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Genome to rhizosphere connections between methanogenesis and arsenic demethylation in flooded rice paddies

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Microbial metabolisms facilitate the production and consumption of methane, contributing significantly to climate change and carbon cycling. At the same time, methane metabolisms can influence trace contaminant biotransformations of importance to human health and food security. This contribution highlights recent connections between methanogenesis and arsenic demethylation in flooded rice paddies, with implications for straighthead disorder and methane emissions during rice cultivation. Across the genome, microbial community, and rice rhizosphere-plant continuum, we investigated the effect of carbon substrates on connections between methanogenesis and arsenic demethylation. At the community-level, we show that amending soil slurries with trimethylamine promoted significant, non-specific couplings between arsenic demethylation and multiple methylotrophic methanogenesis pathways, and that several *Methanosarcina* metagenome assembled genomes (MAGs) were dominant in methyltransferase gene expression (and by inference, arsenic demethylation). In response to toxic (methyl)arsenite intermediates produced during arsenic demethylation, we observed that *Methanosarcina* MAGs simultaneously expressed multiple arsenic detoxification pathways in parallel with methylotrophic methanogenesis genes, with arsenite efflux and methylarsenite oxidation being the dominant detoxification pathways. In more complex rice growth experiments in the greenhouse, we demonstrate that amending natural organic matter (i.e., dried leaves) favored greater net arsenic demethylation in porewater and resulted in less methylated arsenic accumulation in rice grains. Porewater correlations between dissolved methane and arsenic species were consistent with the model of methanogenesis-mediated arsenic demethylation releasing inorganic arsenic into the extracellular environment, enabling the uptake and accumulation of inorganic arsenic in rice. Ongoing methanogen enrichments are being used to test how carbon quality and the extent of arsenic methylation (i.e., the number of methyl groups) influence detoxification pathways and net products of demethylation. Across multiple scales, our findings illustrate how methane dynamics can extend beyond the carbon cycle, offering arsenic biotransformation insights with the potential to alleviate straighthead disorder in rice.