Microbial community development under iron-reducing conditions in wetland sediment microcosms amended with electron shuttles

THEODORE M. FLYNN[1], MARGARET F. SLADEK[1], ZENA D. JENSVOLD[1], CHRISTOPHER W. MARSHALL[1], DIONYSIOS A. ANTONOPOULOS[1], JASON C. KOVAL[1], KENNETH M. KEMNER[1], EDWARD J. O'LOUGHLIN[1]

[1]Argonne National Laboratory, Biosciences Division, Argonne, IL, USA (tflynn@anl.gov, oloughlin@anl.gov)

Dissimilatory metal-reducing bacteria (DMRB) are ubiquitous in sedimentary environments, gaining energy by coupling the oxidation of reduced organic compounds or H_2 to the reduction of iron and other metal oxides. As these minerals are poorly soluble at the temperature and pH ranges typical of many terrestrial environments, many DMRB use soluble electron-shuttling compounds to aid the transfer of electrons to these extracellular electron acceptors. Pure culture studies suggest electron shuttles enhance the overall rate of iron reduction, yet little is known about how these compounds affect native communities of microorganisms under iron-reducing conditions. We created wetland sediment microcosms amended with goethite (α-FeOOH) and either acetate or H_2 to examine the effect of quinone-based electron shuttles with different redox potentials have on the rate of iron reduction, the onset of methanogenesis, and the trajectory of microbial community development. Unlike pure culture experiments, microcosms given 9,10-anthraquinone-2-carboxylic acid (AQC) or 5-hydroxy-1,4-naphthoquinone (lawsone, NQL) showed no increase in the rate of iron reduction relative to control experiments with no shuttle (NS) added. The rate and extent of iron reduction increased significantly, however, in microcosms amended with sulfonated anthraquinones (AQS, AQDS) and 1,2-dihydroxy-9,10-anthraquinone (AQZ). Methanogenesis did not begin until ferrous iron production ceased in all microcosms save those amended with AQC, where it was inhibited entirely. The microbial commmunity in AQC-amended microcosms differed substantially from the others. 16S rRNA sequences classified as *Geobacter* and/or *Desulfuromonas* dominated NS microcosms as well as those amended with AQDS, AQS, AQZ, and NQL, though the relative abundace of specific operational taxonomic units (OTUs) depended on the shuttle used. AQC microcosms were instead dominated by *Pelobacter* (acetate-amended) or *Shewanella*. These results suggest both redox potential and electron donor determine, in part, the extent and mechanism of iron reduction as well as the specific DMRB carrying out this process.