LBNL-58332

Completed Genome Sequence of *Dechloromonas aromatica*: Analysis of a Microbe with Diverse Bioremediative Capability in Anaerobic Environments

J.D. Coates, K. V. Kellaris, W. S. Feil, H. Feil, L.A. Achenbach, R. Chakraborty, C. Shang, E. Alm, K. Huang, M. Price, K. Keller, S. Trong, G. Di Bartolo, A. Arkin, A. Lapidus, P. M. Richardson, F. W. Larimer, and S.M. O'Connor
Dept. Plant and Microbial Biology, Univ. of California, Berkeley, CA

Our previous NABIR-funded studies using pure culture members of the *Dechloromonas* and closely related *Dechlorosoma* genera have demonstrated that radionuclides such as uranium and cobalt are rapidly removed (as much as 80% of the initial 100 μM within 5 days) from solution during the biogenic formation of Fe(III)-oxides resulting from anaerobic nitrate-dependent microbial Fe(II) oxidation. In the case of uranium, x-ray diffraction analysis indicated that the uranium was in the hexavalent form (normally soluble) and was bound to the precipitated Fe(III)-oxides, thus demonstrating the potential of this process. These studies indicate great promise for providing a long-term solution to heavy metal and radionuclide contamination in the environment.

However, to date, nothing is known of the underlying molecular mechanisms or regulatory processes involved in the anaerobic oxidation of Fe(II) by microorganisms. *Dechloromonas aromatica* strain RCB is a β-Proteobacterium found ubiquitously in soil and sediment environments. It is a motile facultative anaerobe, capable of nitrate-dependent Fe(II) oxidation, anaerobic aromatic hydrocarbon degradation, and dissimilatory perchlorate reduction. It was first isolated from Potomac River sediments based on its ability to anaerobically metabolize 4-chlorobenzoate coupled to perchlorate reduction. With its metabolic versatility, *D. aromatica* strain RCB was selected for complete genome sequencing at the DOE Joint Genome Institute, Walnut Creek, CA. The completed sequence consists of a single circular chromosomal DNA structure containing a total of 4.5 Mb of DNA with a G+C content of 60%. Initial draft annotation was conducted at Oak Ridge National Laboratory and the Virtual Institute for Microbial Stress and Survival (http://escalante.lbl.gov), identifying approximately 4,000 open reading frames (ORFs). The closest relative with a completed genome sequence is *Ralstonia solanacearum*, also a gram-negative β-Proteobacterium. *D. aromatica* and *Ralstonia* possess very similar genomic content, duplicative 23S and 16S RNA regions, and identical operon structures for many families of genes. In *Ralstonia*, many catabolic capabilities are thought to be concentrated within plasmid DNA structures. However, *D. aromatica* lacks a large genomic plasmid element (the *Ralstonia* pGMI1000MP plasmid is 2.09 Mb in size), which indicates its metabolic versatility is not dependent on a highly transmissible and mutable plasmid structure. *D. aromatica* genes have been annotated for InterPro domains, EC assignments, TIGRfams, KEGGS pathways, and GO ontologies. Genes that likely reflect the versatility of *D. aromatica* within the environment include a remarkably high number of two-component sensors and regulators (11% of the annotated ORFs), placing it in the top 5% of microbial genomes in this capability. The *D. aromatica* genome has been found to contain RuBisCo, indicating the ability to fix carbon dioxide; however, to date the environmental conditions required for the expression of this phenotype have not been identified.

The availability of the completed and partially annotated genome sequence provides us the opportunity to design and utilize a custom *D. aromatica* microarray to identify genes that are up-regulated under Fe(II)-oxidizing conditions and, thus, presumably involved in this anaerobic metabolism.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under Contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under Contract No. W-7405-ENG-36.