



Steven Short, PhD | Associate Professor & Chair

Department of Biology  
University of Toronto Mississauga

*Viral parasitism of freshwater algae, the ecological churn at the base of aquatic food webs*

JEUDI 10 JUILLET 2025 à 12 h 30

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

**Abstract:**

My research is motivated by the desire to better understand phytoplankton ecology. Through studies of viruses which parasitize and lyse, or kill, phytoplankton, my students and I have uncovered complex microbial dynamics in aquatic food webs. Our earliest, pre-genomic environmental surveys revealed the remarkable diversity of freshwater algal viruses. These results paved the way for studies that demonstrated that even closely related viruses have distinct seasonality and spatial distributions, virus turnover is seasonally variable, and viral activity can at times stimulate primary productivity. Eventually, metagenomics demonstrated that Lake Ontario is home to even greater viral diversity than we imagined and reinforced notions of the highly dynamic nature of aquatic viruses. Together these studies have provided a glimpse into the complex ecology governing freshwater microbial communities. In addition to studies of natural environments, we have also established a model system for lab studies of freshwater algal viruses by isolating from Lake Ontario viruses that infect the freshwater haptophyte *Chrysochromulina parva*. Based on phylogenetic analysis of the virus DNA polymerase gene, this virus named CpV-BQ1 was considered a member of the *Phycodnaviridae*. When we later sequenced *C. parva* virus genomic DNA, we assembled the genome of different virus, CpV-BQ2, and learned that our cultures included three satellite viruses, CpVV-Larry, -Curly, and -Moe, that might parasitize the other viruses. Through various growth experiments, we have recently purified for independent cultivation three distinct CpVs (BQ1, BQ2, and BQ3) and one of the satellite viruses (CpVV-Moe). This has enabled sequencing the genome of the other *C. parva* viruses highlighting their distinct replication strategies and genes that could be involved in inter-virus competition. Purification of individual CpVs has also led to the observation of a lineage of *C. parva* which is resistant to lysis by BQ1, yet produces infectious viruses suggesting a novel, chronic infection strategy. Experiments to study the replication of CpVV-Moe demonstrated its dependence on the replication of one of the other viruses, CpV-BQ3, but also showed that Moe is detrimental to BQ3 highlighting its multi-parasitic lifestyle. Overall, our research has taught us that there exists within this single algal virus-host system the potential for a myriad of interactions that could confound predictions of the ecological dynamics of these aquatic microorganisms. How the interactions of this one freshwater alga and its viruses scale to an entire ecosystem is beyond our current understanding. Nonetheless, when combined with the remarkable diversity of freshwater viruses revealed through metagenomics, the surprisingly complex dynamics of *C. parva* and its viruses highlights our immature understanding of microbial communities and the complex interactions of their constituents.

Hôte: Sylvain Moineau

Responsables: Juan Carlos Villarreal Aguilar et Davoud Torkamaneh  
[juan-carlos.villarreal-aguilar@bio.ulaval.ca](mailto:juan-carlos.villarreal-aguilar@bio.ulaval.ca) et [davoud.torkamaneh.1@ulaval.ca](mailto:davoud.torkamaneh.1@ulaval.ca)