Development of New Tools and Approaches for Determining Mercury Methylation in the Environment

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Recently, we identified two genes responsible for MeHg generation in Bacteria and predicted new methylators in the Firmicutes and Methanogens (1). We confirmed this prediction which increased the diversity of known methylators (2). We have utilized these results and established molecular tools and protocols for the detection and quantification of the methylmercury generating genes *hgcAB* as well as their transcripts in the environment. While construction of "universal primers" was not feasible, degenerate primers spanning both essential genes (*hgcA* and *hgcB*) were constructed specifically for the *Deltaproteobacteria*, the *Firmicutes* and the *Methanogens*. Degenerate qPCR and RT-qPCR primers to quantify the genomic potential and transcribed *hgcAB* by each clade in a given environment were constructed. Sequencing and identification of all *hgcAB* amplicons in coordination with 16S rRNA gene sequencing for each environment may allow determination of each clades contribution to MeHg generation and what fraction of the community in a given environment can methylate. Coordination of the molecular data with geochemical and physiochemical parameters is likely to elucidate new predictive information for Hg methylation potentials.

[1] Parks, J. M. *et al* The genetic basis for bacterial mercury methylation. *Science* 2013, **339** (6125), 1332–1335. [2] Gilmour, C. *et al* Mercury methylation by novel microorganisms from new environments. *Environ. Sci. Technol. 2013*, **47**, 11810–11820