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Porewater Mercury, Particle Size and Mercury Speciation as Predictors for Mercury Methylation in Aquatic Sediments

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Mercury (Hg) can be transformed to methylmercury (MeHg) in aquatic sediments, which can bioaccumulate and biomagnify in the food web. The goal of this research is to develop a simple laboratory assay to experimentally assess biologically available Hg for methylation as well as identifying Hg methylation predictors in different soils and sediments.

Hg methylation was evaluated in jar microcosms for marine, freshwater, and terrestrial floodplain sediments. Microcosms included both native sediments and sediments amended with lactate to enhance microbial activity, ferric iron to encourage iron reducing conditions and sulfate to encourage sulfate reducing conditions. Total Hg (THg) and MeHg were measured in both sediments and porewater at two time periods designed to maximize MeHg formation. Porewater concentrations were measured via DGT devices and in filtered water. The primary results from the microcosm experiments showed that bulk THg was not a good indicator of MeHg production, however porewater THg was positively correlated with MeHg concentration for all sediments after correcting for colloidal/particulate dissolved organic carbon (DOC) (r^2=0.98 and $p < 0.0001$).

The effect of sediment particle size and Hg speciation (assessed by X-ray Absorption Spectroscopy) on methylation potential were investigated. One freshwater river sediment (SS1) containing > 67% organBic thiol-Hg ($Hg(SR)_2$) and one marine sediment (SS7) containing > 65% (β-HgS) were separated into 3 size fractions (< 0.5 μm, 2–45 μm and bulk) and each fraction was analyzed for Hg species. The different size fractions were spiked into a pure culture of Hg methylator bacteria (*Desulfovibrio Desulfuricans* ND132), and after t = 0, 12 and 24 h total MeHg concentrations were evaluated. For SS1, dominated by Hg-thiol species, Hg methylation increased with surface area, however for SS7 dominated by metacinnabar, Hg methylation was similar in the specific size fractions tested. Overall, other factors such as metacinnabar, surface structure or differences between SS1 and SS7 DOC may explain the different trends in methylation observed. In our ongoing work, we will evaluate the relative importance of surface structure and DOC on methylation in sediments.