Community Composition of Iron(III)-Reducing Bacteria from Subsurface Sediments of the Field Research Center

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To test the bioremediation potential of the acidic uranium-contaminated sediment in Area 1 at the FRC, we focused on Fe(III)-reducing bacteria (FeRB), as they represent the indigenous microorganisms capable of immobilizing uranium in situ. Thus, we extracted DNA from more than 20 Fe(III)-reducing MPN tubes cultured at both neutral and low pH. Over 850 clones were screened in order to detect the organisms most suited for in situ bioremediation at this site. Through cloning and sequencing experiments, we found considerable differences in phylotype between Fe(III)-reducing enrichments from background and contaminated FRC sediment. In the background Fe(III)-reducing MPN tubes (pH7), over two-thirds of the 16S rRNA gene sequences obtained were closely related to members of the *Geobacteraceae* family. In contrast, sediment from the contaminated pH 7 Fe(III)-reducing MPN tubes revealed that almost half of the 16S rRNA gene sequences were 96% similar to the halogen-respiring species *Anaeromyxobacter dehalogenenans*, but no *Geobacteraceae* sequences were detected. In the Fe(III)-reducing MPN tubes cultured at low pH (4 to5), only 16S rRNA gene sequences closely related to gram-positive organisms were detected. From the contaminated enrichments cultured at low pH, the most predominant 16S rRNA gene sequences were closely related to the gram-positive organisms *Brevibacillus* and *Paenibacillus*. T-RFLP analysis of enrichment cultures strongly supported the cloning and sequencing results. Our current work is focused on the determination of bioremediation potential by following selected groups of FeRB before and after sediment biostimulation through the addition of selected carbon sources (in conjunction with push-pull experiments being carried out by Istok et al.). Using DNA extracted directly from the sediment, both MPN-PCR and real-time PCR are being conducted in order to quantify the differences in abundance of *Geobacter*-, *Anaeromyxobacter*-, *Paenibacillus*-, and *Brevibacillus*-type 16S rRNA gene sequences. Our results suggest that new model Fe(III)-reducing organisms should be pursued to aid in the ongoing development of bioremediation strategies for uranium contamination in acidic subsurface sediments.