

The Sulfate-Reducing Bacterium *Desulfovibrio desulfuricans* ND132 as a Model for Understanding Bacterial Mercury Methylation

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DOE/Office of Science/Biological & Environmental Research

- The ORNL Mercury Science Focus Area is developing the Hg-methylating bacterium *Desulfovibrio desulfuricans* ND132 as a model organism for a renewed effort to identify and characterize the genes, proteins and biochemical pathways involved in the generation of methylmercury.
- This paper, a companion to the recent genome sequencing announcement, provides basic information of growth, methylmercury production and degradation by strain ND132.



Gilmour C.C., D.A. Elias, A.M. Kucken, S.D. Brown, A.V. Palumbo, C.W. Schadt and J.D. Wall. 2011. The sulfate-reducing bacterium *Desulfovibrio desulfuricans* ND132 as a model for understanding bacterial mercury methylation. *Appl. Environ. Microbiol.* 77:3938-3951 (doi:10.1128/AEM.02993-10).

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- Enriched stable Hg isotopes were used to show that ND132 simultaneously produces and degrades MeHg during growth. Mass balances for Hg and MeHg illustrate how partitioning impacts the availability of each for transformation.
- The ability to produce MeHg is constitutive and does not confer Hg resistance. MeHg produced by cells is mainly excreted.
- Methylation rates for several previously untested *Desulfovibrio* species are presented, and the phylogenetic distribution of Hg-methylation with the genus is examined. Only half of *Desulfovibrio* strains tested to date have the ability to produce MeHg.

