Iron and Molybdenum Metabolism in Se(VI)-Respiring Bacteria

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Introduction: The ability of prokaryotes to perform dissimilatory selenium reduction is a remarkable biological adaptation that allows Se(VI)-respiring microorganisms to populate ecological niches in Earth's subsurface. Advances in genetics and genomics have made it possible to elucidate the mechanisms of microbial Se(VI) reduction and the ancillary metabolic pathways required for selenate reductase activity. This presentation will report the results of our recent studies on the iron-sulfur cluster and molybdopterin biosynthesis genes in Se(VI)-respiring bacteria, and the role of the Fe-S and Mo cofactors in dissimilatory selenium reduction.

Experimental Approach: The catalytic subunit of the selenate reductase is predicted to bind a bis-molybdopterin guanine dinucleotide cofactor and a [4Fe-4S] cluster. To determine if the molybdenum and iron-sulfur cofactors are required for selenate reduction, we examined the selenate reductase activity in mutant strains impaired in the Moa molybdopterin biosynthesis pathway and Isc iron sulfur cluster assembly pathway. Genetic complementations were performed with the mutants deficient in selenate reductase activity to establish the role of specific genes in selenate reduction activity. Mutants strains were grown in defined media containing a known amount of $NaSeO_4$. Selenate reduction activity was monitored by sampling the cultures and quantifying the loss of selenate using ion chromatography.

Results and Discussion: Mutants carrying deletions of the *moaA*, *moaB*, *moaE*, or *mog* gene in the molybdopterin biosynthesis pathway lost the ability to reduce selenate. Deletion of the *iscU* gene in the Isc iron sulfur assembly pathway also resulted in complete loss of selenate reduction activity. Genetic complementation by the wild-type sequences restored selenate reduction activity in the mutant strains. These results study indicate that both the molybdenum and iron-sulfur cofactors are essential for the functioning of the selenate reductase enzyme. The biochemical pathways for molybdenum and iron-sulfur cofactor biosynthesis and the evolution of Se-respiring bacteria will be discussed.