

Title:

Viral biodiversity in glacier-fed streams

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Abstract (300 words maximum): :

Viruses are well known to modulate the biomass, diversity and activity of microbial communities in many ecosystems. Yet, little remains known about their role in stream biofilms. Here, we leverage metagenomic data collected by the Vanishing Glacier Project from 170 glacier-fed streams (GFS) around the world to unravel the diversity and biogeography of benthic dsDNA viral communities. Despite the extreme environmental conditions in GFS, we uncover a large and previously unknown viral diversity. The biogeography of both host and phage communities is structured by spatial isolation, reflected by conspicuous regionalism. The GFS microbiome is characterized by low cell abundances and few but well-adapted bacterial clades. Phages leverage high host specificity, elevated lysogeny and encode auxiliary metabolic genes to interact with their hosts, pointing to the prevalence of mutualistic interactions rather than mere lysis of host cells in GFS. Taken together, our work highlights the co-evolutionary history of phages and their hosts in a cryospheric ecosystem, now threatened by climate change.