

CO-ORGANIZED EVENT

International Conference on **Chronic Diseases**

&  
6<sup>th</sup> International Conference on **Microbial Physiology and Genomics**

August 31-September 01, 2017 Brussels, Belgium

## Archaeal communities from deep-sea sediment in a chemosynthetic biotic community in the southwestern Atlantic Ocean

Adriana Giongo<sup>1</sup>, Renata Medina-Silva<sup>1</sup>, Luiz G A Borges<sup>1</sup>, Adolpho H Augustin<sup>1</sup>, Taiana Haag<sup>1</sup>, Taiz L L Simão<sup>1</sup>, Dennis J Miller<sup>2</sup>, Adriano R Viana<sup>2</sup>, Eduardo Eizirik<sup>3</sup> and João M M Ketzer<sup>1</sup>

<sup>1</sup>Institute of Petroleum and Natural Resources - PUCRS, Brazil

<sup>2</sup>PETROBRAS, Brazil

<sup>3</sup>PUCRS, Brazil

Cold seep areas are widespread around the world's oceans, occurring at different latitudes and depths. Chemosynthesis often occurs in these areas, supporting biotic communities sustained by gases such as methane, generally at temperatures of ~2° - 4°C. Such environments have been studied in the Northern Atlantic and Pacific Oceans; equivalent systems in the Southern Hemisphere have received little attention. We have previously documented a chemosynthetic benthic community in a cold seep pockmark site in the southwestern Atlantic Ocean using clone-based phylogenetic approaches. Here we assessed the archaeal communities from samples inside a pockmark, at the seafloor level and 1 m below the seafloor using high throughput DNA sequencing. After trimming off 16S rRNA sequences shorter than 100 bp and with low quality scores, a total of 510,321 sequences were used in the downstream analysis. The most abundant archaeal phylum was Euryarchaeota representing more than 31% and 34% of the total prokaryotic sequences at the seafloor and 1 m below the seafloor, respectively. From this phylum, OTUs from ANME-1, ANME-2c and ANME-2a-2b groups were the most abundant in these samples. The Marine Benthic Group B (MBGB) belonging to the phylum Crenarchaeota was also observed in abundance in samples, representing an average of 1.65% of the total sequences at the seafloor and 0.26% at 1 m below the seafloor. Our data brings the first report based on metabarcoding analyses on the archaeal diversity of southwestern Atlantic chemosynthetic zone. In some aspects they presented interesting similarities in relation to previous microbial diversity reports from other oceanic regions, but also it brings new venues for the in-depth comparative analysis of these communities, from ecological and evolutionary standpoints.

### Biography

Adriana Giongo coordinates the Geobiology Lab at the Institute of Petroleum and Natural Resources in Brazil. During her MSc and PhD, she has worked with Soil Nitrogen Fixation. For the past 10 years, she has focused in Microbial Ecology from deep-sea samples, using high throughput sequencing to describe microbial communities and the role of microorganism in the carbon and nitrogen cycles.

adriana.giongo@pucrs.br

### Notes: