Analysis of the *Elodea nuttallii* Transcriptome in Response to Mercury and Cadmium Pollution: Development of Sensitive Tools for Rapid Ecotoxicological Testing

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Abstract
Toxic metals polluting aquatic ecosystems are taken up by inhabitants and accumulate in the food web, affecting species at all trophic levels. It is therefore important to have good tools to assess the level of risk represented by toxic metals in the environment. Macrophytes are potential organisms for the identification of metal-responsive biomarkers but are still underrepresented in ecotoxicology. In the present study, we used next-generation sequencing to investigate the transcriptomic response of *Elodea nuttallii* exposed to enhanced concentrations of Hg and Cd. We *de novo* assembled more than 60,000 contigs, of which we found 170 to be regulated dose-dependently by Hg and 212 by Cd. Functional analysis showed that these genes were notably related to energy and metal homeostasis. Expression analysis using nCounter of a subset of genes showed that the gene expression pattern was able to assess toxic metal exposure in complex environmental samples and was more sensitive than other end points (e.g., bioaccumulation, photosynthesis, etc.). In conclusion, we demonstrate the feasibility of using gene expression signatures for the assessment of environmental contamination, using an organism without previous genetic information. This is of interest to ecotoxicology in a wider sense given the possibility to develop specific and sensitive bioassays.