Microbial Extracellular Electron Transfer Mechanism in Hanford Subsurface Geobacter spp.

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Iron (Fe) is abundant (i.e., 3.5-8% by weight) in the subsurface sediments of Hanford 300 area (300A) where Fe(III) and Fe(II) can serve as an oxidant and a reductant for microbial energy generation, respectively. Microbial mediated redox reactions may impact fate and transport of the contaminants, such as Cr, Tc and U, that are commonly found in 300A and other DOE sites. Geobacter spp. were identified as the most abundant Fe(III) -reducing bacteria found in the redox transition zone (RTZ) of 300A sediments and the Fe(III)-reducing bacterium Geobacter sp. FA1 was isolated from the 300A RTZ. The electron transfer mechanisms for extracellular Fe(III) reduction in these 300A microorganisms are, however, essentially unknown.

Genome analysis of the model Fe(III)-reducing bacterium G. sulfurreducens revealed a Geobacter porin-cytochrome (Gpc) protein complex that consisted of a porin-like outer membrane protein, a periplasmic c-type cytochrome (c-Cyt), and an outer membrane c-Cyt, which we predicted was responsible for transferring electrons across the outer membrane. The genes that encode the Gpc proteins are adjacent to each other in the genome of G. sulfurreducens where the gpc1 and gpc2 gene clusters are also co-located. Deletion of both gpc1 and gpc2 gene clusters of G. sulfurreducens has no impact on growth with fumarate as the terminal electron acceptor, but diminishes the ability of G. sulfurreducens to reduce Fe(III)-citrate and ferrihydrite, a poorly crystalline Fe(III) oxide. Complementation with the entire gpc1 gene cluster restores the ability of G. sulfurreducens to reduce Fe(III)-citrate and ferrihydrite. Isolated Gpc protein complexes reconstituted in proteoliposomes are able to transfer electrons across the lipid bilayer from reduced, internalized methyl viologen to external Fe(III). The gpc gene clusters are present in all eight sequenced genomes of Geobacter spp., the Hanford isolate Geobacter sp. FA1 as well as 11 other sequenced bacterial genomes, including the Fe(III)-reducing bacteria Anaeromyxobacter spp. and Desulfuromonas acetoxidans. Furthermore, the characterized function and organization of the Gpc complex are very similar to that of the Mtr porin-cytochrome extracellular electron transfer protein complexes found in the other Fe(III)-reducing bacteria, such as Shewanella spp., and several Fe(II)-oxidizing bacteria, although Gpc and Mtr proteins share no sequence identity. Thus, the porin-cytochrome complex appears to be a common mechanism for transferring electrons across the outer membrane by diverse Fe(III)-reducing and Fe(II)-oxidizing Gram-negative bacteria.