Viral Abundance in Terrestrial Cyanobacteria Differs as a Function of Host Ecology

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Bacteriophages, viruses that infect bacteria, are one of the most abundant entities on Earth and impact many ecosystems. Bacteriophages that follow the lysogenic cycle, when the phage integrates its DNA into the host's genome, are known as prophages. Prophages have been extensively studied in oceans and humans, but few studies have examined prophages in terrestrial ecosystems. My project specifically explored the difference in the number of prophages found within genomes of free-living and symbiotic Nostoc cyanobacteria. Using 45 publicly available genomes of symbiotic and free-living Nostoc, I quantified the number of prophages in each genome using three prophage-identifying tools: Vibrant, VirSorter, and PHASTER. VirSorter and Vibrant found ~500 prophage sequences across all genomes, while PHASTER found only 85. Comparisons of the phage sequences to reference databases suggest that the majority of Nostoc prophages are novel. Of the prophages with matches to previously identified phages, many were similar to phages found from marine cyanobacteria. I also found that non-symbiotic Nostoc contained a greater number of prophages compared to symbiotic Nostoc: VirSorter and Vibrant found ~3 additional prophages per genome of free-living Nostoc compared to prophages per genome of symbiotic Nostoc. Similar results were obtained with PHASTER. My results suggest that that symbiotic Nostoc may be better protected from viral infection compared to free-living Nostoc. My research illustrates the novelty and diversity of prophages within terrestrial cyanobacteria, but additional work is necessary to test the hypothesis about host protection and to understand the ecological impacts of prophages on their host and environment.

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