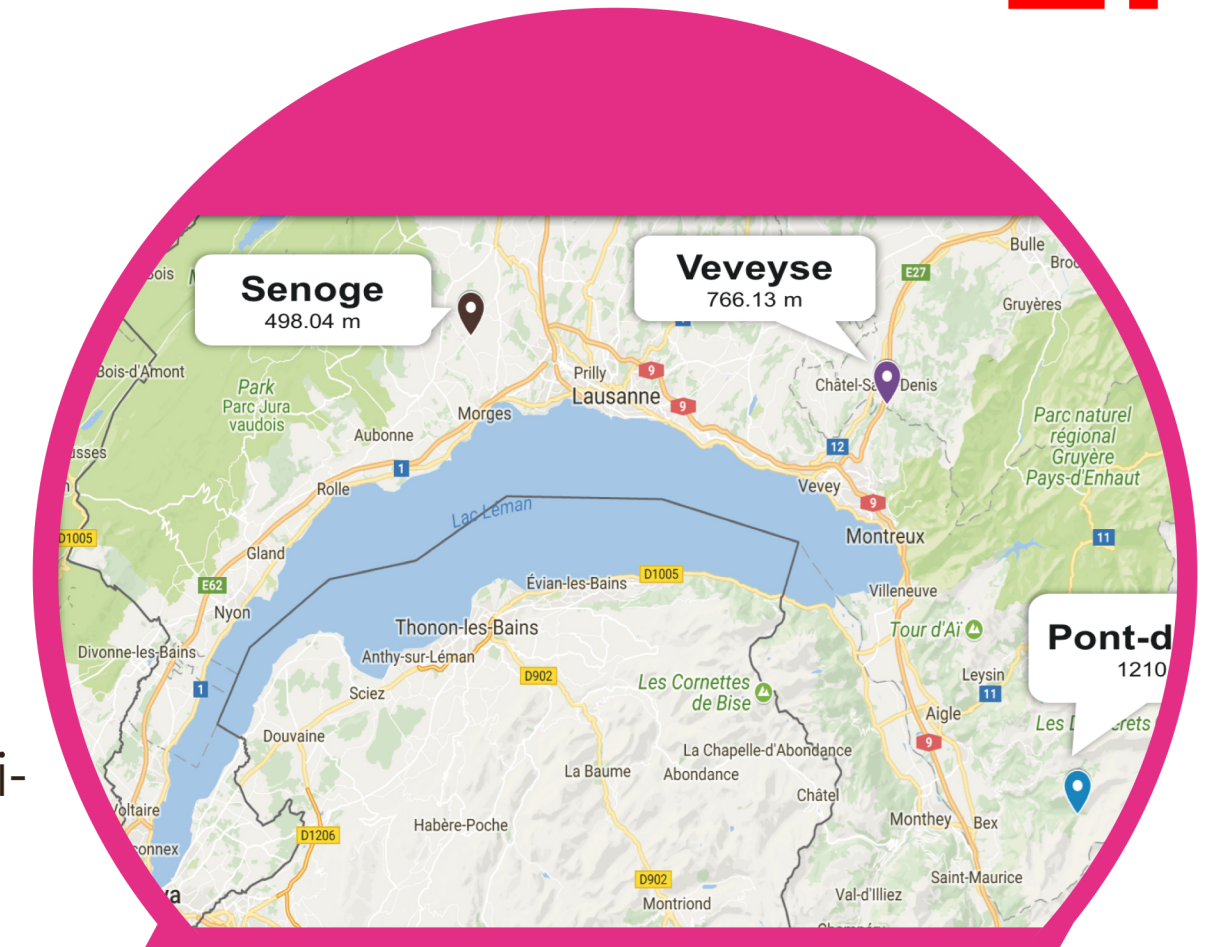


BACKGROUND & AIMS

Viruses are the most abundant biological entities on Earth. They are recognized as important microbial predators that influence global biogeochemical cycles and drive microbial evolution. Their small size, genomic flexibility, rapid evolution and the lack of a common phylogenetic marker make them difficult to study in environmental settings. Despite their potential importance, viruses have not yet been studied in stream biofilms. Here, using recently developed molecular tools, we study the diversity of viruses in stream biofilms and their potential relevance for biofilm structure and function. Our goal is to link viral and bacterial diversity using network approaches and to understand host range and specificity of viruses.



IMPLICATIONS

The discovery of abundant and diverse viruses in stream biofilms may redress our perception of the microbial structure and function of these biofilms.

