Active microbial arsenic methylation

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Arsenic (As) is an ubiquitous environmental toxin and a carcinogen. Given this exposure, most microorganisms have one or more pathways for As resistance [1]. Perhaps the most widespread mechanism is through transmembrane proteins that export arsenite out of the cell: Acr3 and ArsB. As methylation, catalyzed by ArsM, was first regarded as another means of detoxification. Today, parallel to its detoxification role, As methylation under anoxic environments is hypothesized to have evolved for the production of the reduced monomethylarsenite, a potent toxin able to kill surrounding competitors [2].

In addition to its controversial role, As methylation has been studied in rice paddy soils due to the high concentration of these As species in rice. Methylated As is produced by soil microbes and several studies have focused on the *arsM* genes in a attempt to describe the diversity and abundance of the As methylating community [3]. However, harboring this gene may not be a sufficient condition for active As methylation.

We conducted a thorough study to identify active methylating microorganisms. We assessed seven type strains encoding an *arsM* gene for their As methylation capacity and tested their functionality by cloning all *arsM* genes into an arsenic sensitive *Escherichia coli* strain.

The results show that most of the strains were not able to methylate As despite harboring *arsM* genes that encode functional ArsM proteins. We hypothesized that an efficient As efflux system must preclude methylation. We proceeded with the deletion of the transmembrane As transporter gene, *acr3*, in one of the strains. While its As sensitivity and the ArsM expression increased, the Δ*acr3* clone still did not methylate As.

Thus, the regulation of microbial As methylation remains unclear. Work is currently underway to investigate active As methylators in a rice paddy soil enrichments.

[1] Fekih *et al.* (2018) *Front Microbiol.* **9**:2473. [2] Li *et al.* (2016) *Metallomics.* **8**, 1047-1055. [3] Zhai *et al.* (2017) *Sci. Rep.* **7**:42198.