Periphyton biofilms generate methylmercury in a contaminated creek system

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The results of previous SFA research on mercury methylation in East Fork Poplar Creek (EFPC) in Tennessee imply key controls on net methylation occur within the stream or on the stream bed. The large diel variability in dissolved methyl mercury (MeHg) concentration appears to be correlated with the daily photocycle and the sparse wetlands (< 3% watershed area) are poorly connected to the main channel of the creek. Methylmercury is generated in fine-grained channel margin deposits along the creek but the extent of these deposits, coupled with the rates of Hg methylation, suggest these locations account for only a portion of the MeHg in the water. This phase of our research is designed to elucidate the role of periphyton biofilms in MeHg production in the creek. Periphyton is ubiquitous throughout the creek and redox gradients created within them can support Hg-methylating microbial activity. Periphyton growth surfaces deployed at upstream (closer to the historic point source of contamination) and downstream locations (~17 km apart) are collected following ~8 weeks colonization in the creek. These samples are subsequently used in laboratory assays of inorganic Hg methylation and MeHg demethylation. Enriched stable isotopes of Hg are employed to distinguish new activity from ambient background levels during incubations. Subsamples for microbial community analysis and *hgcAB* gene abundance are also collected. Redox gradients within the periphyton samples are quantified using voltammetric microelectrodes. Results to date demonstrate that both mercury methylation and MeHg demethylation occur within the periphtyon biofilms. Both processes are adequately described by pseudo-first-order kinetic expressions. Clear differences in methylation and demethylation activity exist between the upstream and downstream sites and across seasons. Both methylation and demethylation potentials are higher at the downstream site. Pseudo-first-order rate constants are ~100× lower with a 10°C decrease in temperature. Although both methylation and demethylation occur in the periphyton, the rate of methylation is greater than the rate of MeHg demethylation suggesting periphyton is a net source of MeHg to the creek.