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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 km^2, a total storage capacity of 133.39 × 10^6 m^3 of water and an average depth of 9.5 m (http://www.edpjari.com.br/).

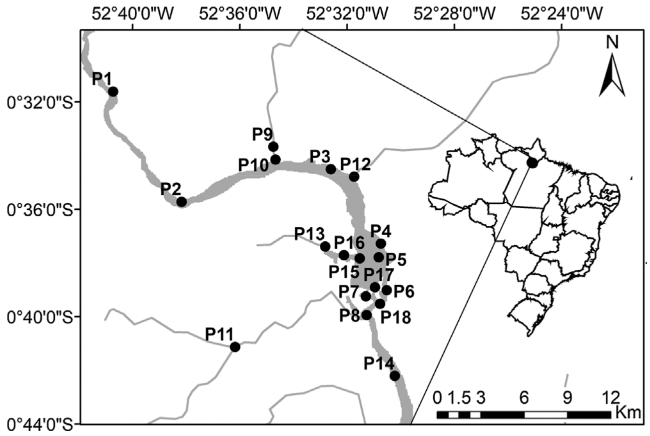

Fig. 1. Santo Antonio do Jari Hydroelectric Power Plant (South America, Brazil, Pará/Amapá states). The reservoir area is shown in gray. Sampling sites are represented as black circles (•).

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 m^3. 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 ordinations generated with data from different zooplankton groups (concordance between communities) and different taxonomic and numerical resolutions (Legendre and Legendre 2012). These analyses were repeated for each site (using sampling campaigns as rows in the original matrices) and for each sampling campaign (using sampling sites as rows in the original matrices). The statistical significance of each test was based on 9999 permutations. In addition to the significance level ($P \leq 0.05$), we adopted a threshold of ≥ 0.7 to consider the results of Procrustes' *r* as strong enough to justify the use of these simplification strategies (as suggested by Heino, 2010). We also evaluated the levels of cross-taxon congruence in species richness using the Spearman rank correlation coefficient. All analyses were conducted using the functions *decostand, vegdist* and *protest* from the *vegan* package (Oksanen et al., 2016) for the statistical software R (R Core Team, 2017).

3. Results

We found a total of 235 zooplankton species during the sampling period. These species were distributed among 93 genera and 44 families (see Table S2). Rotifers were the richest group (95 species), followed by testate amoebae (81 species), cladocerans (49 species) and copepods (10 species). The highest density was recorded in August 2012 (194,342 ind m^{-3}), with a high dominance of rotifers (176,810 ind m^{-3}; see Fig. S1). The highest density was recorded at the sampling site 7 (289,330 ind m^{-3}; see Fig. S2). This result can be explained by considering that this site has low water flow, favoring population growth.

In general, the relationships between the biological matrices at species and genera levels were significant over time (Fig. 2). Similar results were obtained when the matrices were organized for each sampling site (where the rows of the matrices were the sampling campaigns; Fig. 3). The correlation strengths were more variable for testate amoebae and rotifers. For testate amoebae, the correlations were more frequently non-significant.

Similarly, the relationships between species- and family-level data were often significant. The strengths of the relationships (as measured by Procrustes' *r*) also varied temporally (Fig. 4) and spatially (Fig. 5), mainly for copepods and testate amoebae. For cladocerans and rotifers, most values were significant and higher than 0.7. On the other hand, Procrustes' *r* was often lower than 0.7 for copepods and testate amoebae (Figs. 4 and 5).

