Incorporating microbial anomalies into seabed geochemical prospecting in different deepwater settings

Casey R. J. Hubert[1], Carmen Li[1], Deidra K. Stacey[1],
Oye Adebayo[1], Anirban Chakraborty[1], Emily Ellefson[1],
Bernie Bernard[2], James Brooks[2], Adam Macdonald[3],
Jamie Webb[4] & Martin Fowler[4]

[1]Department of Biological Sciences, University of Calgary; [2]TDI Brooks International; [3]Nova Scotia Department of Energy; [4]Applied Petroleum Technology Canada

Offshore oil and gas exploration relies heavily on hydrocarbon seep detection through geochemical analyses of seabed sediment cores. Geochemistry can indicate hydrocarbon potential and the presence of working petroleum systems in prospective areas, but does not eliminate the risk of drilling 'dry holes'. With drilling costs in deep water areas reaching hundreds of millions of dollars per well, additional and complementary tools for prospecting are welcome. Microbiological strategies may offer key insight into the hydrocarbon potential in these areas by revealing anomalous diversity patterns or distributions of indicator taxa to help to pinpoint hydrocarbon seeps. This was tested in deep-sea areas of the Eastern Gulf of Mexico and the Scotian Slope in Atlantic Canada, with samples obtained on piston coring expeditions for surface geochemical prospection. Bacterial community compositions were determined in over 300 sediment samples, from the top few cm down to 10 metres sediment depth through sequencing up to triplicate 16S rRNA gene amplicon libraries on an in-house Illumina MiSeq coupled to in-house bioinformatics using the MetaAmp platform (Dong et al. 2017). Parallel geochemical analyses followed industry standards for assessing the presence and quantity of petrogenic hydrocarbons; this revealed a fraction of sampling locations in both regions having oil indications in the core samples. Distributions of bacterial groups known from growth-based studies to be associated with hydrocarbon-degradation, i.e. members of the *Gammaproteobacteria* and *Chloroflexi*, were relatively uniform in Scotian Slope samples. However, a distinct trend was observed in the dominance (i.e., >20% relative abundance) of a single OTU (defined at 97%) belonging to the relatively undescribed and so far-uncultivated phylum *Atribacteria* in surface and subsurface sediments at sites that were geochemically hydrocarbon-positive. In one instance, where confident geochemical interpretation was impossible, DNA sequencing of the sediment bacterial community reproducibly revealed >30% of the *Atribacteria* OTU. In Gulf of Mexico sediments closely related *Atribacteria* were also detected, and were only in high relative abundance (>5%) in geochemically 'oil positive' locations. These findings demonstrate the value of molecular microbiology, both in comparison to growth based bioassays (i.e. a promising biosensor candidate from uncultivated microbial 'dark matter'), and more broadly as a tool that can support geochemical data interpretation for offshore prospecting.

Dong X, Kleiner M, Sharp CE, Thorson E, Li C, Liu D and Strous M (2017) Fast and Simple Analysis of MiSeq Amplicon Sequencing Data with MetaAmp. *Front. Microbiol*. 8:1461. doi: 10.3389/fmicb.2017.01461