

# **Genome-resolved metatranscriptomics reveals simultaneous methylation and demethylation of arsenic under methanogenic conditions in rice paddy soil**

HYUN YOON<sup>1</sup>, MICHAEL VEGA<sup>2</sup> AND MATTHEW REID<sup>2</sup>

<sup>1</sup>University of California, Berkeley

<sup>2</sup>Cornell University

Presenting Author: [mcr239@cornell.edu](mailto:mcr239@cornell.edu)

Microbial transformations of arsenic (As) in rice paddy soils influence the speciation and toxicity of As in rice grains. Methanogenesis is a dominant microbial metabolism in flooded rice paddy soils, and methanogens have been linked to both As methylation and demethylation. Here, we combine a genome-resolved metatranscriptomic analysis with monitoring of As speciation in anaerobic paddy soil incubations to elucidate the impacts of methanogenic conditions on paddy soil As speciation. Incubations enriched a methanogenic community dominated by *Methanosarcina* co-existing with fermentative bacteria, and the community actively demethylated more than 50% of dimethylarsinic (DMA) amended to incubations. Experiments with 2-bromoethanesulfonate as an inhibitor of methanogenesis confirmed that methanogens were the primary drivers of As demethylation. Amendment of trimethylamine (TMA) as a carbon substrate stimulated methylotrophic methanogenesis and led to an earlier onset of arsenic demethylation. However, the overall extent of demethylation by the end of the three-week incubation was similar in incubations with and without TMA amendment. Dimethylarsinic amendment also stimulated As methylation, with contributions from both fermentative bacteria and select methanogens that co-expressed genes for both methylation and demethylation. This study highlights the complexity of concurrent methylation and demethylation of As in methanogenic rice paddy soils, and suggests that environmental factors stimulating methylotrophic methanogenesis will favor the dominance of inorganic arsenic by enhancing net demethylation.