

Diversity of microbial arsenic and antimony transformation pathways associated with antimony mine tailing

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Arsenic (As) and antimony (Sb) are both naturally occurring toxic metalloids and are considered to be priority pollutants of interest by the USEPA. Antimony is commonly associated with As in the environment and both elements have similar chemistry and toxicity. The trivalent forms, As^{III} and Sb^{III}, are highly reactive with thiol-containing proteins and more toxic to biota than As^V and Sb^V. Despite their toxicity, microorganisms have developed mechanisms to tolerate and catalyze redox transformation of As and Sb. In this study, we characterized microbial metalloid transformation pathways associated with stibnite mine tailing soils (Ehime, Japan). Total concentrations of Sb and As in the surface soils were 2.28 and 1.24 g kg⁻¹, respectively [1]. By conducting enrichment culturing, relevant As and Sb-transforming bacteria, including aerobic Sb^{III}-oxidizing *Pseudomonas* and *Stenotrophomonas* strains and an anaerobic Sb^{III}-oxidizing *Mesorhizobium* strain, were isolated. These Sb^{III}-oxidizing isolates did not oxidize As^{III}, suggesting the involvement of different mechanisms for Sb and As oxidation. In addition, an anaerobic consortium capable of reducing Sb^V in the presence of lactate were obtained and the precipitation of antimonite as antimony trioxide was confirmed by X-ray absorption near-edge structure (XANES). The influence of the co-contamination with Sb and As on mine soil microbial community was also examined. It was shown that the presence of Sb species affected As^{III} oxidation rates and selected distinct As^{III}-oxidizing bacteria with higher tolerance to As and Sb toxicity [2]. Collectively, our study revealed the presence of diverse microbial metalloid transformation pathways associated with polluted environments, and the importance of co-existing metalloid as a factor affecting the redox transformation and mobility of arsenic in natural systems.

[1] Hamamura et al. (2013), *Microbes Environ* 28, 257-263. [2] Kataoka et al. (2018), *Microbes Environ* 33, 214-221.