Biofilm exposure to copper: bioaccumulation and effects on fatty acid profiles and micromeiofauna taxonomic composition

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Introduction

Periphytic biofilms, fundamental components of aquatic ecosystems, host a wide variety of organisms, including the often overlooked micromeiofauna. These small but essential organisms play a crucial role within biofilms. Despite their ecological importance, the response of micromeiofauna to environmental contaminants such as metals remains poorly understood.

Copper, a common industrial pollutant, is essential in trace amounts but toxic at high concentrations. While its effects on primary producers in biofilms are well documented, its effects on micromeiofauna and biofilm fatty acid profiles are not well understood.

This study aims **to identify possible effects of copper on the biodiversity and taxonomic composition of biofilm micromeiofauna.**

As a preliminary study, we conducted a microcosm experiment in which we exposed periphytic biofilms to copper at environmental concentrations.

Methods

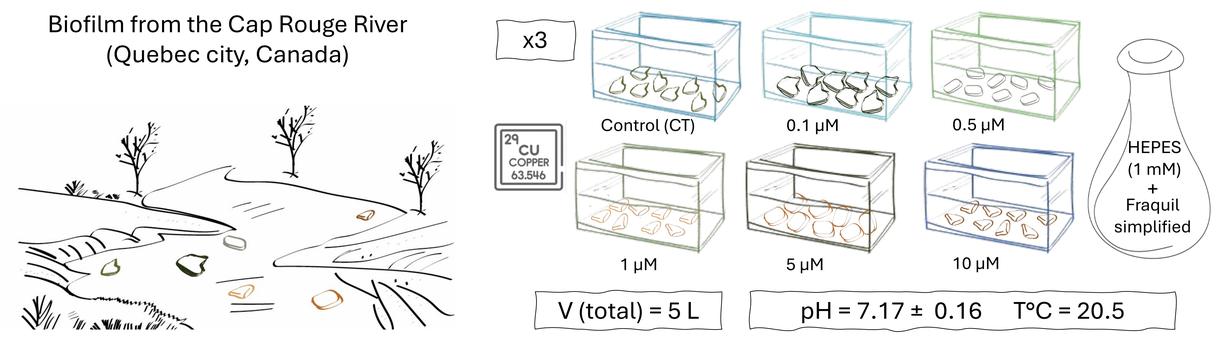

Figure 1: Experimental design for biofilm exposure to copper.

Exposure conditions
3 days of acclimatization
28 days of exposure
Water renewed once / week

Biological measurements & chemical analyses
Taxonomic composition of micromeiofauna and biofilm fatty acids profiles, copper concentrations and bioaccumulation, water physico-chemistry (T°C, pH, conductivity, nutrients)

Results and Discussion

Bioaccumulation

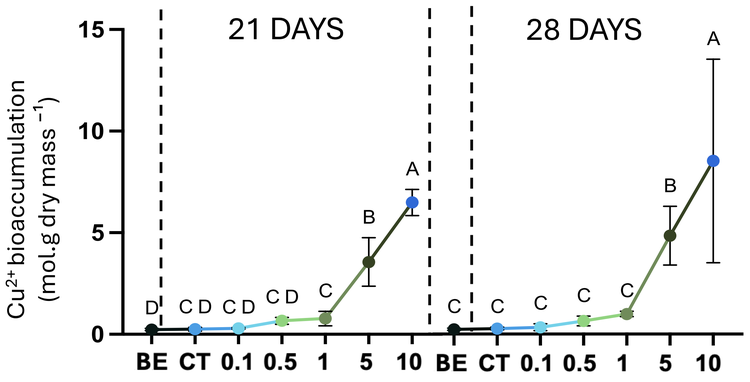

Figure 2: Cu^{2+} bioaccumulation (mol.g dry mass^{-1}) as a function of nominal copper concentrations (µmol.L^{-1}) before exposure (BE) and after 21 days and 28 days of exposure. Controls (CT).

