

## **How omics approaches contribute to the understanding of mercury cycling in the environment**

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The microbial and geoscience research community has invested substantial efforts over the past five decades in understanding the environmental Hg cycle. From the biological point of view, some genetic determinisms are known to be involved in Hg transformations. The *mer* system involved in Hg demethylation and reduction was the first While discovered and the best known so far. Nevertheless, *mer* system is described in aerobic bacteria, biological oxidative Hg demethylation and reduction in anaerobiosis are still unknown. Seven years ago, a major breakthrough has been made with the discovery of genes *hgcA* and *hgcB*, which control mercury methylation in anaerobic Hg methylators. An effort to fully understand their role in mercury environmental transformations should be undertaken. Omics approaches, at model strains or environmental level will allow the research community in Hg field to generate new hypotheses to fully understand Hg cycle. In this talk, an overview of these omics approaches will be presented. Applying those approaches at cellular level will generate mechanistic models, while their use at environmental level will contribute to the understanding of the link between the Hg-methylating organisms and environmental geochemistry. This field being in continuous progress, it will certainly bring key information toward the goal of modeling Hg cycle in the environment.