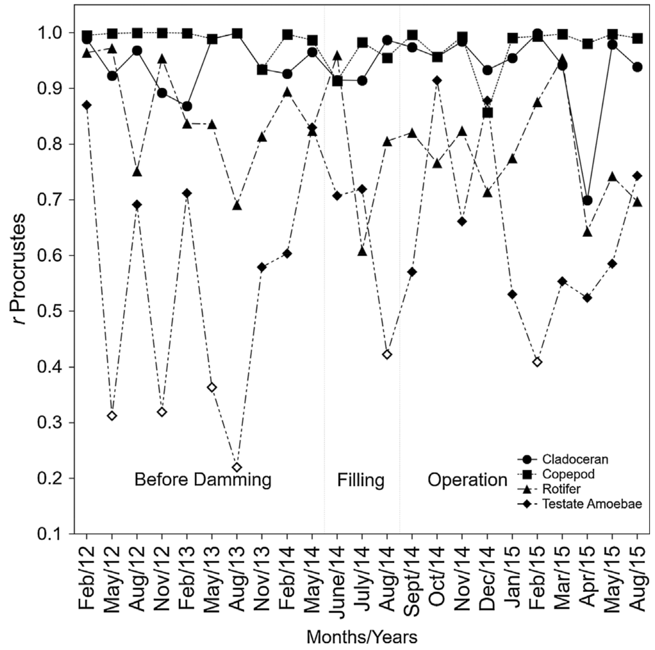

Fig. 2. Variation in the taxonomic sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each sampling campaign the comparisons were made between species-level and genus-level data, considering the sampling sites as rows in the matrices. Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

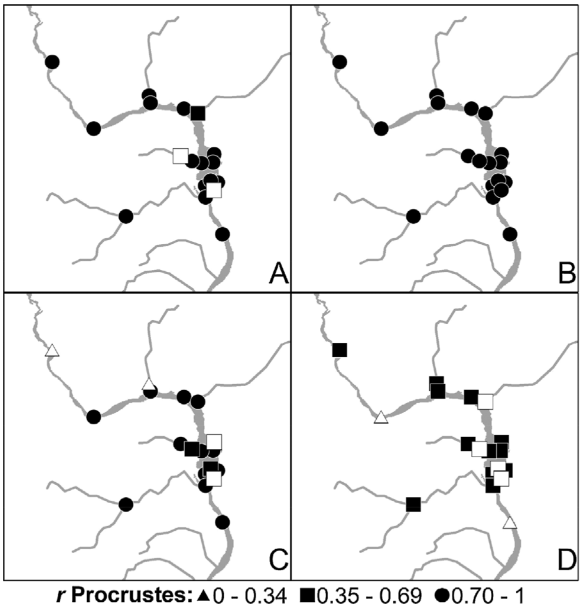

Fig. 3. Variation in the taxonomic sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each site the comparisons were made between species-level and genus-level data, considering the sampling campaigns as rows in the matrices. Shown are results for cladocerans (A), copepods (B), rotifers (C), and testate amoebae (D). Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

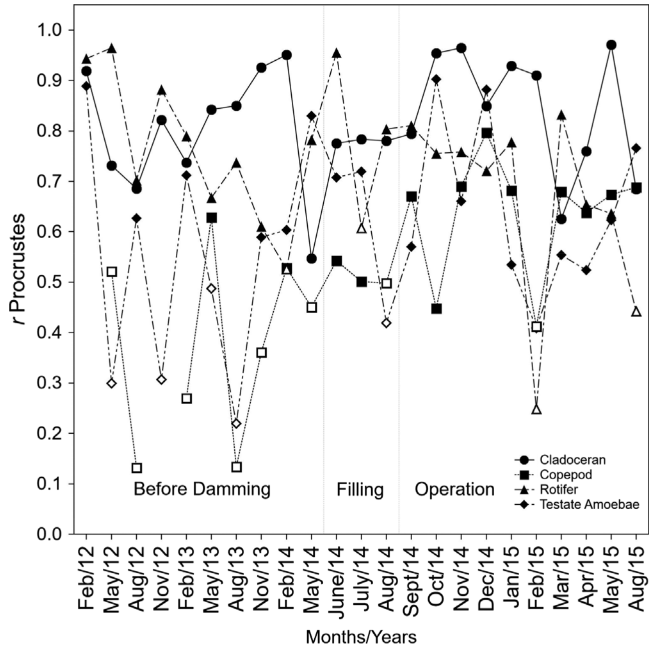

Fig. 4. Variation in the taxonomic sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each sampling campaign the comparisons were made between species-level and family-level data, considering the sampling sites as rows in the matrices. Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

