The sulfate-reducing bacterium *Desulfovibrio desulfuricans* ND132 as a model for understanding bacterial mercury methylation

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The extensive industrial release of mercury into the environment has resulted in sites of contamination across the globe. The fate of Hg is varied but, typically, it is sequestered in sediments and soils where is can be converted to the more mobile, toxic and bioaccumulative methylmercury. Monomethylmercury is produced primarily by sulfate-reducing (DSRB) and Fe(III)-reducing bacteria (DIRB), although only a subset of species within these groups is capable of methylation. DSRB and DIRB play dual roles in the fate of environmental Hg, through both methylation and immobilization in iron sulfides. Hence these anaerobes are important to the fate of Hg in subsurface systems. Despite the importance of this issue, the genes and proteins involved in microbial Hg methylation remain poorly understood. The work described herein is aimed at elucidating these microbial methylation systems in the Hg methylating sulfate-reducing bacterium *Desulfovibrio desulfuricans* ND132 as a model organism. The strain was chosen for its exceptionally high methylation rate, and because of its phylogenetic similarity to *Desulfovibrio desulfuricans* strain LS (now lost), for which methylation pathways have been partially defined. Although methylation rates are strongly dependent on Hg concentration and medium chemistry, ND132 can methylate ~15% of added Hg at ng/ml concentrations. ND132 is also the first DSRB methylator to have its genome sequenced. Hence, we propose to use this organism as a model DSRB for the determination of the Hg methylation pathway. Here we present the physiological characteristics of this bacterium and its Hg methylation rates as compared to other DSRB. Genes selected from the sequenced genome that might be involved in the methylation process are described. Strain ND132 is capable of respiratory growth with a variety of electron donors and acceptors. The optimal salt concentration, pH and temperature for growth were found to be 2% (wt/v), NaCl, pH 7.8 and 37^{o}C, respectively. It is sensitive to a number of antibiotics that are currently being used to develop a genetic manipulation system so as to select for targeted deletion of identified gene targets.