Copper uptake by biofilm is dose-dependent

Toxic effect on micromeiofauna at high copper concentrations

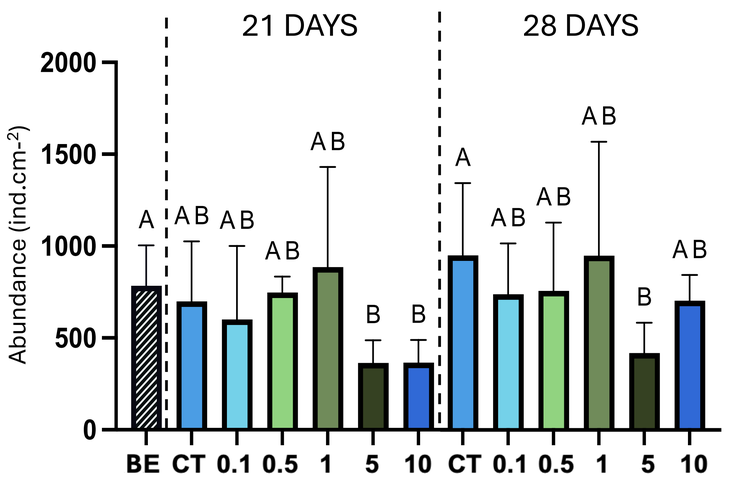

Figure 5: Micromeiofauna abundance (ind.cm-^{2}) as a function of nominal copper concentrations (µmol.L^{-1}) before exposure (BE) and after 21 days and 28 days of exposure. Controls (CT).

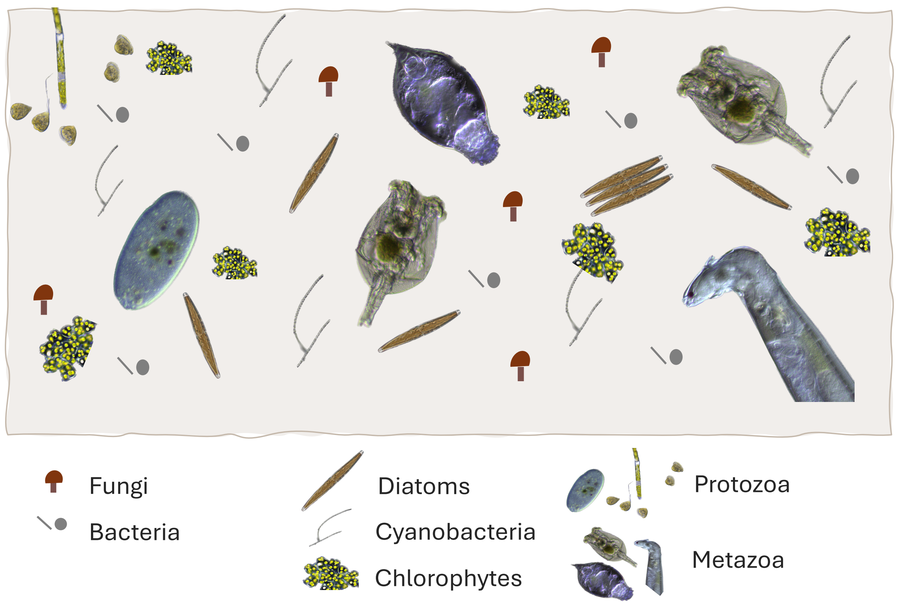

Figure 3: Representation of a mature periphytic biofilm.

Micromeiofauna taxonomic composition

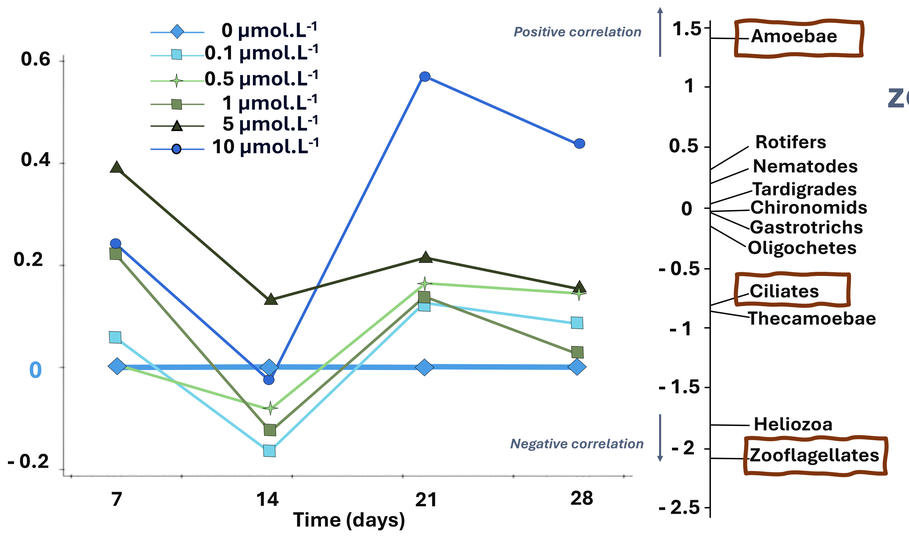

Figure 6: Principal response curves showing the effect of copper on the abundance of micromeiofauna organisms over time. The weight of each group reflects the affinity of the groups with the curves.

