Centre - Eau Terre Environnement

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Differential genetic expression : diatoms and river biofilm as diagnostic tools for metal contamination

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FROM MESOCOSMS TO NUNAVIK
Development of a bioindicator for metal contamination in mining regions

✓ **In the near future, Northern Quebec will be subjected to environmental stress related to metallic contamination due to the development of its mining potential. In order to quantify the impacts caused by the mining development it is crucial to understand ecosystem functioning in this region.**

✓ **Biofilms are composed of different organisms such as diatoms, green algae, cyanobacteria and fungi, and play a key role in river ecosystem functioning through nutrient cycling or primary production.**

✓ **Nevertheless, at the present time, there is a lack of tools for the assessment of metal contamination. Consequently, one objective of the project is to study the effects of metal exposure on biofilms and diatoms.**

✓ **Our team study the relationships between metal contamination and the response of biofilms using traditional community-based descriptors (i.e. bioaccumulation, deformations, presence of tolerant species…) and explore new approaches to assess metal effects on diatoms and biofilms.**

✓ **Another objective of this research project focuses on differential genetic expression of diatoms exposed to metals. Our team is currently developing qPCR tools forestimating induction or repression of specific genes of interest after metal exposure. With this technique, the differential genetic expression is precisely assessed for a limited number of selected genes (basic studies explore the expression of 10 to 20 genes).**

Past and present work on diatoms and qPCR tools

EPOC

qPCR tools have shown their potential to reveal Cd effects on *Eolimna minima*

- **Impacts on genes involved on photosynthesis and mitochondrial metabolism**
- **Effects on diatoms were observed earlier with qPRC than with standard monitoring approaches such as growth**

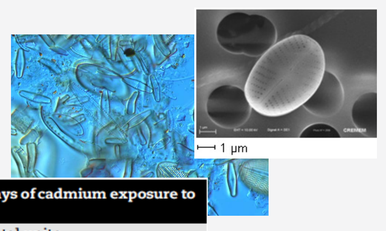


Table 2 – Differential gene expression as compared to actin from *E. minima* after 1, 2, 7 and 14 days of cadmium exposure to 10 and 100 µg Cd/L by direct route[a].

Functions	Genes	Cadmium-contaminated experimental units							
		C_1 (10.0 ± 3.2 µg/L)				C_2 (96.0 ± 34.2 µg/L)			
		1	2	7	14	1	2	7	14
Mitochondrial metabolism	*cox1*	/	/	/	/	/	/	9.5	/
	nad5	/	/	/	2.5	/	/	/	9.5
	12s	/	/	/	/	/	/	15	/
Oxidative stress	*sodMn*	/	/	/	/	/	/	/	/
Photosynthesis	*d1*	/	/	/	2	/	/	5.5	24
	psaA	/	/	/	2.5	/	/	7.5	48
Xenobiotic metabolisation	*cyp1A1*	/	/	/	/	/	/	/	/

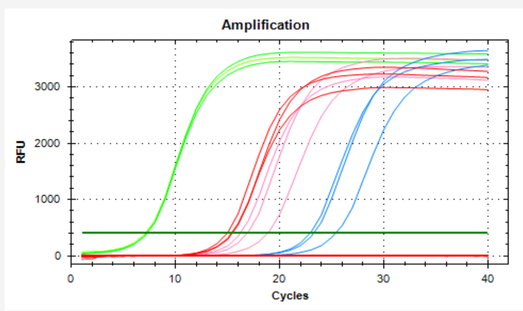
a Significant induction and repression factors are indicated by positive and negative values, respectively compared to the control *E. minima*. /: identical to control levels.

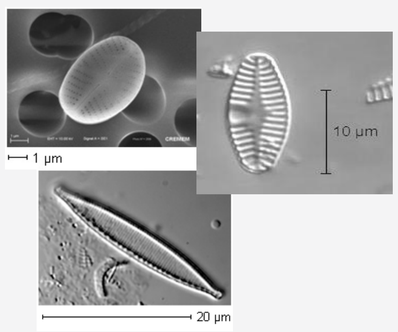
Kim Tiam et al. 2012, Water Research

irstea

Diuron effects were evidenced by qPCR on three different diatom species

- **Impacts on genes involved in photosynthesis and mitochondrial metabolism**
- **Differences in diuron sensitivity among the three species : *E. minima* and *N. palea* appeared to be more tolerant than *P. lanceolatum***





Moisset et al. 2015, SToTEn

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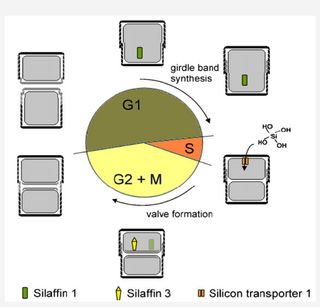
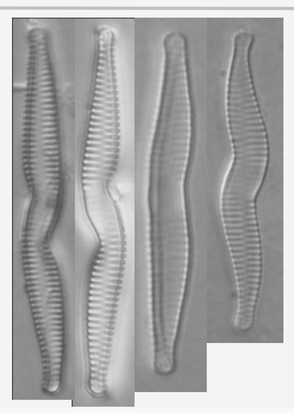
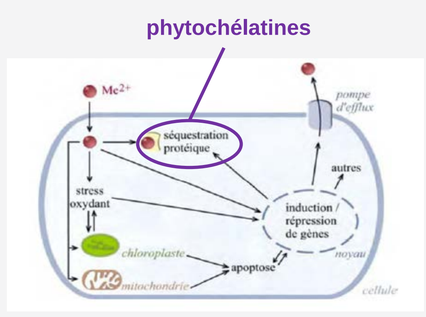
qPCR tools could be used to:

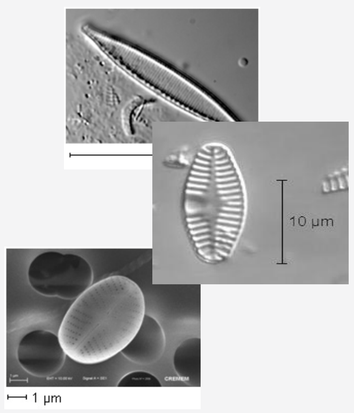
- **Link the observed frustule deformations with metal contamination by studing Sit and Sila genes**
- **Investigate metal detoxification mecanisms by studing PCS genes**







NGS and Metabolomics: toward a more integrative understanding of contaminants effects



NGS

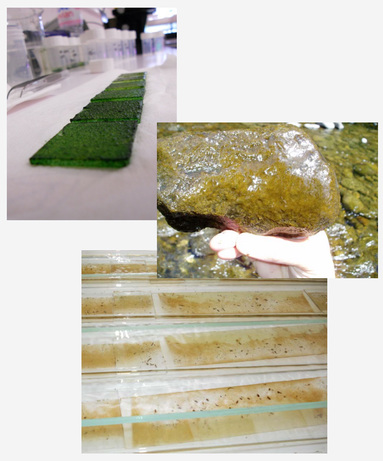
Study of the transcriptome : approach without *a priori*

qPCR

Study in detail of responses of few genes selected with *a priori*

Metabolomics

Study of responses of thousands of genes at the community level



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