Genetic and transcriptomic insights into dissimilatory antimonate reduction by an obligate anaerobe

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Antimony (Sb) is an industrially significant metalloid that has been exploited by humans for the last 3,000 years. In the environment, Sb typically occurs in two main oxidation states, Sb(III) (antimonite) and Sb(V) (antimonate). Unlike its well-known group 15 neighbor, arsenic (As), relatively little is known about the types of microbes that mediate redox transformations of this highly toxic element in nature. In fact, information regarding the reductive side of the Sb cycle had remained elusive until recently. In 2014, we isolated and described the first microbe, *Desulfuribacillus stibiiarsenatis* MLFW-2^T, capable of using Sb(V) as a terminal electron acceptor to support anaerobic respiratory growth [1,2]. Further research with microbial assemblages and pure cultures from different environments has shown that dissimilatory Sb(V) reduction can be coupled to the oxidation of a variety of organic and inorganic electron donors, suggesting that the process is ubiquitous and carried out by a phylogenetically-diverse group of microbes.

The goal of this study was to identify the respiratory Sb(V) reductase in MLFW-2^T. The draft genome of MLFW-2^T contains fourteen genes encoding complex iron-sulfur molybdoenzymes of the dimethyl sulfoxide reductase (DMSOR) family, members of which function as important components of the anaerobic respiratory chains of prokaryotes. We used RT-qPCR to monitor the relative transcription of all fourteen genes during growth of MLFW-2^T on nitrate, Se(VI), As(V), and Sb(V) as electron acceptors. Using this technique, we identified the putative respiratory reductases for each of the electron acceptors tested. Homologs of the putative respiratory Sb(V) reductase were found in six described phyla and two candidate phyla across both domains of prokaryotic life. In addition, we used messenger RNA sequencing to study the physiological response of MLFW-2^T to Sb(V) and As(V), two species with similar chemistry but which elicit signficantly different effects on cellular growth.

[1] Abin & Hollibaugh (2014) *Environ. Sci. Technol.* **48**, 681-688. [2] Abin & Hollibaugh (2017) *Int. J. Syst. Evol. Microbiol.* **67**, 1011-1017.