Anaeromyxobacter dehalogenans Strain 2CP-C Employs Distinct Metabolic Activities for Growth with Metal vs. Non-metal Electron Acceptors

Xiaoxin Liu[3,4], Karuna Chourey[3], Silke Nissen[1,2], Robert Hettich[3,4], Susan Pfiffner[5], and Frank Löffler[1,2,6]

[1] Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA.
[2] Department of Microbiology, University of Tennessee, Knoxville, TN 37996, USA.
[3] Chemical Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA.
[4] Graduate School of Genome Science and Technology, University of Tennessee, Knoxville, TN 37919, USA.
[5] Center for Environmental Biotechnology, University of Tennessee, Knoxville, TN 37996, USA.
[6] Department of Civil and Environmental Engineering, University of Tennessee, Knoxville, TN 37996, USA.

Anaeromyxobacter dehalogenans strain 2CP-C is a facultative Gram-negative Gamma-proteobacterium related to the *Myxobacteria*. Unlike other members of *Myxobacteria*, which were considered obligate aerobes, *A. dehalogenans* is capable of growth and survival in anoxic and suboxic environments. Studies of anaerobic growth of strain 2CP-C revealed tremendous respiratory versatility, as evidenced by the ability to utilize a range of electron donors (e.g. acetate, hydrogen, pyruvate, lactate, succinate, formate) and electron acceptors (e.g. nitrate, fumarate, halogenated phenols, ferric iron, nitrous oxide, etc.). In particular, the dissimilatory metabolic reduction of metals, including radionuclides, by strain 2CP-C spurred interest for *in situ* bioremediation of contaminated soils and sediments.

In order to understand the cellular mechanisms that enable this microbe to survive under different environmental conditions, a mass spectrometry-based proteomics approach was implemented to characterize the proteome profiles of strain 2CP-C grown with various electron acceptors. A total of eight growth conditions were tested, providing a global survey of the proteome-wide responses to different electron acceptors. The pan-proteome consists of 2,846 proteins, representing 65% of predicted open reading frames. The results also revealed a core proteome of 710 proteins that comprise the fundamental cellular machinery needed regardless of varying electron-accepting environments. To visualize proteins significantly changed between growth conditions, differentially abundant proteins were mapped to metabolic pathways in KEGG database using iPath 2.0. Significantly abundant proteins in metal electron acceptor growth mapped to metabolic pathways participating in the TCA cycle, and amino acid, nucleotide and carbohydrate metabolism, whereas significantly abundant proteins in non-metal electron acceptor growth mostly involved in regulatory pathways for translation and cell motility. Metabolic pathways mapping clearly indicated elevated expression of energy production pathways in growth with metal electron acceptors. Amino acid and nucleotide metabolism also demonstrated significant higher abundance levels in metal electron acceptor- growth, which could be a result of overall higher expression of energy-generating pathways in cells grown with metal electron acceptors.

Taken together, the ANOVA analysis and pathway mapping results demonstrated the distinct effects of metal and non-metal growth conditions on the proteome expression of *A. dehalogenans* strain 2CP-C. In particular, growth with metal electron acceptor resulted in elevated abundances for proteins involved in energy production compared to cells using non-metal electron acceptors.