

Mercury Species Transformations by Natural Microbial Communities in a Sulfidic Hydrothermal Spring, Southwest France

JIN-PING XUE¹, ROSANNA MARGALEF MARTI^{1,2},
EMMANUEL TESSIER¹, RÉMY GUYONEAUD¹, AUBIN
THIBAUT DE CHANVALON³, MATHIEU SEBILO^{1,4},
ZOYNE PEDRERO ZAYAS¹ AND DAVID AMOUROUX⁵

¹Universite de Pau et des Pays de l'Adour, E2S UPPA, CNRS, Institut des Sciences Analytiques et des Physico-Chimie pour l'Environnement et les Matériaux (IPREM), Pau 64000, France

²Universitat de Barcelona, Barcelona 08007, Spain

³CNRS/UPPA

⁴Sorbonne Université, CNRS, Institut d'Ecologie et des Sciences de l'Environnement de Paris (IEES Paris), Paris 75005, France

⁵CNRS E2S/UPPA

Presenting Author: jinping.xue@univ-pau.fr

Mercury (Hg) has been recognized as a global pollutant owing to its volatility from anthropogenic sources and long-range transport. Microbial-mediated transformations of Hg species are key processes for understanding the environmental impact of Hg. Until now, effort has been made by using pure cultures, while insight into Hg pathways at the community level is lacking, especially considering the complexity of microbial communities in aquatic environments. We report preliminary results concerning Hg species concentrations (inorganic Hg as iHg(II), monomethylmercury as MMHg) and transformations (e.g., reduction, methylation and demethylation) by natural microbial communities developing close to a sulfidic hydrothermal spring ("Trou de Madame", Préchacq, Southwest France). Given the physical and chemical characteristics of the system (water temperature ~28 °C, O₂ < 10%, sulfides 0–420 μM, pH 7.2–8.0), specific microbial communities comprising of both phototrophs (e.g., cyanobacteria) and sulfate-reducing bacteria were found to dominate the microbial taxonomic abundance in biofilm matrices (~50–60%). Laboratory incubations were performed at ambient conditions on collected biofilms, sediments, and water samples within a 24-hour period, and the extent of Hg species transformations in different incubation systems was obtained using dual addition of isotopically labelled Hg compounds (i.e., i¹⁹⁹Hg(II), MM²⁰¹Hg) at environmentally-relevant concentration levels. Concentrations of iHg and MMHg in water were found to be lower in fall as 0.39–0.49 and 0.026–0.029 ng/L than in early summer (1.91–2.19 and 0.370–0.639 ng/L), respectively. Also, iHg and MMHg concentrations in biofilms and sediment were 28–74 and 0.10–0.24 ng/g (*dw*) in fall, respectively. For Hg transformations by microbial mats communities, MMHg demethylation was mainly detected with demethylation yields of 13–35%. In addition, production of dissolved gaseous ²⁰¹Hg(0) (~0.05% yield) indicated the occurrence of specific biotic MMHg reductive demethylation. Besides, inorganic Hg methylation was not detected for the different biofilms or

sediments incubations (< 0.3% yield). Overall, the variations in iHg and MMHg levels in water indicate that biotic and environmental factors affect the seasonal changes in Hg speciation. Moreover, MMHg demethylation is a significant pathway in biofilms that could involve the metabolism of cyanobacteria and sulfate-reducing bacteria under sulfidic conditions.