttker et al 2015; Tucker et al 2016); supporting our first hypothesis that taxonomic, functional and, partially, phylogenetic β-diversity is non-random. These deterministic processes are probably due to intensive agricultural practices imposing strong environmental filtering on stream fish communities, as observed in other aquatic communities under anthropogenic disturbance conditions (Villéger et al 2010; Wang et al 2013).

Nevertheless, excluding phylogenetic ses.β.$MNTD_{in}$, the phylogenetic β-diversity facet showed signs of stochastic processes across the agricultural gradient (Chase et al 2011; Püttker et al 2015), indicating that processes affecting phylogenetic β-diversity are mostly probabilistic and affected by randomness (Tucker et al 2016). In a broad sense, this suggests that although multiple facets of stream fish communities are ruled mainly by deterministic processes, stochastic processes are also substantial in community assembly. Indeed, it is expected that natural communities are structured by a combination of these two processes (Soininen et al 2007; Vellend et al 2014; Tucker et al 2016), including aquatic organisms under effect of anthropogenic disturbance (Wang et al 2013; Bini et al 2014).

An interesting finding was that not all β-diversity facets affected by deterministic processes exhibited the same pattern of variation in community composition. For instance, mean taxonomic ses.β.RC_{in} values indicated that fish communities were more similar to each other than expected by chance, whereas mean values of taxonomic ses.β.RC_{ab}, phylogenetic ses.β.$MNTD_{in}$ and functional metrics indicated fish communities were more different than expected by chance. This indicates that our second hypothesis that fish communities will be more similar than expected by randomness (Vellend et al 2007; Ekroos et al 2010; Karp et al 2012) was supported only by taxonomic β-diversity based on incidence data (ses.β.RC_{in}). Namely, from the perspective of the taxonomic facet (incidence based), our study suggests that in agricultural landscapes there is an increase of similarity in the stream fish community composition among sites leading to taxonomic homogenization (Ekroos et al 2010; Karp et al 2012; Püttker et al 2015; Siqueira et al 2015).

According to Rahel (2002), taxonomic homogenization of freshwater faunas results from the following interacting processes: introductions of non-native species, habitat alterations and extirpation of native species. The first two processes are clearly acting in our study area: introductions of non-native species, such as *Poecilia reticulata*, *Xiphophorus maculatus* (Poeciliidae), *Crenicichla semifasciata*, *Oreochromis niloticus* and *Tilapia rendalli* (Cichlidae), have been widely reported (Garutti 1988; Casatti et al 2009; Roa-Fuentes et al 2015b; this study), and habitat alterations, such as reduction of habitat heterogeneity and absence of riparian forest, are extensive (Casatti et al 2009; Zeni and Casatti 2014). Even though extirpations of native species are very plausible, there is no documentation of these in the studied drainage basin. Extirpations may be overlooked or underestimated because the first registers on the fish fauna in this region started in the 1980s (Garutti 1988), when habitats had already been transformed since a century ago (Victor et al 2005). It is not surprising that the most sensitive species to disturbance had already been extinct at this extent (Brook et al 2003).

When abundance data for the taxonomic facet (ses.β.RC_{ab}) was included, a different pattern emerged (i.e., communities were more different than expected by chance), indicating that species dominating each community differed between sites (Püttker et al 2015; Siqueira et al 2015). Evidence of this is that of the 51 species collected in the 43 streams, 14 different species (≈ 30%) were dominant in almost one site, for example, *Poecilia reticulata* (10 sites), *Imparfinis* cf. *schubarti* (1), *Astyanax altiparanae* (8), *Hypostomus ancistroides* (2), *Aspidoras fuscoguttatus* (7), *Moenkhausia sanctaefilomenae* (1), *Astyanax fasciatus* (1), *Characidium zebra* (1). This pattern may result from different non-mutually exclusive niche-based factors (Püttker et al 2015), such as inter-specific competition (Götzenberger et al 2012; Püttker et al 2015) or differential dispersal limitation among species (Gilbert and Lechowicz 2004; Püttker et al 2015). In addition, since species sorting is typically the main mechanism structuring stream communities (Heino et al 2015a; Carvalho and Tejerina-Garro 2015a; but see Saito et al 2015), mechanism that includes among its assumptions that the resource gradients or patch types generate differences in the local demography of species (Leibold et al 2004), it is expected that each site had unique levels of species abundances (Janzen and Schoener 1968; Tucker et al 2016).

Discordance between different facets of β-diversity has been previously reported, mainly in studies comparing taxonomic and functional facets (Tobias and Monika 2011; Sonnier et al 2014). For instance, in temperate forests, functional β-diversity unexpectedly remained constant through time (50 years), despite evident declines in taxonomic α- and β-diversity (measured as variation in composition among a set of communities), indicating that forest communities have experienced clear taxonomic but no functionally homogenization (Sonnier et al 2014). Similar results have also been reported for temperate herb layer communities (Tobias and Monika 2011). Among the reasons for discordance between different facets are: (i) changes in taxonomic and functional β-diversity are a priori independent of each other (e.g., a taxonomic homogenization could induce a functional differentiation if the species added to only one assemblage fill a unique portion of the functional space; Villéger et al 2014). And (ii) the species shifts that account for taxonomic similarity (i.e., homogenization) are distinct from those that account for variations in functional β-diversity (Tobias and Monika 2011 but see Pool and Olden 2012). The latter suggests that the effect of a particular species on multiple β-diversity facets (homogenizing or differentiating) is product of its: frequency of occurrence, variation in abundance, the commonness or rareness of trait values and the interactions between these variables (Tobias and Monika 2011). Accordingly, we attribute discordance between taxonomic (incidence data) and functional and, partially, phylogenetic β-diversity facets to the combined effect of environmental heterogeneity in individual stream reaches and to the contribution of rare and not co-occurring species that are functionally and/or phylogenetically ‘unique’ (i.e., species that contributed disproportionately to functional/phylogenetic β-diversity). On the one hand, individual sites with greater environmental heterogeneity can create distinct gradients of resource variability, resulting in the occurrence of very dissimilar functional groups (Willis et al 2005; Passy and Blanchet 2007; Montaña and Winemiller 2010) and also likely lead to evolutionarily distinct species. On the other hand, rare and not co-occurring species as *Pseudopimelodus mangurus, Pimelodella* cf. *avanhandavae, Apareiodon affinis, Parodon nasus* and/or *Apareiodon piracicabae* that are functionally dissimilar (located on the periphery of the functional space and dendrogram, see Figs. S5 and S6) possibly contribute disproportionately to generate a greater functional β-diversity, and it will be subject to further analysis.

Influence of environmental and spatial predictors

We observed increase of β-diversity among sites and some authors argued that this condition can result from strong dispersal limitation (Nekola and White 1999; Genner et al 2004; Soininen et al 2007), even in highly disturbed tropical environments (i.e., with 4% of remaining forest cover; Arroyo-Rodríguez et al. 2013). However, in our case, this is probably not the underlying reason because the stream network distance-β-diversity relationship and pure distance effect was weak or not significant. Another possibility is that high variation rates might be explained by pronounced environmental gradients because similarity decays with distance since of decreasing similarity in environmental characteristics (Soininen et al 2007; Wang et al 2008; Wang et al 2013). This explanation is more suited our findings since we found that, independent of the analytical method considered (i.e., Mantel and partial Mantel tests, slopes obtained from Gaussian generalized linear models or MRM analysis), all β-diversity metrics were positively correlated with environmental distance rather than with stream network distance. This result supports species-sorting mechanisms as the primary drivers of stream fish community structure. Species sorting mechanisms typically prevail in structuring aquatic communities, particularly in streams (Bini et al 2014; Heino et al 2015a; but see Saito et al 2015). Under these mechanisms, the resource gradients or patch types produce sufficiently strong dissimilarities in the local demography of species so that the species are filtered by environmental features to occur at environmentally suitable sites (Leibold et al 2004; Heino et al 2015a). In addition, local biotic interactions caused by patch quality and sufficient dispersal together affect local community composition (Leibold et al 2004).

Considering the relative importance of environmental variables measured at different spatial scales, the influence of pure local-scale features was always higher than pure catchment-scale features, including landscape dynamical indicators, whereas shared variance was always low. Considering variables measured at small spatial scales, Genner et al (2004) indicated that pure local environmental variables explained a small portion of the variation in cichlids β-diversity from Lake Malawi (≈6%). The same outcome has been described for tropical plants β-diversity (e.g., Tuomisto et al 2003). That is, independent of the assessed groups apparently the trend is that pure local environmental features explain little variation of β-diversity, but at the same time indicates that these have an important role in determining it (Genner et al 2004). This reasoning apparently does not apply for catchment-scale features, which had little or no influence on the different facets of β-diversity. For α-taxonomic facet of stream biota, previous studies have demonstrated that the past (i.e., decades ago) land cover in the catchment is a better predictor of biodiversity than current land cover in agricultural regions (Harding et al 1998; Surasinghe and Baldwin 2014). It is also possible that this reasoning also applies to β-diversity, but it remains to be fully explored. Additionally, since of the four land cover classes in our study area two were highly dominant (≈73%) - sugarcane (mean proportion = 0.38) and pasture (mean proportion = 0.35) – it is possible that catchment variables presented little variability and hence did not overwhelm the effect of local environmental variables on β-diversity. This is also suggested in cases of weak effects of catchment features on α-diversity of stream communities (e.g., Heino et al 2008; Casatti et al 2015; Chapter 1).

