The role of sulfate-reducing bacteria in arsenic biomethylation in rice paddies: Implications for uptake into rice plants

MATTHEW C. REID[1]*, PHU LE VO[2], ALICIA GAYOUT[1] AND RIZLAN BERNIER-LATMANI[1]

[1]Environmental Microbiology Laboratory, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland (*correspondence: matthew.reid@epfl.ch)
[2]Ho Chi Minh City University of Technology - VNU, 268. Ly Thuong Kiet, Dist. 10, Ho Chi Minh City, Vietnam

Arsenic (As) contamination of rice is a growing public health concern, particularly in regions in South and Southeast Asia where the use of As-contaminated groundwater for irrigation has led to widespread contamination of rice paddy soils, and where rice is a dietary staple. The methylation of As by soil microorganisms reduces As toxicity and also influences the mobility and fate of As within soil-plant systems [1]. At present, there is limited knowledge of how As methylation is regulated by soil environmental conditions, and thus it is unclear how soil and water management practices in rice paddies affect As methylation dynamics.

There is evidence from enrichment culture experiments [2] as well as microarray-based genomic surveys [3] that sulfate-reducing bacteria (SRB) may be key drivers of As methylation in anaerobic systems, but this link has not been tested experimentally. In this contribution, we evaluate the role of SRB in As methylation using a systematic and well-controlled set of anaerobic batch experiments with soil collected from a contaminated rice paddy in the Mekong Delta in Vietnam. We combine As speciation analysis using HPLC-ICP-MS with an analysis of the abundance of *arsM* (the gene that encodes the ArsM enzyme which catalyzes methylation) in the presence of varying sulfate and organic carbon concentrations.

Taken together, this set of geochemical and microbial analyses yield process-level insights into the microbial community and soil conditions promoting As methylation. We discuss these results in the context of efforts to reduce As toxicity and/or its bioavailability for plant uptake through soil water and nutrient management practices.

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[2] Bright *et al* (1994) *Appl. Organomet. Chem.* **8**, 415-422.
[3] Zhao *et al* (2013b) *Environ. Sci. Technol.* **47**, 7147-7154