

Marie-Ange Moisan¹, Jérôme Comte¹, Alexander I. Culley², François Guillemette³, Stéphanie Guilherme⁴, Manuel Rodriguez⁵, Camilo A. Herrera¹, Isabelle Laurion¹

¹ Centre Eau Terre Environnement, Institut national de la recherche scientifique, Québec, Québec; ² Département de biochimie, de microbiologie et de bio-informatique, Université Laval, Québec, Québec; ³ Département des sciences de l'environnement, Université du Québec à Trois-Rivières, Trois-Rivières, Québec; ⁴ Department of Civil Engineering, University of Ottawa, Ottawa, Ontario; ⁵ Département d'aménagement du territoire et de développement régional, Université Laval, Québec, Québec

Northern communities are facing new challenges for drinking water supply as the climate changes, both in terms of water quality and quantity.

Surface water browning is caused by the increasing addition of terrestrial organic matter to aquatic ecosystems. This phenomenon reported in temperate and boreal regions is now observed at higher latitudes. Northern water browning, related to permafrost thawing, hydrological cycle intensification and changes in terrestrial productivity, can cause major changes in the functioning of aquatic ecosystems, and may favor certain microorganisms such as toxic cyanobacteria.^{1,2,3} Thawing permafrost may also release microbes and pathogens previously trapped in soils into aquatic ecosystems.⁴ Collectively, these changes represent risks for drinking water quality in northern communities.^{5,6}

Objectives

We aim to evaluate the **implications of browning on drinking water quality** by **assessing the microbial composition (virus and bacteria)** along the drinking water supply system (from source to tap) and explore its relationship with dissolved organic matter (DOM).

This project aims to identify the environmental conditions leading to water quality issues and eventually forecast future changes in response to the changing climate in order to support northern communities in adapting to the impacts of climate change.

Hypotheses

- I. Browning is causing an increase in microbial abundance in drinking water sources
- II. Microbial abundance and composition change from source to tap and respond to DOM composition
- III. Bacterial regrowth in house tanks is supported by a community relying on recalcitrant DOM

Methods

The **collaborative work with the communities** will allow us to sample the water at different times of the year, and to identify and monitor alternative sources of drinking water (neither treated nor monitored)



- Microbial abundance is measured by flow cytometry
- Viral and bacterial composition is assessed by nucleic acids extraction and new generation sequencing
- DOM characterization (concentration, optical properties and composition); part of Camilo A. Herrera's project, is used to interpret the microbial composition

Preliminary results

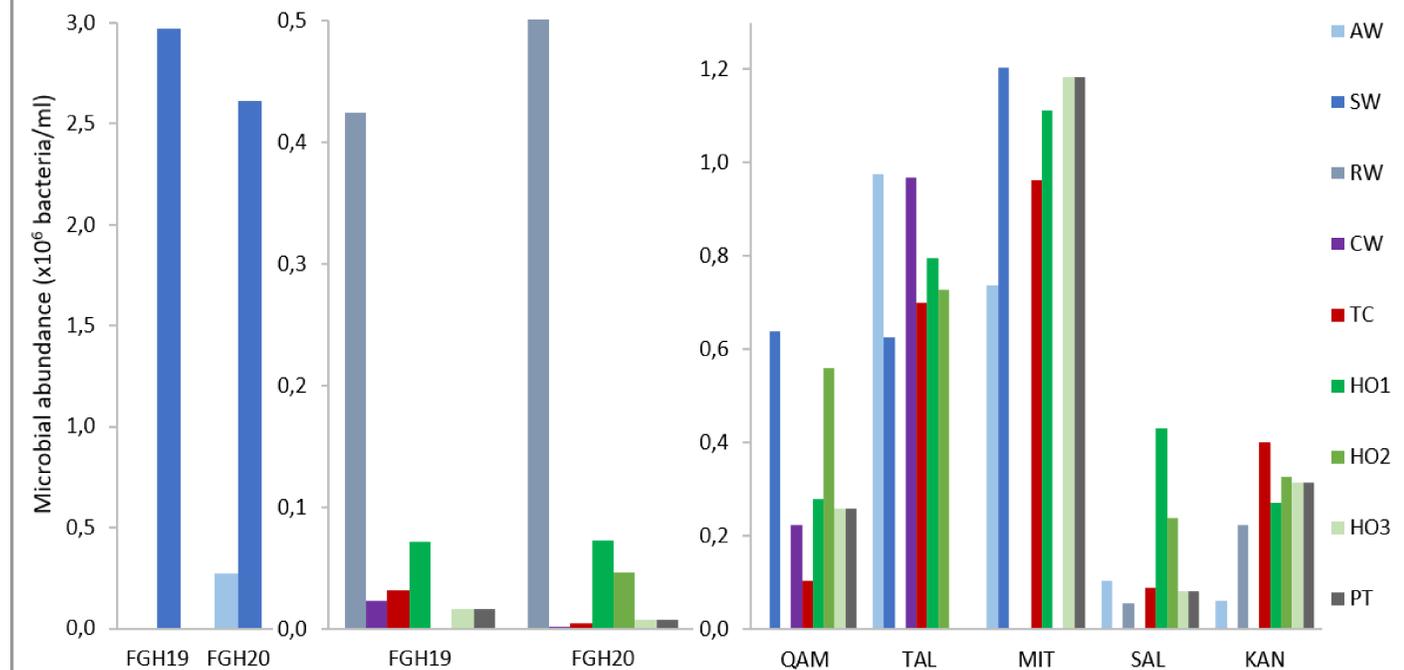


Figure 1. Microbial abundance of water **source waters** (SW), **alternative sources** (AW), **raw water** before chlorination (RW), **chlorinated water** (CW), water in **truck** (TC), **house tap** water (HO) and **public tap** water (PT) of 6 northern communities sampled in 2019 (FGH in 2019 and 2020).

- In FGH there is an important reduction of bacterial abundance between the source water (composed of natural microbes having a significant ecosystem function; the Mackenzie River) and raw water (the city reservoir, a reduction of 6 fold on average) and between the raw water and the chlorinated water (a reduction of 75 fold on average).
- In QAM, there is lower bacterial abundance in all chlorinated waters (CW, TC, HO, PT) compared to the source water (Baker Lake) but to a smaller extent than in FGH.
- In TAL and MIT, there is similar bacterial abundance all along the treatment circuit from source to tap water.
- In SAL and KAN, there is higher microbial abundance in some chlorinated waters compared to raw water that may be explained by some degree of bacterial regrowth in household cisterns.

To come:

- Perform the DNA sequencing analysis to identify if any threatening microorganisms are present along the treatment circuit and describe their functional diversity
- Analyse the relationships between microbial composition and DOM concentration and composition
- Present our results to the communities and organize water outreach activities in schools
- Establish collaborative work to generate more samples despite the pandemic over the coming winter

Acknowledgements

The research team thanks the authorities of the participant communities for their welcoming, collaboration and help during this sampling campaign.

Questions? marie-ange.moisan@ete.inrs.ca