

Alkylation of mercury by isolated microorganisms from the gut of *Eisenia foetida*

Burkhard Knopf, Elisabeth Kaschak and Helmut König

Institute for Microbiology and Wine Research
Johannes Gutenberg University, Becherweg 15
D- 55128 Mainz, Germany
e.kaschak@web.de

The qualitative speciation and determination of organomercury compounds at ultra trace levels are of special interest, because toxicity, bioavailability and detoxification depend mainly on the chemical form of this element. Alkylated mercury species can cross the blood-brain barrier and cause heavy intoxications. Much is known about the mercury cycle of aquatic systems and the microbial methylation but less about the bioavailability in soil and the effect on soil feeding invertebrates. The circle of mercury in soil is of special interest because of a high methylation potential by microorganisms. Mainly sulphate reducing bacteria are responsible for the methylation of mercury. This omnipresent of microorganism in the gut of soil living and feeding invertebrates is a way to alkylate mercury and accumulate higher concentrations of organomercury compounds. As an invertebrate model organism the annelidae *Eisenia foetida* was chosen. First studies of the potential alkylation of mercury by the model organism show an increase of methylmercury in the tissue of the worm. For this reason aerobic and anaerobic microorganisms were isolated and different microbiological methods were used to produce pure cultures. Following to the isolation these cultures were screened for their potential to alkylate inorganic mercury. The speciation of the alkylated mercury species in the biological samples were done by GC-ICP-MS. For this water soluble organomercury compounds were transferred into peralkylated by a derivatization with sodium tetra-(n-propyl)-borate and extracted with hexane.