

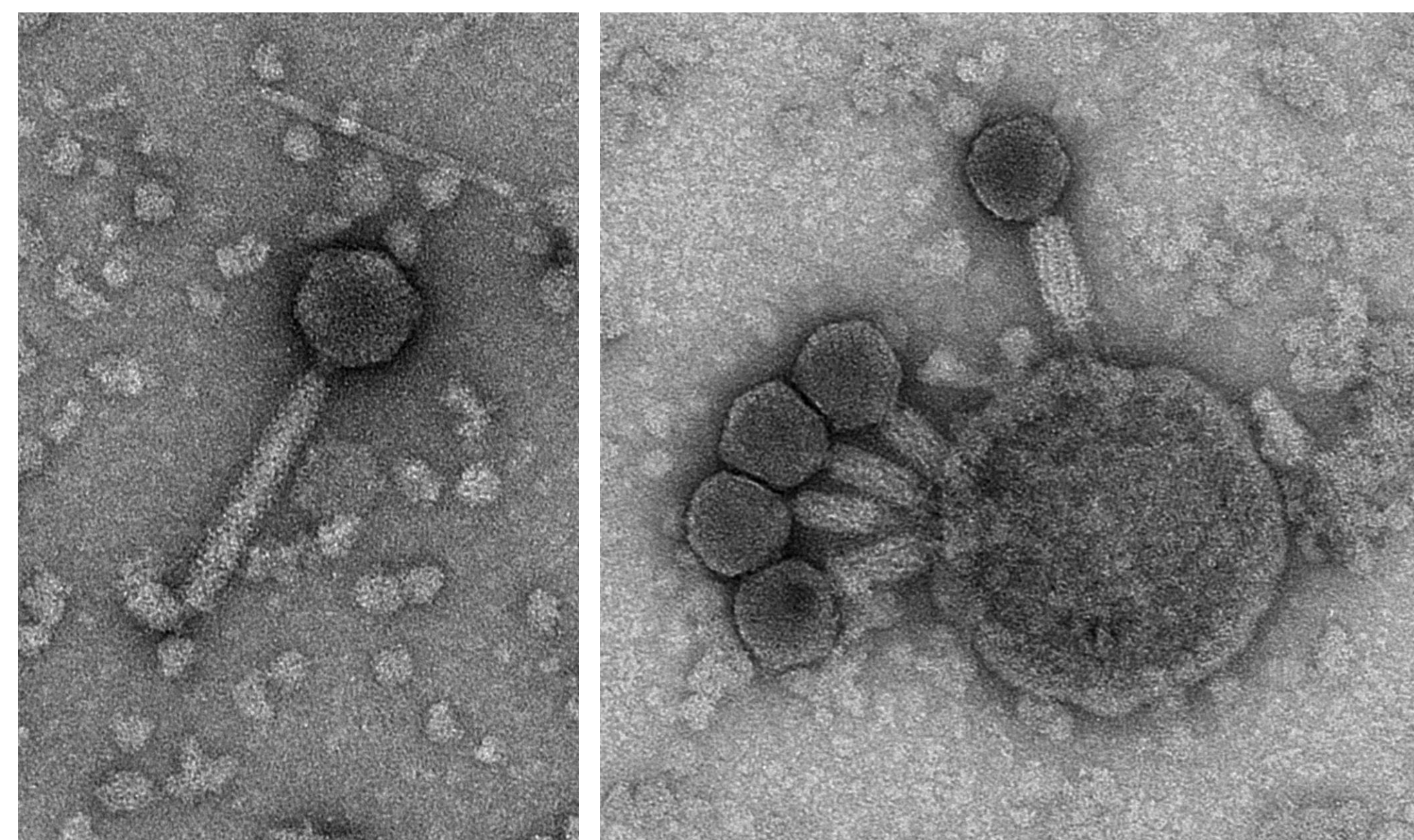