Viral Ecology of Stream Biofilms

METHODS

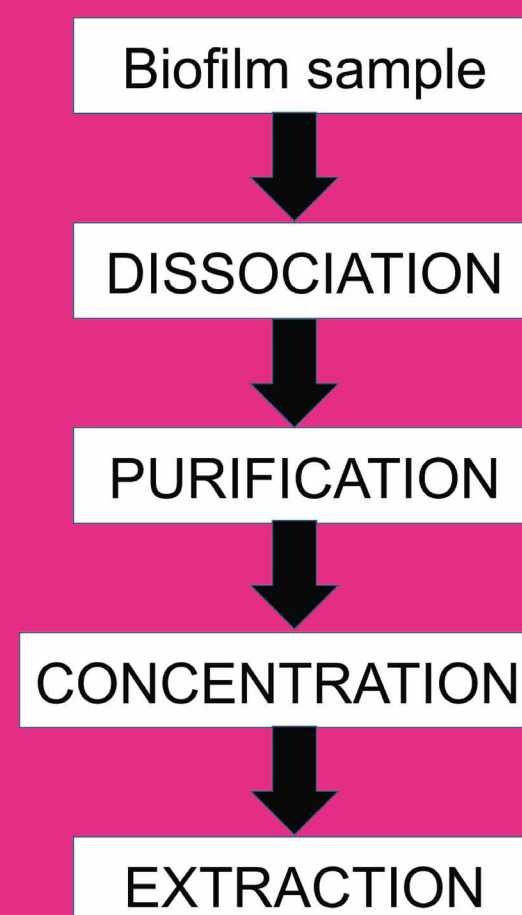
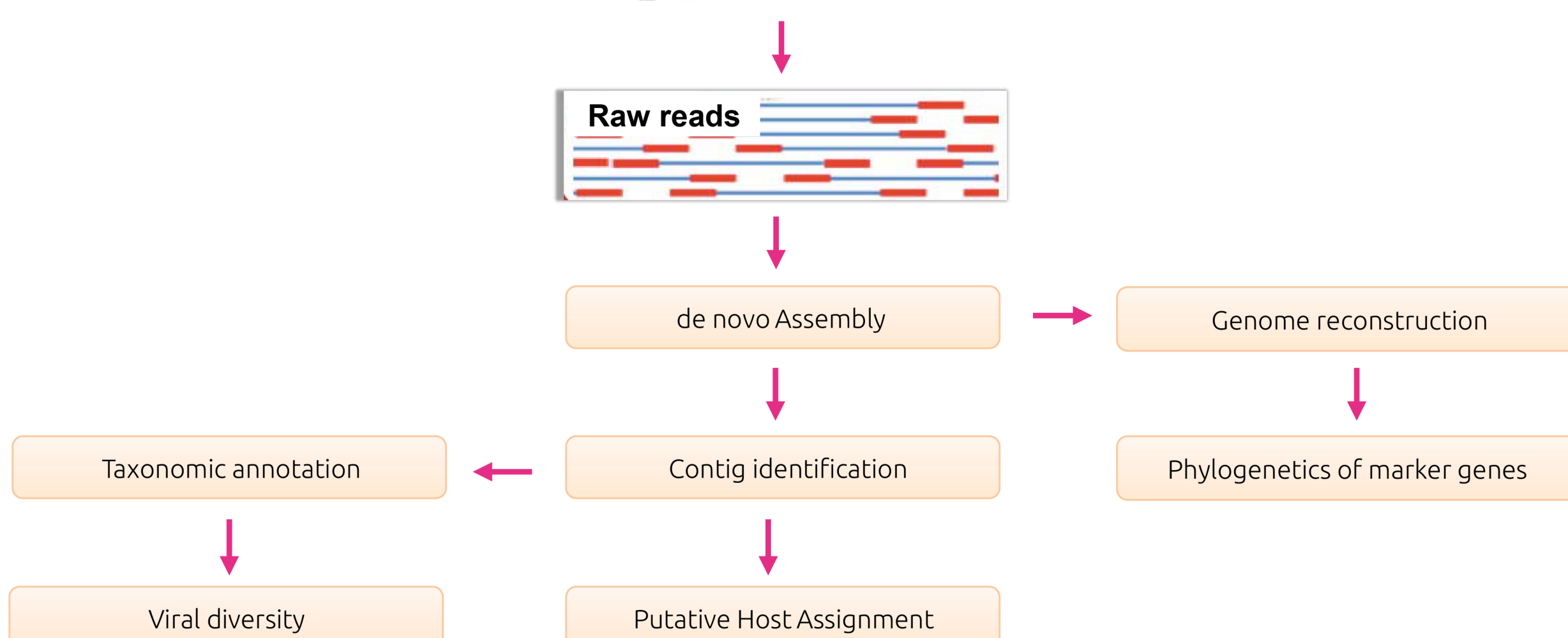
We developed a protocol tailored to the extraction and purification of viral single- and double stranded DNA from stream biofilms. Epifluorescence and Transmission Electron Microscopy is used to estimate virus abundance. Metagenomic sequencing and sophisticated bioinformatic pipelines are used to classify viruses and their hosts.

RESULTS

Our first findings show the presence of viruses in stream biofilms. Microscopy has unraveled and unexpectedly high abundance of viruses in stream biofilms. Concomittantly, first results from metagenome sequencing indicate highly diverse viral communities.



METAGENOMIC SEQUENCING



METHODS

Methods for extraction of high quality viral DNA are developed and benchmarked using epifluorescence microscopy counting.