

Original Articles

Biodiversity shortcuts in biomonitoring of novel ecosystems



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ABSTRACT

Hydropower reservoirs are novel ecosystems that present different challenges for the design of biomonitoring programs. To ensure long-term programs and wide spatial coverage, it is important to test the reliability of different cost-saving strategies that have been widely evaluated among researchers, such as taxonomic sufficiency, numerical sufficiency and surrogate groups. Using data on zooplankton composition, our objective was to test whether these strategies could be applied to increase the efficiency of biomonitoring programs in reservoirs. Zooplankton data were collected at the Santo Antônio do Jari Hydroelectric Plant, which is located between the states of Pará and Amapá (Amazon region, Brazil), over 23 months between 2012 and 2015. The data were organized in different taxonomic groups (cladocerans, copepods, rotifers and testate amoebae) and matrices by decreasing the taxonomic resolution (from species to genera and families) and the numerical resolution (from species abundance to species presence/absence) of the data. The ordination patterns obtained with Principal Coordinate Analysis for the different matrices were compared using Procrustes analyses. Our results suggest that ordination patterns using genus-level data were similar to those obtained with species-level data. However, analyses based on family-level data were often unable to reproduce results based on species-level data. Ordination patterns using presence/absence data were similar to those obtained from abundance data. We also found that the strengths of the relationships between ordinations derived from different taxonomic groups (e.g., rotifers and cladocerans) were low and often not significant. We conclude that the use of zooplankton genera and presence/absence data may be a reliable strategy to monitor reservoirs. However, our results highlight the need to monitor different zooplankton groups, as the ordination patterns depicted by a given group were poorly related to those generated by a second zooplankton group.

1. Introduction

River regulation by dams is an important driver of biodiversity loss in freshwater systems (Dudgeon et al., 2006). The change in hydrology caused by impoundments triggers several other changes in water quality, ecosystem processes and structure of aquatic communities. For instance, one can anticipate the creation of reservoir zones with different limnological characteristics (Kimmel et al., 1990) and periods with water stratification, mainly close to the dam (i.e., in the lacustrine zone), that were negligible or completely absent before damming. In terms of ecosystem processes, an increase in the primary productivity rate is also predicted, and this increase can be exacerbated due to eutrophication. Changes in aquatic communities are also pervasive and

include the decline of migratory fish populations (Agostinho et al., 2008) and the transformation of pseudoplanktonic into euplanktonic communities (Lodi et al., 2014; Silva et al., 2014; Simões et al., 2015). All these changes are enough to classify reservoirs as “novel ecosystems” (Hobbs et al., 2009, 2006). According to Seastedt et al. (2008), to manage these novel ecosystems, the pace of information transfer from the scientific community to stakeholders and policy makers should increase. Therefore, the implementation of efficient environmental monitoring programs is of paramount importance (Kallimanis et al., 2012).

Strategies to improve the efficiency and celerity of biomonitoring programs include the use of the higher taxa approach (e.g., Lovell et al., 2007; Mazón, 2016; Zhang et al., 2015), which consists of using

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biodiversity data at taxonomic levels higher than species. When the use of the higher taxa approach is proven to be reliable (e.g., when the patterns observed with species-level data are reproduced using genus-level data), then biomonitoring programs are thought to be simpler, faster and more cost-efficient (Bennett et al., 2014; Carneiro et al., 2013). Tests on the efficiency of higher taxa (i.e., data with lower taxonomic resolution) have indicated that this approach is reliable for different biological groups such as macroinvertebrates (Marshall et al., 2006; Sánchez-Moyano et al., 2006), phytoplankton, testate amoebae, copepods, cladocerans, rotifers (Machado et al., 2015) and ciliate communities (Jiang et al., 2016; Xu et al., 2014; Zhang et al., 2015).

The use of low numerical resolution has also been tested to increase the efficiency of biomonitoring programs (Gomes et al., 2015; Heino, 2014; Landeiro et al., 2012; Melo, 2005). In an extreme case, this approach relies on the use of simple incidence (presence/absence) data instead of abundance data (Blanchet et al., 2016). In addition to reducing sample processing time, Joseph et al. (2006) argue that the use of presence/absence data can be an interesting approach to increase the spatial extent of biomonitoring programs (Joseph et al., 2006: “the presence-absence data can be collected at more sites because the surveyor is not obliged to spend a fixed amount of time at each site”).

A growing number of studies have also tested the validity of surrogate groups (see Heino, 2010 and Westgate et al., 2014 for reviews and Corte et al., 2017 for a recent example). Currently, these tests are based on concordance (or cross-taxon congruence) analysis between pairs of biological communities defined taxonomically (e.g., Bae et al., 2014; Bini et al., 2008; Gioria et al., 2010; Grenouillet et al., 2008; Paavola et al., 2006). Proponents of this approach argue that data from different taxonomic groups are redundant in detecting natural and anthropogenic changes, while opponents argue that different groups are needed to detect subtle environmental changes (Bowman et al., 2008). However, it appears that a large number of studies support the view of the “opponents” (e.g., Backus-Freer and Pyron, 2015; Guareschi et al., 2015; Kimmel and Argent, 2016; Rosa et al., 2014; Vilmi et al., 2016) instead of the view of “proponents” of the surrogacy approach (e.g., Kilgour and Barton, 1999).