The effect of decreasing the numerical resolution of the data (from species abundance to species presence/absence data) was higher for testaceans than for the other zooplankton groups, especially when the analyses were conducted for each sampling campaign (Fig. 6). In

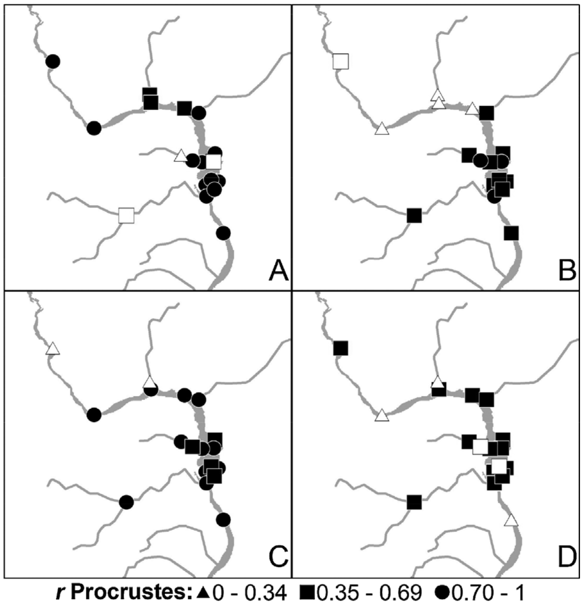

Fig. 5. Variation in the taxonomic sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each site the comparisons were made between species-level and family-level data, considering the sampling campaigns as rows in the matrices. Shown are results for cladocerans (A), copepods (B), rotifers (C), and testate amoebae (D). Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

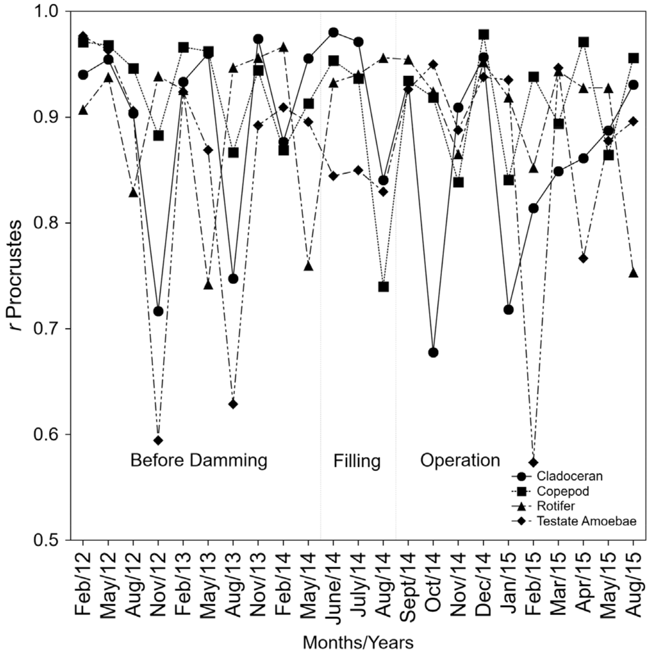

Fig. 6. Variation in the numerical sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each sampling campaign the comparisons were made between abundance and presence/absence data, considering the sampling sites as rows in the matrices. Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

