Mercury Methylation Growth State and Potential Hg Transporters Identified

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Objective

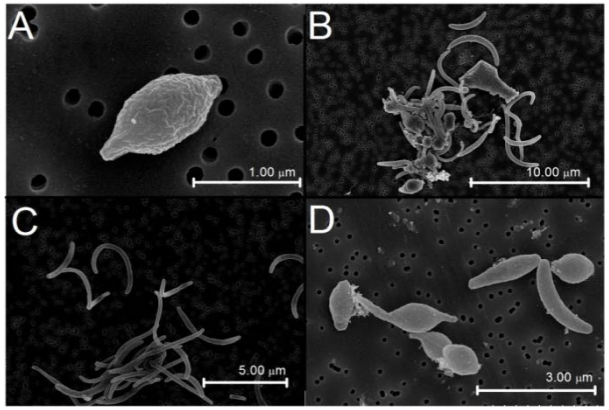
- Determine pleiomorphy effect on Hg methylation and identify genes up-regulated with Hg exposure in *Desulfovibrio africanus*.

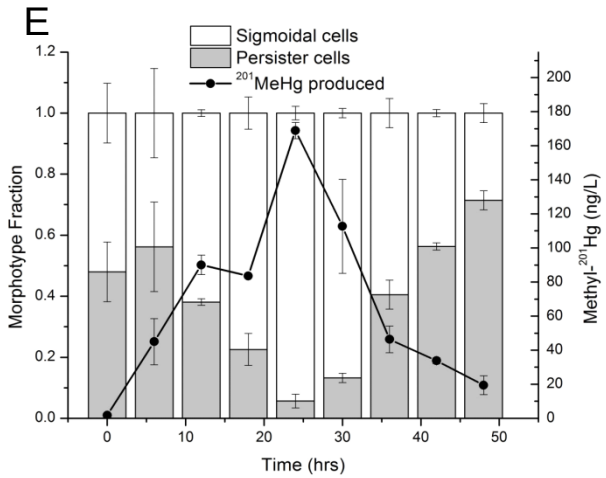
New Science

- Hg methylation was strongly correlated with the active (sigmoidal) cells during exponential growth.
- Iron transport genes (FeoAB) were amongst very few genes up-regulated with Hg exposure versus no exposure during exponential growth. This suggests that ferric iron transport genes may be used to bring Hg into the cell.

Significance

- While much is known about Hg methylation in the field, the genes and proteins involved in transport, methylation and anaerobic demethylation are unknown. This work verifies that methylation occurs during specific growth periods and has revealed high value targets for Hg transport.





(A) The persister (lag-phase) and (B) mixture of sigmoidal and persister morphotypes (early exponential), (C) sigmoidal (mid-exponential), and (D) predominantly persister (stationary phase). (E) Changes in persister (shaded bars) and sigmoidal (white bars) morphotype fractions with methyl-^{201}Hg produced (closed circles).

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The biogeochemical transformations of Hg are a complex process, with the production of methylmercury (MeHg), a potent human neurotoxin, repeatedly demonstrated in sulfate- and Fe(III)- reducing as well as methanogenic bacteria. However, little is known about the morphology, genes or proteins involved in MeHg generation. *Desulfovibrio africanus* strain Walvis Bay is a Hg-methylating δ-proteobacterium with a sequenced genome and has unusual pleomorphic forms. In this study, a relationship between pleomorphism and Hg methylation was investigated. Proportional increases in the sigmoidal (regular) cell form corresponded with increased net MeHg production, but decreased when the pinched cocci (persister) form became the major morphotype. Microarrays indicated that the ferrous iron transport genes (*feoAB*), as well as ribosomal genes and several genes whose products are predicted to have metal binding domains (CxxC), were up-regulated during exposure to Hg in the exponential phase. While no specific methylation pathways were identified, the finding that Hg may interfere with iron transport and the correlation of growth-phase dependent morphology with MeHg production are notable. The relationships between differential gene expression, morphology, and the growth phase dependence of Hg transformations suggests that actively growing cells are primarily responsible for methylation, and so areas with ample carbon and electron-acceptor concentrations may also generate a higher proportion of methylmercury than more oligotrophic environments. The observation of increased iron transporter expression also suggests that Hg methylation may interfere with iron biogeochemical cycles.

Moberly, J.G., C.L. Miller, S.D. Brown, A. Biswas, C.C. Brandt, A.V. Palumbo, and D.A. Elias. Role of morphological growth state and gene expression in *Desulfovibrio africanus* strain Walvis Bay mercury methylation. Environ. Sci. Technol. 46:4926-4932 (doi: 10.1021/es3000933).