Hydrocarbon seep-associated microbes for offshore oil and gas exploration

Carmen Li[a], Oyeboade Adebayo[a], Deidra K. Ferguson[a], Scott Wang[a], Francisco D. Davila[a], Martin Fowler[b], Jamie Webb[b], Calvin Campbell[c], Natasha Morrison[d], Adam MacDonald[d], Casey R.J. Hubert[a]*

[a]Department of Biological Sciences, University of Calgary.

[b]Applied Petroleum Technology Canada.

[c]Natural Resources Canada, Geological Survey of Canada-Atlantic.

[d]Nova Scotia Department of Natural Resources and Renewables, Government of Nova Scotia

Summary

Deep sea oil and gas exploration relies predominantly on conventional geochemical analyses of subsurface marine sediments to identify the presence of a working petroleum system and de-risk exploratory drilling. In this study, DNA-based microbiological methods were investigated as a complementary tool for hydrocarbon seep detection.

Piston coring was performed in >2500 m water depth at 19 geographic locations along the Scotian Slope resulting in samples from the upper 10 metres below seafloor (mbsf). Sediments were assessed for hydrocarbon liquids and gases that typically signify seepage and for microbial biodiversity in >400 sediment subsamples.

Select sites showed strong evidence of both biogenic and thermogenic hydrocarbons. Significantly different microbial communities were detected in the presence of hydrocarbons, characterized by anaerobic methane-oxidizing archaea (ANME). ANME groups were observed in high relative abundance in hydrocarbon seepage-positive sediments and were notably absent in hydrocarbon seepage-negative sediments, suggesting that specific taxa within ANME lineages can signal the presence of hydrocarbons. Furthermore, differential abundances of these ANME taxa can distinguish between hydrocarbons of thermogenic- and biogenic-origin. These findings suggest that microbial DNA sequencing has the potential to play a key role in offshore exploration.

Theory / Method / Workflow

Marine sediments down to 1000 cmbsf were collected by piston coring at 19 deep sea locations in the Atlantic Ocean where water depths exceeded 2500 m. Geochemical analysis of headspace gases and sediment extracts revealed the presence and type of hydrocarbons such that sites were ranked as positive (thermogenic or biogenic), negative, or inconclusive (i.e., weak geochemical signals). Microbial DNA sequencing of archaeal 16S rRNA genes was performed on >400 sediment samples ranging from 0 cmbsf to 1000 cmbsf. Biodiversity assessments of amplicon sequence variants (ASVs) in these microbial communities were compared through bioinformatics analyses.

Results, Observations, Conclusions

Of the 19 sampled seafloor locations, geochemical evidence of biogenic hydrocarbons was found at two sites and of thermogenic hydrocarbons at two sites. Five sites had weak evidence of hydrocarbons, such that they were classified as inconclusive. The remaining ten locations were non-seep sites.

Microbial communities in non-seep and seep sediments are distinct. The difference between microbial communities in sediments with biogenic hydrocarbons and sediments with thermogenic hydrocarbons is less obvious.

