**The impact of uranium and malic acid on soil microbial communities and a *Mesorhizobium* isolate**

**R.E. Linares-Jiménez,\*** **T.-S. Wei, R. Steudtner, A. Cherkouk, T. Stumpf, S. Sachs**

*Helmholtz-Zentrum Dresden-Rossendorf, Institute of Resource Ecology, Bautzner Landstraße 400, 01328 Dresden, Germany*

\* *r.linares-jimenez@hzdr.de*

Radionuclides (RNs) that are released into the environment, for example, from contaminated sites or due to accidental events, can migrate via the groundwater into the surface soils. There they may interact with indigenous microorganisms and plants, potentially entering the food chain and posing health risks to humans. Accurate modeling of the RN uptake by plants requires a thorough understanding of the mechanisms governing their transport and accumulation, including the role of soil microorganisms. Both soil microbes and plant root exudates can alter the speciation of RNs in the soil, affecting their mobility and bioavailability [1, 2]. Microorganisms exhibit different mechanisms to interact with RNs, which enable them, for instance, to increase their survival rates in unfavorable environments. The main microbe-heavy metal interaction processes, which also apply to RNs, are biosorption, bioaccumulation, biotransformation, and biomineralization [3].

In this study, we investigate the impact of uranium (U) and malic acid (MA), as an example of a common plant root exudate, on the composition of the microbial community in a reference soil (Refesol 01-A, Fraunhofer IME) based on 16S rRNA gene analysis as well as the interaction of U with a selected soil microorganism. The soil community comprised three main phyla: Firmicutes, Actinobacteriota, and Proteobacteria. However, after 28 days of exposure with 1.8 or 7.1 mg U/kg soil and 20 mg MA/kg soil, no apparent changes in the abundance of these three phyla in the soil were observed. *Mesorhizobium* sp. DNB0012 was isolated from the U exposed soil and is used to study its interaction with U and MA. *Mesorhizobium* spp. are mainly found in association with legume rhizosphere systems [4]. The bioassociation of 100 µM U to *Mesorhizobium* sp. DNB0012 was studied by batch experiments as a function of the exposure time.  *Mesorhizobium* sp. DNB0012 showed a rapid biosorption of U reaching an equilibrium after only 2 hours with about 38% of the initial U adsorbed to the biomass. The results of a viability assay with live/dead staining exhibited a significant toxicity of U to the cells compared to control cells without U. Time-resolved laser-induced fluorescence spectroscopy (TRLFS) is used to determine the U(VI) speciation in the presence of *Mesorhizobium* sp. DNB0012. First TRLFS results confirmed the presence of one U(VI) species in the cell pellet indicating the bioassociation of U. Further studies on the impact of *Mesorhizobium* sp. DNB0012 and MA on the U speciation are in progress.

This study assess the interaction between U, MA and soil microorganisms on a molecular level and its impact on the bioavailability of U. Knowledge about the interaction of U with a plant-associated microorganism will be provided. The results can help to improve radioecological models for the assessment of the RN transport and transfer in the environment to the food chain.

This study is funded by the German Ministry of Education and Research under contract No. 15S9437C.

References:

[1] Gupta (2017), *Rev. Environ. Contam. Toxicol. 241*, 139-160.

[2] Banala (2021), *Environ. Technol. 21*, 101254.

[3] Lloyd (2003), *FEMS Microbiol. Rev. 27*, 411-25.

[4] Laranjo (2014), *Microbiol. Res. 169*, 2-17.