

## 4.3.18

### Biosynthesis and dietary uptake of PUFAs by piezophilic bacteria, implications for marine biogeochemistry

J. FANG<sup>1</sup>, O. CHAN<sup>1</sup>, N. AGARKAR<sup>1</sup>, C. KATO<sup>2</sup> AND T. SATO<sup>2</sup>

<sup>1</sup>Department of Geological and Atmospheric Sciences, Iowa State University, Ames, Iowa 50011, USA  
(jsfang@iastate.edu)

<sup>2</sup>Department of Marine Ecosystems, Japan Marine Science and Technology Center, 2-15 Natsushima-cho, Yokosuka 237, Japan

The biochemistry of piezophilic bacteria is unique in that the piezophiles produce polyunsaturated fatty acids (PUFAs). A pertinent question is if piezophilic bacteria synthesize PUFA de novo, through dietary uptake, or both. This study was undertaken to examine the biosynthesis and cellular uptake of PUFAs by piezophilic bacteria. A moderately piezophilic (*Shewanella violacea* DSS12) and two hyperpiezophilic bacteria (*S. benthica* DB21MT-2 and *Moritella yayanosii* DB21MT-5) were grown under 50 MPa (megapascal) and 100 MPa, respectively, in media containing marine broth 2216 supplemented with arachidonic acid (AA, sodium salt) and/or antibiotic cerulenin. There was active uptake and cellular incorporation of AA in the hyperpiezophilic bacteria DB21MT-2 (14.7% of total fatty acids) and DB21MT-5 (1.4%), but no uptake was observed in DSS12. When cells were treated with antibiotic cerulenin, all three strains incorporated AA into cell membranes (13 to 19%). The biosynthesis of monounsaturated fatty acids was significantly inhibited (10 to 37%) by the addition of cerulenin, whereas the concentrations of PUFAs increased by 2-4 times. These results suggest that piezophilic bacteria biosynthesize and/or incorporate dietary polyunsaturated fatty acids that are important for their growth and piezoadaptation. The significance of these findings is also discussed in the context of phenotypic classification of piezophiles.

## 4.3.21

### Changes in microbial response for natural organic matter promoted metal inhibition during Fe(III)-oxide bioreduction

J.J. STONE<sup>1</sup>, W.D. BURGOS<sup>2</sup>, AND S.S. RUEBUSH<sup>3</sup>

<sup>1</sup>Department of Civil and Environmental Engineering, South Dakota School of Mines and Technology  
(James.Stone@sdsmt.edu)

<sup>2</sup>Department of Civil and Environmental Engineering, The Pennsylvania State University (bburgos@psu.edu)

<sup>3</sup>Department of Biochemistry and Molecular Biology, The Pennsylvania State University (ssr123@psu.edu)

A developing technology for the in situ treatment of metal and radionuclide contaminants is the stimulation of dissimilatory metal-reducing bacteria (DMRB) to reduce solid phase iron oxides which promote Fe(II) induced chemical reduction of contaminants. Natural organic matter (NOM) can stimulate the biological reduction of solid-phase iron oxides by serving as an electron shuttle and by complexing biogenic Fe(II). The addition of NOM to contaminated zones has been proposed to further stimulate iron reduction and the fortuitous reduction and immobilization of contaminants. However, little research has been conducted on quarternary systems that contain DMRB, ferric oxides, NOM, and metals or radionuclides. The effect of zinc, a common US-Department of Energy contaminant, on the biological reduction of hematite by two different DMRB species, *Shewanella putrefaciens* CN32 and *Shewanella oneidensis* MR1 was studied. Previous work with CN32 demonstrated that, in the presence of NOM, increased inhibition of hematite bioreduction occurred with increasing concentrations of zinc. However, similar experiments performed with MR1 showed that NOM decreased zinc inhibition. Additional experiments were performed with cell membrane fractions isolated from anaerobically-grown MR1, capable of solid-phase Fe(III)-reduction, and incubated with hematite, zinc and NOM. These experiments also demonstrated that NOM did not increase zinc toxicity. These results suggest differences in cell outer membranes between these two DMRB species must account for contradictory responses to metal-NOM complexes.