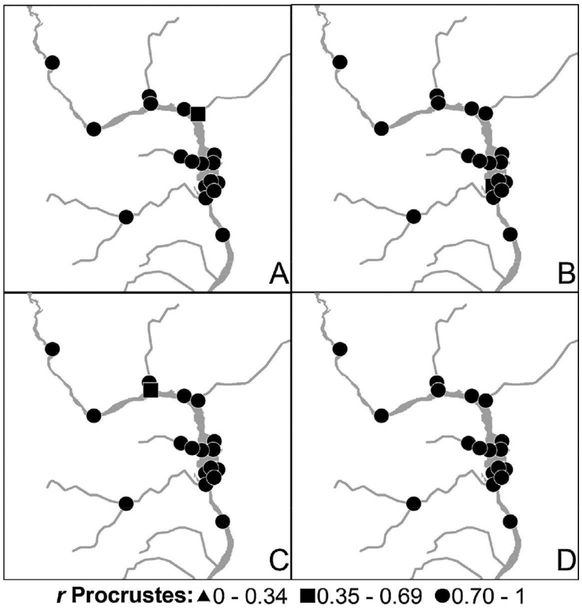

Fig. 7. Variation in the numerical sufficiency strength (as measured by Procrustes' *r*) for different zooplankton groups in the Santo Antonio do Jari Reservoir. For each site the comparisons were made between abundance and presence/absence data, considering the sampling campaigns as rows in the matrices. Shown are results for cladocerans (A), copepods (B), rotifers (C), and testate amoebae (D). Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

general, when the analyses were conducted for each sampling site, Procrustes' *r* values were higher than 0.7 for all zooplankton groups (Fig. 7).

The relationships between matrices of different biological groups (concordance analysis) varied conspicuously over time and space; however, most were not statistically significant (Figs. 8 and 9). We also found that species richness congruence varied conspicuously in time (Fig. S3) and space (Fig. S4). In general, the highest levels of species richness congruence were found for cladocerans and copepods, cladocerans and rotifers, and copepods and rotifers. However, weak and non-significant relationships were found for most comparisons (Figs. S3 and S4).

4. Discussion

4.1. Taxonomic resolution

We found evidence to support the use of the higher taxa approach in biomonitoring programs of novel ecosystems, as reported in other studies (Carneiro et al., 2013; Valente-Neto et al., 2016; Vilmi et al., 2016). However, this inference should be restricted to microcrustaceans and rotifers. Our results indicate that the information provided by species-level data is consistent with that provided by genus-level data. In contrast, the use of family-level data for these groups is not advisable due to the decline in the correlation strengths when data at this level of taxonomic resolution were used. We are confident in our results because, unlike most previous studies (Gomes et al., 2015; Machado et al., 2015), we analyzed the level of taxonomic sufficiency when the data were organized in different ways (i.e. spatially or temporally). Thus, the high correspondence between species and genera-level datasets was not anecdotal, minimizing the likelihood of false-positives (i.e., a circumstantial and random correspondence between datasets with different taxonomic resolutions).

High correlations for copepods (close or equal to 1.0) were found in some analyses due to the similar number of species (10) and genera (8) identified, and the inclusion of larval forms (nauplii) and juveniles (copepodites) in the analyses (see Rosser, 2017 for a discussion on the effect of species to higher taxa ratio on taxonomic sufficiency analysis). In practice, these immature forms are always counted, even when the interest is at the species, genus or family level. An important reason to consider them is their numerical importance to the zooplankton community, as these immature forms are often the most abundant among copepods (Lansac-Tôha et al., 2009). For example, in the present study we recorded 414,905 nauplii and copepodites (85.86%) and only 68,293 adults (14.14%).

