

Title: HOLOBIOME OF THREE MARINE SPONGES FROM THE NORTH COAST OF SÃO PAULO

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ABSTRACT: Marine sponges perform several processes that contribute to the functioning and health of the benthic ecosystems. They also harbor diverse archaeal, bacterial and fungal communities in which complex interactions are established and aid the host to grow and develop. Conversely, little is still known about the diversity and community structure of this microbiota. As such, there is a need to disclose their taxonomic and functional diversities within these animals. To tackle this, the sympatric species *Aplysina fulva*, *A. caissara* (endemic) and *Tedania ignis* were collected along with surrounding seawater and sediment at Praia Preta, in the north coast of São Paulo. The sponge species were identified using morphological characteristics and by barcoding using the genes cytochrome oxidase subunit 1 (*cox-1*), cytochrome *b* (*cob*), and the internal transcribed spacer regions (ITS, including ITS1, 5.8S, ITS2). The DNA from the sponges, seawater and sediment were extracted and subjected to Illumine MiSeq platform using the phylogenetic markers 16S (prokaryotic communities) and ITS (eukaryotic communities – Fungi). Even though three genes were used to identify the sponge species, only *cob* was capable to separate *A. fulva* and *A. caissara* into two distinct clusters. The Illumine sequences were analyzed with MOTHR and showed that the highest Shannon diversity index and CHAO richness was observed for sediment, followed by seawater, *Aplysina* species and *T. ignis* for both 16S rRNA and ITS genes. The most abundant bacteria phyla were *Acidobacteria*, *Actinobacteria*, *Chloroflexi*, *Cyanobacteria* and *Proteobacteria* (*Gammaproteobacteria*, *Alphaproteobacteria*); whereas *Crenarcheota* was the dominant phyla in the Archaea domain. The abundance of these phyla was different between sponge species and environmental samples. For fungi the *Agaricomycetes* and *Basidiomycetes* were the major phyla associated with sponge species, where *Zygomycetes* dominated the environmental samples. When OTUs were assigned, it clearly showed that the holobiome associated with sponge species were distinct from the detected in seawater and sediment. This survey addressed for the first time the holobiome of the São Paulo sponge species and it demonstrated that the microbial communities associated with sponges were host-specific.

Keywords: Porifera, microbial ecology, South-western Atlantic, metagenomics, high-throughput sequencing

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