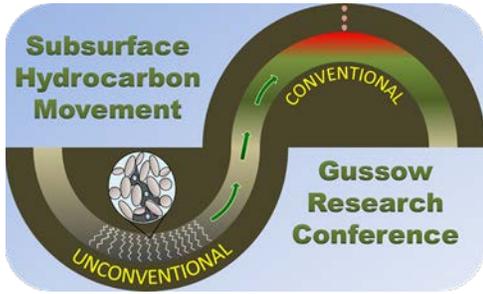


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Hydrocarbon Degrading Bacteria: Potential Indicators for Oil and Gas Prospection in Deep Sea Sediments

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Introduction

The migration of hydrocarbons from subsurface petroleum reservoirs to the surface enables hydrocarbon seep detection as an exploration tool in oil and gas industry. The increased hydrocarbon supply creates conditions favorable for the development of bacterial populations with the capacity to utilize hydrocarbons for carbon and energy. Hydrocarbon oxidizing bacteria in sediments can thereby be an indicator of oil and gas reservoirs in the deeper subsurface and hence offer a useful tool to identify undetected micro seepages and aid characterization of reservoirs. This additional exploration strategy can be integrated into existing exploration data sets or become useful to pre-select specific areas, reducing risks associated with cost-intensive exploration techniques. This study examines the distribution of hydrocarbon-degrading populations in sediment samples from the Scotian Slope off Canada's east coast.

Theory and/or Method

Deep sea sediments (2500 – 3500 m water depth) from the Scotian Slope in Atlantic Canada were sampled from five different locations by piston coring, and were examined at different depths within the top 10 metres for the presence and potential of aerobic hydrocarbon-degrading microbial communities. Enrichment cultures were established by combining sediments with growth medium amended with naphtha (a mix of short chain alkanes, long chain alkanes and monoaromatic hydrocarbons) and incubated at 4°C, the temperature of the deep-sea bed.

Examples

Hydrocarbon degradation was observed in all treatments after four months of incubation at 4°C, with the extent of naphtha removal being variable, as revealed by headspace GC-MS. Patterns of hydrocarbon compound removal were not uniform and suggest variability in the degradation pathways and/or microbial key players. Community analyses via 16S rRNA gene amplicon sequencing revealed a predominance of *Gammaproteobacteria* in all instances, however operational taxonomic units (based on a 97% sequence identity cutoff) within the genera *Pseudomonas* and *Alteromonas* showed differential enrichment patterns in different locations and sediment depths.

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Conclusions

The study shows the presence and distribution of deep-sea microbes capable of hydrocarbon utilisation and highlights the potential roles of specific bacterial taxa. Further studies to quantify metabolic genes associated with hydrocarbon biodegradation in different samples will provide information to sharpen the diagnostic accuracy of the identified taxa and reliable differentiation between background and anomalous microbial populations in deep sea sediments.