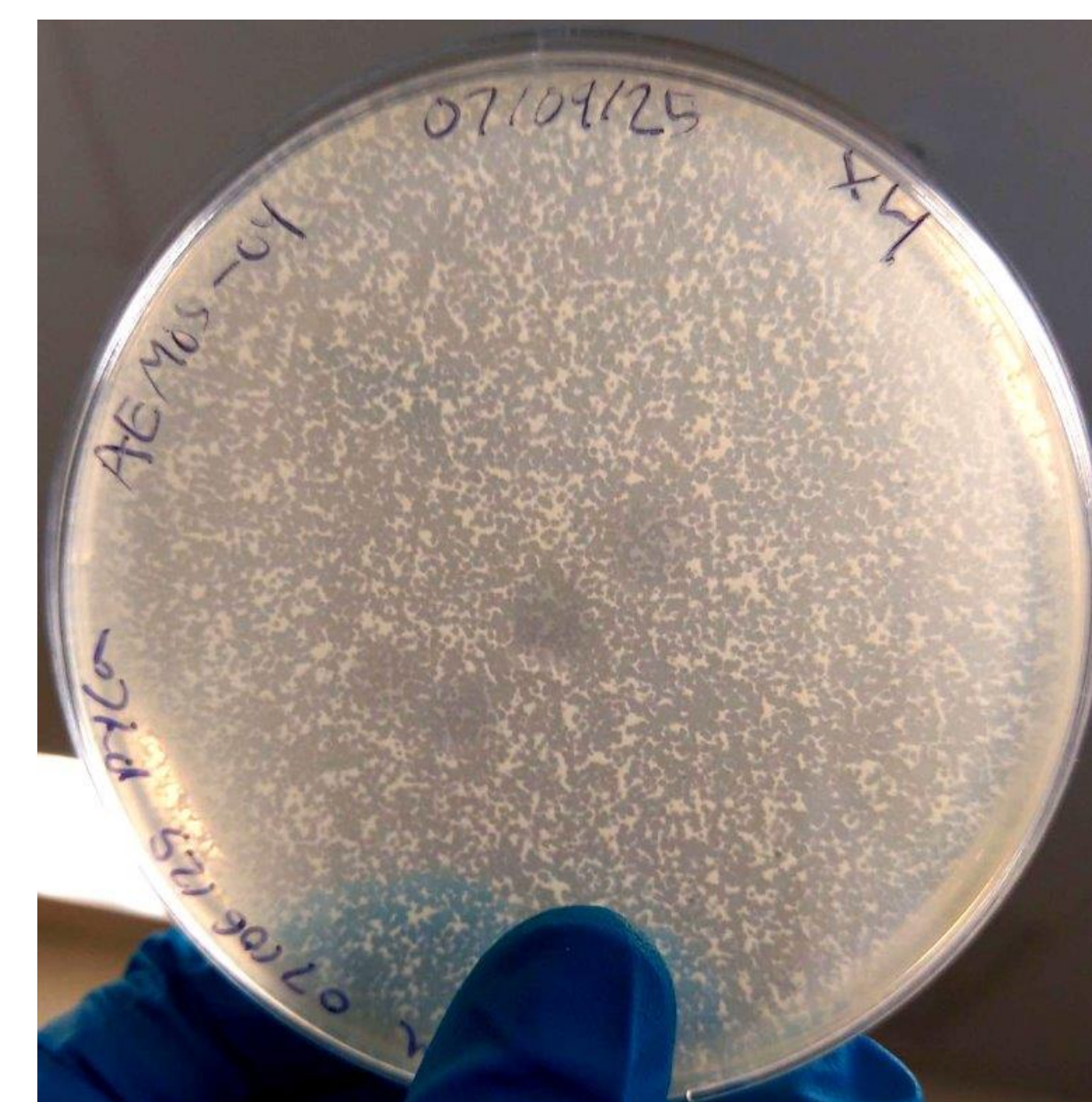
Background

