Natural uranium ores host iron-reducing and iron-oxidizing bacteria as demonstrated by high throughput sequencing and cultural approaches.

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We investigated the influence of uranium on the indigenous bacterial communities in natural uranium ores by conducting an in-depth analysis of soil samples collected in the region of Bessines, one of the most important natural uranium deposits in France. Soil samples exhibiting 1.5 to 25.5% U in mass were compared with nearby control soils containing trace uranium. EXAFS and XRD analyses of soils revealed the presence of U(VI) and uranium-phosphate mineral phases, identified as sabugalite and meta-autunite.

A comparative analysis of bacterial diversity using DGGE [1] and high throughput pyrosequencing of 16S rRNA genes revealed the presence of complex populations in both control and uranium-rich samples. Among the 232.000 reads analyzed by pyrosequencing, 23 bacterial phyla were detected with *Proteobacteria*, *Acidobacteria* and *Chloroflexi* being predominant. Statistical analyses of the DGGE fingerprints and pyrosequencing data showed that bacterial communities of uranium-rich samples differ from that of controls. An enrichment of sequences related to iron- and uranium-reducing bacteria as well as iron-oxidizing species in uranium-rich samples was evidenced by both methods. Several iron-reducing anaerobic isolates related to *Pelosinus, Clostridium* and *Enterobacter* were cultured from the uranium-rich soil samples and characterized.

Taken together, these results demonstrate that uranium shapes bacterial diversity and suggest the existence of an iron and/or uranium redox cycle mediated by bacteria in the soil.

[1]Mondani *et al*. (2011) *PLoS ONE* 6(10): e25771. doi:10.1371/journal.pone.0025771

Towards Understanding Magnetite Biomineralisation: The Effect of Short Chain Peptides on the {100} and {111} Magnetite Surfaces

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Biomineralisation is the process by which living organisms form minerals. The earliest known example of biomineralisation is that of the biosynthesis of magnetite [1]. A major step forward in understanding the principles of magnetite biomineralisation occurred with the discovery of Magnetotactic bacteria (MTB) [2]. Despite this, much of the detailed atomistic mechanism by which the process occurs is unknown.

Numerous commercial applications for bacterial MNPs have been suggested, including the removal of radionuclides and heavy metals from waste water, MRI contrast agents, magnetic antibodies and drug and gene delivery. However, such applications are not commercially viable at present. In order to produce MNPs more economically the biomineralisation processes need to be further understood. Therefore, we are developing an atomistic model for the system, in an attempt to understand the processes involved.

Magnetite formation within Magnetospirillum magneticum AMB-1 occurs under the influence of the Mms6 protein. It was previously discovered that the Mms6 protein was linked to the control of the morphology and size of the magnetite crystals within the M.magneticum AMB-1 [3]. The acidic C-terminal region of this sequence is of particular interest due to its potential linkage to iron binding. It is hypothesised that if key iron binding sites within the C-terminus of the Mms6 protein are substituted for alanine, the protein's overall iron binding ability is diminished.

In this study, an atomistic model of Mms6-driven magnetite formation was developed, using molecular dynamics (based on classical atomistic potentials), to study the attachment of a series amino acid repeats (alanine-alanine, alanine-glutamic acid & glutamic acid-glutamic acid) to the {100} & {111} magnetite surfaces and investigate the effect on iron binding ability.

[1] J.W. Schopf *et al*. , *Science*, 1965, 149, 1365, [2] R. Blakemore, *Science*, 1975, 190, 377, [3] A. Arakaki *et al*., *J. Colloid Interface Sci*., 2010, 343, 65.

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