The aim of the present study was to test three strategies to increase the efficiency of biomonitoring programs in reservoirs: taxonomic sufficiency, numerical sufficiency and taxonomic surrogacy. We used a four-year dataset on zooplankton groups (cladocerans, copepods, rotifers and testate amoebae) collected in an Amazonian hydroelectric reservoir in Brazil. Based on previous evidence (Table S1), we predicted strong relationships between datasets with high (species-level) and low (genus- or family-level) taxonomic resolutions, and between datasets with high (abundance data) or low (presence/absence data) numerical resolution. We also anticipated that taxonomic surrogacy (based on concordance analysis or cross-taxon congruence) would not be advisable because the strength of the relationships between biological communities tends to be low. One strength of our study is that we based our conclusions on repeated tests conducted at different sampling points in space and time. Thus, these conclusions were not only based on snapshot surveys.

2. Materials and methods

2.1. Study area

This study was conducted in the Santo Antonio do Jari Hydroelectric Power Plant (SAJHPP), which impounded a 28 km long stretch of the Jari River (a tributary of the Amazon River; located between the states of Pará and Amapá; Fig. 1). Reservoir construction concluded in 2015, and the system operates as a “run-of-the-river reservoir”, with a low water residence time (ca. 1.5 days). The reservoir has a total area of 31.7 km², a total storage capacity of 133.39 × 10⁶ m³ of water and an average depth of 9.5 m (<http://www.edpjari.com.br/>).

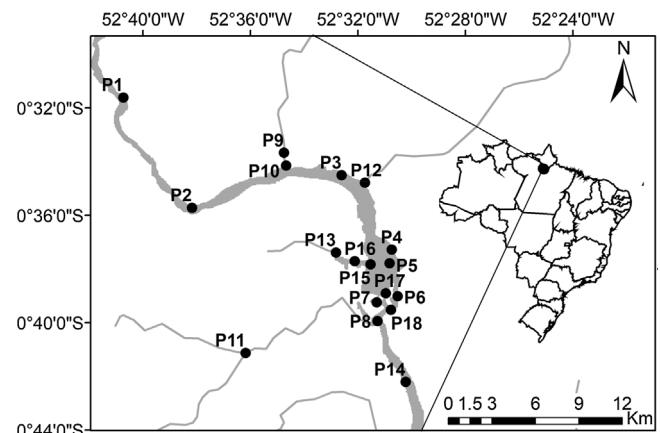


Fig. 1. Santo Antonio do Jari Hydroelectric Power Plant (South America, Brazil, Pará/Amapá states). The reservoir area is shown in gray. Sampling sites are represented as black circles (•).

2.2. Sampling

We conducted 23 sampling campaigns: nine before the impoundment (from February 2012 to February 2014), three during the filling period (May–July 2014) and eleven during the operation period (August 2014–August 2015) of the SAJHPP. The number of sampling sites varied from 14 during the beginning of the study to 18 sites after the filling of the reservoir. The sampling sites were distributed along the main axis of the reservoir and along some tributaries of the Jari River.

In each sampling site, a zooplankton sample was collected at a depth of 0.5 m by filtering 1000 L of water through a 68 µm plankton net. Samples were fixed with a 4% solution of calcium carbonate-buffered formaldehyde. For species identification and abundance analyses, zooplankton samples were concentrated to volumes ranging from 75 mL to 300 mL, depending on the concentration of suspended sediment in the samples. Larger volumes were necessary to observe specimens in samples with high suspended sediment concentrations. Prior to analysis, the samples were stained with Rose Bengal to facilitate the visualization of the organisms. Samples were analyzed under a microscope (Olympus CX31–400x) to determine zooplankton composition and abundance using Sedgwick-Rafter chambers. Five sub-samples of 1.5 mL (7.5 mL in total) obtained with a Hensen-Stempel pipette were analyzed, and the results were expressed as individuals per m³. Samples with very low densities were analyzed entirely (Bottrell et al., 1976).

2.3. Data analysis

We organized different matrices for each sampling campaign and for each zooplankton group (cladocerans, copepods, rotifers and testate amoebae) with varying taxonomic (family-, genera- and species-level) and numerical resolutions (presence/absence and abundance data). We repeated the process for each sampling site using months as the rows of the biological matrices. We log-transformed the abundance data after the addition of a constant (1.0). We used the Hellinger distance to calculate the compositional dissimilarity between samples when the analyses were based on abundance data (Legendre and Gallagher, 2001). According to Legendre and De Cáceres (2013), the Hellinger coefficient has multiple desirable properties (e.g., double-zero asymmetry and positivity; see their Table 2 for a complete list of properties). These authors also argue that a community-composition distance matrix based on the Hellinger coefficient is entirely “suitable for ordination by principal coordinate analysis (PCoA), which will not produce negative eigenvalues and complex axes”. For presence-absence data, we used the complement of the Jaccard coefficient. Afterward, we used these distance matrices to ordinate the samples with a PCoA. Based on the scores from the PCoA, we used Procrustes analyses to compare

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