## TITLE: THE MICROBIOME OF SPONGES FROM THE AMAZON REEF SYSTEM

AUTHORS: SOARES, A.C.S.<sup>1</sup>; THOMPSON, F.L.<sup>2</sup>; SETUBAL, J.C.<sup>1</sup>

**INSTITUTION:** <sup>1</sup>LABORATÓRIO DE BIOINFORMÁTICA, INSTITUTO DE QUÍMICA, UNIVERSIDADE DE SÃO PAULO (AV. PROF. LINEU PRESTES, 748 - BUTANTÃ, SÃO PAULO - SP, 05508-000), <sup>2</sup>LABORATÓRIO DE MICROBIOLOGIA, INSTITUTO DE BIOLOGIA, CCS, UNIVERSIDADE FEDERAL DO RIO DE JANEIRO (ILHA DO FUNDÃO, RIO DE JANEIRO - RJ, 21944970 ).

## ABSTRACT:

The Amazon Reef System is located on the Brazilian continental shelf underneath the Amazon River plume. This environment has a benthic community mainly formed by sponges and calcareous algae. Sponges are ubiquitous organisms and the main members of the marine benthic community. Through filtration of large amounts of water, sponges are important links between the column water and benthic compartments. They are able to influence nutrient cycling by removal, processing and release of the filtrated materials. Sponges are known to harbor a large abundance of microbes. The microbial abundance can be 3 to 4 orders of magnitude higher than the density in the surrounding water. Most of microorganisms associated with sponges are species specific. Among the functions of these microbial communities are those related to the symbiotic lifestyle, such as nutrient supply, degradation of complex carbohydrates, sponge skeletal stabilization, waste processing and production of secondary metabolites involved in sponge defense. Using a metagenomics approach, the main goal of this study is to evaluate the microbial diversity associated with sponges from the Amazon Reef System in terms of taxonomy, genomic and functional metabolism. A total of 232.198.141 good quality paired-end sequences were generated for 35 metagenomes from 18 sponge species. Taxonomic assignments showed a higher contribution of Actinobacteria, Eurvarchaeota. Chloroflexi and Planctomycetes, besides the classes Betaproteobacteria and Deltaproteobacteria. This taxonomic profile was distinct between the sponges and surrounding water, showing that sponges harbour their own unique microbial community. From the metagenome data we obtained 115 metagenome-assembled genomes, revealing new species of bacteria and archaea. The sponge microbiome also showed an enrichment of genes related to carbon and nitrogen metabolism. These results bring new knowledge about marine sponge microbial symbionts.

Key words: marine sponge, microbiome, metagenomics, microbial diversity

## **Development Agency: CAPES**