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# Comparative Transcriptomic Analysis of the Response of *Dunaliella acidophila* (Chlorophyta) to Short-Term Cadmium and Chronic Natural Metal-Rich Water Exposures

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*acidophila*. We employed Illumina sequencing for a de novo transcriptome assembly and to identify changes in response to high cadmium concentrations and natural metal-rich water. The photosynthetic performance was also estimated by pulse amplitude-modulated (PAM) fluorescence. Transcriptomic analysis highlights a number of processes mainly related to a high constitutive expression of genes involved in oxidative stress and response to reactive oxygen species (ROS), even in the absence of heavy metals. Photosynthetic activity seems to be unaltered under short-term exposition to Cd and chronic exposure to natural metal-rich water, probably due to an increase in the synthesis of structural photosynthetic components preserving their functional integrity. An overrepresentation of Gene Ontology (GO) terms related to metabolic activities, transcription, and proteosomal catabolic process was observed when *D. acidophila* grew under chronic exposure to natural metal-rich water. GO terms involved in carbohydrate metabolic process, reticulum endoplasmic and Golgi bodies, were also specifically overrepresented in natural metal-rich water library suggesting an endoplasmic reticulum stress response.

**Fig. 1**

**Fig. 2**

**Fig. 3**

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## Electronic Supplementary Materials

Below is the link to the electronic supplementary material.

### Fig. S1

Differential Biological Process (BP) GO-Term distribution. Relative proportions of significantly up-regulated transcripts belonging to each Gene Ontology category for the three transcriptomic libraries. The x-axis contains the proportion of significantly up-regulated transcripts in each category, the y-axis shows the GO-categories. GO IDs are presented in parenthesis. (DOCX 17 kb)

### Fig. S2

Differential Molecular Function (MF) GO-Term distribution. Relative proportions of significantly up-regulated transcripts belonging to each Gene Ontology category for the three transcriptomic libraries. The x-axis contains the proportion of significantly up-regulated transcripts in each category, the y-axis shows the GO-categories. GO IDs are presented in parenthesis. (DOCX 17 kb)

### Fig. S3

Differential Cell Component (CC) GO-Term distribution. Relative proportions of significantly up-regulated transcripts belonging to each Gene Ontology category for

## Table S2

Significant differentially expressed transcripts in *D. acidophila* with significant blast homologies and gene-ontology (GO) terms. When many isoforms from the same Trinity subcomponent shared the same blastx result, only the one with the highest expression in each condition was reported. LogFC values were obtained from Trimmed-Mean-of-M-values (TMM) - normalized expresion values by using the edgeR function "predFC".(XLSX 503 kb)

## Table S3

Significant differentially expressed transcripts in *D. acidophila* with significant blast homologies and gene-ontology (GO) terms. When many isoforms from the same Trinity subcomponent shared the same blastx result, only the one with the highest expression in each condition was reported. LogFC values were obtained from Trimmed-Mean-of-M-values (TMM) - normalized expresion values by using the edgeR function "predFC".(XLSX 24.1 kb)

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