

## Molecular effects of inorganic mercury on freshwater microalgae: an omics approach

C. GUEGUEN<sup>1\*</sup>, V. MANGAL<sup>1</sup>, M.E. DONALDSON<sup>2</sup>, B. SAVILLE<sup>3</sup>

<sup>1</sup>Departement de Chimie, Université de Sherbrooke, Qc J1K 2R1, Canada (\*correspondence: celine.gueguen@usherbrooke.ca; vaughn.mangal@utoronto.ca)

<sup>2</sup>Environmental and Life Sciences Program, Trent University, Peterborough, Ontario, Canada (michaeldonaldson@trentu.ca)

<sup>3</sup>Forensic Science Program, Trent University, Peterborough, Ontario, Canada (barrysaville@trentu.ca)

Mercury (Hg) is of major concern in aquatic system due to its conversion to neurotoxin methylmercury (MeHg) that can be biomagnified and bioaccumulated in the food chain. In this study, we assess the metabolomics and transcriptomic changes in the green algae *Gracilis* in response to Hg stress. The nontargeted Fourier Transform Ion Cyclotron Resonance Mass Spectrometry (FT ICR MS) analyses showed a clear distinction between the metabolic profiles of Hg-exposed and control algae samples. Some pathways including carbon fixation, assimilation of ammonia, and oxidative stress mitigation were affected by Hg stress. We performed RNA-sequencing on Hg-exposed and control algae samples. Analysis of that data identified 1413 differentially expressed genes, 727 of which were up-regulated in Hg-exposed samples. Integrating metabolomic and transcriptomic approaches provided valuable information to gain a better understanding of interactions of *Euglena* with Hg.