



Original Articles

Cross-taxon congruence in benthic communities: Searching for surrogates in marine sediments



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ABSTRACT

Cross-taxon congruence has been suggested as an efficient tool in conservation planning and biodiversity monitoring. It corresponds to the degree to which patterns in assemblage structure in a set of sites are similar among different taxonomic groups. If different groups ordinate the sampling sites similarly, they are concordant and this information is frequently used as an indicative that one group could be used as a surrogate for the other. Using spatiotemporal benthic data from a biodiverse coastal ecosystem (the Araçá Bay in southeast Brazil), we first assessed if macro- and meiofaunal assemblages inhabiting marine soft-sediments show concordant patterns. Then, we used multi- and univariate analysis to examine the relationship of both groups with the environment. Macro- and meiofaunal assemblages exhibited strong congruent patterns in all periods analyzed. Moreover, both groups responded to similar environmental features and their ordination patterns matched those generated by the environmental data. These results show that the patterns of concordance are probably mediated by similar responses to environmental gradients. Overall, our results suggest the potential for use of the surrogacy approach in conservation planning and monitoring purposes of marine benthic biodiversity, and that macro- and meiofauna can be used as a surrogate for each other.

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1. Introduction

Biodiversity loss is currently a major threat to the structure and functioning of ecosystems (Chapin et al., 2000; Larsen et al., 2012). Over the past few decades, the accelerating extinction rates have induced an increasing effort into assessing biodiversity (Pereira et al., 2010). The limited funding for conservation, the lack of taxonomic specialists and the time-consuming work to sample and identify organisms (Myers et al., 2000; Heino 2010; Vieira et al., 2015), however, usually preclude a complete biodiversity assessment. To reconcile the opposite forces of complexity and practicality, it is therefore necessary that a translation of the diversity associated with ecological communities into fast and cost effective measures can be used for nature conservation and monitoring (Siqueira et al., 2012).

A common alternative to provide practical, less costly and more quickly obtainable measures of biodiversity is to base broad-scale assessments on well-known surrogate taxa (Paavola et al., 2006; Dolph et al., 2011). Studies testing the effectiveness of surrogate taxa have generally been based on the cross-taxonomic level surrogacy, whereby indicator species, genera or families are used as indication of the overall biodiversity of an ecosystem (Dufrière and Legendre, 1997; Sánchez-Fernández et al., 2006; Heino, 2010). Nevertheless, single taxonomic levels represent only a facet of the community and may fail to adequately represent the local biodiversity (Allen et al., 1999; Su et al., 2004; Bilton et al., 2006). To avoid wrong conclusions regarding both the fundamental ecology and management requirements, researchers started to consider the cross-taxon surrogacy (known as community concordance or cross-taxon congruence), by which whole assemblages are used as biodiversity surrogates. This approach is based on the degree to which different assemblages show congruent ordination patterns in a set of sampling sites (Jackson and Harvey, 1993; Paavola et al., 2006; Bini et al., 2007). Strong congruence is expected to happen when different taxa respond to the same ecological processes, and is

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therefore an indication of the validity of the surrogate taxa for conservation planning and monitoring purposes (Jackson and Harvey, 1993; Bini et al., 2007).

In aquatic ecosystems, studies evaluating cross-taxon congruence have been mostly realized with freshwater communities inhabiting streams, lakes and ponds (e.g.: Jackson and Harvey, 1993; Heino et al., 2003; Paavola et al., 2006; Bini et al., 2007, 2008; Dolph et al., 2011; Lopes et al., 2011; Larsen et al., 2012; Vieira et al., 2015). Marine soft sediments comprise one of the largest and oldest ecosystems in the world (Gray, 2002), and the benthic (bottom-living) species that reside within the sediments (infaunal species) form one of the richest species pools on Earth (Snelgrove, 1997). Yet, remarkably little is known about their patterns of species richness (Gray, 2002) and, to our knowledge, no study has investigated cross-taxon congruence among infaunal benthic assemblages thus far.

Infauna of the marine benthic system is traditionally divided in two major components: macro- and meiofauna. Although this division is based on sizes, being macrofauna composed by individuals larger than 0.5 mm and meiofauna by organisms ranging from 0.04 mm to 0.5 mm, they represent ecologically different compartments (Warwick et al., 2006; Giere, 2008). Given their benthic nature, both groups are linked to sediment characteristics and related variables, such as grain size, pollutant concentration, and microphytobenthic primary production (Defeo and McLachlan, 2005; Fonseca et al., 2014). They are also relevant food sources for higher trophic levels, and essential for ecosystems services such as nutrient cycling and environmental stability (Danovaro et al., 2007; Brown and McLachlan, 2010; Bonaglia et al., 2014; Amaral et al., 2016). Because of their widespread distribution, high biodiversity, limited mobility and specific ecological requirements, macro- and meiofaunal assemblages have been extensively used in environmental impact assessment studies (e.g. Frontalini et al., 2011; Alves et al., 2013; Patrício et al., 2012; Pinna et al., 2013; Semprucci et al., 2013). However, sampling and taxonomic efforts needed to study each group are fundamentally different, and most studies on the diversity and community structure of benthic assemblages focused on only one of their components (Fonseca and Netto, 2006; Curini-Galletti et al., 2012; Sutcliffe et al., 2012).

