

The microbial and geochemical architecture of Scotian Slope cold seep Site 2A-1, Scotian Slope, Canada

GREGORY TODD VENTURA¹, **ELISH REDSHAW¹**,
UNYMIE UMOH¹, **NARGES AHANGARIAN¹**, **GAMRA**
OUESLATI¹, **ANIRBAN CHOWDHURY¹**, **JEREMY**
BENTLEY¹, **NATASHA MACADAM²**, **ADAM W. A.**
MACDONALD², **MARTIN FOWLER³** AND **PATRICIA**
GRANADOS¹

¹Saint Mary's University

²Nova Scotia Department of Natural Resources and Renewables

³Previously at Applied Petroleum Technologies (APT) Ltd.,
Canada

Cold seeps are globally occurring sites of low temperature, reduced fluid seepage along the seabed of continental margins. These features sustain oasis-type ecosystems in highly redox stratified sediments that are unique to the larger surrounding seafloor. In this study, the microbial soft sediment architecture of Site 2A-1 [1], a deep-water Scotian Slope cold seep, is reconstructed as a 600 m long, six-push core transect along an environmental gradient using porewater ion geochemistry in conjunction with targeted and untargeted lipidomic surveys. Downcore profiles of nine porewater ion species were measured using ion chromatography and photometry. Additionally, 23 tentatively identified lipid classes of predominately archaeal origin were identified and quantitated. These data were compiled as spatially resolved 2D-heatmaps to illustrate vertical and lateral changes in the subsurface geochemical and microbiological architecture of the seep structure. Porewater ion concentrations and specific ion diffusion fluxes were calculated to designate microbially mediated metabolic zones of denitrification, microbial sulfate reduction, and anaerobic methane oxidation. All porewater ion fluxes were highly influenced by the high rates of methane seepage from the seep site. Additionally, intact polar lipids, core lipids, core lipid degradation products, and chlorophyll were measured across the transect. Lipidomic diversity patterns and biomarker proxy data revealed a heavily zoned archaeal community, with diversity increasing as a function of seepage rate. Lipidomic signatures indicated the seep is dominated by ANME-1 communities. Biomarker proxies and bulk sediment stable carbon isotopes provided insights into seepage evolution and its impact on carbon cycling and microbial zonation dynamic across the seep structure. High methane index values for both core and intact polar lipids were observed across the seep structure indicating sustained active point source macroseepage with an asymmetrical apron of microseepage. The elevated methanotrophy impacted the bulk organic carbon isotope concentrations of the seep surface sediments. Lower chlorophyll concentrations on the seep structure marking higher rates of heterotrophy that further indicate elevated rates of microbial activity as compared with the surrounding ambient sediments. These spatial changes highlight the complex interplay of micro- and macroseepage conditions within these deep-sea