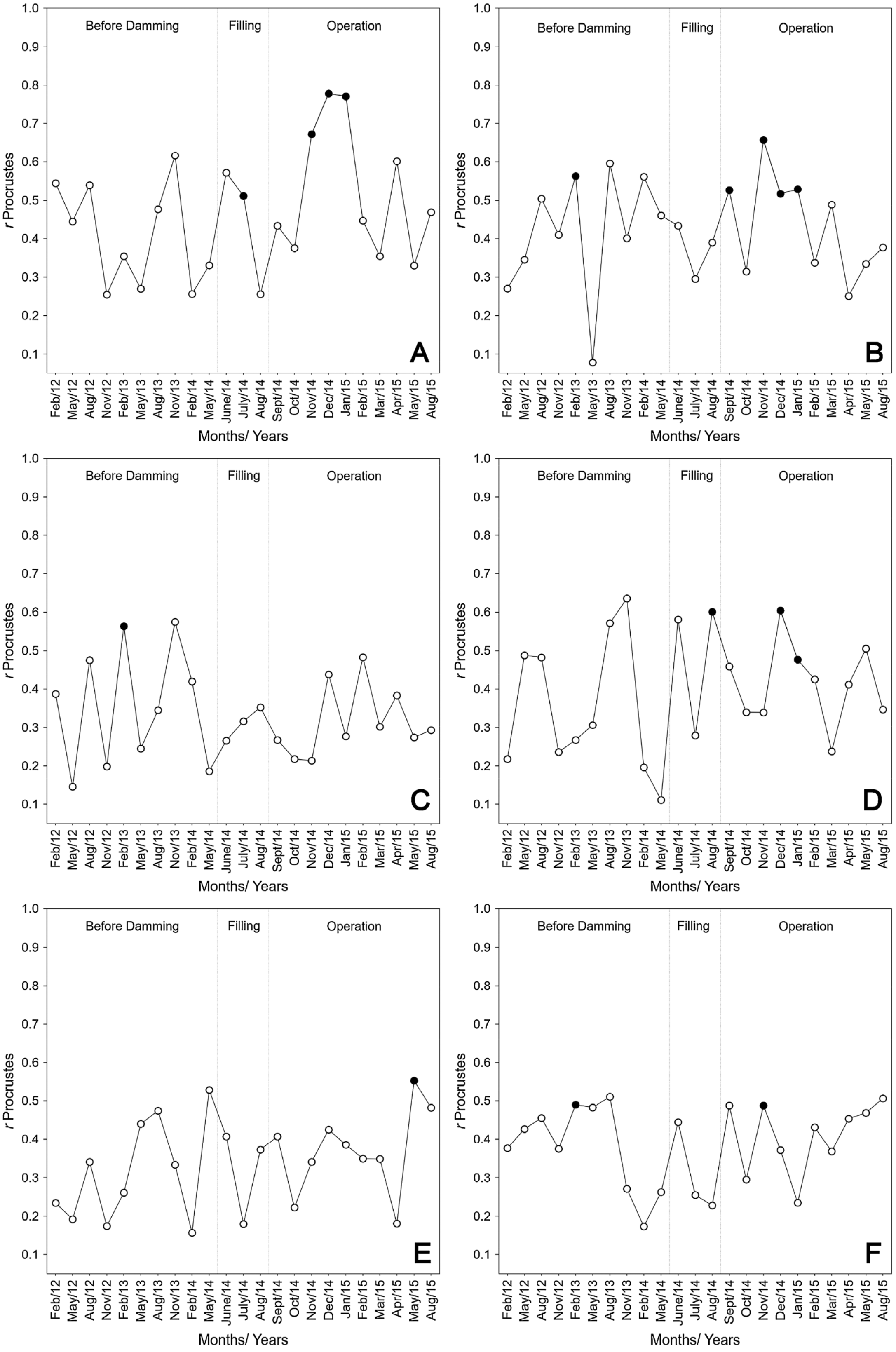

Fig. 8. Variation in the strength of community concordance (as measured by Procrustes' *r*) between different zooplankton groups in the Santo Antonio do Jari Reservoir. For each sampling campaign the comparisons were made between cladocerans x copepods (A), cladocerans x rotifers (B), cladocerans x testate amoebae (C), copepods x rotifers (D), copepods x testate amoebae (E) and rotifers x testate amoebae (F), considering the sampling sites as rows in the matrices. Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