Bacteriophages, or phages, are viruses that infect and kill a host bacterium. Numerous phages have been discovered and studied, such as those targeting bacterial species of the phylum Actinomycetota, but many millions remain undiscovered. The goal of this research was to discover novel phages that infect different types of water bacteria and to provide a functional annotation of their genomes.

Results

Bacteriophage Northmill

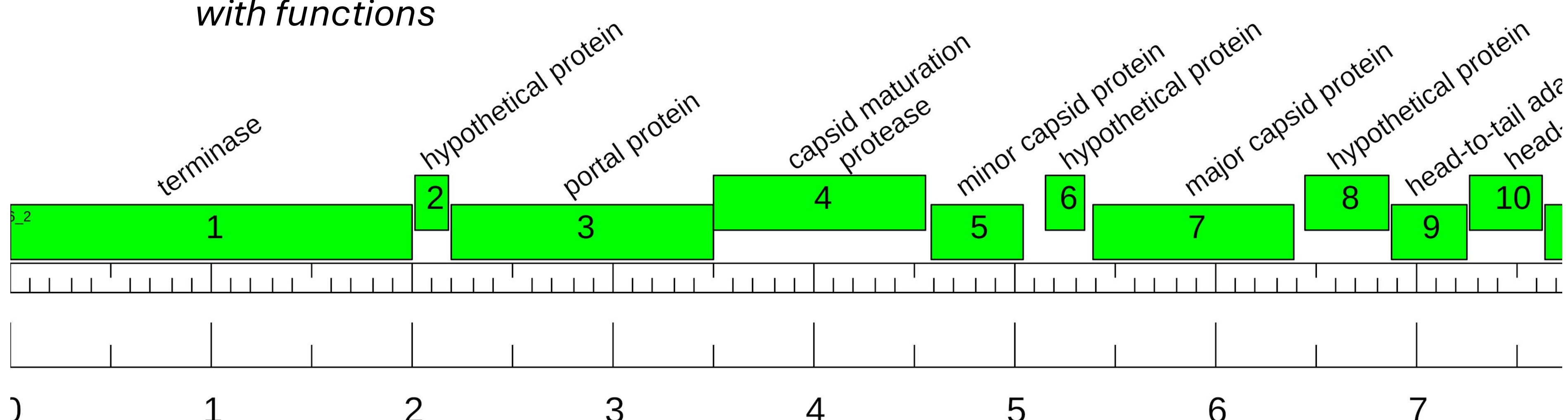
- Myoviridae phage
- Host bacterium: *Serratia fonticola* (gram-negative bacteria)
- Phage isolated from the North Sawmill Swamp in Atkinson, NH
- Host bacterium isolated from the Pete Bog in Londonderry, NH
- 53997 bp long
- 86 genes identified
- Functions assigned to 37 of 86 genes



Top: Northmill plaques at a high conc.

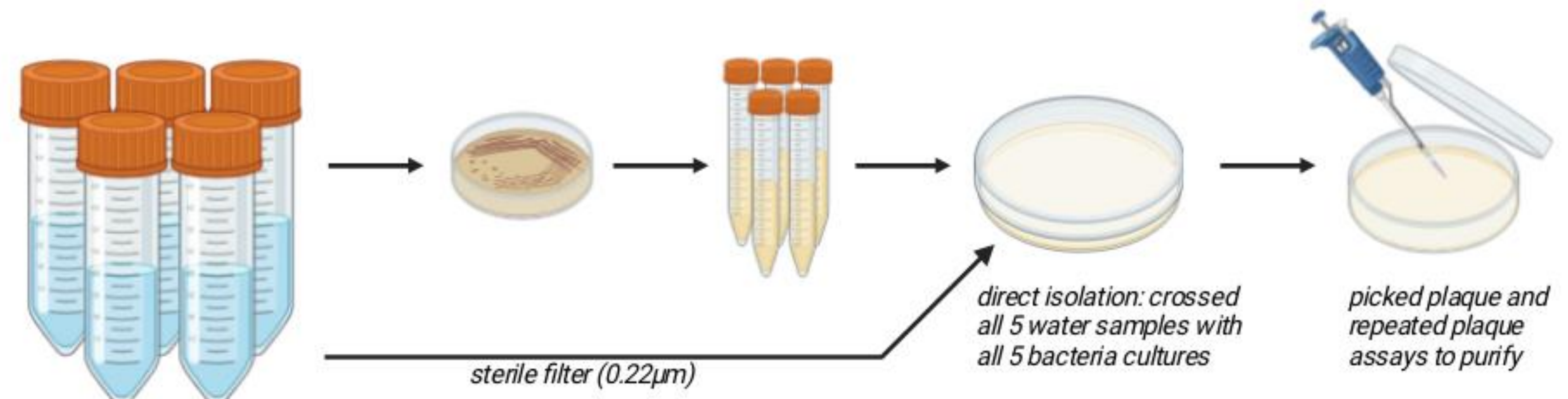
Middle: TEM images of Northmill

Bottom: genome map for first 10 genes with functions



Methods

Step 1: purify bacterial cultures and isolate Northmill (using SEA-PHAGE protocols)



Step 2: isolate & sequence DNA, TEM imaging

Step 3: analyze genome and assign functional annotations to Northmill



Discussion

The discovery of Northmill demonstrates a process in which novel phages can be discovered and characterized, expanding our understanding of natural phage diversity and opening the door to further exploration of biomedical phage applications. Northmill's annotated sequence data will be submitted to GenBank, and we plan to publish a scientific paper on the discovery of this phage in the future as well.

References & Acknowledgements

We gratefully acknowledge NH-INBRE for funding and support of lab space, which made this research possible. We also acknowledge the SEA-PHAGES Program for their phage isolation and bioinformatics guides (<https://seaphages.org>). Some figures were created with BioRender (<https://biorender.com>).