Contribution of microbial compartments (biofilms, suspended matters, surface sediments) to monomethylmercury formation in subarctic thermokarst (Nunavik, Quebec) and temperate (Lorraine, France) ponds

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Monomethylmercury, a potent neurotoxic form of mercury, is predominantly produced by anaerobic microbial activities in aquatic systems. In arctic and sub-arctic areas, which are exposed to the thawing permafrost, the rate of mercury methylation could increase due to the rise of microbial activities.

The originality of this work is the evaluation of the contribution of different microbial compartments (biofilms, suspended matters, surface sediments) on the potential methylation rates in subarctic thermokarst ponds (Nunavik, Quebec) and in temperate ponds (Lorraine, France). Samples were incubated for seven days with a spike of $^{199}Hg^{2+}$ and were analyzed for $^{199}CH_3Hg^+$ by GC-ICP-MS.

The potential methylation rates determined were of the same order of magnitude in subarctic thermokarst ponds and in temperate ponds. However, the microbial communities in surface sediments emerged as the main contributor in mercury methylation. Iron-reducing and sulfate-reducing bacteria were identified as active methylators by combining the analysis of *hgcA* gene diversity with a metabolic approach (use of specific inhibitors). In the microbial biofilm compartment, green rust (Fe^{II}-Fe^{III} phase) can be biogenerated and thus would compete with the formation of monomethylmercury.