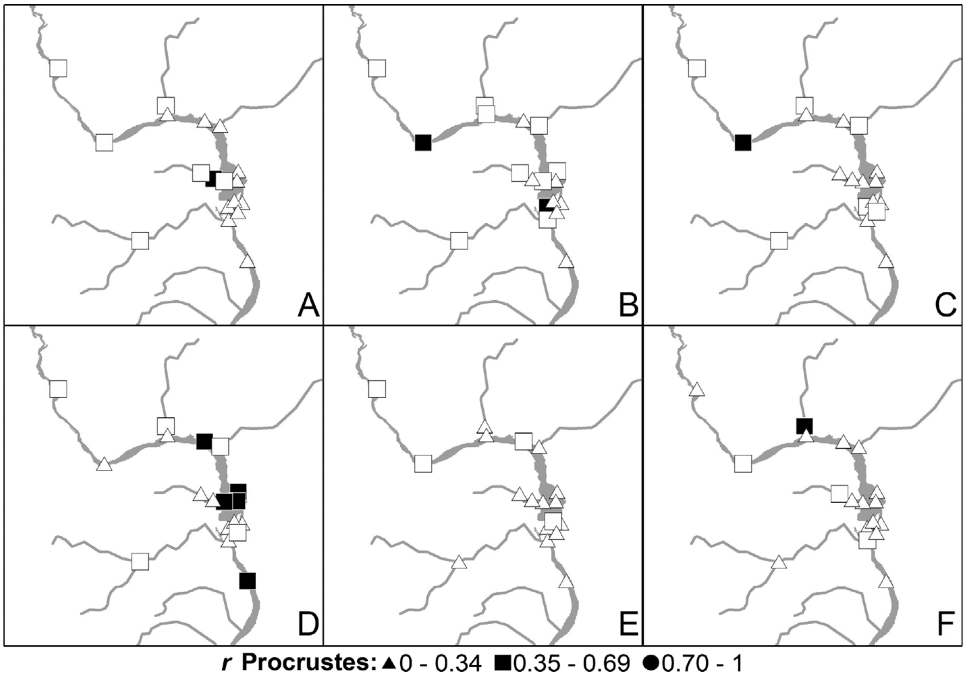

Fig. 9. Variation in the strength of community concordance (as measured by Procrustes' *r*) between different zooplankton groups in the Santo Antonio do Jari Reservoir. For each site the comparisons were made between cladocerans x copepods (A), cladocerans x rotifers (B), cladocerans x testate amoebae (C), copepods x rotifers (D), copepods x testate amoebae (E) and rotifers x testate amoebae (F), considering the sampling campaigns as rows in the matrices. Non-significant values ($P \geq 0.05$) are indicated by unfilled symbols.

The use of a lower taxonomic resolution in biomonitoring programs may be beneficial in different aspects. First, the sample processing time can be substantially reduced and data from biological samples can be delivered faster. This is especially valuable in highly dynamic systems like reservoirs. Second, the resources saved by using a lower taxonomic resolution can be used instead to expand the biomonitoring program by increasing the number of sites, the sampling frequency and the number of taxonomic groups monitored. Third, the use of a lower taxonomic resolution tends to be more robust to variations in the level of expertise of the personnel involved in a biomonitoring program. For example, in a long-term biomonitoring program the personnel in charge of the taxonomic determinations will likely change over time (e.g., due to retirements and job change; Straile et al., 2013). Thus, despite standardization efforts with the new personnel, the differences in taxonomic expertise may be substantial enough to compromise the comparability of the time series. In this situation, a strong "change" in community structure over time may simply reflect the change in personnel.

