

Biotechnology-2013: Hydro-Bio-Geo-Chemistry - George Ivey - Ivey International Inc.

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Principles regarding soil, sediment and groundwater contamination not taught in colleges or Universities. This is achieved through a visually driven and interactive presentation approach in which the audience learns water is not H₂O, what really affects contaminant solubility, and the important role of contaminant sorption in soil, sediments, and groundwater and how this all forms of remediation including bioremediation. Attendees with limited chemistry, biochemistry, or microbiology experience will learn a new 'easy to use' set of principles to accurately predict the behaviour and solubility of most contaminants in soil, sediments, and groundwater, how to change the properties of water, and how to improve contaminant solubility to increase its Physical, Chemical and Biological Availability for in-situ and ex-situ remediation.

Introduction

Hydrothermal activity can generate a variety of reduced compounds, including low molecular weight hydrocarbons, which can be produced abiotically through water–rock interactions under high temperature and pressure . It was recently discovered that Fe²⁺ in hydrothermal systems is oxidized by water formed oxygen to give magnetite (Fe₃O₄), while the water is reduced to H₂. Ultimately, the H₂-dependent reduction of CO₂ leads to the generation of hydrocarbons (C₂–C₁₁), methane, and aromatics using Fe₃O₄ as the catalyst . Long carbon chain alkanes and polycyclic aromatic hydrocarbons (PAHs) can also be generated in the deep subsurface via thermogenic processes . For instance, numerous hydrocarbons have been observed in the vent fluids and sulfide deposits of the Rainbow vent field at the north Mid-Atlantic Ridge (MAR), including C₉–C₁₄ n-alkanes, C₉–C₁₃ branched alkanes, C₉–C₁₁ cycloalkanes, C₇–C₁₂ nonaromatic hydrocarbons, naphthalene, methyl-naphthalene, and C₁₃–C₁₆ PAHs (fluorene, phenanthrene, and pyrene). Similarly, a high abundance of n-alkanes of C₁₅–C₃₀ chains, and three- or four-ring PAHs were detected in the hydrothermal sediments from the Lost City vent field at the northern part of the MAR.

The deep biosphere may be partially energetically supported by hydrocarbons ; however, we know little about this unique ecosystem. Deep-sea hydrothermal vent areas may foster harvesting of deep matter and energy, by unique extremophiles and provide clues to understand the coupling of deep-sea life and abiotic and biotic processes under the seafloor. Recently, alkane oxidation genes that encode short-chain alkane monooxygenases, degradation pathways for corresponding alcohols, and short-chain fatty acids were found to be abundant in the hydrothermal plume metatranscriptome and metagenome,

and these genes may be derived from the uncultivated bacterial group SAR324 . In addition, a high diversity of alkane monooxygenases that were phylogenetically affiliated with enzymes involved in C₁–C₄ alkane oxidation was observed in the Guaymas Basin hydrothermal plume . Moreover, genes involved in anaerobic hydrocarbon degradation were also detected among several phyla in Guaymas Basin sediments, including Bacteroidetes, Chloroflexi, Deltaproteobacteria, and the candidate phylum Latescibacteria (WS3) . Metagenomic and metatranscriptomic approaches revealed the presence of diverse methyl-coenzyme M reductase-based alkane-oxidizing archaea, including the multi-carbon alkane oxidizer *Ca. Syntrophoarchaeum* spp., anaerobic methane-oxidizing archaea (ANME-1 and ANME-2c), and sulfate-reducing bacteria (HotSeep-1 and Seep-SRB2) coexisting with sulfate-reducing bacteria and showed the potential for alkane oxidation in Guaymas Basin hydrothermal sediments . However, these advances are mainly based on metadata, while few hydrocarbon-oxidizing microbes have been isolated from deep ecosystems.

In the past decade, we have explored the bacterial diversity involved in PAH degradation in deep-sea sediments of the MAR the west Pacific [, and the Arctic , as well as in the deepwater columns of the southwest Indian Ridge. diversity of bacteria that may be driven by hydrocarbons in situ. Here we report the microbial diversity of aliphatic and aromatic hydrocarbons degrading bacteria in the vent plumes, chimney sulfides, and nearby sediments, and confirm their activity under in situ conditions. The results extend the body of knowledge of the potentially hydrocarbon-utilizing microbial community inhabiting the hydrothermal vent ecosystem, and promote understanding of their interactions with extreme environments.

Materials and methods

Samples and their descriptions are provided in Table S1 and and the Supplementary Materials and Methods. Detailed descriptions of the chemicals and enrichment media are also described in the Supplementary Materials and Methods.

Hydrocarbon analysis

To determine the hydrocarbon concentrations in hydrothermal plume samples, a method that combined stir bar sorptive extraction, thermal desorption–gas chromatography–mass spectrometry, and the Hydro-CARB® software package (IFP, Rueil-Malmaison, France) was used. The details of these procedures are described in the Supplementary Materials and Methods.

Enrichment of hydrocarbon-degrading bacteria at high pressure

Deep-sea-mimicking cultivation was conducted under high pressures and low temperatures in the chamber of a HP vessel as described in the Supplementary Materials and Methods.

Stable-isotope probing experiments

Stable-isotope probing (SIP) experiments for the above plume, sulfide deposit, and sediment enrichments were performed with ^{13}C -labeled alkanes and PAHs, yielding a total of 12 samples. The details of these procedures are described in the Supplementary Materials and Methods.

Isolation of heterotrophic hydrocarbon-degrading bacteria

Serial dilutions of enrichments were streaked onto M2 agar plates, then incubated at $15\text{ }^{\circ}\text{C}$ until the formation of bacterial colonies was observed. Colonies exhibiting unique morphological features were selected and re-streaked onto M2 plates to obtain pure cultures that were then preserved at $-20\text{ }^{\circ}\text{C}$ for further analyses. The bacterial community composition of the plume samples of the newly discovered hydrothermal field named Deyin-1 on the south MAR (15°S) is shown in . In the rising plume sample (SAP-1_S), the 16S rRNA gene sequences related to gamma-proteobacteria (31.5%) and epsilon-proteobacteria (19.2%) were highly abundant. Among the

detected gamma-proteobacteria, levels of the following genera were relatively high: Alcanivorax (7.4% of the total), Glaciecola (6.7%), Marinobacter (3.7%), SUP05 clade sequences (3.7%), Cycloclasticus (2.3%), and Alteromonas (1.8%). Among the epsilon-proteobacteria sequences, the genera Sulfurimonas (11.9%), Sulfurovum (4.9%), and Arcobacter (2.1%) were present at relatively high concentrations. Additionally, the SAR324 clade (4.4%) of delta-proteobacteria and the SAR202 clade (3.2%) of Chloroflexi were detected in the rising plume sample.

Biography

George Ivey doing his current research on hydro-geo-biochemistry at Ivey International Inc. Canada.

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