Microbiome analysis to identify species and biomarkers for water quality monitoring and bioremediation

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Innovative techniques are required

- Mining development, agricultural intensification and population growth are threatening our watersheds with environmental degradation.
- Moving forward sustainably requires innovations in biomonitoring and bioremediation that will address the needs of a variety of water quality stakeholders: mining & industry developers, farmers, fishers, recreational users, basic drinking water needs, etc.
- Using metagenomic sequencing, we are profiling microbial taxa and genes across contaminated watersheds to identify specific genetic biomarkers of pollution associated with agriculture, urbanization, and mining.

Metagenomics allows unbiased profiling of microbial communities

- Metagenomics is the study of all genetic material (DNA) recovered directly from an environmental sample, without culturing.
- DNA is sequenced and analysed to build a microbial profile of the composition of the community and the gene function categories present (Fig. 2).

Sampling microbial response along contamination gradients

- We have collected a year of monthly river water samples from seven sites in protected, urban, and agricultural watersheds in Southwestern Canada, plus hourly samples in selected months.
- We have also collected riverbed biofilm from up and downstream of a point source of copper contamination.
- For each sample, we have recorded physical, chemical and biological water quality data and are surveying bacteria using metagenomics (Illumina MiSeq with 250 bp paired-end reads). Viruses and protists were also studied for the year-long river water study. Using this data, we are identifying taxa and genes that are differentially abundant between sites and that correlate with environmental conditions.
- We are using these relationships in the agriculturally- and urban-affected data to develop a panel of qPCR biomarkers to assess water quality.
- In the metal-affected data, we are investigating how these relationships might reveal a microbial role in this instance of natural copper depletion and whether this system could inform future bioremediation strategies.

Copper contamination shifts bacterial community, indicates possible bioremediation with native species

- Naturally occurring copper at a proposed mining site enters an uncontaminated river. Dissolved copper concentration spikes then declines too quickly to be explained by physiochemical processes.
- Biofilms can immobilise dissolved metals – possibly occurring here.
- Microbiome sequencing reveals riverbed biofilm bacterial community is dominated by one family after copper contamination occurs.
- This microbe will be further studied for potential utility for bioremediation at this proposed mining site.

Baseline temporal bacterial variation supports development of testing guidelines

- Examined river microbial community changes over hourly and monthly time scales
- Observed relatively small changes in microbial composition on an hourly timescale, with notable changes occurring seasonally (Fig. 6).
- Variability indicating testing may need to occur multiple times a day in some seasons while not in others.

Biomarkers identified for clean and agriculturally contaminated water

- Detected differentially abundant taxa in an agricultural watershed in upstream versus polluted and downstream samples
- Difference was stable over 6 monthly samples (Fig. 7)
- PCR tests have been developed based on these taxa and validated in the lab.

Conclusions and comments

- Metagenomics analysis can provide meaningful insight into watershed ecology and response to environmental changes. These findings will support the development of:
  - More accurate water quality tests that could save millions of dollars in monitoring costs, as well as ensure long-term sustainability of our watersheds and their surrounding ecosystems.
  - Fundamental knowledge of microbial communities under copper-rich and acidic conditions, which will support the development of new bioremediation approaches, including the use of native microorganisms at a potential mining site.
- This work is the most comprehensive analysis of watershed microbiomes over space and time to date and moves towards development of robust environmental monitoring & bioremediation techniques.