

Deep-sea sediment microbial communities at Hook Ridge hydrothermal vent in the Bransfield Strait, Northwestern Antarctic Peninsula

Diego Franco¹, Camila N. Signori¹, Wânia Duleba², Vivian H. Pellizari¹

¹Oceanographic Institute, University of São Paulo, São Paulo, Brazil; diecasfranco@usp.br

²School of Arts, Sciences and Humanities, University of São Paulo, São Paulo, Brazil

At Hook Ridge (HR), a submarine volcanic edifice at the eastern end of the Central Bransfield Basin were detected anomalies indicating low-temperature hydrothermal discharge. Despite the macrofaunal diversity has been reported at this vent site, the microbial community is not well-known. The aim of this study was to describe and compare microbial communities across geochemical parameters of deep-sea sediments influenced by hydrothermal activity in the Bransfield Strait. Sediment samples were collected at two sites of HR separated by a distance of 1725 m, HR6 (1190 m depth, reported to be the only hydrothermally active sediment) and HR4 (1090 m depth, off-vent site). Based on the V4 region of 16S rRNA, amplicons were sequenced on the MiSeq Illumina sequencing platform, and resulted in 180,585 sequences of varied length. High quality and non-chimeric sequences were clustered into OTUs by setting a 97% of similarity and classified using SILVA 128. Based on taxonomic relative abundances, Chloroflexi (30.4%), Proteobacteria (15.1%), Atribacteria (9.9%), Aminicenantes (6.9%) were the major bacterial phyla at HR6, whereas Proteobacteria (36.6%), Actinobacteria (25.0%), Chloroflexi (11.7%), Planctomycetes (9.7%) were the most abundant taxa at HR4. Archaeal communities were very similar at both sites, and composed by Woesearchaeota (74.0% at HR4 and 64.0% at HR6) and Thaumarchaeota (23.8% and 7.5%, respectively). In addition, HR6 sample presented some unique archaeal taxa such as Bathyarchaeota, Hadesarchaea, Lokiarchaeota, Parvarchaeota and euryarchaeotal class WSA2, which are related to chemosynthetic metabolism. Our results show an influence of geochemical settings of sediments on the microbial community composition at HR6 and their potential role in chemosynthesis at HR.