Catchment land cover and landscape dynamical indicators were generally not correlated with β-diversity metrics. We therefore suggest that the recent sugarcane expansion in São Paulo State (Rudorff et al 2010), and possible connected impacts as annual forest change rate (q index) and/or patterns of change of forest cover (FCCP index), probably have not critically affected stream fish β-diversity facets. This reasoning is in line with findings for freshwater communities of lentic systems where the conversion of pastures to sugarcane fields apparently did not affect α-diversity (Schiesari and Corrêa 2016). Although it is possible that the sugarcane plantations do not represent a different environmental filter than pastures, under the conditions of this study, it is also likely that this has not been noticed due to one of the following factors or by their interactions:

(i) due to the relatively recent expansion of sugarcane to the region the effects are not yet detectable; (ii) trade regulation for sugarcane demands some sustainable rules regarding forests protection (Goldemberg et al 2008), contrary than pasture or other crops; and (iii) the effects of sugarcane may be more pronounced in the rainy season. The latter because episodic runoff events, more frequently in the rainy season, represent a major input path for agrochemicals in small streams situated in agricultural matrices (Liess and Von Der Ohe 2005; Beketov et al 2013).

Rather weak relationship between environmental distance and β-diversity may also indicate that the pronounced agriculture-related environmental gradient is not the main driver of higher variation among sites. It is possible that *unmeasured* environmental variables are governing variation in community composition (Wang et al 2013) or that environmental heterogeneity between sites was not quantified as perceived by the organisms of interest (Heino et al 2013). We believe, however, that this would not be so in our case since (i) the partial Mantel coefficients related to network distance were non-significant for 9 of the 10 metrics, suggesting that *unmeasured* spatially-structured environmental variables have little influence over community composition (see Wang et al 2013 for details), and (ii) we measured environmental factors known to influence α-diversity (Montaña and Winemiller 2010; Carvalho and Tejerina-Garro 2015b; Cruz et al 2013) and β-diversity components (Genner et al 2004) of tropical freshwater fish communities. Thereby, weak environmental-β-diversity relationship might rather indicate that other processes and factors might also be controlling community β-diversity (Heino et al 2013; Bini et al 2014). For instance, randomness related to frequent flood disturbances, a typical event in streams of the study area (Marques et al 2013) and streams in general (Heino et al 2013), or other environmental disturbance (e.g., high pesticides concentration, increased water temperatures, low oxygen concentrations) that lead to strong priority effects, direct mortality or temporary extinctions of some species from a stream reach (Heino et al 2013; Hawkins et al 2015). This again emphasizes the importance of stochastic events to assembly processes in the studied stream fish communities.

Management implications

In tropical agroecosystems, β-diversity patterns in all of its facets are largely unknown (Karp et al 2012; Fugère et al 2016). Furthermore, according to Fugère et al (2016), the effects of environmental disturbance on β-diversity in streams are much more difficult to predict because there is scarce empirical evidence, and competing theories suggests opposite responses (e.g., stochasticity in community assembly could lead to high β-diversity; Chase 2010). However, our study has clear implications for protection of regional fish diversity and would be integrated into stream management in different ways, for example, indicating which key environmental features must be restored or preserved (Socolar et al 2016). Specifically, since variation in community composition were explained mainly by local-scale environmental gradient conservation schemes would ideally attempt to protect enough sites to capture this entire gradient (Gutiérrez-Cánovas et al 2013). Furthermore, because rare species that are functionally and/or phylogenetically ‘unique’ possibly contributed disproportionately to the functional/phylogenetic dissimilarity among sites this group of species deserve special attention for conservation. Rare species are more susceptible to extinctions, at least locally, and in our study area its loss would signify a loss of functional traits that contribute exceptionally to the maintenance of ecosystem functioning and resulting in a substantial loss of evolutionary information (Mouillot et al 2013; Winter et al 2013).

In conclusion, our study stresses the previous suggestions that much remains to be known about β-diversity patterns in tropical streams environments. Also, our results highlight the importance to incorporate multiple facets in biodiversity assessments because changes in one facet do not necessarily represent changes in the same direction in the other facets. This indicates that one facet cannot be used as a proxy for the other as has already been suggested in other studies (Higgins 2010; Tobias and Monika 2011; Villéger et al 2014). This suggestion is also true in the case in tropical streams fish communities in human-modified landscapes, where understanding biodiversity and community assembly certainly benefited from the multi-facet approach.

Supplementary material

Tables

Table S1. Description of land cover classes.

Land cover class	**Description**
Native forest	Areas occupied by the different native forest found in the study area (i.e., Savanna and Semi-deciduous seasonal forest).
Herbaceous and shrub vegetation	Areas occupied by herbaceous and shrub vegetation, which also included species of cattail (*Typha* spp.).
Pasture	Areas used for intensive and extensive livestock, also including areas covered by native grasses but to a lesser extent.
Sugarcane	Areas covered with sugarcane culture (*Saccharum* spp.) or that showed evidences of being used for this culture.
Perennial culture	Areas covered with perennial cultures (e.g., *Citrus* spp., *Hevea* spp., *Coffea* spp.).
Reforestation	Included planted forests and restored areas with *Eucalyptus* spp. or *Pinus* spp..
Urban area	Include towns and villages.
Other land cover	It groups rural installations, temporary cultures, highways and exposed soil.

Table S2. Predictor variables measured at the 43 sampling sites, Turvo-Grande and São José dos Dourados River basins at the northwest region of São Paulo State, southeastern Brazil.

Category	**Variable**	**Unit**	**Transformation**	**Code**
	Catchment-scale variables			
Entire catchment	Native forest	proportion	logit	Cfor
	Pasture	proportion	logit	Cpas
	Sugarcane	proportion	logit	Csug
	Other land cover	proportion	logit	Coth
Landscape dynamic indicators	Mean annual forest change rate	-	-	q
	Forest change curvature profile	-	-	FCCP
	Local-scale variables			
Stream physical habitat condition	Physical Habitat Index	absolute value	square root	phi
Mesohabitat	Pool	proportion	logit	pool
Physicochemical descriptors	Water temperature	°C	square root	tem
Substratum	Unconsolidated substrate: clay, silt and sand	proportion	logit	usu
Stream morphology	Mean width	m	square root	wid
	Standard deviation of width	-	-	widSD
	Mean depth	m	square root	dep
	Mean water velocity	m/s	square root	vel
	Standard deviation of water velocity	-	-	velSD
Marginal vegetation	Grasses (mostly *Brachiaria* spp.)	proportion	logit	gra

Table S3. Traits used for the description of each fish species. Trait type codes: Nominal (N); Quantitative (Q); Ordinal (O).

Traits	Statistical type	Attributes
Compression index (CI)	Q	MBD/MBW
Relative area of pectoral fin (RAPF)	Q	PFA/BA
Pectoral fin aspect ratio (PFAR)	Q	LPF/WPF
Relative eye position (REP)	Q	DEM/HD
Relative depth (RD)	Q	MBD/SL
Index of ventral flattening (IVF)	Q	MMD/MBD
Fineness coefficient (FC)	Q	$\frac{SL}{\sqrt{\text{MBD x MBW}}}$
Trophic guild	O	1 = Algivores; 2 = Detritivores; 3 = Aquatic insectivores; 4 = Terrestrial insectivores; 5 = Lepidophagous; 6 = Periphytivores; 7 = Piscivores; 8 = Omnivores
Size	O	1 = 1 - 50 mm standard length (SL); 2 = 51-100mm SL; 3 = > 101 mm SL
Preference for substrate	N	0 = Unconsolidated; 1 = Consolidated
Preference for water velocity	O	0 = Low; 1 = Medium; 2 = Fast
Adaptation to anoxic conditions	N	0 = No; 1 = Yes

Codes for morphological measurements: BA: body area; DEM: depth of the eye midline; HD: head depth; LPF: maximum length of pectoral fin; MBD: maximum body depth; MBW: maximum body width; MMD: maximum midline depth; PFA: pectoral fin area; SL: standard length; WPF: maximum width of pectoral fin.

Table S4. Subsets of environmental variables best correlated (Pearson's correlation (r)) with stream fish β-diversity. Selection was performed using 'bioenv' function of 'vegan' package (Oksanen et al 2015). For selected variables codes see Table S2.

	Selected variables	r
Taxonomic		
ses.β.RC_{in}	pool, gra, tem, vel, velSD, Q, FCCP	0.384
ses.β.RC_{ab}	pool, usu, tem, dep, vel, Q	0.397
Phylogenetic		
ses.β.MPD_{in}	tem, dep, Q	0.249
ses.β.MPD_{ab}	phi, tem, dep	0.253
ses.β.$MNTD_{in}$	phi, dep, Cpas	0.272
ses.β.$MNTD_{ab}$	phi, dep	0.265
Functional		
ses.β.MPD_{in}	gra, phi, tem, vel, Cfor	0.165
ses.β.MPD_{ab}	usu, gra, phi, vel, Cfor	0.257
ses.β.$MNTD_{in}$	phi, tem, vel	0.200
ses.β.$MNTD_{ab}$	gra, phi, vel, Coth	0.268

Table S5. Fish species sampled in the 43 stream reaches. In bold, species and family that were not sampled in the 43 stream reaches mentioned in this chapter but that were recorded for the same study area in 2013 (for details see Chapter 1).

