The Properties of and Microbial Interactions with Natural Organic Matter Extracted from Oak Ridge FRC

Romy Chakraborty[1]* (rchakraborty@lbl.gov), Xiaoqin Wu[1], Sindhu Jagadamma[2], Terry C. Hazen[2], Nicholas Justice[1], Stefan Jenkins[1], Trent R. Northen[1], Matthew W. Fields[3], Patricia Fox[1], Peter Nico[1], Adam P. Arkin[1] and **Paul D. Adams**[1]

[1]*Lawrence Berkeley National Laboratory, Berkeley CA;* [2]Oak Ridge National Laboratory, Oak Ridge, TN & University of Tennessee, Knoxville, TN; [3]Montana State University, Bozeman, MT

Project Goal: Natural organic matter (NOM) availability and transformations determines much of the carbon (C) flux in subsurface environments. However, the molecular signature of this pool of C is largely unknown, and the microbial activities that regulate NOM turnover are still poorly resolved. The goal of this discovery project was to ascertain physical and chemical characteristics of NOM, using minimally destructive techniques that retains the originality of the material, and to use it as a C source in enrichments to study it's turnover by microbial communities at Oak Ridge FRC. Discovery projects are short term, high impact, investigatory efforts to drive changes in science or technological capability that deeply impact the program in some way.

NOM was obtained by extracting FW305 and FW306 sediment samples from different depths using MilliQ-water via shaking and sonication. Using this extraction, total organic C in NOM was 0.4% in the surficial layers and dropped to 0.15% in the deeper layers. The amount of inorganic C in extracted NOM decreased significantly with depth. Results from UV and FTIR analyses showed that extracted NOM mainly contained aromatic and unsaturated compounds in shallower depths and mostly polysaccharides in deeper sediments. HPSEC was used to study the molecular weight distribution of the NOM and a stirred ultrafiltration cell was used to fractionate the extracted NOM based on molecular weight. Extracted NOM was provided as the sole C source to microbes present in background well waters of Oak Ridge FRC. Analysis of the enriched microbial community, and transformed NOM metabolites was carried out. Several fine-scale chemical techniques including FTIR, LC-TOF-MS, and Orbitrap were used to characterize the metabolites, and 16S rRNA sequencing and metatranscriptomics were used to identify the changes in microbial communities in these enrichments.

This material by ENIGMA- Ecosystems and Networks Integrated with Genes and Molecular Assemblies (http://enigma.lbl.gov), a Scientific Focus Area Program at Lawrence Berkeley National Laboratory is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological & Environmental Research under contract number DE-AC02-05CH11231