Skepticism regarding the use of a low taxonomic resolution is, however, well-founded (Maurer, 2000; Verdonschot, 2006; Rosser, 2017). We agree that for basic research (e.g., studies on beta diversity), the use of the highest possible level of taxonomic resolution is needed (Li et al., 2006). Additionally, the effects of subtle environmental impacts may pass unnoticed with the use of low taxonomic resolution data. However, stronger environmental changes that are characteristic of reservoirs (e.g., water level variation) are likely to be detected with low taxonomic resolution data (Bowman and Bailey, 1997; Ferraro and Cole, 1990; Mendes et al., 2007; Wright and Ryan, 2016).

4.2. *Numerical resolution*

Our results agree with previous studies regarding the negligible information loss caused by the use of species presence/absence data instead of abundance data, both across temporal and spatial scales. For example, similar results were obtained for phytoplankton (Carneiro et al., 2010), plants (Landeiro et al., 2012), zooplankton (Gomes et al., 2015) and macroinvertebrates (Rosa et al., 2014). Similar to the discussion on taxonomic resolution, the use of a low numerical resolution reduces the sample processing time. We believe that the use of presence/absence data or partial-abundance data (e.g., Blanchet et al., 2016) can be cost-effective for monitoring biological communities in reservoirs. However, for specific applications (e.g., monitoring of harmful algae), abundance data are indispensable.

4.3. *Surrogates*

Our third prediction was also supported, as we did not find strong and consistent relationships between the biological matrices of the different zooplankton groups: in general, the ordination patterns generated for a biological group were unrelated to those generated by a second group. The results based on congruence in species richness pointed in the same direction (see also Westgate et al., 2014). Even the relationships between cladocerans and copepods that are more phylogenetically related to one another than to the other analyzed groups (see, for example, results from Bini et al., 2008), were often not significant (mean Procrustes' $r = 0.46$; s.d. $= 0.15$). We agree with Heino (2010) that a much stronger relationship (> 0.7) would be required to justify the use of a surrogate group as an indicator of overall biodiversity patterns. In general, our results caution that assessments of the reliability of surrogate groups based on snapshot surveys may be misleading. For instance, during December 2014 and January 2015 (operation phase) we found strong and highly significant relationships between cladocerans and copepods ($r = 0.78$ and 0.77, respectively). However, these results were clearly circumstantial as the strength of the relationships during other sampling months were low and non-significant. If the evaluation of the reliability of surrogate groups had been based on these particular campaigns, the conclusion would have been wrong (see also Padial et al., 2012). The unreliability of the surrogacy approach is gaining strong support. For instance, using a meta-analysis that included 15 studies, Westgate et al. (2014) found a very low average correlation ($r = 0.27$; s.d. $= 0.26$). Despite studies indicating the reliability of surrogate groups (Su et al., 2004), our results suggest, in accordance with a growing body of evidence (Gioria et al., 2010; Paavola et al., 2003; Ruhí and Batzer, 2014; Vilmi et al., 2016), that this approach should be avoided.

5. Conclusion

Reservoirs are novel ecosystems (Turgeon et al., 2016) as complex as natural systems. Thus, biomonitoring programs for these systems should be designed cautiously. Our results suggest that the biomonitoring program of the zooplankton community in the SAJHPP based on genera and presence/absence data is defensible. We speculate that this recommendation can be extrapolated to other reservoirs in the Amazon region. However, we also recommend that this strategy be tested first using pilot surveys before it is adopted elsewhere. Once evidence has been produced to support this recommendation (i.e., the use of zooplankton genera and presence/absence data), a biomonitoring program, within the context of adaptive monitoring (Lindenmayer and Likens, 2009), could be reframed to, for instance, increase sampling frequency and spatial coverage. These are important issues given the high temporal dynamics and spatial complexity of reservoirs (Kimmel et al., 1990). Finally, our results suggest that the use of a particular zooplankton group to predict others is unreliable. The resources saved with the use of cost-effective strategies could then be directed to support the monitoring of a range of biological groups.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.ecolind.2017.07.025.

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