Isolation and Genomic Analysis of Bacteria that drive biogeochemical cycling in Prairie Pothole Lake sediments

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Introduction and Background

• Prairie pothole lakes (PPLs) are small wetlands in the upper Midwest/Northern Great Plains of the United States, and southern Canada that cover approximately 750,000 km².
• Biogeochemistry of the PPLs is characterized by reducing conditions coupled with high concentrations of dissolved organic carbon (DOC) and varying sulfur species, including sulfide, sulfur, sulfites, and polysulfides.
• Lake sediments and waters contribute to the global cycles of carbon and sulfur by releasing large amounts of greenhouse gases including methane and carbon dioxide, resulting from the microbial breakdown of complex carbon sources.
• Sulfide reducers are energetically favored in the competition for substrates with microorganisms involved in the methanogenic degradation pathways, resulting in a considerable diversion of the carbon flow from methane to carbon dioxide.
• Sulfide is a toxic compound not typically found excessively in freshwater media (FW).

Measurements of sulfide in PPL sediments and pore waters are frequently recorded between 2-3 mM.

The environment.

Biogeochemistry of the PPLs is characterized by reducing conditions coupled with high concentrations of dissolved organic carbon (DOC). Freshwater media (FW), including lakes and rivers, can further begin to comprehend the role and impact of microorganisms involved in the microbial breakdown of complex carbon sources.

Substrate utilization.

Sulfate

• Two isolates resulted from enrichments including a SRB (denoted 1L) and a fermenter, YPD1. 16S rRNA was extracted and confirmed 1L and YPD1 as close neighbors to Desulfovibrio magneticus. Genomic DNA for YPD1 was sent for sequencing to the Joint Genome Institute (JGI) and established its identity as a strain of Proteobacteria; Desulfovibrio.
• In February 2016, genomic DNA was extracted from 1L and sent for sequencing to the Genomics Shared Resource (GSR) facility at the Ohio State University using the Illumina HiSeq2500 sequencing platform. A genome with an estimated 3900 genes resulted.

A maximum likelihood tree was constructed with neighbors from the SILVA and NCBI BLAST databases for isolate 1L.

By understanding microbial processes in lake sediments that drive carbon and sulfur cycles, we can further begin to comprehend the role and impact of freshwater wetland systems on the global carbon cycle and apply our knowledge of PPL to similar systems in other parts of the world.

Identification of Isolates

Physiology and Characterization

The physiology of 1L was characterized by experiments for sulfide tolerance, salinity tolerance, and growth on various organic and inorganic substrates.

1L: Genomic Preview

The draft genome of isolate 1L was annotated and resulted in a predicted ~3900 genes across 232 scaffolds. The following are genes of interest currently identified. Further analysis via the program ITEP (An integrated toolkit for exploration of microbial pan-genomes) will be used to observe genes conserved across related organisms.

Sulfate Reduction Process

Ability to reduce multiple oxidized sulfur species (sulfate, thiosulfate)

DNRA (dissimilatory nitrate reduction to ammonium)
Mechanism for disposing of excess redundant in environments with abundant electron donor

Direction and Discussion

We successfully isolated a sulfate-reducing bacterium and a fermenter under anaerobic conditions. Physiological experimentation has helped us understand 1L’s metabolic capabilities, with this isolate showing some tolerance to elevated aqueous sulfide concentrations. Further analysis of this microorganism’s genome will enable further hypotheses to be developed and tested, and will enable inferences to be made regarding interactions between such SRB and other community members in PPL sediments and pore waters. Such interactions likely play key roles in carbon and sulfur cycling in these systems and also regulating contaminants and compounds.

Future Research Goals

• Expand our knowledge of isolate 1L by exploring its genome
• Derive a relationship between isolate 1L and other community members (methanogenic archaea)
• Use our scaled system to test our hypotheses about larger scale biogeochemistry in the Prairie Pothole Lake region