Microbial Communities in Methane Hydrate-Bearing Sediments from the Alaskan North Slope

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Abstract

High latitude soils and sediments often contain large quantities of methane as well as microbial communities capable of producing and consuming the methane. We studied the microbial communities collected from hydrate-bearing sediments on the Alaskan North Slope to determine how abiotic variables (e.g., grain size, hydrate presence, original depositional environment) may control the type and distribution of microbes in the sediments. The soils were acquired from sub-permafrost, Eocene (25-36 million years ago [Ma]) sediments laid down as a marine transgressive series within which hydrates are believed to have formed 1.3 Ma. Forty samples, eight of which contained hydrates, were acquired from depths of 606–666 meters below land surface. Five samples from drilling fluids were recovered and then amplified using polymerase chain reaction with primers specific for bacterial and archaeal 16S rDNA. Only bacterial DNA amplicons were detected. Terminal-restriction fragment length polymorphism (t-RFLP) was used to measure bacterial diversity in the respective samples. Non-metric multidimensional scaling (NMDS) was then used to determine the factors that may have influenced bacterial diversity. NMDS analysis revealed that sediment samples were distinct from those obtained from drilling fluids suggesting that the samples were not contaminated by the drilling fluids. All samples had evidence of microbial communities and sample depth, temperature, and hydrate presence appeared to have some influence on community diversity. Samples sharing these environmental parameters often shared common t-RFLP profiles. Further examination of selected samples using clone libraries should help to identify the key taxa present in these unique sediments and yield a better understanding of the biogeochemistry of these gas-bearing systems.

Objective: Determine how abiotic variables (e.g., grain size, hydrate presence, original depositional environment) may control the type and distribution of microbes in subpermafrost sediments.

Methods

Sample site and sample collection
- Mt. Elbert drill site on the Alaskan North Slope (Figure 1)
  - From 154 m of vertical core, 40 samples were preserved and shipped in liquid N2 (Figure 2)
  - Eight samples contained hydrate, all of which were from between 607 and 646 mbls.
- Cores were subcored to obtain pristine material (Figure 3)

Molecular methods
- DNA was extracted using Power Soil kits from six grams of each sediment sample
- DNA yield was >1 ng DNA/g sediment
- PCR amplification (bacterial primers 8F and 928R; 35 cycles) and dilution of the DNA (Figure 4) indicated that PCR inhibitors were minimal
- Terminal-restriction fragment length polymorphism (t-RFLP) was used to measure bacterial diversity in the respective samples. Non-metric multidimensional scaling (NMDS) was then used to determine the factors that may have influenced bacterial diversity. NMDS analysis revealed that sediment samples were distinct from those obtained from drilling fluids suggesting that the samples were not contaminated by the drilling fluids. All samples had evidence of microbial communities and sample depth, temperature, and hydrate presence appeared to have some influence on community diversity. Samples sharing these environmental parameters often shared common t-RFLP profiles. Further examination of selected samples using clone libraries should help to identify the key taxa present in these unique sediments and yield a better understanding of the biogeochemistry of these gas-bearing systems.

Next Steps and Future
- Completion of 16S rDNA clone libraries developed from DNA extracted from selected or representative cores
- Consideration of sample mineralogy to determine importance of this factor in structuring microbial communities
- Continuous coring and sampling from the surface through the permafrost and into the hydrate zone beneath would provide a complete picture of microbial communities and their functional potential in this sensitive environment.

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References


Figure 1. Location of Mt Elbert gas hydrate well site.

Figure 2. Depth profile for samples acquired from the Mt Elbert gas hydrate well showing geographic formations and microbiology sample locations (red circles, far right).

Figure 3. Results of PCR amplification following dilution of two selected samples.

Figure 4. Generalized strategy for terminal restriction length polymorphism (t-RFLP) analysis of DNA from complex communities (from Gruntzig et al. 2002. Mich. State Univ.).

Figure 5. NMDS plot of t-RFLP data. Samples from hydrate zones (red), non-hydrate zones (green), and drilling fluids (green, circled) are shown.

Figure 6. NMDS plot of t-RFLP data (drilling mud samples excluded). Environmental factors included in the analysis include depth, hydrate presence, grain size, density derived porosity, temperature, mud gas methane, drilling rate, and gamma (mg. Environmental factors that align consistently with axis 2 are depth (R=0.63), hydrate presence (R=0.46), and temperature (R=0.82).

Figure 7. NMDS plot of t-RFLP data showing the operational taxonomic units (OTUs) or terminal restriction fragments (t-RFs) that define respective clusters of samples as highlighted in blue boxes.