Potential of Hg(II) methylation/demethylation by biofilms *versus* planctonic cells and surface sediments

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The mercury methylation in aquatic systems has been linked to the growth of several anaerobic microbes such as iron reducers, sulfate reducers and methanogens, while both biotic and abiotic processes describe the demethylation. Although many studies have focused on pure microbial cultures, few investigations have been performed with biofilms, which are one of the major microorganism life in aquatic systems. Some previous works showed a greatest mercury methylation potential in biofilms than with planktonic bacteria in water column. However, this issue is still under discussion.

This present study investigates the potential of Hg(II) methylation and demethylation in biofilms *versus* planktonic cells in the water column and surface sediment in an eutrophic pond. Water, sediments, and/or intact or dispersed biofilms, were incubated with spikes of $^{199}Hg^{2+}$ and $CH_3{}^{201}Hg^{2+}$ for seven days. These isotope species were monitored by GC-ICP-MS over the time. The Hg(II) methylation and demethylation potentials were normalized in relation to the cell density in order to achieve specific rates. The results showed that preserved biofilms have a greatest Hg(II) methylation rate than ultrasound dispersed biofilms and planktonic cells. Moreover, planktonic cells exhibited a higher demethylation rate than sediments or biofilms. Therefore, this study highlights that planktonic cells and biofilms have a different contribution to the net methylation of Hg(II).