Fatty acids

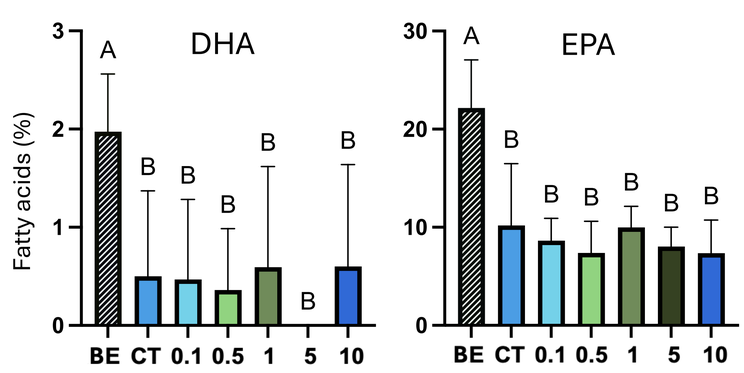

Figure 4: DHA (docosahexaenoic acid, C22:6n-3) and EPA (eicosapentaenoic acid, C20:5n-3) fatty acids (%) as a function of nominal copper concentrations (µmol.L^{-1}) before exposure (BE) and after 28 days of exposure. Controls (CT).

Loss of nutritional quality over time exposure (diatoms)

Compared to amoebae and ciliates, zooflagellates appear to be more sensitive to Cu

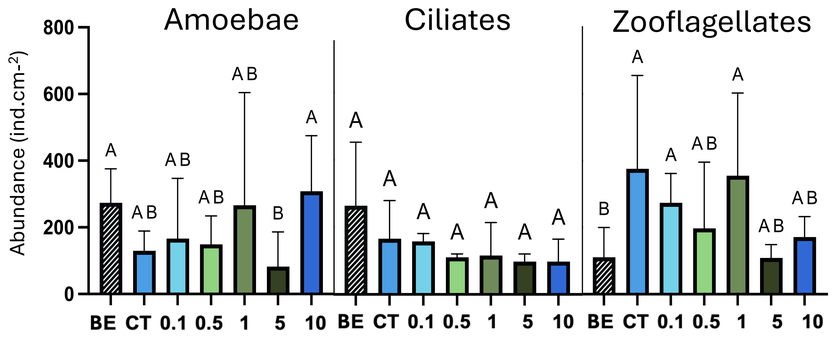

Figure 7: Abundance of amoebae, ciliates and zooflagellates as a function of nominal copper concentrations (µmol.L^{-1}) before exposure (BE) and after 28 days of exposure. Controls (CT).

Conclusions and Perspective

Increasing copper bioaccumulation correlates with a decrease in micromeiofaunal abundance at high concentrations, indicating copper toxicity. Copper had no effect on DHA and EPA, suggesting that trophic relationships did not influence micromeiofaunal abundance. Thus, the reduction in micromeiofauna seems to be due to a direct toxic effect. Studies on micromeiofauna based on microscopic observations are limited in number and scope due to the technical limitations of preserving these organisms. Identification of micromeiofauna requires fresh (live) material, is time-consuming, and requires meticulous handling and taxonomic expertise. Metabarcoding is a promising approach to study microbial diversity. Metabarcoding will be performed on our samples using 16S (bacteria), 18S (eukaryotes), COI (proto-metazoans) and ITS (fungi). The comparison of DNA-based community assessment of biofilm organisms with our microscopic observations and fatty acid profiles will improve our understanding of copper-induced changes in the biofilm matrix. Assessing the relative proportions of algal groups will also help to better interpret our results. These future perspectives will enrich our understanding of the effects of copper on the biofilm matrix.

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