

Environmental parameters as drivers of bacterial communities responsible for arsenic removal from acid mine drainage

Vincent Tardy, Corinne Casiot, Lidia Fernandez-Rojo, Eléonore Resongles, Angélique Desoevre, Marina Hery

Laboratoire HydroSciences Montpellier, HSM, UMR 5569 IRD, CNRS, Université Montpellier, CC 57, 163 rue Auguste Broussonet, 34090 Montpellier, France, vincent.tardy@univ-montp2.fr, casiot@msem.univ-montp2.fr

Extended Abstract

Arsenic (As) is one of the most toxic pollutants commonly associated with mine tailings and Acid Mine Drainage (AMD), with concentration ranging from $< 1 \mu\text{g}\cdot\text{L}^{-1}$ to hundred $\text{mg}\cdot\text{L}^{-1}$ in mine water [1]. Considering the toxicological effects of Arsenic on organisms, it is essential to develop remediation strategies specifically dedicated to the treatment of As-rich AMD. In the former mine of Carnoules (Gard, France), AMD formation coincides with the creek of the Reigous stream. Natural attenuation of As occurs at this site *via* a coprecipitation with iron (III) [2,3]. This natural process, based on bacterial oxidation of iron and arsenic, represents a promising strategy for the development of biological treatment of AMD. In this context, it is necessary to better understand the influence of biological and environmental parameters on the diversity and activity of iron and arsenic oxidizing bacterial populations involved in As and Fe removal.

In the present work, we have hypothesized that the influence of environmental parameters (temperature increase and nutrient supply) will have a significant impact on the composition or activity of bacterial communities and consequently on the processes of iron and arsenic oxidation. To test this hypothesis, we conducted a batch experiment with AMD water collected at the Reigous spring. We have tested three biotic conditions: (i) incubation at 35°C corresponding to optimal temperature for arsenic oxidizing bacteria, (ii) nutrient supply ($0.2 \text{ g}\cdot\text{L}^{-1}$ of yeast extract) used for heterotrophic growth and (iii) control conditions (20°C , which corresponded to summer field water temperature, without nutrient supplement). For each conditions tested, abiotic controls have been performed in parallel with filtered-sterilized DMA water. Dissolved As and Fe concentrations in batches were monitored during eight days. At the end of the experiment, the speciation of As (As(III)/As(V) ratio) was determined in the precipitates that formed in the batches and the composition of bacterial community in water was characterized by high throughput sequencing of 16S rRNA ribosomal gene.

No changes in soluble Fe and As concentrations were observed in the abiotic controls, confirming the key role of microorganisms in arsenic and iron removal. At the end of the experiment, 100% of arsenic was precipitated in the batches heated at 35°C and in the batches supplied with nutrients, whereas only 68% of arsenic was precipitated in the control batches. In contrast, iron precipitation was higher in the control (96%) than in the 35°C and nutrient conditions (73% and 23%, respectively). Arsenic speciation in the precipitates also revealed differences, with higher proportion of As(V) when nutrients were added. These findings suggest that nutrient addition stimulated arsenic oxidation by heterotrophic bacteria whereas iron oxidation, mainly due to autotrophic bacteria, was inhibited. To characterize the modifications induced in the bacterial community composition by the treatments (temperature and nutrients), 16S rRNA genes were sequenced using high throughput approach and *aioA* gene was quantified. In conclusion, our study opened new research perspectives for the development of a biological treatment process taking into account the influence of key parameters (temperature, nutrients) on the composition and activity of bacterial communities involved in iron and arsenic removal in AMD.

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Key words: Acid Mine Drainage, bacterial composition, iron and arsenic removal

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