Correlating microbial community profiles with geochemical data in highly stratified sediments from the Arctic Mid-Ocean Ridge

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AUTHOR SUMMARY

Marine sediments host the largest reservoir of organic carbon and the largest number of microorganisms in the world (1, 2). These microorganisms form highly complex communities with a metabolic activity that profoundly affects global biogeochemical cycles. Understanding their function and structure is crucial for predicting the fate of carbon and other essential elements in the marine system. However, the vast majority of subsurface microorganisms are poorly characterized, and their physiological activities remain unknown. Here, we show that the structure of the microbial community correlates directly with geochemistry, allowing us to determine factors that shape the composition and to predict metabolic properties of the most abundant microbial taxa in deep-sea sediments.

The geochemical and physical properties of the sediments are considered the main determinants of microbial community structures, because they influence the availability of the various electron donors (e.g., organic carbon) and acceptors (e.g., iron oxide) required to sustain specific energy-yielding metabolic pathways. However, finding direct quantitative correlations between overall community structure and geochemical variation has remained challenging.

We investigated the link between geochemistry and microbial communities in two 3-m-long sediment cores from the ultraslow-spreading Arctic Mid-Ocean Ridge system. The cores were retrieved 15 km southwest and 15 km northeast of the active hydrothermal field Loki's Castle (Fig. P1A) (3). The site is one of only a few localities where substantial sediment accumulates in a rift valley and where hydrothermal material is deposited. The unusually strong geochemical layering within relatively shallow cores (Fig. P1 B and C) allowed us to study how large changes in sediment geochemistry relate to changes in the microbial communities.
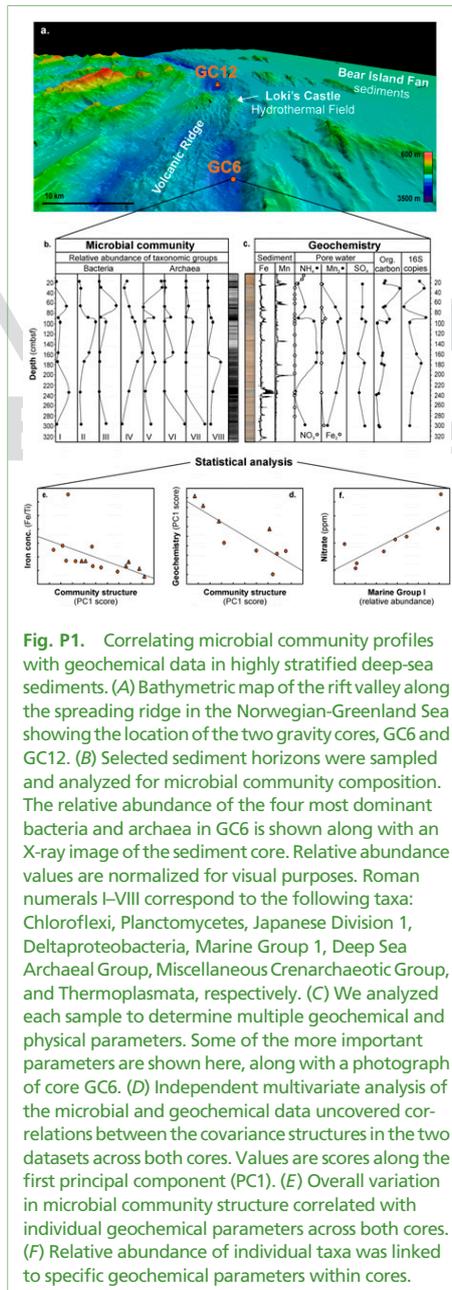

Fig. P1. Correlating microbial community profiles with geochemical data in highly stratified deep-sea sediments. (A) Bathymetric map of the rift valley along the spreading ridge in the Norwegian-Greenland Sea showing the location of the two gravity cores, GC6 and GC12. (B) Selected sediment horizons were sampled and analyzed for microbial community composition. The relative abundance of the four most dominant bacteria and archaea in GC6 is shown along with an X-ray image of the sediment core. Relative abundance values are normalized for visual purposes. Roman numerals I–VIII correspond to the following taxa: Chloroflexi, Planctomycetes, Japanese Division 1, Deltaproteobacteria, Marine Group 1, Deep Sea Archaeal Group, Miscellaneous Crenarchaeotic Group, and Thermoplasmata, respectively. (C) We analyzed each sample to determine multiple geochemical and physical parameters. Some of the more important parameters are shown here, along with a photograph of core GC6. (D) Independent multivariate analysis of the microbial and geochemical data uncovered correlations between the covariance structures in the two datasets across both cores. Values are scores along the first principal component (PC1). (E) Overall variation in microbial community structure correlated with individual geochemical parameters across both cores. (F) Relative abundance of individual taxa was linked to specific geochemical parameters within cores.

We generated an extensive geochemical dataset and performed a comprehensive microbial profiling from 15 distinct sediment horizons. Determining the sequences of ~60,000 microbial 16S rRNA genes provided detailed taxonomic information across both prokaryotic domains (Fig. P1B). By determining the relative abundance of taxonomic groups within each sample, we were able to characterize changes in community structure quantitatively. This analysis demonstrated that the sediments were dominated by several microbial groups known to be ubiquitous in marine sediments. However, the relative abundances of these groups varied substantially among horizons and fluctuated between Bacteria- and Archaea-dominated communities. Moreover, the two cores differed markedly in both geochemical and microbial profiles.

To compare microbial and geochemical variation directly, we distilled the covariance structures of the relative microbial abundance and geochemical data independently by using principal component analysis. We found a significant correlation between changes in the overall geochemical

composition and changes in the overall community structure across the two cores (Fig. P1*D*). We identified four individual geochemical parameters tightly linked to the taxonomic distribution of microorganisms: total organic carbon, iron content (Fig. P1*E*), manganese content, and sulfate concentration in the pore water. Therefore we concluded that organic carbon and mineral (iron and manganese) content are key determinants of microbial community structure. Conversely, the community structure is a likely determinant of the sulfate concentration. This dataset can be used to build hypotheses about the energy metabolism of uncharacterized groups of organisms, including two of the most abundant archaeal groups: the Deep Sea Archaeal Group and sediment lineages of potentially anaerobic Marine Group I (Fig. P1*F*). We predict that heterotrophic iron oxide reduction and anaerobic ammonia oxidation are the most likely metabolic activities of these two groups, respectively.

The detailed molecular and chemical study of these highly stratified sediment cores offered a unique possibility to correlate stratigraphic variation in geochemical properties directly to stratigraphic variation in microbial community structure as well as to the relative abundance of individual taxa. Our findings shed light on key factors that shape community structure and help constrain possible metabolisms of the most typical and abundant prokaryotic lineages found in marine sediments. Improved understanding of microbial function and structure in this system is crucial for predicting the long-term fate of carbon and other essential elements in the face of global environmental changes.

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