Order and families, species and authors	Codes
Characiformes	
Parodontidae	
Apareiodon affinis (Steindachner 1879)	Apaaff
Apareiodon piracicabae (Eigenmann 1907)	Apapir
Parodon nasus Kner 1859	Parnas
Curimatidae	
Cyphocharax vanderi (Britski 1980)	Cypvan
Steindachnerina insculpta **(Fernández-Yépez 1948)**	**Steins**
Anostomidae	
Leporinus friderici **(Bloch 1794)**	**Lepfri**
Leporinus lacustris **Amaral Campos 1945**	**Leplac**
Crenuchidae	
Characidium gomesi Travassos 1956	Chagom
Characidium zebra Eigenmann 1909	Chazeb
Characidae	
Astyanax altiparanae Garutti & Britski 2000	Astalt
Astyanax fasciatus (Cuvier 1819)	Astfas
Astyanax paranae Eigenmann 1914	Astpar
Astyanax schubarti **Britski 1964**	**Astsch**
Bryconamericus stramineus **Eigenmann 1908**	**Brystr**
Hasemania sp.	Hassp
Hemigrammus marginatus Ellis 1911	Hemmar
Hyphessobrycon anisitsi **(Eigenmann 1907)**	**Hypani**
Hyphessobrycon eques (Steindachner 1882)	Hypequ
Knodus moenkhausii (Eigenmann & Kennedy 1903)	Knomoe
Moenkhausia sanctaefilomenae (Steindachner 1907)	Moesan
Oligosarcus pintoi Amaral Campos 1945	Olipin
Piabina argentea Reinhardt 1867	Piaarg
Planaltina britskii Menezes, Weitzman & Burns 2003	Plabri

Order and families, species and authors	Codes
***Roeboides descalvadensis* Fowler 1932**	**Roedes**
Serrapinnus heterodon (Eigenmann 1915)	Serhet
Serrapinnus notomelas (Eigenmann 1915)	Sernot
Acestrorhynchidae	
Acestrorhynchus lacustris (Lütken 1875)	Acelac
Erythrinidae	
Erythrinus erythrinus (Bloch & Schneider 1801)	Eryery
Hoplias malabaricus (Bloch 1794)	Hopmal
Lebiasinidae	
Pyrrhulina australis Eigenmann & Kennedy 1903	Pyraus
Siluriformes	
Callichthyidae	
Aspidoras fuscoguttatus Nijssen & Isbrücker 1976	Aspfus
Callichthys callichthys (Linnaeus 1758)	Calcal
Corydoras aeneus (Gill 1858)	Coraen
Hoplosternum littorale (Hancock 1828)	Hoplit
Lepthoplosternum pectorale (Boulenger 1895)	Leppec
Megalechis thoracata (Valenciennes 1840)	Megtho
Loricariidae	
Hisonotus francirochai (Ihering 1928)	Hisfra
Hypostomus ancistroides (Ihering 1911)	Hypanc
Hypostomus cf. *nigromaculatus* (Schubart 1964)	Hypnig
Pterygoplichthys ambrosettii (Holmberg 1893)	Pteamb
Pseudopimelodidae	
Pseudopimelodus mangurus (Valenciennes 1835)	Pseman
***Pseudopimelodus pulcher* (Boulenger 1887)**	**Psepul**
Heptapteridae	
***Cetopsorhamdia iheringi* Schubart & Gomes 1959**	**Cetihe**
Imparfinis cf. *schubarti* (Gomes, 1956)	Impsch
Pimelodella cf. *avanhandavae* Eigenmann 1917	Pimava
Rhamdia quelen (Quoy & Gaimard 1824)	Rhaque
Gymnotiformes	

Order and families, species and authors	Codes
Gymnotidae	
***Gymnotus inaequilabiatus* (Valenciennes 1839)**	**Gymina**
Gymnotus paraguensis Albert & Crampton 2003	Gympar
Gymnotus cf. *sylvius* Albert & Fernandes-Matioli 1999	Gymsyl
Sternopygidae	
Eigenmannia trilineata López & Castello 1966	Eigtri
Cyprinodontiformes	
Rivulidae	
Melanorivulus pictus (Costa 1989)	Melpic
Poeciliidae	
Phalloceros harpagos Lucinda 2008	Phahar
Poecilia reticulata Peters 1859	Poeret
***Xiphophorus maculatus* (Günther 1866)**	**Xipmac**
Synbranchiformes	
Synbranchidae	
Synbranchus marmoratus Bloch 1795	Synmar
Perciformes	
Cichlidae	
Cichlasoma paranaense Kullander 1983	Cicpar
Crenicichla britskii Kullander 1982	Crebri
Crenicichla haroldoi Luengo & Britski 1974	Crehar
***Crenicichla semifasciata* (Heckel 1840)**	**Cresem**
Geophagus brasiliensis (Quoy & Gaimard 1824)	Geobra
Laetacara araguaiae Ottoni & Costa 2009	Laeara
Oreochromis niloticus (Linnaeus 1758)	Orenil
Satanoperca pappaterra (Heckel 1840)	Satpap

Table S6. Mean values of taxonomic, phylogenetic and functional β-diversity metrics among sites. Significant differences from expected value of zero for random data were assessed through a series of one sample *t-test* ($P < 0.05$).

	Mean	95% confidence interval		*t*	df	*P*
		Lower	Upper			
Taxonomic						
$ses.\beta.RC_{in}$	-0.31	-0.39	-0.22	-7.32	42	< 0.001
$ses.\beta.RC_{ab}$	0.49	0.42	0.57	12.60	42	< 0.001
Phylogenetic						
$ses.\beta.MPD_{in}$	0.00	-0.20	0.19	-0.01	42	0.990
$ses.\beta.MPD_{ab}$	0.09	-0.13	0.30	0.82	42	0.416
$ses.\beta.MNTD_{in}$	0.28	0.11	0.44	3.37	42	0.002
$ses.\beta.MNTD_{ab}$	0.14	-0.04	0.32	1.56	42	0.127
Functional						
$ses.\beta.MPD_{in}$	0.72	0.60	0.84	12.23	42	< 0.001
$ses.\beta.MPD_{ab}$	0.38	0.25	0.51	5.95	42	< 0.001
$ses.\beta.MNTD_{in}$	0.32	0.20	0.44	5.29	42	< 0.001
$ses.\beta.MNTD_{ab}$	0.16	0.06	0.25	3.24	42	0.002

Table S7. Relative importance of environmental features, grouped as local-scale and catchment-scale, on fish β-diversity. This table includes multiple R^2, P-value (*P*), beta coefficients (β), structure coefficients (r_s), each predictor's total unique (U), total common (C), and total variance (Total) in the regression equation. When the number of regressors was < 2 commonality analysis was not conducted. Note that only environmental features best correlated with fish β-diversity (see Table S4), grouped as local-scale and catchment-scale, are used as predictor variables.

					Commonality analysis*		
β-diversity facet	Scale	β	*P*	r_s	U	C	Total
Taxonomic							
ses.β.RC_{in} (R^2=0.15; P<0.001)	Local	0.165	<0.001	0.837	0.103	-0.001	0.10
	Catchment	0.116	0.010	0.544	0.044	-0.001	0.04
ses.β.RC_{ab} (R^2=0.13; P<0.001)	Local	0.218	<0.001	-	-	-	0.13
Phylogenetic							
ses.β.MPD_{in} (R^2=0.05; P=0.035)	Local	0.227	0.035	-	-	-	0.05
ses.β.MPD_{ab} (R^2=0.06; P=0.008)	Local	0.291	0.008	-	-	-	0.06
ses.β.$MNTD_{in}$ (R^2=0.08; P<0.001)	Local	0.315	<0.001	0.906	0.056	0.007	0.06
	Catchment	0.170	0.006	0.517	0.014	0.007	0.02
ses.β.$MNTD_{ab}$ (R^2=0.07; P<0.001)	Local	0.364	<0.001	-	-	-	0.07
Functional							
ses.β.MPD_{ab} (R^2=0.07; P<0.001)	Local	0.209	<0.001	-	-	-	0.07

β-diversity facet	Scale	β	*P*	r_s	Commonality analysis* U	Commonality analysis* C	Total
ses.β.MNTD$_{in}$ (R^2=0.04; *P*=0.002)	Local	0.198	0.002	-	-	-	0.04
ses.β.MNTD$_{ab}$ (R^2=0.07; *P*<0.001)	Local	0.222	<0.001	-	-	-	0.07

*Unique effects (U) represent the amount of variance in the response variable that is uniquely accounted for by a single explanatory variable. Common effects (C) represent the amount of variance in the response variable that can be jointly explained by two or more predictors together. Total (Total = (U + C)) represents the total contribution of a predictor to the response variable irrespective of collinearity with other variables (Prunier et al 2015).

Figures

Figure S1. Composite phylogeny for 63 stream fish species (i.e., including species collected in other 42 different catchments localized in the same basins, for details see Chapter 1). For species codes see Table S5.