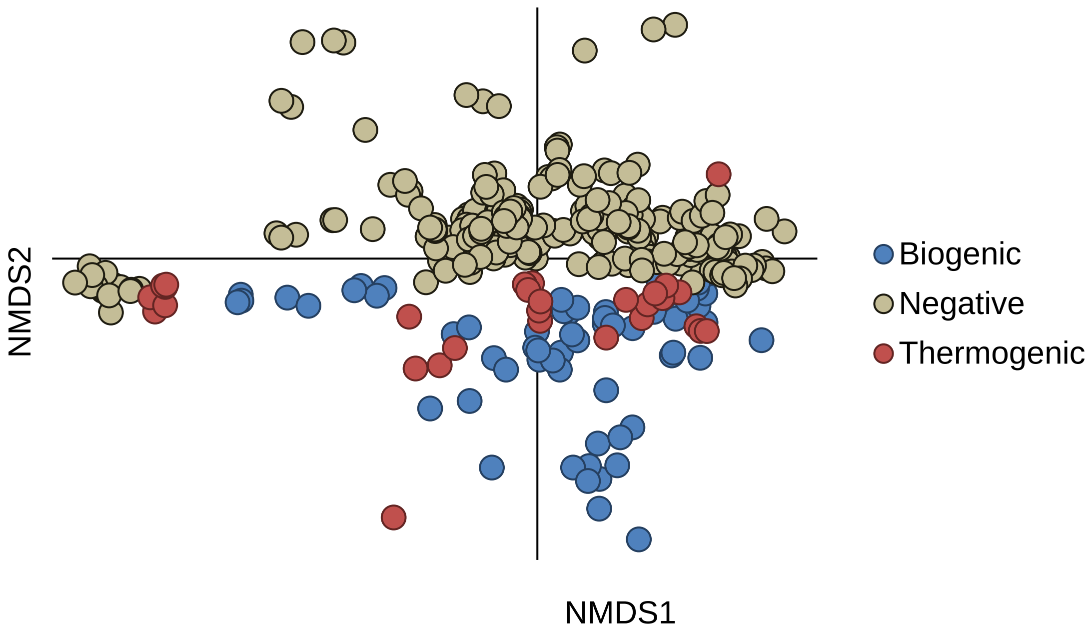

Figure 2. Non-metric multidimensional scaling (NMDS) ordination of variation in archaeal community structure of 401 sediment samples. Ordination is based on Bray-Curtis dissimilarities among samples. Points represent samples and colours represent hydrocarbon-status.

Anaerobic methanotrophic archaea (ANME) are significant members defining the difference between microbial communities in non-seep and seep sediments. Select ANME are also differentially abundant in seep sediments with some ANME being detected only in sediments with either biogenic or thermogenic hydrocarbons. These ecological patterns suggest that these ANME can be used as biological indicators for the presence of hydrocarbons and that they can furthermore differentiate between biogenic and thermogenic hydrocarbon seepage.

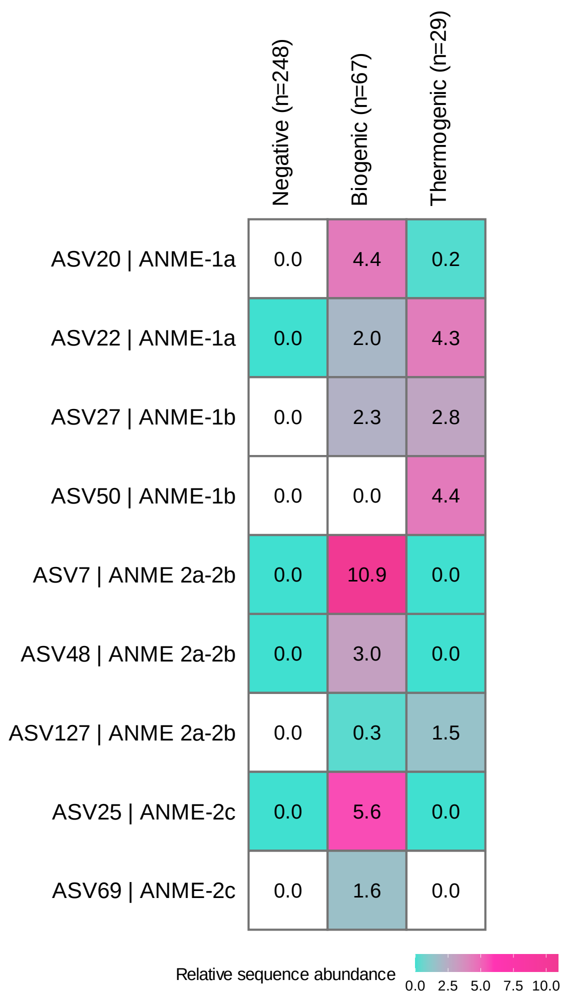

Figure 2. Heatmap of relative 16S rRNA gene sequence abundances of nine indicator ASVs compared between non-seep, biogenic hydrocarbon-seepage, and thermogenic-hydrocarbon seepage sediments.

Novel/Additive Information

This study demonstrates that DNA-based microbial diversity patterns in seabed sediments can be used as bioindicators for thermogenic hydrocarbon seeps in the deep sea and provide a complementary tool for de-risking offshore oil exploration.

Acknowledgements

Bedford Institute of Oceanography, Canadian Coast Guard, Natural Resources Canada, Genome Canada, Genome Alberta, Genome Atlantic, Geological Survey of Canada, Fisheries and Oceans Canada, Government of Nova Scotia – Department of Energy and Mines