Genomic and physiological characterization of *Desulfovibrio vulgaris* strains isolated from a metal contaminated lake.

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Abstract:

Nine *Desulfovibrio vulgaris*-like bacteria (DP1-9) were isolated from a heavy metal impacted field site (Lake DePue, Illinois) on a lactate medium. All had identical 16S rRNA and *dsrAB* genes that were virtually identical to the orthologous genes of *D. vulgaris* Hildenborough (DvH). Their growth rates at different temperatures on B3 medium supplemented with lactate and sulfate were comparable. Characterization of resistance to $ZnCl_2$, using the Omnilog™ System, revealed no difference among isolates and little or no difference to the closely related reference organism *D. vulgaris* Hildenborough. However, pulse field gel electrophoretic analysis of I-CeuI whole genome digests identified a large deletion in the genomes of all isolates. Complementary whole-genome microarray hybridization revealed that approximately 300 deleted genes were distributed in six regions of the chromosome, annotated as conserved/ hypothetical or phage related genes in DvH. These deletions were also confirmed by PCR analysis, using primers complementary to regions flanking the deletions. One of the "phage-deficient" *D. vulgaris* strains (DP4) has been demonstrated to serve as host for latent viruses of *D. vulgaris* Hildenborough. Two distinct phage morphotypes have so far been identified by EM.