

## Biogeochemical arsenic cycling unraveled by microbial genome analysis

\*Seigo Amachi<sup>1</sup>, Tatsuya Tsuchiya<sup>1</sup>, Yasuhiro Kasahara<sup>3</sup>, Natsuko Hamamura<sup>2</sup>

1. Chiba Univ., 2. Kyushu Univ., 3. Hokkaido Univ.

Arsenic is released from anaerobic sediments into groundwater as As(III) (arsenite), which threatens the health of millions of people in southern Asia. It is widely accepted that certain anaerobic bacteria, such as dissimilatory iron-reducing bacteria and dissimilatory As(V) (arsenate)-reducing bacteria, play important roles in arsenic release in nature. Although respiratory arsenate reductase genes (*arrA*) closely related with *Geobacter* species have been detected frequently in arsenic-rich sediments, it is still unclear whether they directly participate in arsenic release, mainly due to lack of pure cultures capable of arsenate reduction. Previously, we isolated *Geobacter* sp. OR-1 from Japanese paddy soil. Strain OR-1 also utilized soluble Fe(III) and ferrihydrite as electron acceptors, and catalyzed dissolution of arsenic from arsenate-adsorbed ferrihydrite. Furthermore, inoculation of strain OR-1 into sterilized paddy soil successfully restored arsenic release. In this study, we analyzed draft genome sequence of strain OR-1, and found two distinct “arsenic islands”, the genomic regions highly enriched with arsenic-metabolizing genes. One consisted of *arrAB*, and they are also flanked with genes for arsenic resistance (*arsADR* and *acr3*). Another island consisted mainly of genes for arsenic resistance including that for a detoxifying arsenate reductase *ArsC*. Transcriptional analysis revealed that most of these genes were expressed specifically in the presence of arsenic, and that the expression of *arrA* was more than 30 times higher in the presence of arsenic. Comprehensive proteomic analysis by means of 1D SDS-PAGE and LC-MS/MS showed that not only arsenic-metabolizing proteins but also those involved in oxidative stress response, protein folding, molecular chaperones, phosphate uptake, and sulfur metabolism were expressed cooperatively in the presence of arsenic. Our results shed light on how microbes cope with this toxic metalloid, and play an important role in the biogeochemical cycling of arsenic.

Keywords: arsenic, microbes, genome analysis, arsenate reduction, transcriptional analysis, proteomic analysis