To better understand the associations among marine benthic assemblages, we investigated whether macro- and meiofaunal assemblages inhabiting marine soft-sediments exhibit concordant patterns of community structure and respond similarly to environmental variables. Our main goal was to evaluate if both assemblages show a concordant spatial and temporal structure. This is important information to implement effective conservation and monitoring programs in marine ecosystems (Paavola et al., 2006; Bini et al., 2008). Additionally, we aimed to further expand the cross-taxon congruence approach by combining multi- and univariate analyses to investigate trends in different assemblages. Community concordance studies usually test the relationship between each assemblage and environmental drivers based on species data tables (i.e., multivariate datasets). This approach allows researchers to distinguish changes of assemblages in response to an environmental gradient. However, it does not necessarily show if each assemblage respond similarly to the environment in terms of univariate metrics such as abundance and species richness. Benthic assemblages can have very similar relationships to each other in terms of their community structure; however, they can show different patterns with respect to their univariate attributes (Warwick and Clarke, 1991). Consequently, it is possible that different taxa may respond to the same environmental gradient (for example organic enrichment or sediment features) and have congruent ordination patterns, however, one assemblage may respond positively (i.e., higher number of species and individuals) while the other responds negatively to the environmental gradient. In this context, the combined use of multi-

and univariate analyses would be useful to achieve a more complete comprehension of the responses of different assemblages to multiple ecological processes, and to provide more detailed information to be used in conservation programs.

2. Material and methods

2.1. Study area

This work was done at Araçá Bay (23° 49'S, 45° 24'W), a diverse coastal ecosystem (534.500 m²) located in the central area of the São Sebastião Channel, state of São Paulo, Southeast Brazil (Fig. 1). A number of habitats are represented in Araçá Bay such as mangrove, wide intertidal flat and rocky shores (Amaral et al., 2015). This area has a gentle slope reaching a maximum depth of 30 m in the channel. The tides range from average levels of 2.06 m to −0.04 m (Gubitoso et al., 2008).

2.2. Sampling

Samples were taken during the low tide from thirty-seven georeferenced sites arranged in an irregular sampling grid ($n = 4 \times 37$) from the intertidal to 25 m deep (Fig. 1). Sampling was performed in October 2012, February, June and September 2013, totaling 148 samples (4 periods \times 37 samples). At shallow sites (≤ 3 m depth), samples were collected manually, and at deeper sites a multi-corer was used for sampling. At each sampling site, samples were collected simultaneously for the investigation of macrofauna, meiofauna (nematode), microphytobenthos and granulometry.

For macrofauna analysis, four sediment samples were taken using a corer of 10 cm inner diameter and 20 cm depth. Each sample was placed in a plastic bag and taken to the laboratory, where they were sieved with a 0.3 mm mesh. Although the standard size for macrofauna is 0.5 mm, we used a smaller mesh because it is more effective to collect juvenile macrofauna individuals. The fauna retained was sorted in taxonomic groups and fixed in 70% ethanol. All individuals were identified to the species level.

For meiofauna analysis, one sediment sample was taken using corer of 2.5 cm inner diameter and 5 cm depth. Samples were immediately fixed in 4% formaldehyde. In the laboratory, samples were washed through a 45 μ m mesh sieve and extracted by flotation with Ludox TM 50 (specific density 1.18) (Heip et al., 1985). The retained material was stored in 4% formaldehyde and stained with Rose Bengal. The meiofauna was predominantly composed of nematodes, with a lower contribution of Copepoda, Kinorhynca and Tardigrada. Nematoda is the most dominant and diverse group of the meiofauna in soft sediments (often >50% of the total meiofauna, up to >90% in deep-sea sediments) and is thought to be closely connected to other faunal compartments of the benthic system (Balsamo et al., 2012). Therefore, Nematoda is expected to be a good representation of benthic biodiversity (Boucher and Lamshead, 1995; Giere, 2008). Thus, in order to improve taxonomic identification to species level, we have opted to use only nematode individuals for the analysis. Nematodes were counted, identified to genus level and further separated into morphospecies. From each sample, a total of 100 nematodes were randomly picked, evaporated slowly in anhydrous glycerol and mounted on permanent slides for identification. After identification, the proportion of each taxon per sample was multiplied by the total number of individuals per sample to achieve the total number of individuals of each species.

For microphytobenthic analyses, five samples of the top 1 cm of the sediment were taken using a corer measuring 2 cm inner diameter and conditioned in dark bottles. These samples were kept on ice and stored at −20 °C. Microphytobenthic biomass was estimated from phaeopigments and chlorophyll a concentrations according

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