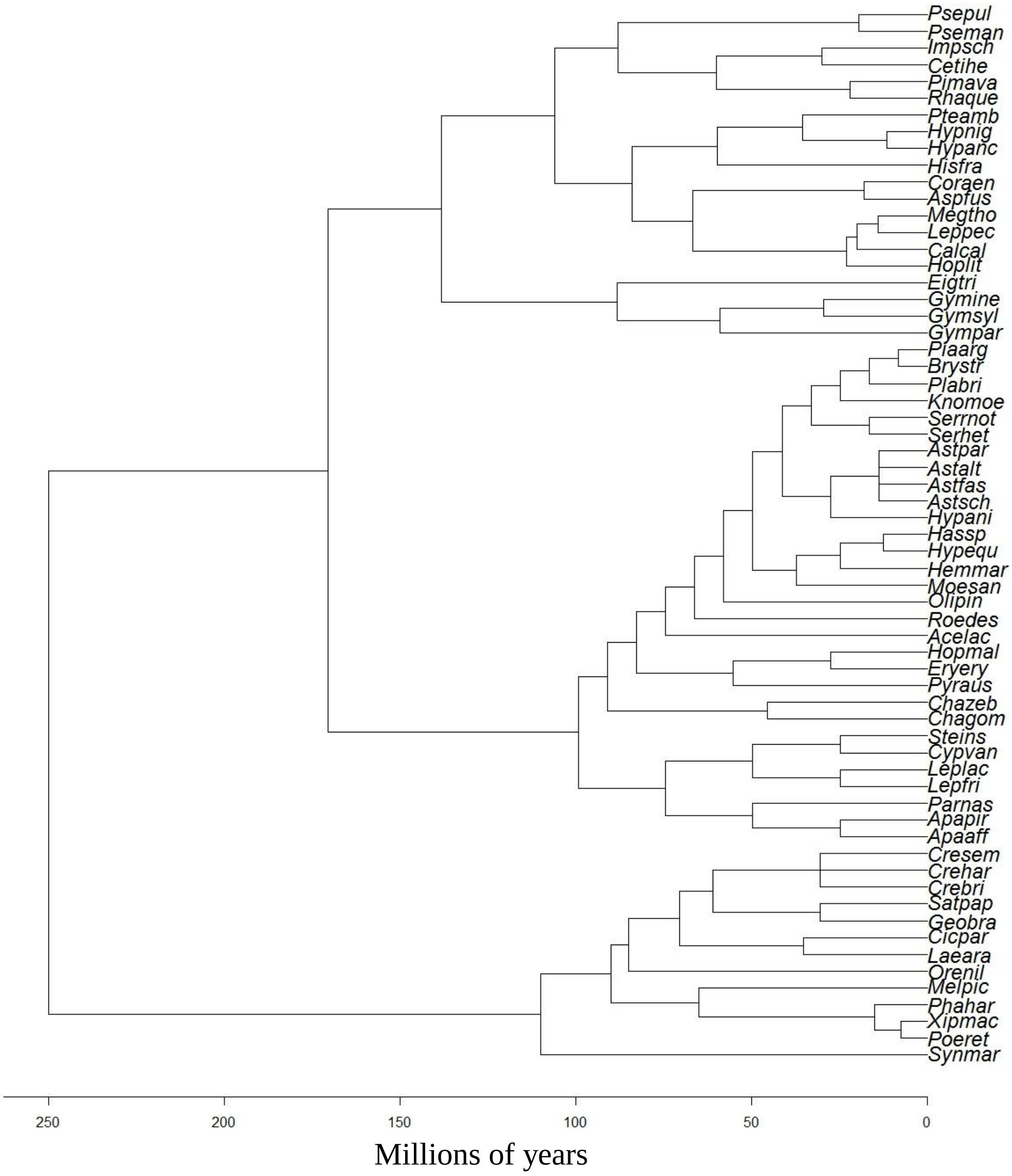


Figure S2. Schematic representation of the analysis procedure. For details see the main text.

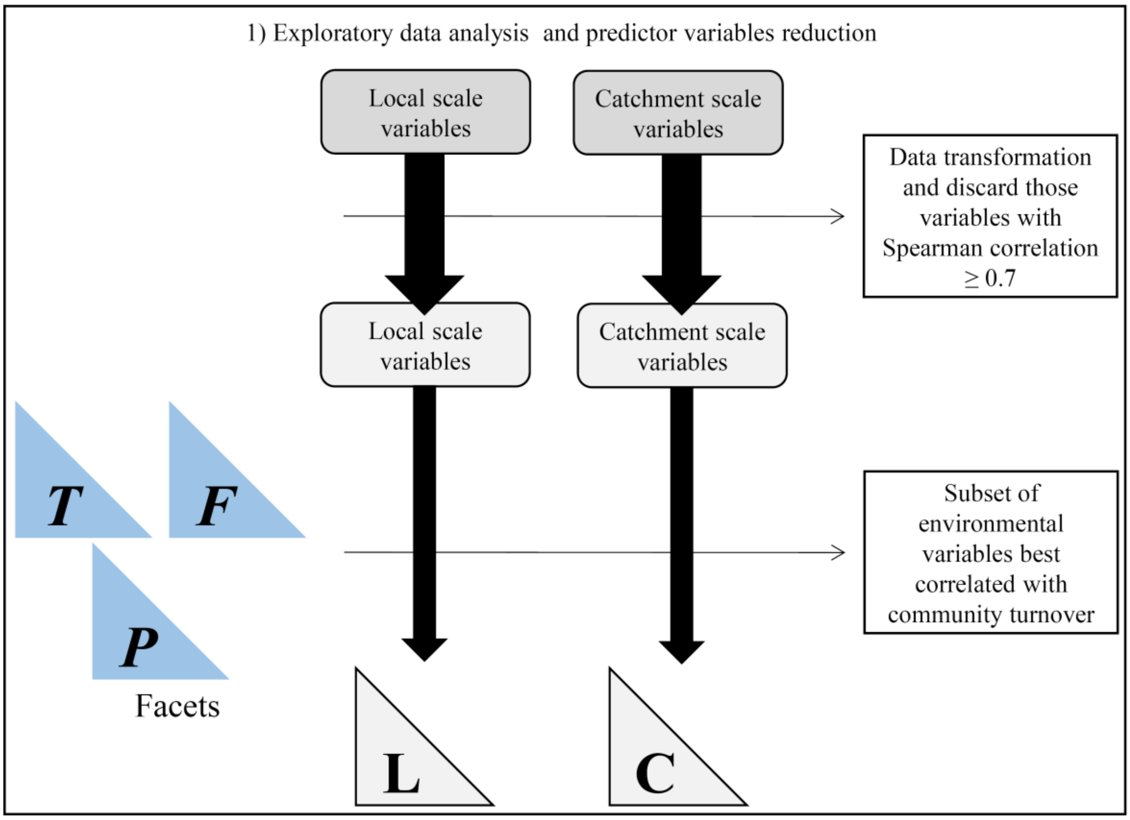


Figure S2 (continue)**.** Schematic representation of the analysis procedure. For details see the main text.

