Study of the transformation and localization of Hg species in different sub-cellular fractions of *Desulfobulbus propionicus*

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Bacterial methylation is one of the major process which transform inorganic mercury Hg(II) into toxic monomethylmercury MeHg. The methylation potential of some bacteria, as well as their MeHg assimilation potential could be directive to evaluate their impact on the ecosystem. However, the Hg methylation mechanisms by bacteria are still poorly understood and further investigations are required to better understand the fractionation of mercury species between the cellular compartments and the metabolic pathways involved. The advantages of the use of multiple isotopic tracers can be exploited in order to study the localisation (partitioning) and the origin of the different mercury compounds after incubation.

In this work, a pure bacterial strain *Desulfobulbus propionicus* MUD10 (DSM 6523) was incubated during 90 hours under sulphate reducing conditions in presence of isotopically labeled mercury species (100 µg g^{-1} of ^{199}Hg(II) and 10 µg g^{-1} of ^{201}MeHg). Hg speciation analyses in each sub-cellular fraction (membranes, cytoplasm) were carried out by GC-ICP-MS, and quantification was performed by reverse species-specific isotope dilution analysis. Ultrasound probe sonication and French press were used for the extraction of soluble cytoplasmic mercury-containing proteins and efficiencies of both methods were compared. Size Exclusion Chromatography-ICP-MS was investigated to obtain mercury-containing proteins patterns in cytosolic extract.

This study confirms the use of isotopically labeled Hg species as a valuable tool to follow their transformations due to metabolic process.