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アンチモンによる土壌性細菌群集及びヒ素酸化能への影響
Effect of antimony on arsenite oxidation by soil microbial community

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Antimony (Sb) and arsenic (As) are naturally occurring toxic elements in the earth’ s crust, and both elements exist commonly in sympatric environment. The chemical properties and the mode of toxicity of those elements depend on their oxidation states. Although both oxidation states are toxic, trivalent is more toxic than pentavalent chemical form. The microbiological oxidation of As(III) can impact on the geochemical cycling of arsenic in the contaminated environment, and more than 30 phylogenetically diverse As(III)-oxidizing bacterial strains have been isolated. Although natural microbes are exposed to multiple contaminants in situ, the effect of co-contamination on microbial As(III)-oxidation activity is not well understood. To gain insight into the microbial roles in the biogeochemical cycles of As, we evaluated the effect of co-contamination of Sb and As on the microbial community and their As-oxidizing activity by using solid-phase culturing which was inoculated with antimony mine tailing soil (Ichinokawa, Ehime, Japan). As(III) oxidation rates increased exponentially and reached steady state at day-8 in which 0.15 mM As(III) was oxidized to As(V) in 22.9 hrs. The addition of antimonite tartrate (Sb[III]-tar, 0.15 mM) at day-9 inhibited arsenite oxidation, which was then reduced to 40% by day-15. Successional changes in bacterial community compositions were observed after Sb(III)-tar addition by 16S rDNA- and arsenite oxidase gene (aioA)-targeted analyses. Total of 69 As(III)-oxidizing strains were isolated from the solid samples obtained before and after the Sb(III)-tar addition, and the Sb(III)-tar tolerance of representative isolates were determined. Various As(III)-oxidizing strains exhibited different levels of Sb(III)-tar tolerance in growth response and As(III)-oxidation rates. These results indicated that the co-contamination of As and Sb affect the community composition and activity of As(III)-oxidizing microbial population reflecting the differences in cellular responses among strains to Sb toxicity.

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