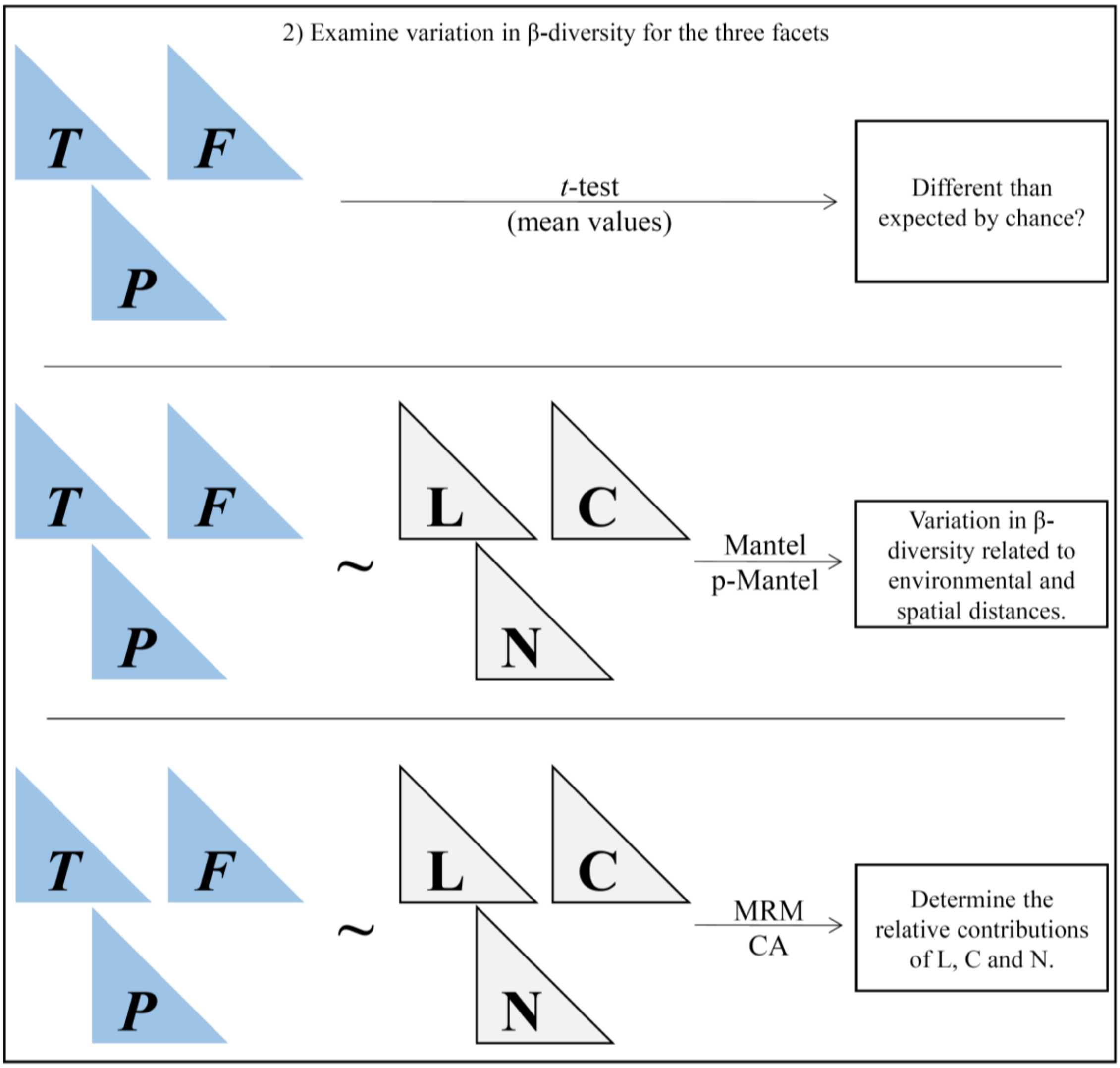
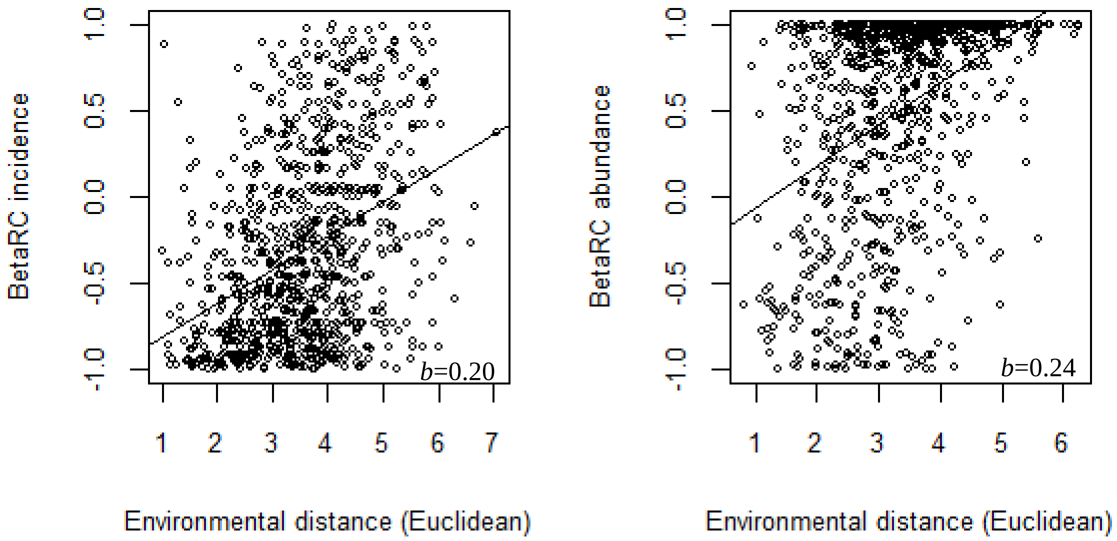
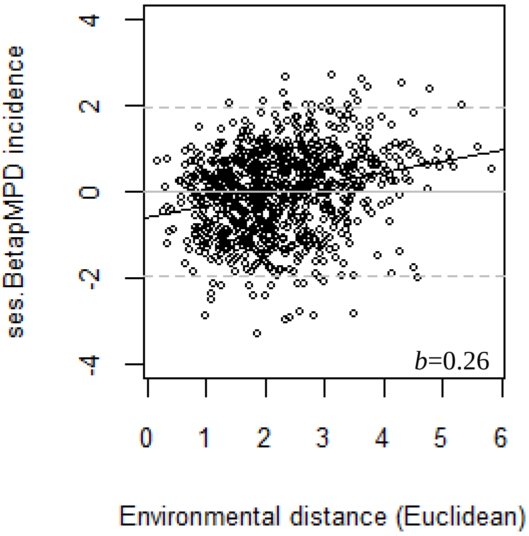


Figure S3. Relationship between pairwise β-diversity and environmental distance. All regression slopes (*b*) of the linear relationships are based on Gaussian generalized model were significant (Mantel test, Pearson's correlation, 10,000 permutations, $P < 0.05$). Slopes (*b*) are shown in each β-diversity metric panel. Detailed Mantel statistics are shown in Table 1. For phylogenetic and functional β-diversity metrics, the dotted gray line (>+1.96 or <-1.96) represents the 95% confidence intervals around the expectation under a null model.

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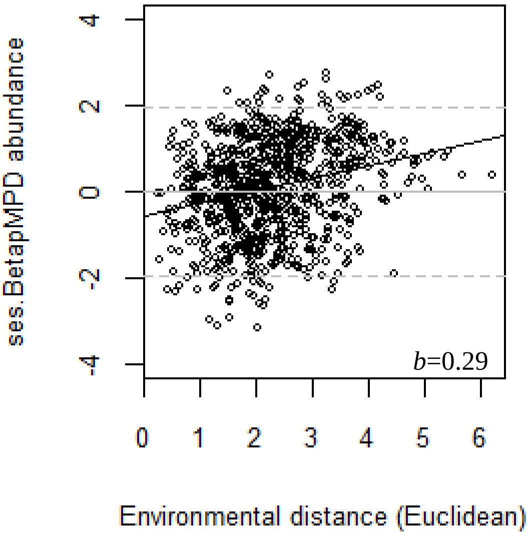
4
2
0
-2
-4
b=0.26
0
1
2
3
4
5
6
Environmental distance (Euclidean)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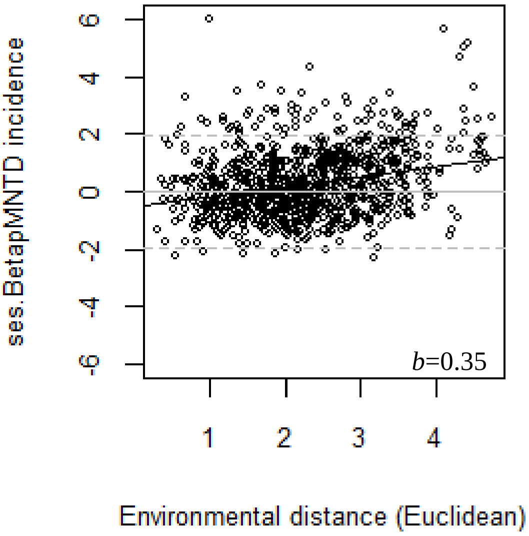
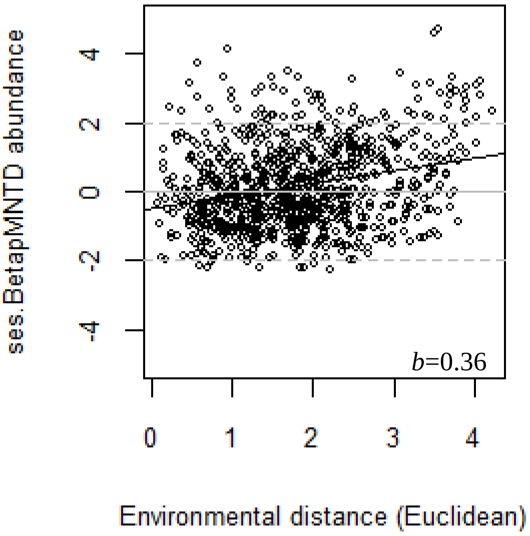
2
0
-2
-4
b=0.29
0
1
2
3
4
5
6
Environmental distance (Euclidean)


ses.BetapMNTD incidence
6
4
2
0
-2
-4
-6
b=0.35
1
2
3
4
Environmental distance (Euclidean)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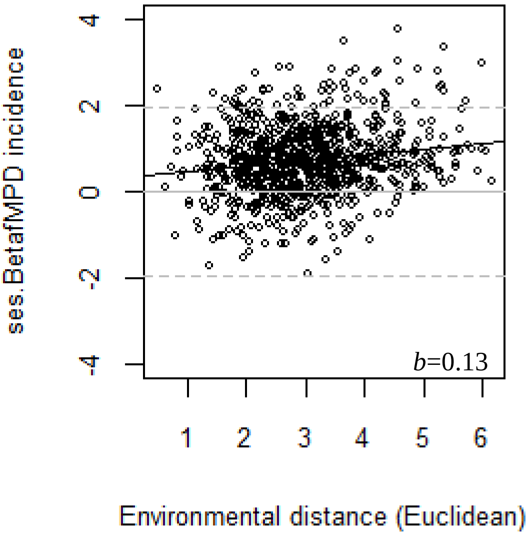
0
-2
-4
b=0.36
0
1
2
3
4
Environmental distance (Euclidean)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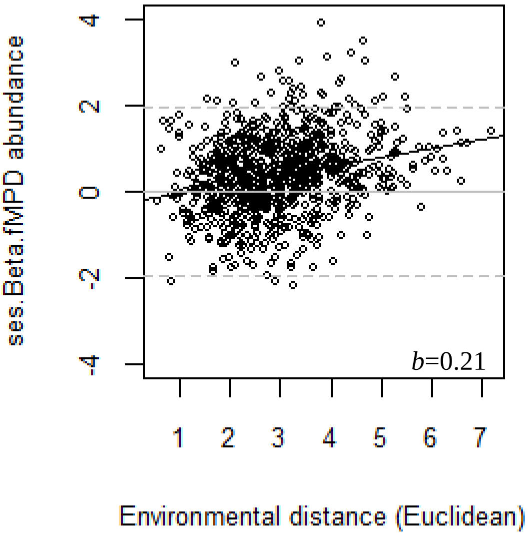
2
0
-2
-4
b=0.13
1
2
3
4
5
6
Environmental distance (Euclidean)


