**Virus diversity in metagenomes of a lichen symbiosis (*Umbilicaria phaea*):**

**complete viral genomes, putative hosts, and elevational distributions**

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Viruses can play critical roles in symbioses by initiating horizontal gene transfer, affecting host phenotypes, or expanding their host’s ecological niche. However, knowledge of viral diversity and distribution in symbiotic organisms remains elusive. Here we use deep-sequenced meta-genomic DNA (PacBio Sequel II; two individuals), paired with a population genomics approach (Pool-seq; 11 populations, 550 individuals) to understand viral distributions in the lichen *Umbil-icaria phaea*. We assess 1) viral diversity in lichen thalli, 2) putative viral hosts (fungi, algae, bacteria), and 3) viral distributions along two replicated elevation gradients. We identified five novel viruses, 28% - 40% amino acid identity to known viruses, tentatively belonging to the families Caulimoviridae, Myoviridae, Podoviridae and Siphoviridae. Our analysis suggests that the Caulimovirus is associated with green algal photobionts (Trebouxia) of the lichen, and the remaining viruses with the bacterial microbiome. We did not detect viral sequences in the my-cobiont. Caulimovirus abundance decreased with increasing elevation, a pattern reflected by a specific algal lineage putatively hosting this virus. Bacteriophages showed population specif-ic patterns. Our work provides the first comprehensive insights into viruses associated with the mycobiont, photobiont and microbiome of a lichen, and suggests an interplay of viral hosts and environment in structuring viral distributions.