Goldschmidt 2023 Abstract
https://doi.org/10.7185/gold2023.18910

Elevated antimony concentration in soils may stimulate microorganisms to utilize Sb(V) for anaerobic respiration

YIDAN ZHANG[1], MAXIM I BOYANOV[2], EDWARD J O'LOUGHLIN[2], KENNETH M. KEMNER[2], HAN-SUK KIM[1] AND MAN JAE KWON[1]

[1]Korea University

[2]Argonne National Laboratory

Presenting Author: yidanzhang@korea.ac.kr

Antimony (Sb) is a toxic metalloid that mainly exists in natural environments as Sb(III) and Sb(V). Redox activities of Sb essentially control the ecotoxicity and mobility of Sb species since Sb(III) is considered more toxic than Sb(V). The study of Sb redox behavior contributes to the management of Sb as a contaminant. In subsurface environments where oxygen is scarce, the fate of Sb is largely controlled by specific microorganisms that can enzymatically reduce Sb(V) to Sb(III). These microorganisms, termed as Sb(V)-reducing bacteria (SbRB), couple the reduction of Sb(V) to the oxidation of organic acids or molecular hydrogen and can gain energy for cell growth. Currently, only a few strains of SbRB have been identified, while the metabolic pathway behind biotic Sb(V) reduction is unclear either. Here we present a new strain of SbRB, temporarily named YZ-1, which was isolated from soils contaminated with elevated Sb concentration. YZ-1 utilizes Sb(V) as terminal electron acceptor and acetate as electron donor for anaerobic respiration. 16S rRNA sequencing showed that YZ-1 is over 99% similar to *Rhodoferax ferrireducens* T118, a strain previously only identified as iron reducing bacteria. XRD indicates the end product of biotic Sb(V) reduction by YZ-1 as a mixture of valentinite and senarmontite, both being Sb(III)-bearing minerals. XAFS results suggest that the biomineralization process during biotic Sb(V) reduction involves a transformation from valentinite to senarmontite. Full genomic sequencing of YZ-1 showed it contains the whole arsenic (As) metabolism cluster, *ars* operon. T118 also possesses *ars* cluster but could not reduce Sb(V) in this study. Through RT-qPCR we found the As(V) reductase, *arsC* was highly expressed within YZ-1 during Sb(V) reduction, therefore we proposed the *ars* cluster within YZ-1 may facilitate the Sb(V) reduction and *arsC* could promote Sb(V) reduction as well. This study provides the biomineral formation during biotic Sb(V) reduction, and a new metabolic pathway that is utilized by SbRB during microbial Sb(V) reduction.