ses.Beta.fMPD abundance
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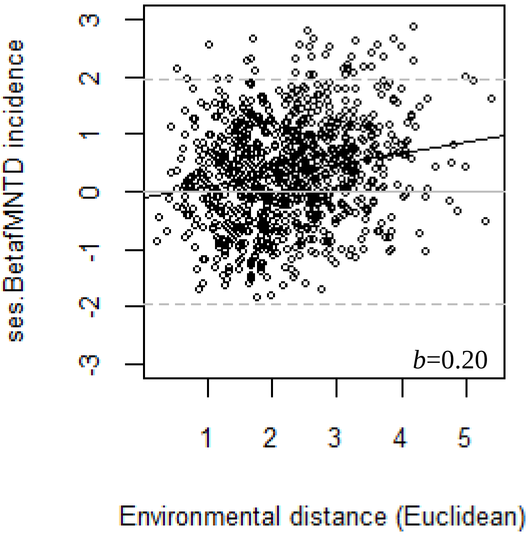
2
0
-2
-4
b=0.21
1
2
3
4
5
6
7
Environmental distance (Euclidean)


ses.BetafMNTD incidence
3
2
1
0
-1
-2
-3
b=0.20
1
2
3
4
5
Environmental distance (Euclidean)

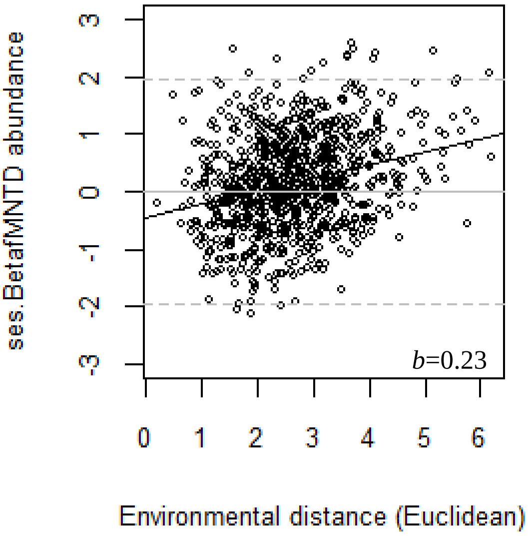
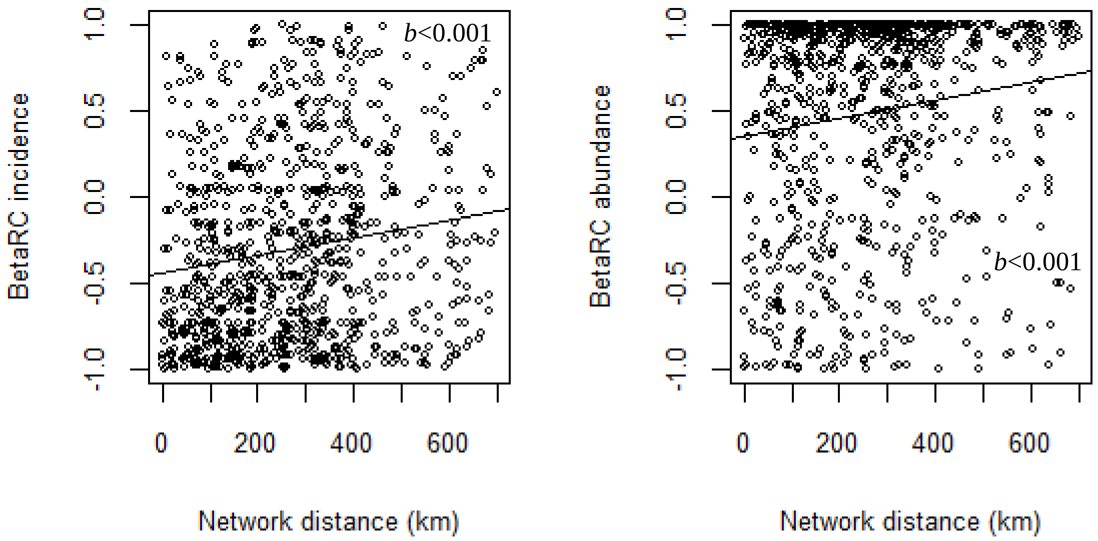
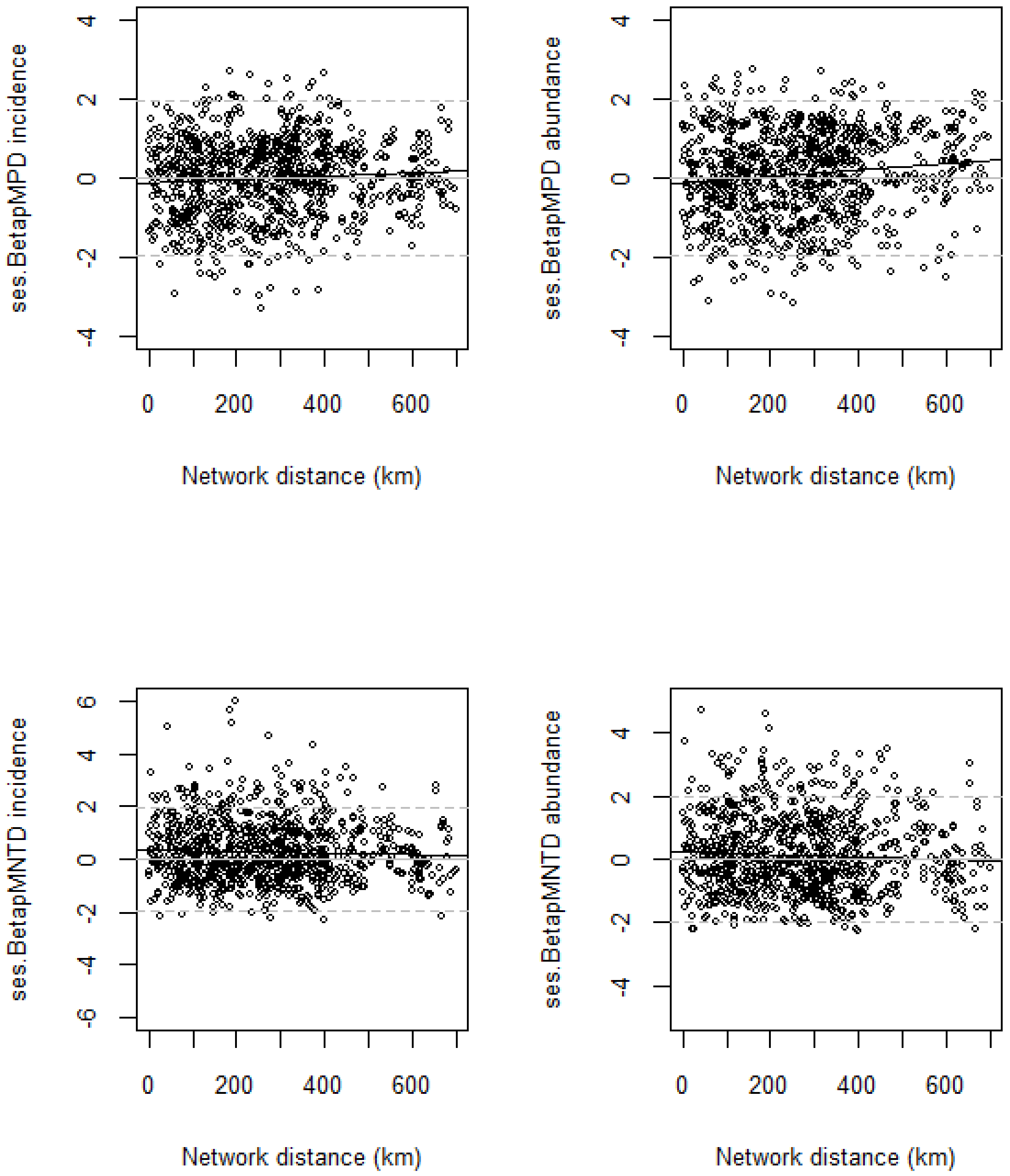
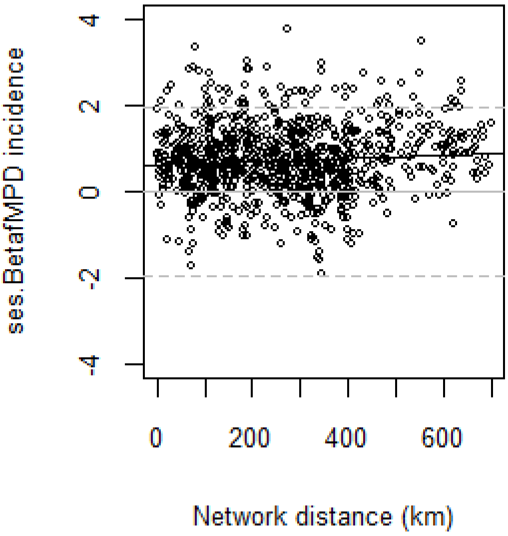
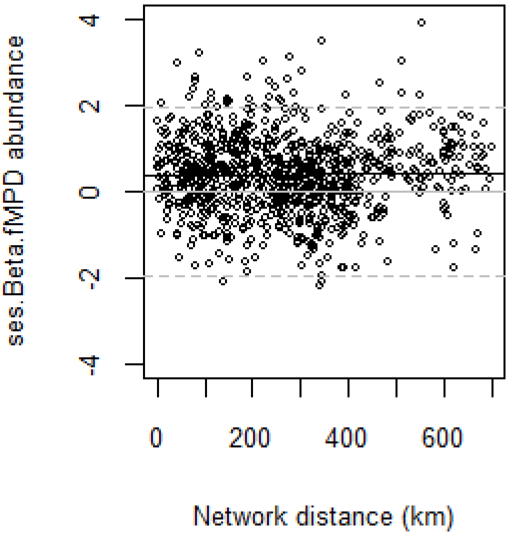

