Arsenic methylation by the sulfate-reducing bacterium *Desulfotomaculum acetoxidans*

MATTHEW C. REID[1]*, KARIN MEIBOM[1], LADINA DONATSCH[1], LEIA FALQUET[1], ADRIEN MESTROT[2], AND RIZLAN BERNIER-LATMANI[1]

[1]Environmental Microbiology Laboratory, École Polytechnique Fédérale de Lausanne, Lausanne 1015, Switzerland (*correspondence: matthew.reid@epfl.ch)

[2]Soil Science Group, Institute of Geography, University of Bern, Bern 3012, Switzerland

The biomethylation of arsenic (As) influences its toxicity, mobility, and fate in soil and aquatic environments. There is particular interest in the methylation dynamics of As in rice paddy soils, since methylated As species are translocated to and accumulate in rice grains to a greater extent than inorganic As [1]. Despite the importance of methylated As species in anoxic paddy systems, few studies probe As methylation by anaerobic microorganisms or investigate the impact of soil biogeochemical variables on methylation rates, and the distribution of methylated species [2].

In this contribution, we characterize As methylation by the spore-forming and sulfate-reducing bacterium (SRB) *Desulfotomaculum acetoxidans*, which is commonly found in anaerobic soil systems including rice paddies, and which has the arsenite S-adenosylmethionine methyltransferase (*arsM*) gene required for enzymatic As methylation. *D. acetoxidans* was grown with inorganic arsenite concentrations ranging from 0 – 25 μM to span a range of environmentally-relevant As concentrations. Aqueous and volatile As species were measured with HPLC-ICP-MS, and the expression of the *arsM* gene was characterized through reverse transcription quantitative PCR.

D. acetoxidans methylated up to 5% of the As present in the medium over six days, and the fraction of methylated As increased as a function of total As in the medium. Trimethylarsine oxide was the primary methylated product, and smaller amounts of monomethylarsonic acid were also formed. Dimethylarsinic acid was not detected. The effect of varying total As concentrations on *arsM* expression will also be discussed.

This work shows that SRB can contribute to As methylation in anoxic environments and underscores the potential importance of methylated species in paddy soils.

[1] Zhao et al. (2013). *Environ. Sci. Technol.* **47**, 3957 - 3966

[2] Wang et al. (2015). *FEMS Microbiology Letters* **362**, 1-8