

# Mercury Methylation by Novel Microorganisms from New Environments

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DOE/Office of Science/Biological & Environmental Research

## Objective

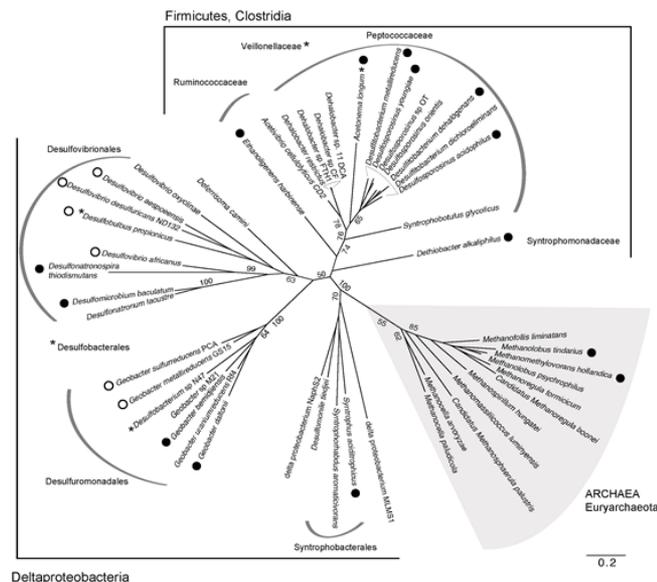
- Validate the prediction of the newly determined and expanded capability of bacteria to methylate mercury.

## New Science

- Validated the newly discovered predictability of bacteria to methylate mercury based upon the presence of two genes; *hgcAB*.
- Determined for the first time that fermenting and methanogenic bacteria can methylate mercury.
- Provided explanation for earlier results showing Hg methylation in low sulfate, Fe environments such as methanogenic rice patties.

## Significance

- Verification of the predictability greatly expands the ability to quantify the potential to methylate Hg in any environment.
- Allows for the use of *hgcAB* as a biomarker and for the development of molecular probes for gene quantification (ongoing effort at ORNL).



White dots: established Hg-methylators,  
Black dots: newly established Hg-methylators.

Gilmour, C.C., M. Podar, A.L. Bullock, A.M. Graham, S.D. Brown, A.C. Somenahally, A. Johs, R.A. Hurt, K.L. Bailey, and D.A. Elias. 2013. Mercury methylation by novel microorganisms from new environments. *Environ. Sci. Technol.* 47:11810-11820 (doi:10.1021/es403075t).

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Microbial mercury methylation transforms a toxic trace metal into the highly bioaccumulated neurotoxin methylmercury (MeHg). The lack of a genetic marker for microbial MeHg production has prevented a clear understanding of the distribution of Hg-methylating organisms in nature. Recently, a specific gene cluster (*hgcAB*) was linked to mercury methylation in two bacteria. Here we test whether the presence of *hgcAB* orthologs is a reliable predictor of Hg methylation capability in microorganisms, a necessary confirmation for the development of molecular probes for Hg-methylation in nature. Although orthologs of *hgcAB* are rare among the several thousand available microbial genomes, the encoding organisms are much more phylogenetically and environmentally diverse than previously thought. By directly measuring MeHg production in several bacterial and archaeal strains encoding *hgcAB* we confirmed that the presence of *hgcAB* predicts Hg methylation capability. For the first time, we demonstrated Hg methylation in species other than sulfate- and iron-reducing bacteria, including methanogens, and syntrophic, acetogenic and fermentative *Firmicutes*. Several of these species occupy novel environmental niches for Hg methylation, including methanogenic habitats such as rice paddies, the animal gut, and extremes of pH and salinity. Identification of these organisms as Hg methylators now links methylation to discrete gene markers in microbial communities.

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