Impact of different micro-organisms (bacteria, archaea) on the Platinum (Pt) speciation

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ABSTRACT

The anthropogenic use of platinum (Pt) has significantly altered its biogeochemical cycle over recent decades[1], leading to its increased dispersion in the environment. Microorganisms, ubiquitous in ecosystems, strongly influence metal speciation. While some metals are essential for microbial metabolism, their transformations can also generate toxic forms that microorganisms detoxify through chelation or redox processes[2]. However, the impact of microorganisms on Pt speciation remains poorly understood, despite Pt's high affinity for sulfur-bearing ligands[3].This study investigates the influence of the common bacterium *Escherichia coli* and of the hyperthermophilic archaeon *Thermococcus kodakarensis*, on Pt and S speciation. These species compass a diversity of metabolic pathways: *E. coli* is a ubiquitous mesophilic bacterium common to human and animals, and the hyperthermophilic *T. kodakarensis*, relies on S-assisted fermentative metabolism.

X-ray absorption spectroscopy (XAS) at the Pt L_3-edge revealed that both microorganisms, when exposed to 100 µM of Pt(IV) in nutritive media, can reduce Pt(IV) to Pt(II) within 1 hour and to Pt(0) after 24 hours, involving S-bearing ligands in *E. coli*. In contrast, *T. kodakarensis* reduced Pt(IV) directly to Pt(0) within 1 hour, indicating faster reduction kinetics. These independent analyses also showed a more reduced intracellular sulfur pool in *T. kodakarensis* than in *E. coli* Similarly, XAS analyses at the S K-edge, performed under the same Pt(IV) exposure conditions (100 µM), revealed an increase in reduced S(-II) and a decrease in oxidized S(+V) species in *E. coli*, whereas *T. kodakarensis* exhibited the opposite trend, highlighting the key role of sulfur in microbial Pt detoxification.

This work provides new insight into the microbial S metabolism driving distinct Pt transformation pathways and emphasizes the key role of microbial diversity on Pt environmental mobility by comparing two phylogenetically and metabolically different microorganisms.

REFERENCES

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