Low temperature nucleation of ferric arsenate using microorganisms

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Introduction

The safe dispoal of arsenic is important for the metal extraction industry worldwide. Previous work has shown that crystalline ferric arsenate ($FeAsO_4 \cdot 2H_2O$), which is a synthetic version of the natural mineral scorodite, fulfils most of the criteria for safe disposal. Presently, this requires the use of expensive pressurised equipment in industrial applications. There is increasing evidence that microorganisms play an important part in the geochemical cycle of As. In environmental samples, bacteria are often closely associated with mineral precipitates, as well as in bioleaching samples.

Method

Strains of acidophillic bacteria (*Acidithiobacillus* spp., *Sulfobacillus* spp. and *Thiomonas* spp.) have been enriched and isolated in liquid and on solid media from rock samples from former mine sites in the Czech Republic and the UK, and experiments carried out to determine whether the bacteria can catalyse the formation of ferric arsenate.

Results

No distinct mineral phases have been identified by XRD, and there is no variation in crystallinity with varying conecntrations or valences of arsenic species. FTIR analyses of precipitates have identified no crystalline mineral phases, and there is no increase in crystallinity with age over the months during which the precipitates have been studied.

Conclusions

To date we have no evidence that the selected bacteria can precipitate ferric arsenate on solid media, despite varying concentrations of As added as As^{3+} or As^{5+}. Material formed has been x-ray amorphous due to rapid formation, and FTIR analyses have shown no increase in crystallinity with age over the months in which the precipitates have been studied.

References

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FT-IR investigation of the uranium S-layer interaction in aqueous solutions

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Many bacteria possess so-called surface layer (S-layer) proteins, forming paracrystalline lattice structures on the cell wall [1]. Beside its ecological relevance for the retention of toxic metals, they are a good model system for investigations of the interaction of bio-ligands, e.g. proteins, with uranium in aqueous solutions. Several S-layers from different *Bacillus* strains were proved to have high binding capacity to uranium. But there is still little knowledge of the interactions between the functional groups of the protein with the actinyl ions at a molecular level [2].

In this work we present results of batch experiments where the uranium binding capacities of different S-layer protein from different *Bacilllus* strains were determined. The experiments were carried out at different pH values (pH 4, 6, and 8) for each isolated S-layer protein. It was found that the uranium binding capacities of each gram S-layer range from 5.0 mg and 63.9 mg, from 11.1 mg and 561.1 mg, and from 14.2 mg and 33.5 mg at pH 4, 6, and 8, respectively, depending on the respective S-layer.

For a deeper understanding of the molecular binding of the uranyl ion to the protein we used Attenuated Total Reflectance Fourier-transform Infrared spectroscopy (ATR-FTIR) which allows vibrational spectroscopic investigations of aqueous solutions containing actinide ions and disolved proteins as well [3, 4]. The spectra clearly demonstrate carboxyl groups are the major functional groups which interact with the uranyl ions at pH 4. Additionally, the infrared spectra suggest the formation of different uranium-protein complexes depending on the incubation period (1 h vs. 48 h) which can be observed by a peak shift of the absorption band representing the antisymetric uranyl stretch to lower wavenumbers.

This spectroscopic approach constitutes the foundation of more detailed investigations on the impact of the pH value and of other functional groups (e.g. phosphate or amino groups) on the uranium complexation by bio-systems.

References

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