Mercury Methylation by *hgcAB+* Methanogens

CYNTHIA C. GILMOUR[1], ALLYSON BULLOCK[1], ALYSSA WETTERAUER[1], MIRCEA PODAR[2] AND DWAYNE ELIAS[2]

[1]Smithsonian Environmental Research Center, 647 Contees Wharf Rd, Edgewater, MD, USA 21307

[2]Oak Ridge National Laboratory, 1 Bethel Valley Road, Oak Ridge, TN, USA 37831

Recently, a specific gene pair (*hgcAB*) was linked to Hg methylation in mercury-methylating sulfate (SRB) - and iron (FeRB) reducing bacteria (1). Orthologues of *hgcAB* were identified in two other groups of microorganisms, methanogens and Firmicutes, which had not previously been associated with methylmercury (MeHg) production. By directly measuring MeHg production in several related bacterial and archaeal strains with and without *hgcAB*, we confirmed that the presence of the gene pair accurately predicts Hg methylation capability (2). Despite the expanded diversity of Hg-methylating organisms and environments, orthologues of *hgcAB* are rare among available microbial genomes.

Here we begin to evaluate how important methanogens may be in Hg methylation in the environment. As a first approach, we measured Hg-methylation rates by *hgcAB+* methanogens in pure culture, using organisms from culture collections with available genomes. Based on available genomes, we identified 12 *hgcAB+* methanogens, all Class *Methanomicrobia*). Using a standardized approach to measuring methylation, the first two cultures we tested (*Methanolobus tindarius* and *Methanomethylovorans hollandica*) were relatively weak methylators (2-5% methylation of a 1 nM Hg spike to a culture) relative to most *hgcAB+* SRB and FeRB (typically more than 50%)(2). However, evaluation of additional cultures showed much higher methylation rates in some strains (up to ~25%), supporting the idea that methanogens may be important contributors to MeHg production in certain environments. We also began to evaluate how Hg complexation impacts Hg uptake and methylation. Early results suggest that sulfur complexes are critical controls on Hg methylation by methanogens, as they are in SRB and FeRB.

[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