ses.BetafMNTD abundance
3
2
1
0
-1
-2
-3
b=0.23
0
1
2
3
4
5
6
Environmental distance (Euclidean)

Figure S4. Relationships between pairwise β-diversity and stream network distance. All regression slopes (*b*) of the linear relationships based on Gaussian generalized model. The significant slopes (*b*) are shown in each β-diversity metric panel (Mantel test, Pearson's correlation, 10,000 permutations, *P* < 0.05). Detailed Mantel statistics are shown in Table 1. For phylogenetic and functional β-diversity metrics, the dotted gray line (>+1.96 or <-1.96) represents the 95% confidence intervals around the expectation under a null model.




ses.BetapMPD incidence
ses.BetapMPD abundance
ses.BetapMNTD incidence
ses.BetapMNTD abundance
-6
-4
-2
0
2
4
6
0
200
400
600
Network distance (km)


ses.BetafMPD incidence
4
2
0
-2
-4
0
200
400
600
Network distance (km)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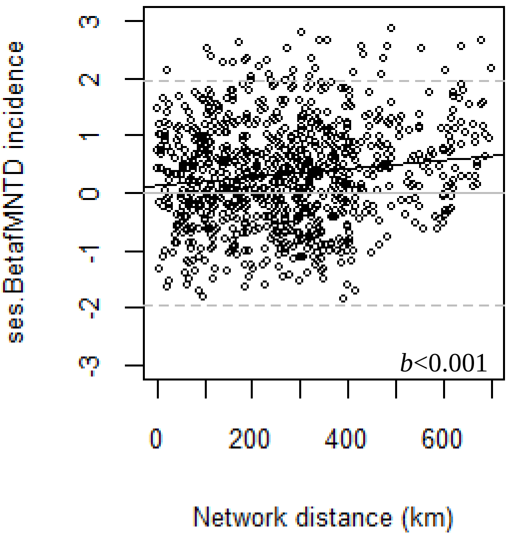
4
2
0
-2
-4
0
200
400
600
Network distance (km)


ses.BetafMNTD incidence
3
2
1
0
-1
-2
-3
b<0.001
0
200
400
600
Network distance (km)

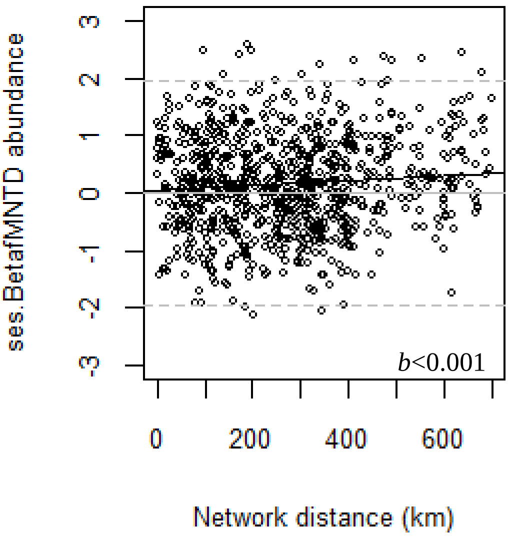

ses.BetafMNTD abundance
3
2
1
0
-1
-2
-3
b<0.001
0
200
400
600
Network distance (km)

Figure S5. Principal coordinates analysis (PCoA) representing functional distance among species. Note that rare species as *Pseudopimelodus mangurus* (Pseman), *Pimelodella* cf. *avanhandavae* (Pimava), *Apareiodon affinis* (Apaaff), *Parodon nasus* (Parnas) and/or *Apareiodon piracicabae* (Apapir) are functionally dissimilar (located on the periphery of the functional space) and possibly contribute disproportionately to functional β-diversity. For species codes see Table S5.

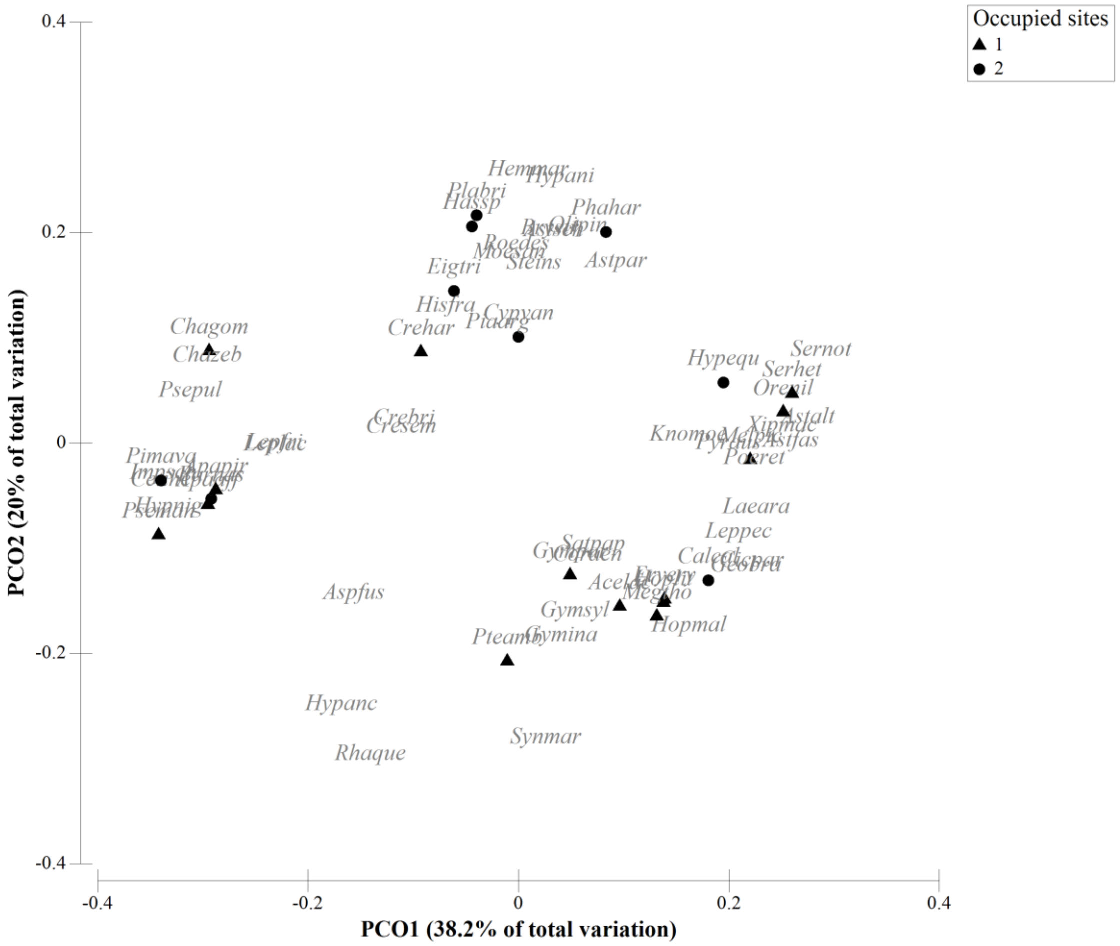
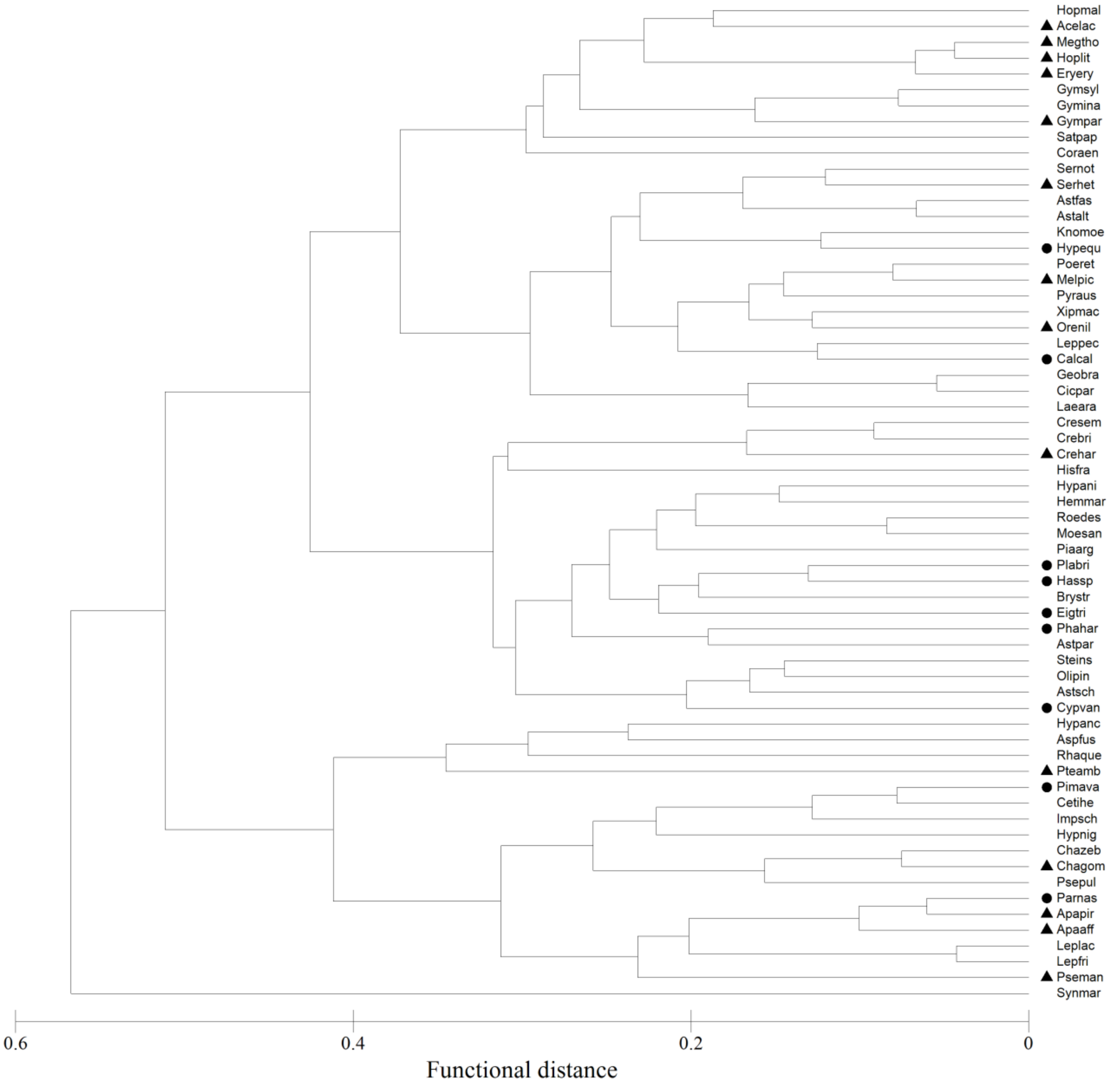


