Title: **Methylation Potential of Mercury for Different Groups of the Methylating Microbial Community**

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Project Abstract:

Methylmercury (MeHg) is a highly bioaccumulative form of mercury (Hg), and the mitigation of risk at contaminated sites requires tools to quantitatively predict MeHg production. This study examined the factors influencing microbial methylation of mercury (Hg) in freshwater wetland ecosystems with the goal of developing geochemical and biomolecular markers for net MeHg production potential. We are testing the hypothesis that mercury methylation potential in sediments can be predicted through a combination of diffusive gradient in thin-film (DGT) passive samplers (for bioavailable Hg flux) with genomic analysis of Hg-methylating microbial communities. We constructed three simulated freshwater wetlands in an outdoor field research station at Duke University. Each mesocosm comprised a 3.7×1.2×0.8 m^3 (length×width×height) slant-bottom box, filled with soil and water to create a gradient of water saturation conditions and was populated with freshwater macrophytes, mosquitofish, and associated macrofauna. After establishment of the simulated wetlands, each mesocosm box was amended with four different geochemically relevant and isotopically labelled inorganic Hg species to represent a gradient of different Hg methylation potentials across the four isotopes. Over several months, after the initial spike of mercury forms in the wetland mesocosms, we monitored each isotopically labelled Hg endmember for: (1) Accumulation into water, sediment and biological components in the mesocosm; (2) Conversion to MeHg in water and sediments; and (3) Accumulation of total Hg and MeHg on DGTs deployed for one week periods in the mesocosms. The results showed that most of the added Hg from each isotope accumulated in the top few centimeters of surface sediment in the first month after dosing. Greater conversion to MeHg was generally observed for the isotopes originating from dissolved forms ($^{202}Hg^{2+}$, ^{201}Hg-humic acid complex) than for isotopes originating from particulate forms (nanoparticulate ^{200}HgS and ^{199}Hg adsorbed to FeS). Also, the uptake of inorganic Hg in DGTs were generally consistent with trends for methylated Hg, indicating that DGT passive samplers might be useful as an empirical tool to evaluate Hg bioavailability for methylating organisms. Ongoing work will attempt to establish changes in the sediment microbial community during the 12-month period after Hg dosing, and compare to the observed changes in the extent of Hg methylation during this time frame.