Goldschmidt 2026 Abstract
https://doi.org/10.46427/gold2026.34451

The impact of bacterial metabolic state on mercury methylation by *Geobacter sulfurreducens*

JOANA GONÇALVES, ISABEL SANZ-SÁEZ, MADELEINE RAMSTEDT AND ERIK BJÖRN

Umeå University

Microbial mercury (Hg) methylation is the main process controlling the formation of methylmercury (MeHg), a potent neurotoxin that bioaccumulates in aquatic foods webs and rice. The iron-reducing bacterium *Geobacter sulfurreducens* PCA resides in anoxic environments, where metal reduction is an important process, and it is a widely used model organism in Hg methylation studies. The *hgcAB* gene cluster has been well established as the genetic determinant for microbial Hg methylation[1], but the physiological conditions that modulate cellular MeHg production remain insufficiently understood. In particular, the influence of bacterial metabolic state, shaped by nutrient availability, electron flow and redox conditions is a critical but understudied factor.

In this work, we investigate how different metabolic states of *G. sulfurreducens* PCA affect Hg methylation. Using controlled laboratory cultures, the metabolic states were manipulated by varying the electron acceptor or nutrient availability. Three different conditions were established: (i) a minimal composition medium with an intracellular electron acceptor, (ii) an enriched vitamin medium with an intracellular electron acceptor, and (iii) a minimal composition medium with an extracellular electron acceptor. Across these states, cell growth was determined, metabolic changes monitored and MeHg production was quantified. Our results demonstrate that the methylation capacity of *G. sulfurreducens* PCA varies substantially across metabolic states, indicating that Hg methylation is not only determined by the presence of *hgcAB* genes, but also linked to cellular metabolism. Cultures with an intracellular electron acceptor present a significantly higher methylation capacity compared to cultures with an extracellular electron acceptor, demonstrating an influence of different electrons transport pathways and redox gradients at the cell surface on MeHg formation.

These findings highlight the importance of metabolic context in controlling microbial Hg transformations, suggesting that environmental factors shaping microbial metabolism may exert stronger control over methylation potential than previously appreciated. By linking bacterial metabolic state to methylation capacity, this work provides new insight into how geochemical conditions regulate the microbial Hg cycle.

1. Parks, J. M. *et al.* The Genetic Basis for Bacterial Mercury Methylation. *Science* **339**, 1332–1335 (2013).