Identification of Metal Reductases and Determination of Their Relative Abundance in Subsurface Sedimentary Systems Using Proteomic Analysis

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Heavy metal and radionuclide contamination at U.S. Department of Energy (DOE) sites nationwide constitutes a major environmental problem. Of particular interest are U and Tc, as well as Fe and Mn due to their potential direct and indirect effects on contaminant biogeochemical behavior. For the past decade bacteria that utilize metals as terminal electron acceptors have been isolated and identified. These bacteria include members of three major anaerobic groups: the denitrifying, sulfate-reducing, and Fe(III)-reducing bacteria. The electron transfer pathways within these bacteria are still not well understood. Moreover, this lack of information substantially impedes efforts to increase in situ bioremediation efficiency. Hence, identification of metal reductases and determination of their similarity among these bacterial groups are essential for understanding these mechanisms and assessing bioremediative potential at DOE sites. We have begun to utilize the genomic sequence available for these organisms in conjunction with mass spectrometry-based proteomics approaches to determine the complement of metal reductases expressed in these bacteria.