

Microbial communities in shallow-sea hydrothermal environment of the Kueishantao Island, Taiwan

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Shallow-sea hydrothermal systems provide easy access to investigating the extent of microbial communities residing in oceanic crustal environments, and the biotic and abiotic interactions along steep physiochemical gradients. This study analyzed venting fluids, pore fluids, surface biofilms and sediments collected from the yellow and white vent areas of the Kueishantao hydrothermal field offshore northeastern Taiwan. Molecular screening of 16S rRNA genes revealed that bacteria and archaea existed ubiquitously in nearly all samples (except for the absence of archaea in biofilms). Of all sequences detected, the bacterial members were affiliated with *Proteobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Chloroflexi*, *Verrucomicrobia*, and *Firmicutes*, whereas the archaeal members were related to *Thermococci*, *Thermoplasmata*, and *Thermoprotei*. Communities in the yellow vent area were composed of all phyla and classes described above. In contrast, only ϵ -*Proteobacteria*, *Firmicutes*, *Thermococci*, and *Thermo-plasmata* were detected in the white vent area. The ϵ -*Proteobacteria* related sequences generally constituted a significant proportion of bacterial libraries, and were more abundant in the white vent area. Thirty strains were isolated from enrichments incubated at 40 °C. These strains were phylogenetically affiliated with α - and γ -*Proteobacteria*, and grew autotrophically or organotrophically by using H₂/O₂, S⁰/O₂, As³⁺/O₂, or complex organic carbon for energy acquisition at acidic or neutral pH. Sequences related to these strains only constituted a small proportion of bacterial libraries in some samples. Overall, the prevalence of potential sulfur-respiring microorganisms, such as ϵ -*Proteobacteria* and *Thermococci* suggests elemental sulfur as an important energy source, and is consistent with the enriched content of elemental sulfur observed during sampling. The contrasting diversities in different areas and highly similar structures within individual areas further indicate that hydrothermal fluids might entrain variable fractions of seawater along different circulation pathways, enabling the proliferation of microbial communities sustained by distinct energy sources and geochemical characteristics.

'Biogenic natural gas' formation in a pressurized lab scale reactor

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It is known that methanogenic micro-organisms produce biogenic natural gas by degrading organic matter in natural gas fields. Methanogens also produce biogas in anaerobic digestion technology [1]. However, biogas generally consists of 55-65% CH₄, ~35% CO₂, and some H₂O, H₂S and NH₃. Our aim was to simulate biogenic natural gas formation in a lab scale pressurized reactor vessel, to see whether natural gas quality could be obtained in a single step reactor system. To do so, pressure reactors were used to simulate CH₄ and CO₂ production from organic matter by mixed culture methanogenic biomass under varying reactor conditions. Temperature, pressure and pH were monitored online with pressure resistant sensors. The lab-scale setup allowed sampling at short time intervals under varying environmental conditions. To determine microbiological organic intermediates, CH₄ and CO₂ production, HPLC and GC were used. Cryo-SEM EDX, FT-IR and TGA-MS were used to acquire information on carbonate precipitates.

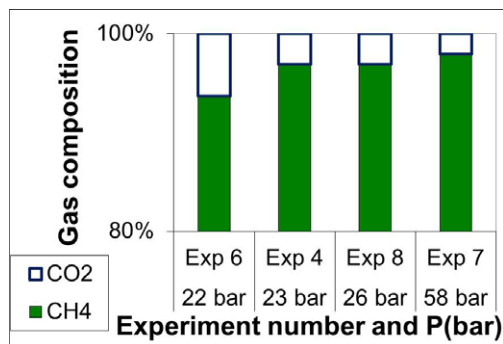


Figure 1: Overview of some experimental gas compositions

Discussion of results

The combination of analytical results highlighted the influence of microbe-mineral interactions on lab-scale biogenic natural gas formation. As a consequence, we found a way to biologically generate pressures up to 90 bar, with 80-97% CH₄-content within a week [2], only limited by the reactor safety limitations.

[1] Stams & Plugge (2009) *Nature Review Microbiology* 7, 568–577. [2] Lindeboom *et al.* (accepted for publication) *Water Science & Technology*.