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Arsenic detoxification in the model alga *Euglena gracilis*: key role of the glutathione pathway evidenced by XAS.

J. Miot (1), G. Morin (1), F. Skouri-Panet (1), C. Férard (1), G. Ona-N'Guema (1), F. Guyot (1), Gordon E. Brown (2, 3).

1. Institut de Minéralogie et de Physique des Milieux Condensés, UMR 7590, CNRS and IPGP, Paris, France, (2) Surface and Aqueous Geochemistry Group, Department of Geological and Environmental Sciences, Stanford University, USA, (3) Stanford Synchrotron Radiation Laboratory, SLAC, USA.

(Jennyfer.Miot@impmc.jussieu.fr / Phone: +33-144279832)

Assessing arsenic speciation in model plants and algae is a major issue to elucidate the detoxification mechanisms accounting for their adaptation to high levels of toxic metal(loid)s under natural conditions. For instance, the acidophilic protozoan *Euglena mutabilis* is naturally exposed to high arsenic concentrations, i.e. 80-250 mg.L-1 As(III) at the Carnoulès acid mine drainage (Gard, France).

In the present study, we investigated arsenic coordination in the model photosynthetic protozoan, *Euglena gracilis* (phylogenetically close to *E. mutabilis*) exposed to arsenite at concentrations ranging from 10 to 200 mg.L-1 As(III) (conditions similar to those encountered in AMD systems). *E. gracilis* was shown to be tolerant to concentrations up to 200 mg.L-1. X-ray Absorption Spectroscopy results at the As Kα-edge showed that, in the cells, arsenic mainly binds to sulphur ligands, in the form of arsenic-tris-glutathione (As-(SG)3) or arsenic-phytochelatin (As-PC) complexes, and to a much lesser extent, to carbon ligands, presumably in the form of methylated arsenic compounds. Additionally, we observed a progressive depletion of the thiols pool in the cells with increasing initial As(III) concentration in the culture medium, which was attributed to a greater production of As(SG)3 or arsenic-phytochelatin complexes.

The major role of the glutathione pathway in As(III) detoxification was confirmed by the lower growth rate of *E. gracilis* cultures exposed to arsenic, in the presence of buthionine sulfoximine, an inhibitor of glutathione synthesis. Eventually, we evidenced that arsenic does not accumulate in the cells.

These spectroscopic results set a methodological framework to decipher microbial detoxification processes both under laboratory and natural conditions.