



## Geomicrobiology of Fe-rich crusts in Lake Superior sediment

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The limnological puzzles of Lake Superior are increasingly attracting scientists, and very little is known about the sediments and their associated microflora. The sediments are organic poor (less than 5% C) and the lake is deep oligotrophic, with water temperatures at the bottom around 3°C. Previous studies reveal Fe-rich layers in the sediments at multiple locations around the lake. The origin and mechanisms of formation of this layer remain unknown. In this study we investigated geochemical and microbiological processes that may lead to the formation of a two cm thick iron layer about 10 cm below the sediment surface. Sediment cores from two stations (EM, 230m water depth and ED, 310m water depth) in the East Basin were used. We monitored oxygen and pH depth profiles with microsensors, porewater and sediment solid matter were analyzed for nutrient and metal contents. Furthermore, phosphorus and iron sequential extractions of sediment cores have been performed. The total cell count was determined using DAPI epifluorescence microscopy. DNA was extracted from the sediment samples and 16S ribosomal RNA amplicons were analyzed with denaturing gradient gel electrophoresis (DGGE). For a more in depth analysis, DNA samples from 8-10 cm and 10-12 cm were sent to the Research and Testing Lab (Texas) for pyrosequencing of 16S rRNA gene amplicons amplified using barcoded universal primers 27f-519r.

The scanning electron microscope (SEM) images from the iron layer 10-12cm show filaments that were encrusted with spheres ca. 20 nm in diameter. SEM observations of thin sections also indicate the presence of very fine particles showing various morphologies. Analyses of the deposit material by SEM and energy dispersive X-ray spectroscopy (EDS) indicate that bacteria cells surfaces served as nucleation surfaces for Fe-oxide formation. EDS line-scans through bacterial cells covered with precipitates reveal phosphorus and carbon peaks at interface between cell surface and Fe-particles.

The cluster analysis performed on the DGGE separation of ribosomal RNA gene fragments revealed that the two iron layers were not highly similar to each other. We obtained a total of 26,062 16S rRNA gene sequence reads from the two iron layers and the layers directly above them, which were clustered into operational taxonomic units sharing 80% similarity or more. 64-70% of these clusters could not be classified below the phylum level. While the 8-10 cm sediment layers were dominated (46.5% of reads) by relatives of Paenibacillus, the iron layers contained far fewer gram positive organisms, far more proteobacteria, and a high proportion of Nitrospira species which show relatively high similarity to organisms found in an iron II rich seep.