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Investigation of electron transport proteins in the Geobacteraceae

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Abstract

Biological Fe(III) reduction is an environmentally significant process, but the mechanisms of electron transfer to Fe(III) are poorly understood. While soluble electron acceptors like oxygen and nitrate diffuse into the cell, dissimilatory Fe(III) reducers transfer electrons onto an insoluble, and therefore extracellular, electron acceptor. Mechanisms of electron transfer in *Geobacter* species are of interest because these species are the predominant Fe(III)-reducing microorganisms in a variety of environments, including aquatic sediments, aquifers contaminated with organic pollutants or with toxic metals, and current-harvesting electrodes. Proteomic, genetic, and genomic approaches were used to identify components of the electron transport chains to Fe(III) and other electron acceptors in *Geobacter sulfurreducens* and *Geobacter metallireducens*. For *G. sulfurreducens* , the fumarate reductase was identified and its dual function as the succinate dehydrogenase was discovered. Growth by fumarate reduction was induced in *G. metallireducens*, which cannot naturally respire fumarate, by the expression of a dicarboxylate transporter that allowed the succinate dehydrogenase to function as a fumarate reductase. A *c*-type cytochrome that was abundant in Fe(III) but not fumarate reducing cells was partially purified and the encoding gene was identified. A strain lacking this gene was severely impaired in Fe(III) reduction, but was unaffected in fumarate reduction or growth under oxidative stress. The conservation of electron transport proteins between *G. sulfurreducens* and *G. metallireducens* was determined. All genes in the pathways of acetate oxidation were well conserved, as were genes involved in electron and proton transport within the inner membrane. However, those genes encoding cytochromes, which are the periplasmic and outer membrane electron carriers to Fe(III), were not well conserved, including those required for Fe(III) reduction in *G. sulfurreducens*. Finally, an 300 kb island present in the *G. metallireducens* but not the *G. sulfurreducens* genome was shown to encode genes for aromatics degradation, and the pathways for toluene, phenol, *p*-cresol, and benzoate oxidation were annotated. Genes encoding the aromatic ring reduction enzyme, the benzoyl-CoA reductase, could not be identified. Gene expression levels were compared between cells grown with acetate or benzoate as the electron donor, and were used to identify candidate genes for the missing enzyme.^

Subject Area

Microbiology

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