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Potential for aqueous uranium(VI) removal by indigenous bacteria in deep granitic groundwater

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Understanding the biogeochemical U redox process is crucial for controlling U mobility and toxicity under conditions relevant to deep geological repositories (DGRs). In this study, we examined the interactions between indigenous bacteria and aqueous U(VI) (($U(VI)_{aq}$) under anaerobic conditions with addition of 20 mM sodium acetate for 24 weeks. Three indigenous bacteria obtained from granitic groundwater at depths of 44–60 m (S1), 92–116 m (S2), and 234–244 m (S3) were applied for $U(VI)_{aq}$ removal. The highest $U(VI)_{aq}$ removal efficiency of 57.8% was observed in S3, followed by S2 (43.1%) and S1 (37.7%). The incomplete $U(VI)_{aq}$ removal was attributed to the presence of the thermodynamically stable uranyl carbonate complex. High throughput 16S rRNA gene sequencing analysis revealed shifts in bacterial community structure after the anaerobic reaction. In particular, the bacterial community structure of S3 was clearly distinguished from the others owing to the presence of sulfate-reducing bacteria (SRB). Two SRB species, *Thermodesulfovibrio yellowstonii* and *Desulfatirhabdium butyrativorans*, became dominant in the S3 sample, and played a key role in the bioreduction of $U(VI)_{aq}$ by precipitating U(VI) as U(IV)-silicate nanoparticles. The Fe(II)-mediated abiotic U(VI) reduction by *Pseudomonas peli* and *Simplicispira hankyongi* is suggested as another possible mechanism for the removal of $U(VI)_{aq}$. These results demonstrated that considerable removal of U(VI)aq is possible by stimulating the activity of indigenous bacteria in the DGR environment.