Micro-Parasites from the Past
A portrait of viruses in ancient Arctic seawater

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INTRODUCTION
Viruses in polar aquatic habitats
Microbial communities dominate polar aquatic ecosystems, and the most abundant constituents are viruses.

These naturally occurring viruses, “wild viruses”, can play major roles in the dynamics of the aquatic foodweb by redirecting the nutrients produced by lysis into the microbial loop. This will alter the circulation of energy to higher trophic levels and eventually be reflected in biogeochemical cycles.

Viruses also have an important impact on microbial communities by regulating their host’s biomass, influencing their metabolic activity during infection and driving their evolution through gene transfers and pressure of infection.

A High Arctic lake enclosing ancient seawater
Lake A is a meromictic lake composed of an anoxic salt water bottom layer covered by freshwater accumulating from the spring melts and the runoff of the catchment area.

Previous studies have shown that the lake contains very distinct microbial communities in each layer. The freshwater layer is home to cyanobacteria, α-β-proteobacteria, archaea and protists including chrysophytes. The saltwater layer harbours various marine-clades of δ-proteobacteria, green-sulfur bacteria, archaea and protists.

OBJECTIVE
-describe the viral diversity of Lake A, taking into account the complexity of the water-column:
  - Can we identify the environmental parameters that may drive viral community composition?
  - How do the viral communities match the potential host (microbial) communities?
  - How do they compare to viral communities from other aquatic environments like other polar freshwater lakes or seawater?

RESULTS and DISCUSSION
Figure 2: Characteristics of the microbial community of Lake A
The pigment concentration graph shows the concentration of pigment characteristic of ecologically relevant microbial groups through HPLC. For example, bacteriochlorophyll-E (characteristic of green-sulphur bacteria) is very abundant in the ancient sea water, as well as its associated carotenoid, isorenieratene.

The microbial abundance graph shows the abundance of relevant microbial groups determined by flow cytometry. Here, cyanobacteria, abundant in the freshwater, are less abundant in the ancient seawater. In place, autotrophic eukaryotes become very abundant. Heterotrophic bacteria are very abundant in both layers, but are less so in the transition zone. Viruses follow a similar pattern.

Figure 3: Clustering of the reads from each sample with Fizkin.
Samples are clustered according to the similarity of their read content through a bayesian social network. Samples containing similar sequences will cluster together and very divergent samples will be drawn apart.

Figure 4: Taxonomy of the viral sequences
A taxonomy is assigned to assembled raw sequences by using blastx and the number of sequences assigned to each taxa is represented in a radial chart.

Conclusions
- The viral community structure of Lake A changes with depth:
  - The freshwater layer and the ancient seawater layer are strikingly distinct indicating important differences in their viral sequence composition
  - Two other divergent viral communities exist in the transition zone
  - The analysis with Fizkin shows tight clustering among replicate samples
  - The classification of viral sequences reflects the dominant host groups in each respective body of water

METHODS
Sampling:
(July 2016, 82 cm of ice)
CTD measurements done with RBR
Concerto and Hydrolab sampling devices
1. Collect triplicates of ~2L at 5 depths
2. Pre-filter water with 0,22μm filter

Laboratory work:
1. Extract DNA directly from filters
2. Prepare libraries with NEBNext Ultra II kit and sequence with Illumina HiSeq 2500

Bio-informatic analysis:
1. Check reads for quality, trim and error-correct reads

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Figure 1: a) Map of northern Canada showing in box (b) the localisation of Lake A on the north coast of Ellesmere Island. c) Picture of Lake A showing most of the water catchment including inflow from Lake B as well as outflow to the Arctic Ocean.

NEXT STEPS
- Assemble and filter for specifically viral sequences
- Classify the viral sequences through taxonomic or functional annotation
- Estimate the abundance of viral sequences in different layers of the water-column
- Compare the viral communities of Lake A to other viral communities in aquatic environments across the world
- Survey the viral communities of Lake A for ecologically relevant genes

References: