

# Potential Mercury Methylating Bacteria Identified in Contaminated Streams

Contact: Dwayne Elias ([eliasda@ornl.gov](mailto:eliasda@ornl.gov), 865-574-0956)  
DOE/Office of Science/Biological & Environmental Research

## Objective

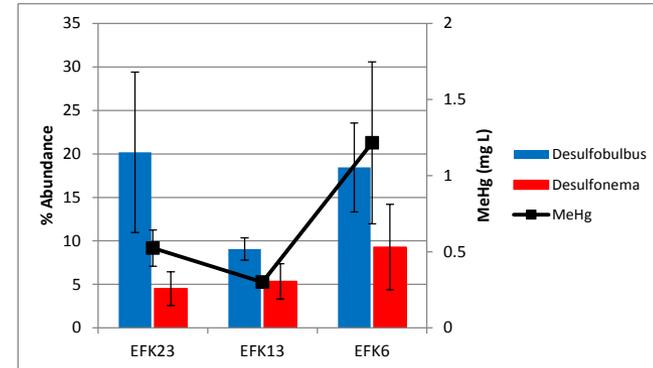
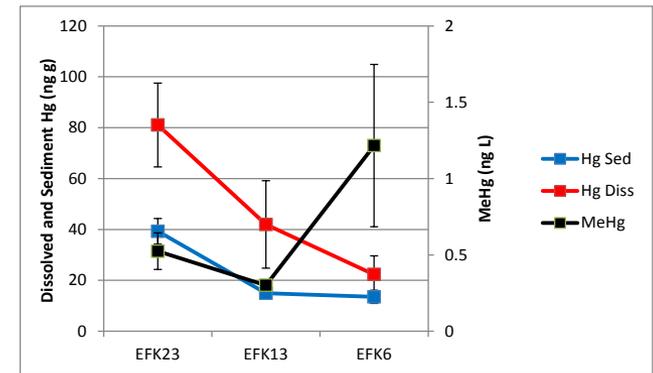
- Provide insight into the types of bacteria that methylate mercury in contaminated environments.

## New Science

- The phylogenetic composition of the sediment bacterial community was examined over three quarterly sampling periods (36 samples) at 5 stream sites in Oak Ridge using 16S rRNA genes pyrosequencing to identify the presence of Deltaproteobacteria, which methylate Hg.
- The majority of Deltaproteobacteria sequences present at the contaminated sites were either known potential metal-reducers/methylators or metal tolerant species with *Desulfobulbus* spp. the most numerous sequence found.

## Significance

- Given the abundance relative to other known mercury methylators and the association with methylmercury, *Desulfobulbus* spp. is considered a prime candidate involved in mercury methylation in these streams.



(A) Concentrations of dissolved Hg, sediment Hg and methylmercury (MeHg) in East Fork Poplar Creek (EFK) sites moving downstream of point source. (B) Abundance of *Desulfobulbus* spp. (% of total Deltaproteobacteria) and MeHg concentrations in corresponding EFK sites.

Mosher, J.J., T. A. Vishnivetskaya, D.A. Elias, M. Podar, S.C. Brooks, S.D. Brown, C.C. Brandt and A.V. Palumbo. 2012. Characterization of the Deltaproteobacteria in contaminated and uncontaminated surface stream sediments and identification of potential mercury methylators. *Aquat. Microb. Ecol.* 66:271-282 (doi: 10.3354/ame01563).

# Potential Mercury Methylating Bacteria Identified in Contaminated Streams

**Contact: Dwayne Elias ([eliasda@ornl.gov](mailto:eliasda@ornl.gov), 865-574-0956)**  
**DOE/Office of Science/Biological & Environmental Research**

Microbial communities were examined in surface stream sediments at five contaminated sites and one control site near Oak Ridge, TN, to identify bacteria that could contribute to mercury (Hg) methylation. The phylogenetic composition of the sediment bacterial community was examined over three quarterly sampling periods (36 samples) using 16S rRNA genes pyrosequencing. 3,064 sequences (0.85% of the total community) were identified as Deltaproteobacteria, the only group known to methylate Hg, at a 99% confidence threshold. Constrained ordination found statistically significant positive and linear correlations between *Desulfobulbus* spp., *Desulfonema* spp. and *Desulfobacca* spp. and methyl-Hg concentrations in the Hg contaminated sites. The distribution of organisms related to *Byssovorax* spp. were significantly correlated to inorganic carbon, nitrate and uranium concentrations, but not to Hg or methyl-Hg. Overall, the abundance and richness of Deltaproteobacteria sequences were higher in uncontaminated sediments, while the majority of the members present at the contaminated sites were either known potential metal-reducers/methylators or metal tolerant species. Given the abundance relative to other known Hg methylators and the association with methyl-Hg, *Desulfobulbus* spp. is considered a prime candidate involved in Hg methylation in these streams.

Mosher, J.J., T. A. Vishnivetskaya, D.A. Elias, M. Podar, S.C. Brooks, S.D. Brown, C.C. Brandt and A.V. Palumbo. 2012. Characterization of the Deltaproteobacteria in contaminated and uncontaminated surface stream sediments and identification of potential mercury methylators. *Aquat. Microb. Ecol.* 66:271-282 (doi: 10.3354/ame01563).