Cadmium Toxicity Impacts the Transcriptome and Global Mineral Homeostasis in *Chlamydomonas reinhardtii*

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Project Goals: One mechanism for removing cadmium from polluted sites is phytoremediation, which works by extraction of the contaminant from the soil or water, using plants or algae[1]. The use of plants (or algae for contaminated water) offers the advantage of low cost and carbon neutrality. The ultimate objective of this project is understanding cadmium metabolism in relation to essential metal homeostasis in algal and plant cells with the long term goal of promoting phytoremediation strategies for Cd.

The 2015 World's Worst Pollutant Problems report identified Cd as one of the top 6 toxic threats to human's health[2]. Human exposure to Cd primarily occurs from food consumption as Cd enters the food web from contaminated soil and waters. Cd exposure in humans results in kidney and renal damage, osteoporosis, cancer, and cardiovascular disease. In plants, Cd toxicity diminishes growth, photosynthesis, and crop yield and causes an alteration in mineral nutrition[3]. Phytoremediation of Cd contaminated sites via plants and algae is of great interest as it is a low cost, solar energy driven clean up technique. *Chlamydomonas reinhardtii* is an excellent reference organism for understanding the metabolic responses to Cd exposure because it has been extensively studied at the cellular lever and it grows in a simple well-defined salts medium.

We have identified two Cd conditions that elicit a phenotypic vs a non-symptomatic response in Chlamydomonas (sub-toxic vs. toxic). Our goal is to identify the mechanisms utilized for tolerance/resistance to Cd and the overall impact of Cd toxicity in the cell. Stress markers such as growth, photosynthesis, GSH/GSSG, and phytochelatin production were used to determine the impact of Cd in the cell. Cd at toxic levels alters the elemental composition profile of Chlamydomonas resulting in the hyper-accumulation of Fe and Cu and in a reduction of P and Ca content. The genome-wide analysis via RNA-Seq of sub-toxic vs. toxic Cd exposed cells identified both overlapping and unique responses to Cd.

References

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This work was supported by the Department of Energy (DE-FC03-02ER63421) and by the National Institutes of Health (GM42143).