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Concordance among zooplankton groups in a near-pristine floodplain system

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ABSTRACT

The search for biological surrogate groups has been an active and contentious area of research. A surrogate group is defined as one that allows researchers to detect a known spatial and temporal environmental gradient and to represent the responses of other biological groups to those gradients. Using spatiotemporal zooplankton data from a near-pristine floodplain (the Araguaia River floodplain in Central Brazil), we first assessed the capacity of four zooplankton assemblages (Cladocera, Copepoda, Rotifera and Protozoa) to depict the effects of flooding. Second, we evaluated whether, during each hydrological period, ordination patterns derived from an assemblage matched those patterns shown by a second assemblage and by the environmental dataset. All four assemblages satisfactorily detected the environmental differences caused by the flood event. Most pairs of assemblages were significantly concordant. Additionally, the ordination patterns generated by these assemblages matched those generated by the environmental data. These results suggest that the patterns of concordance were mediated by similar responses to environmental gradients. However, the strengths of concordance between the assemblages, albeit significant, were low. Our results suggest the potential for use of the surrogacy approach in monitoring hydrological changes. However, due to the low strengths of concordance, the biodiversity pattern revealed by a specific assemblage is unlikely to be a good predictor of another. We also highlighted that conducting a formal meta-analysis on strengths of concordance between assemblages would be a promising avenue for further research.

1. Introduction

Aquatic biomonitoring programs often rely on the use of different biological assemblages and environmental variables. The choice of a biological assemblage for a particular biomonitoring program should be influenced by the kind of environmental problem involved and, according to Resh (2008), "ultimately depends on the characteristics of the area to be studied and the program objectives". Although we generally agree with this statement, in different situations, idiosyncratic reasons, such as the availability of a taxonomic specialist in a given region, may also explain why a particular assemblage has been monitored. Moreover, due to the lack of taxonomic knowledge and financial hindrances, in most cases, only a few biological groups are used as surrogates of biodiversity patterns in space and time (Paavola et al., 2003).

However, the use of a single group in many biomonitoring programs, generally defined in terms of taxonomic relatedness, presupposes that this group covaries with other biological assemblages in space and time. This presumption is testable, albeit rarely. It is verified when different groups are concordant or, specifically, when they exhibit similar patterns in species richness or community structure across a set of sites or through time (Allen et al., 1999; Jackson and Harvey, 1993). Beyond evaluating the reliability of surrogate groups for biomonitoring (Gioria et al., 2010; Kilgour and Barton, 1999), analyses of concordance between assemblages provide important insights on community organization (Paszkowski and Tonn, 2000). One mechanism responsible for concordance is a shared response to environmental gradients

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(Paavola et al., 2006). The strength of concordance is expected to be stronger for weakly dispersing groups than for highly dispersing ones (Grenouillet et al., 2008). Recent studies have also shown that biological interactions may influence community concordance (Padial et al., 2012), primarily when biological groups under analysis respond differently to environmental variables (Grenouillet et al., 2008).

Different frameworks can be used to study patterns of concordance (Gioria et al., 2011) and surrogacy capacity (i.e., "the capacity of a single group of taxa to represent other components of biodiversity"; see Hermoso et al., 2012). For instance, seasonal flood pulses have been shown to strongly shape the structure of floodplain-dwelling communities, and due to overwhelming environmental differences, periods of low and high water are recurrently characterized by different species compositions (Junk et al., 1989; Thomaz et al., 2007). Therefore, a potential surrogate group should, at least, be able to represent this major change in hydrological, sedimentological and physical–chemical factors. In addition to its capacity to detect seasonal patterns, a potential surrogate group should also allow us to recover the spatial patterns depicted by different biological groups.

The construction of dams is an important source of impacts to freshwater biodiversity. Dams can disrupt river connectivity, weaken the flood pulse in floodplain systems and cause biodiversity loss. For example, the Tocantins River, one of the longest rivers in the Brazilian territory and belonging to the Tocantins-Araguaia Basin, is already impacted by several dams (Barrow, 1987; Ribeiro et al., 1995). On the other hand, the Araguaia River, where this study was undertaken, still does not present any dam along its entire course, thereby generating an increasingly rare opportunity to study the functioning of relatively natural ecosystems, focusing on changes in biological composition caused by the flood pulse.

