

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.

Keywords: Heavy metal pollution, Arsenic, Antimony, Solid phase advective culturing, Soil bacterial community

Bacterial community structure in different subsurface sediments of the southern Kanto Plain

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Ground source heat pump (GSHP) systems have become popular because of their efficiency in energy conservation and reduction of CO₂ emission. GSHP utilizes the groundwater or subsurface sediment, with an almost constant temperature during the year, as the heat source or sink. Although the temperature changes in subsurface would affect geological structure, groundwater quality, and subsurface microorganisms, very few studies have addressed temperature effects on subsurface biophysical processes. For evaluation of subsurface environmental effects and ensuring overall sustainability of GSHP use, it is essential to investigate how the temperature change may affect the subsurface microbial community structure. Before that, however, it is necessary to know the subsurface microbial community structure that has not yet been affected by temperature change. The purpose of this study was therefore to investigate initial (non-thermal-change-affected) bacterial community structure in deep boring core samples from three different sites in southern Kanto plain. The three sites were the university campuses of College of Humanity and Science, Nihon University (NU; Setagaya-ku, Tokyo), Saitama University (SU; Saitama-city) and Fuchu campus of Tokyo University of Agriculture and Technology (TAT; Fuchu-city, Tokyo). At all three sites, tests of GSHP systems and their environmental response are planned in the near future.

At each site, 10 to 12 sediment core samples were collected from different depths, and whole DNA was extracted from those core samples. PCR-amplified V2-V3 region of bacterial 16S rRNA gene was analyzed by pyrosequencing. The results showed that bacterial community structures of 0-30 m depth were distinctly different among the three boring sites. At the NU site, bacteria belonging to Actinobacteria and Firmicutes accounted for more than half of the whole bacteria population. On the other hand, Chloroflexi, γ -, and δ -proteobacteria were predominant at the SU site, and α -, β -, and γ -proteobacteria were mainly detected at the TAT site. Especially, OTUs assigned to the classes Dehalococcoidetes and Anaerolineae (both belonging to phylum Chloroflexi) were predominant in a wide range of depths at the SU site, and they were particularly detected in former marine sediment. Below 30-m depth, β -, and γ -proteobacteria were predominant at all sites. The relative amounts of some taxonomic groups of bacteria were correlated with depth, pH, electric conductivity of pore water, and particle size distribution. Thus, the variety of bacterial community structure could be attributed to the differences of the depositional ages and environments and/or present subsurface environment at each site. The fundamental data on subsurface bacterial community structures in the southern Kanto Plain from this study will be a useful platform for evaluating the future GSHP-induced temperature change effects on the subsurface environments.

Keywords: subsurface microorganisms, ground source heat pump, next generation DNA sequencing, bacterial community structures