Figure S6. Dendrogram representing functional distance among species. Species that occurred in a site are identified by triangle; species that occurred at two sites are identified by circle. Note that rare species as *Pseudopimelodus mangurus* (Pseman), *Pimelodella* cf. *avanhandavae* (Pimava), *Apareiodon affinis* (Apaaff), *Parodon nasus* (Parnas) and/or *Apareiodon piracicabae* (Apapir) are functionally dissimilar (located on the periphery of the functional dendrogram) and possibly contribute disproportionately to functional β-diversity. For species codes see Table S5.



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SYNTHESIS

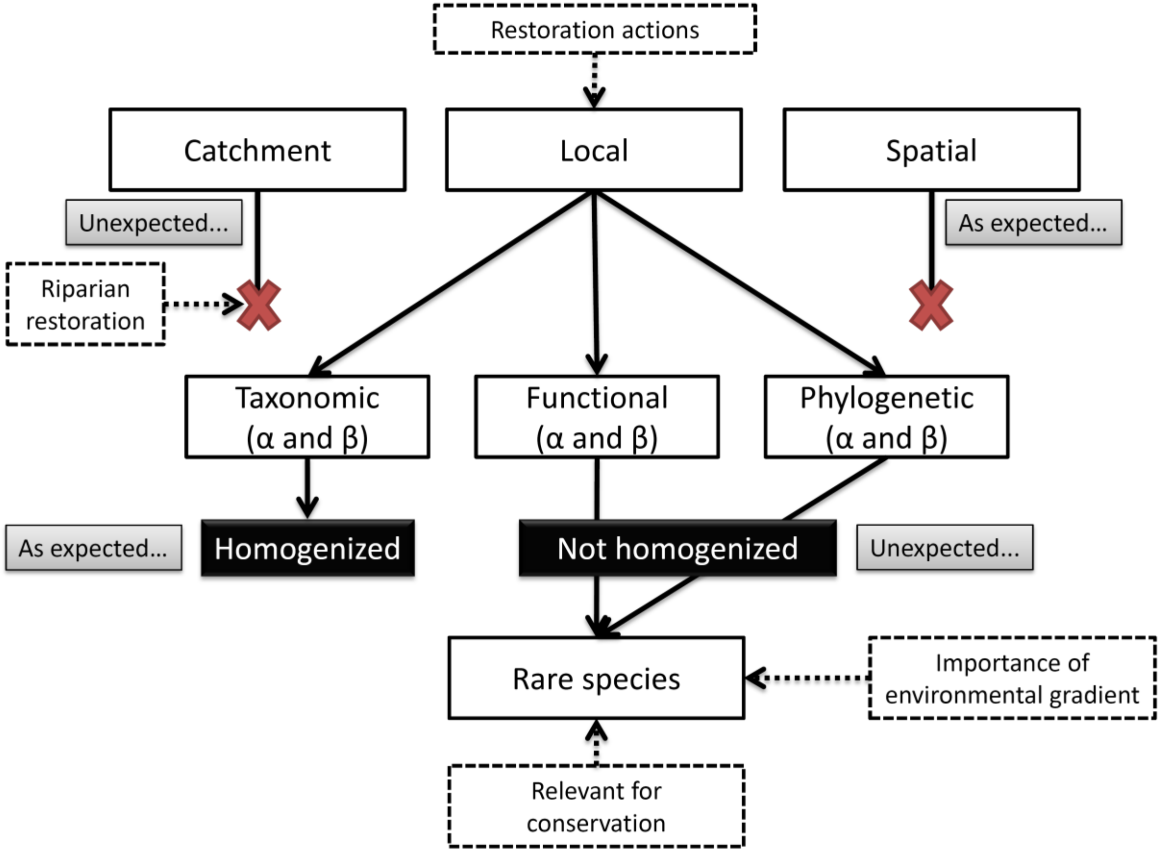
Commonly, understanding Neotropical streams has been ruled on a single catchment or few reaches and it has been based just on α-component of the taxonomic facet. In order to contribute to this field, this thesis focused on the influence of environmental variables, considered in a hierarchical form, and spatial patterns to the variation in three diversity facets, and their α- and β-components, of Neotropical stream fish in an agricultural landscape.

The main findings indicate, in a consistent way, that for almost all biodiversity facets, and their respective α- and β-components, local environmental factors explained a substantial fraction of variance, whereas spatial structuring contributed little to the variation, as it was expected (Fig. 1). However, in an unexpected way, land cover variables were not determining for the structure of stream fish communities (Fig. 1). The study area has been affected over a century by several human activities, including a sequence of deforestation for establishment of coffee crops, subsequently by pastures for livestock and, lately, by sugarcane for ethanol and sugar production. The time since first occupation of this land and the aggressive form in which it occurred may be the main factors behind the weak response of the fish fauna to landscape variables (such as native forest, pasture and sugarcane in the catchment and in the riparian buffer). The ultimate explaining factor for this is that initial contact to anthropogenic disturbances could lead to the extinction of sensitive species, resulting in communities composed by resilient species to future disturbances. It is not difficult to suppose that, along time, this may come happening multiple times, like a vortex.

On the other hand, and as far as is known, this thesis provides the first evidence of taxonomic homogenization for the study area. As expected for taxonomic facet, fish communities are more similar to each other than expected by chance (Fig. 1). However, when considered complementary dimensions of biodiversity, like the functional facet, conclusions are driven in a different way: fish communities are functionally more dissimilar to each other than expected by chance (Fig. 1). This probably highlights the contribution of rare species that are functionally very different for the beta component of diversity.

The findings of this thesis have clear implications for the conservation and management of stream fish in tropical agricultural regions. First, manipulation of local-scale variables, with the goal of ecological restoration of the streams, may have strong effects on the taxonomic, functional and phylogenetic fish community structure. Second, indicate that the riparian zone of streams in the region has no significant effect on fish biodiversity and, therefore, efforts to riparian re-establishment are necessary. Third, the results stress the importance of rare species for ecosystem functioning and as storage of evolutionary history of a community, therefore, efforts towards the conservation of these species and the environmental gradient exploited by these species must be, at least, maintained. Finally, this study may be a preview of what to expect in the coming decades for tropical drainages that have been rapidly deforested, without considering aquatic biodiversity.

Figure 1. Graphical synthesis with the main results of this thesis.



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São José do Rio Preto, 08/11/2016

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Camilo Andrés Roa Fuentes