

Characterization of mercury species and microbial communities in sediments and suspended particulate matter from historically contaminated river systems

JAN G. WIEDERHOLD¹, LORENZ GFELLER¹, NICHOLAS MARQUARDT¹, ALEXANDRA ALTEN², STEPHAN KRISCH¹, ANDREAS BREIDENBACH¹, ANDREAS SCHÜTTLER¹, JENS HAHN¹, SEBASTIAN BUCHINGER¹, ARNE WICK¹, HARALD BIESTER² AND LARS DUESTER¹

¹Federal Institute of Hydrology (BfG)

²Technical University of Braunschweig

Presenting Author: wiederhold@bafg.de

Many river systems worldwide are affected by mercury (Hg) contamination from a variety of anthropogenic sources. Environmental regulations have become stricter in many countries, leading to a decrease in direct industrial Hg discharges into rivers. However, Hg concentrations in riverine environments often remain elevated due to large amounts of legacy Hg residing in sediments. In Germany, all large rivers exceed the environmental quality standard of the EU Water Framework Directive for Hg in fish. A major obstacle towards improving this situation is the incomplete understanding of the pathways and biogeochemical processes controlling the remobilization, transfer and transformation of Hg species from contaminated sediments into the rivers' food web. Here, we present results from summer and winter sampling campaigns collecting suspended particulate matter (SPM) and sediments from the river Elbe and its tributaries Saale and Mulde in Germany. For comparison, riverine SPM was sampled both by flow-through centrifugation over several hours as well as in sedimentation boxes over one-month periods. Freezing all samples on site with liquid nitrogen ensured preservation of the Hg speciation as well as the microbial community. Analyses included total Hg and other element concentrations, the characterization of mobile and potentially bioavailable Hg fractions by selective chemical extractions and of inorganic Hg binding forms by pyrolytic thermodesorption (PTD) as well as PacBio full-length 16S rDNA sequencing to assess the microbial community composition. Analyses of methyl-Hg and further microbial parameters (e.g., *hgcAB* genes) are still ongoing. First results revealed that despite only relatively small differences in total Hg concentrations between SPM collected via centrifugation and in sedimentation boxes (overall range: 0.4 to 4.3 mg kg⁻¹ Hg), clear differences in PTD release curves and microbial community compositions were observed, particularly in SPM samples containing higher levels of algal biomass collected during the summer months. The relative abundance of known Hg methylators was found to be distinctly different between sediment samples, SPM collected in sedimentation boxes, and SPM centrifugation samples, with proportions of approximately 1.7%, 0.8%, and 0.4%, respectively. Our ongoing research aims to further elucidate the