

## Geochemical and microbial context of gassy sediments in the Ría de Arousa (NW of Spain)

Víctor Cartelle (1), David Barros-García (2), Ángel S. Comesáñ (3), Alejandro de Carlos (2), and Soledad García-Gil (1)

(1) Department of Marine Geoscience, University of Vigo, Vigo, Spain, (2) Department of Biochemistry, Genetics and Immunology, University of Vigo, Vigo, Spain, (3) CACTI, University of Vigo, Vigo, Spain

Microbial communities and their associated metabolic activity in marine sediments have a profound impact on global biogeochemical cycles. Data obtained from high-resolution seismic profiles, gravity core analysis, including sedimentology and geochemistry, radiocarbon dating and metagenomics, has been used to establish the geochemical and microbial context of gassy sediments in the Ría de Arousa, which is located in the Atlantic Margin of Galicia (NW of Iberia). It is a drowned valley of 230 km<sup>2</sup> with water depths ranging from 5-10 m in the inner part to 50-60 m at the mouth. The ria is affected by upwelling events from May to October, which bring up nutrient-rich cold water from the shelf. A total of 48 km<sup>2</sup> of acoustic blanking and turbidity areas were mapped. These gas-related anomalies were identified mainly in the youngest seismic unit from the sedimentary infill of the ria, which corresponds to the last 6000 yr. The geochemical zonation and prokaryotic composition of gravity cores are conditioned by the availability of organic matter, which in turn depends on its input, sedimentation rate and also sedimentary facies. The gassy sediments show conspicuous sulphate-methane transition zones (SMTZ) at different core depths (ranging from 0.4 to 1.4 mbsf), which act as methane sinks. Certain amounts of methane (up to 27  $\mu$ M) can be detected near the surface of non-gassy sediments, suggesting surface methanogenesis processes. Archaeal community composition of internal and external gassy, and external non-gassy sediments was assessed at various depths through multiplexed 16S rRNA gene sequencing on an Ion Torrent Personal Genome Machine. The SILVA ngs data analysis service was employed to map sequence reads to taxonomy with a resolution down to the genus level. Depth profiles of relative abundance of archaeal classes and named environmental groups show that the composition is linked to the sediment type. Uncultured archaea common to the marine sub-sea floor like Marine Benthic Group D/Thermoplasmatales are dominant in these organic-rich sediments. Bathyarchaeota increase their presence in the lower layers from the estuarine to the shallow marine sites. The main orders of methanogens are detected along the sedimentary columns, being Methanosaecinales the most abundant. The presence of ANME is conspicuous, especially in the sulphate-methane transition zones of the gassy sediments, indicating anaerobic oxidation of methane processes.

Acknowledgments: This work was supported by grant CGL2012-33584 (Spanish Ministry of Economy and Competitiveness) and also by European Regional Development Fund through contract GRC2015/020 (Xunta de Galicia).