

Microbial communities from deep subsurface uranium deposit in the Tono area

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Microbial activity plays an important role in the fate and transport of uranium in natural and contaminated environments. Sulfate reducing bacteria (SRB) are capable of immobilizing dissolved uranium directly as part of their metabolism or indirectly as a result of metabolic byproducts, including changes in pH. Culture-dependent and -independent methods were used to determine the activity and diversity of the microbial community in groundwater samples collected from the Tono uranium deposit. Molecular signatures of organisms present in the samples were detected by using selective PCR primers for SRB, Bacteria, and Archaea. Sequence analysis of the dissimilatory sulfite reductase (DSR) genes was used to determine the diversity of the SRB community. This analysis revealed that more than 80% of the cloned DSR genes from the deeper part of the sedimentary formations are not closely related to any previously characterized DSR genes. We also observed a dominance of archaeal methanogens in the clone libraries. The highest sulfate reduction rates, as inferred from groundwater incubation experiments, were observed near the boundary between the marine facies and lignite rich layers. The non-acetate oxidizing SRB *Desulfovivrio* and *Desulfotomaculum* were the most dominant DSR genes detected at this depth. These microbial communities may contribute indirectly for the long-term immobilization of uranium in this deposit.