We gathered temporal and spatial data in the near pristine floodplain system of the Araguaia River in Central Brazil to address two questions: (1) are different zooplankton assemblages (cladocerans, copepods, rotifers and protozoans) able to detect the environmental differences caused by a flood event, and (2) are these assemblages concordant independently of the hydrological period? We expected all assemblages to respond similarly to the effect of flooding (i.e., differences between hydrological periods would be well represented in ordination plots by all groups). This response would result from the strong effects of floods on assemblage structure, environmental factors and processes in floodplain systems (Junk et al., 1989; Neiff, 1990; Ward et al., 1999). Therefore, all assemblages should be able to reflect these differences between hydrological periods. Beyond the differences resulting from water level variation, a reliable surrogate group should also be able to represent the spatial patterns of different aquatic assemblages and do so during both low and high water level periods.

2. Materials and methods

2.1. Study area

The Araguaia River drains the central highlands of Brazil, with a basin of 377,000 km^2. The regional climate is humid tropical (Koppen Aw), with two distinct hydrologic seasons characterized by wet summers and dry winters. The mean annual discharge of the Araguaia River is ca. 6400 m^3/s (Aquino et al., 2005), with peak discharges occurring from November to April (Latrubesse and Stevaux, 2002). The Araguaia River floodplain encompasses a variety of aquatic habitats (e.g., blocked valleys, channels, oxbow lakes and meander lakes) characterized primarily by the Cerrado Biome (Brazilian Savanna) (Latrubesse and Stevaux, 2002).

A salient feature of the Araguaia River floodplain is the absence of dams along the entire river. This characteristic is key to one of the primary goals of this study, i.e., to assess the ability of different aquatic assemblages to detect a seasonal pattern. Patterns of hydrological variation are therefore nearly unaltered.

2.2. Sampling

This study was carried out in January 2006, during a period of high water level (with a mean water flow of ca. 2542 m^3/s), and July 2006, during a period of low water level (with a mean water flow of ca. 567 m^3/s). For each period, we sampled 22 lakes of the Araguaia River floodplain (Fig. 1 – lake 1 S15°00′56.16″/W51°21′47.1″ and lake 22 S12°50′52.1″/W50°34′14.0″). The Instituto Brasileiro do Meio Ambiente e dos Recursos Naturais Renováveis (IBAMA) and Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio) issued the permits for sampling and access to each location. All lakes were permanently connected to the main river channel.

Zooplankton samples were gathered at subsurface (ca. 50 cm) by pumping 2000 L of water (1000 L were taken from the middle and from near the shores of each lake) through a plankton net of 68 μm mesh size and were fixed in a solution of 4% formaldehyde buffered with calcium carbonate. Densities of cladocerans, copepods, rotifers and protozoans (ind/L) were estimated by counting subsamples (2.5 ml) taken with a Hensen-Stempel pipette. At least 200 individuals of each group were counted per sample using a Sedgwick-Rafter cell (Bottrell et al., 1976). Organisms were identified to the lowest possible taxonomic level (usually species).

In the field, near the middle of each lake, we measured water depth (m). Also near the middle of each lake and at subsurface (ca. 50 cm), we measured the following variables: water temperature (°C), pH, turbidity (NTU), and conductivity (μS/cm). Water samples were analyzed for total phosphorus (μg/L), total nitrogen (μg/L) and chlorophyll-*a* (μg/L) (Golterman et al., 1978; Mackereth et al., 1978).

2.3. Data analysis

A log $(y+1)$ transformation was applied to abundance data before statistical analysis to minimize the effect of extreme values. For the whole dataset and for each assemblage (Cladocera, Copepoda, Rotifera and Protozoa), compositional dissimilarities between lakes were calculated using the Bray–Curtis coefficient. We then subjected each Bray–Curtis distance matrix to a principal coordinate analysis (PCoA; Legendre and Legengre, 2012) to ordinate the samples. We also used each Bray–Curtis distance matrix in a permutational multivariate analysis of variance (PERMANOVA; Anderson, 2001) to test for differences in assemblage structure between hydrological periods. An indicator species analysis (Dufrene and Legendre, 1997) was used to characterize the species composition of each period.

To quantify and test the strengths of concordance between pairs of assemblages for each period, we used the PCoA scores from each assemblage in a Procrustes Analysis (Jackson, 1995; Peres-Neto and Jackson, 2001). The residual sum-of-squares statistics (m^2), derived from a Procrustes Analysis, was transformed in r_P by calculating $r_p = \sqrt{1 - m^2}$. The higher the r_P, the higher the similarity between the ordination patterns generated by the assemblages under comparison.

With the exception of pH, the environmental variables were log-transformed. The standardized Euclidean distances between sampling sites were then subjected to a principal coordinate analysis (PCoA). To test for relationships between biological and environmental datasets, we also used Procrustes analysis on PCoA scores (summarizing the environmental and the biological datasets; see above). Next, the standardized Euclidean distances