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## Recent Work

### Title

Genomic Comparisons Between a Metal-resistant Strain of *Desulfovibrio Vulgaris* and the Type Strain D. *Vulgaris* Hildenborough

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## Genomic Comparisons Between a Metal-resistant Strain of *Desulfovibrio vulgaris* and the Type Strain *D. vulgaris* Hildenborough

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A sulfate-reducing bacterium closely related to *Desulfovibrio vulgaris* Hildenborough was isolated from heavy-metal impacted lake sediments located in northern Illinois (Lake DePue). Initial characterization revealed differences in genome content and structure between this strain (DePue) and strain Hildenborough, despite a very high level of 16S rRNA sequence similarity (>99%). Phenotypic analyses of this strain revealed significant differences in minimum inhibitory concentrations for a variety of compounds when compared with strain Hildenborough. Strain DePue exhibited greater tolerance towards Cr(VI) and increased sensitivity to nitrate. Small differences were observed in growth rates, although not sensitivity, for sodium between the two strains. Genome sequencing of strain DePue indicated that the majority of genes (approximately 88 - 92%) share a high level of similarity (>98%) to genes found in strain Hildenborough. However, the genome of strain DePue exhibits multiple genome inversions and rearrangements, as well as the presence of a several hundred novel genes not found in strain Hildenborough. Current analyses verified that strain DePue lacks at least six phage regions found in strain Hildenborough, but also suggests at least two unique phage regions, one of which contains putative multi-drug efflux genes. Further curation of the genome, as well as mutant analysis should inform the basis for increased metal-tolerance of strain DePue and metal-resistance among *Desulfovibrio* in general.