

Public Abstract

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Examination of Metabolic and Regulatory Networks of *Desulfovibrio* Species

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The sulfate-reducing bacteria are a morphologically diverse group of organisms characterized by the ability to couple the enzymatic reduction of sulfate to energy production and growth. This metabolic activity has profound economic and environmental consequences such as the corrosion of metal structures and the souring of petroleum reserves. The sulfate-reducing bacteria are also among a select group of organisms that may be used as tools for the bioremediation of toxic heavy metal contaminants from the environment. To understand the mechanisms through which these bacteria impact our environment both positively and negatively, genomic studies have been undertaken to predict the metabolic and regulatory networks of two species of the genus *Desulfovibrio*. Studies have focused on the elucidation of carbon metabolic pathways, the role of CRP-FNR proteins in the regulation of *Desulfovibrio* metabolic pathways, and the prediction of global regulatory networks using bioinformatics techniques. Surprisingly, several hexose metabolic genes were found despite the fact that biochemical evidence suggests that these bacteria do not use hexose sugars as growth substrates. This physiological paradox was explored. Possible redox regulation by a putative CRP-FNR protein was explored by analysis of a mutation in the gene which suggested a role for this protein in the metabolism of ethanol by *Desulfovibrio*. A computational analysis of the promoter regions of *Desulfovibrio* genes revealed putative regulatory protein binding motifs homologous to the *Escherichia coli* CRP and GalR binding sites as well as motifs that may be unique to *Desulfovibrio*.