



Influence of U(VI) and nitrate on microbial communities of uranium mining wastes

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Changes in the structure of the microbial community of a soil sample from the uranium mining waste pile Haberland near the town Johanngeorgenstadt in Germany were investigated after addition and incubation with uranyl or sodium nitrate. For this purpose a sample with a natural uranium content of 26 mg/kg was treated with uranyl and sodium nitrate solutions (pH 4.0) and incubated under aerobic and anaerobic conditions for different periods of time. Afterwards total DNA was extracted from both treated and untreated samples, 16S rRNA gene fragments were amplified by PCR using primers specific for the domains of *Bacteria* or *Archaea* and then cloned. The predominant microbial populations were identified by restriction fragment length polymorphism and their 16S rRNA genes were sequenced and phylogenetically affiliated. The 16S rRNA gene retrieval revealed that representatives of *Acidobacteria* and of *Alphaproteobacteria* were dominating the bacterial community of the untreated sample. The increasing of the uranium content up to 100 mg/kg with a subsequent incubation for four weeks under aerobic conditions stimulated a propagation of *Pseudomonas* spp., *Arthrobacter* spp., and *Geobacter* spp. In a parallel sample supplemented with sodium nitrate under the same conditions mainly denitrifying and nitrate reducing populations of *Actinobacteria* and of *Bacteroidetes* were induced. In another sample, which was longer incubated (14 weeks) even with a higher uranium content, U-sensitive *Bacteroidetes* and alphaproteobacterial populations were predominant. The latter indicates that at that later stages of incubation the added U(VI) was not anymore bioavailable. In a parallel sample incubated under anaerobic conditions mainly *Betaproteobacteria* were stimulated. Additionally, some sequences closely related to *Clostridium* spp. were found in the anaerobic sample. Archaeal diversity in the uranyl and sodium nitrate treated samples decreased in comparison to the untreated sample.

All retrieved archaeal sequences were closely related to representatives of *Crenarchaeota*. Our results represent the first cultivation-independent analysis of changes in the structure of a natural microbial community of a particular environment induced by the addition of uranyl or sodium nitrate.