Studying Bacterial Selenium Methylation at Environmental Relevant Concentrations

Ying Liu*,**, Andreas Schäffer**, Markus Lenz*

*Institute for Ecopreneurship, School of Life Sciences, University of Applied Sciences and Arts Northwestern Switzerland, Hofackerstrasse 30, 4132 Muttenz, Switzerland (ying.liu@fhnw.ch)
**Institute for Environmental Research (Biology V), RWTH Aachen University, 52074 Aachen, Germany

The trace element selenium (Se) which acts as a component of major metabolic pathways is essential for animals and humans health. However there are abundant Se deficiencies worldwide and millions of people may be affected by the accompanying endemic diseases (Fairweather-Tait et al., 2011). Methylation and subsequent volatilization is an important Se cycle process in natural environments which may lessen available Se in soils, ultimately limiting its entry into the food chain (Winkel et al., 2012). Se methylation is mostly regarded as a detoxification process for organisms since volatilization decreases the intracellular Se content. Previous studies of Se volatilization were performed using Se concentrations 10^3 - 10^6 fold higher (sub-ppm / ppm) than those commonly found in the environment (Luxem et al., 2017; Vriens et al., 2016). Se volatilization fluxes based on those experiments using high concentrations may have limited relevance for most environments which only contain trace amounts of Se.
Here, we developed a method to study Se methylation using a *Pseudomonas* strain with treatment of different concentrations of SeIV in sub-ppb to ppb range. The substrate ^{74}Se-selenite were synthesized from elemental ^{74}Se through a nitric acid oxidation reaction. Headspace SPME-GC-MS was used to quantify methylated ^{74}Se compounds while ^{80}Se methylated from the background Se in the culture medium was measured. Using Se stable isotope allowed distinguishing external from endogenous Se methylation and for the first time studying microbial selenium methylation at environmental relevant concentrations.

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