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Characterization of microbiological community in natural REE-containing matrixes

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Biochemistry of REE is very poorly understood. As microbes drive biogeochemistry in many ecosystems it can be expected with various yet unknown organisms that play a role in REE biogeochemistry. Thus these environments are a promising source for the recovery of microbes that are suitable candidates for their application in REE extraction and recycling. The microbial community is a close metabolic network, where some of the organisms actively contribute to the carbon, nitrogen, sulfur, and phosphorus cycle and other microorganisms interact with minerals, metals, and pollutants. On the one hand such a microbial community is well adapted to environment and on other hand it is influenced by the geochemical parameters. Investigation of microbial community of REE containing matrixes has to be accompanied by (geo)-chemical analyses. Geochemical and structural soil parameters like organic compounds, ion exchange or water holding capacity and porosity influence the microbial population. Moreover daily or seasonal changes of physical matrix properties force the microbial community to adapt. Reflection of environmental circumstances is one challenge describing natural microbial community. The most sensitive describing tools are culture independent genomic methods. These genomic methods describe and characterize the majority of microorganisms including even the uncultivated microorganisms. Generated metagenomic data will be matched with already existing genomic databases. Up to now genetic methods like PCR fingerprinting techniques and fluorescence *in situ* hybridization used to identify and quantify microorganisms interacted with REE containing ore. Nevertheless genomic information of energetic metabolism, phosphate, sulfur and iron metabolism, quorum sensing, and genes involved in metal resistance and amino acid biosynthesis pathways were identified. As already mentioned the data base for comparative genomics is small. To extent this fundamental it is necessary to extract single strains, to cultivate them and to analyze their genomes.

Biography

Sabine Kutschke has studied Bioengineering at the Moscow State Institute of Food Production. She has finished her PhD in Biochemistry at the Universität Leipzig in 2002. Focus of her research is on the interaction of microorganisms with metals. Other research topics are the characterization of natural microbial communities using DNA-based and culturing techniques. As a senior scientist she supervised diploma and master students and worked in several projects in the field's resource ecology, resource technology and technology transfer. She has published 13 peer-reviewed publications and one patent is pending. Her work was awarded in 2011 with the Technologiepreis des Helmholtz-Zentrums Dresden-Rossendorf.

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