

Microbial diversity of the Grímsey High-Temperature Vent Field on the Subpolar Mid-Atlantic Ridge

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Background

One of the most active neovolcanic centers on Earth can be found in Iceland, which is dominated by the subaerial expression of the Mid-Atlantic Ridge (MAR) system crossing the Iceland hot spot. Active spreading in the North of Iceland is found along on a 75 km wide area known as the Tjörnes Fracture Zone. During two cruises of R/V Poseidon in 1997 and 1999, a very large area of hydrothermal activity was discovered at shallow depth east of Grímsey Island, right across the Arctic Circle.

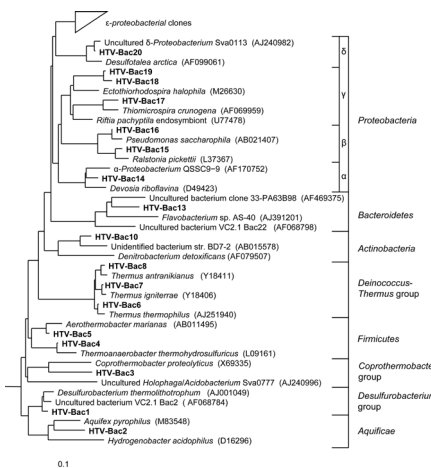
The Grímsey vent field is characterized by emission of high-temperature fluid (250°C) through large anhydrite chimneys, associated with vast zones of percolation hot water (50 to 80°C) through thick layers of mixed glacial and volcanic sediments and large anhydrite deposits at 400 m depth. Grímsey vent fields differ from other hydrothermal sites close to the Equator by depth and the presence of a large geographical barrier constituted by the Icelandic continental shelf splitting the MAR in two.

In situ bacterial colonization experiments were conducted at 394 m depth by a 2-man research submersible JAGO and the research vessel R/V Poseidon (Cruise 253). DNA was extracted from the concentrated biomass samples and clones were sequenced.

Results

Species composition of the Bacteria

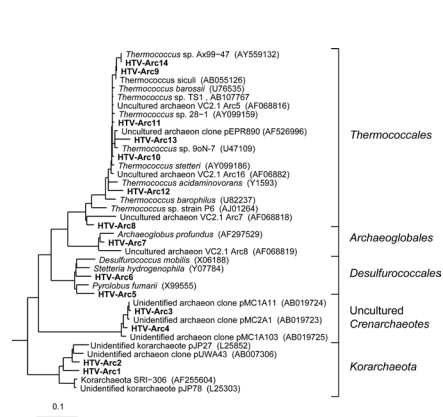
A total of 219 partial (~500–600 nt) or nearly full-length (~1400 nt) clones were obtained from two libraries. Sample JO7-8 was almost exclusively composed of OTUs related to μ -Proteobacteria whereas JO7-9 contained all other bacterial phylotypes as well as μ -Proteobacteria. No distinct particularities in the μ -proteobacterial species composition could be observed between samples JO7-8 and JO7-9.



Evolutionary neighbour-joining phylogenetic dendrogram of the bacterial 16S rRNA sequences detected in the Grímsey high-temperature vent field.

Species composition of the Archaea

Archaeal ribosomal genes were successfully amplified from sample JO7-8 but not from sample JO7-9 despite many attempts. The Archaea 16S rRNA gene library from JO7-8 was largely dominated by clones related to Thermococcales (91%), and the few other clones assigned to the Archaeoglobales (1%), Thermoproteales (2%), uncultured Crenarchaeota group (4%) and Korarchaeota (2%) (Table 2 and Figure 3).



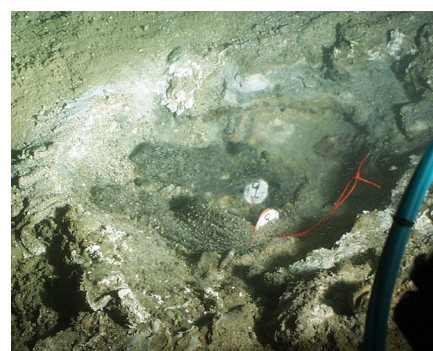
Evolutionary neighbour-joining phylogenetic dendrogram of the archaeal 16S rRNA sequences detected in the Grímsey high-temperature vent field.



The submersible JAGO about to dive



Photo on chimney structure in the ocean floor vent field near Grímsey



In situ enrichment was performed at a zone with shimmering hot water

Conclusions

This study brings the first results on the microbial diversity high-temperature vent field of Grímsey. The results suggest that the bacterial communities in the Grímsey vent field are most likely characterized by isolated populations due to geographical discontinuities between hydrothermal sites. The geological uniqueness of the hydrothermal vent field is reflected by presence of distinct populations, in particular among the μ -Proteobacteria and much lower microbial diversity than in hydrothermal or pelagic sediments.