Environmental toxicogenomics – linking toxicity and adaptive responses of silver-exposed *Chlamydomonas reinhardtii* across the transcriptome, proteome and phenotype

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ABSTRACT

Understanding mechanistic and cellular events underlying a toxicological outcome allows predicting the impact of environmental stressors on organisms living in different habitats. A systems based approach allows characterizing molecular events, and thereby the cellular pathways that have been perturbed. However, mapping just adverse outcomes of a toxicant in an organism falls short of describing the stress response that is mounted to maintain homeostasis on perturbations and may confer resistance to the toxic insult. Silver is a toxicant which is a potential threat to aquatic organisms, at least partly due to the increasing use of silver-based nanomaterials, which release free silver ions. In this study, we have derived a mechanistic understanding of the temporal dynamics and pathways involved in toxicity, detoxification and repair in the unicellular green algae, *Chlamydomonas reinhardtii*, exposed to silver.

We could show that silver uptake through copper transporters is fast, with intracellular levels rising several orders of magnitude above exposure levels. These high levels almost immediately cause a loss of energy in the cells and reduced photosynthetic yield and growth. At the same time the cells instigate a fast transcriptome and proteome response to combat oxidative stress and to eliminate silver via efflux transporters. Depending on the exposure levels, this regulation of genes and proteins allowed the algae to partly recover, as seen by the reactivated photosynthetic machinery, while growth and elimination of silver from the cells was still negatively affected. This indicates a certain resilience of the cells to silver exposure but raises concern about the transfer of silver through algae in the aquatic food chain and fitness of algae exposed to silver for extended times.