Biology

Outcomes

Since 2016, freshmen students have isolated, purified, and characterized a total of 48 novel bacteriophages found in the soil in and around Winthrop University, Rock Hill, South Carolina. See the Actinobacteriophage Database for individual phage information.

Each phage was amplified in the bacterial host *Mycobacterium smegmatis* mc^2155, *Microbacterium foliorum* or *Microbacterium liquefaciens*. The phage were characterized following DNA extraction using restriction enzyme digests and gel electrophoresis. Electron microscopy demonstrated that most phages had long, flexible tails and belong to the Siphoviridae group of bacteriophages.

After studying the electron micrographs, the digestion patterns, and quality of the DNA, two of the most potentially unusual phages each year are chosen to be sequenced at Pittsburg State University (PSU). In the following semester, research continues and both genomes are annotated using DNA Master Software and several homology search programs, including BLASTp and HHPred, to predict gene locations and determine gene function.

The genomes are then ready to be submitted for peer review and ultimately deposited and published at the National Library of Medicine's database, GenBank.

The next part of the project is SEA-GENES (**S**cience **E**ducation **A**lliance-**G**ene-function **E**xploration by a **N**etwork of **E**merging **S**cientists). Here, our SEA students return to the bench to explore phage gene function using a variety of cutting edge molecular and genetic techniques.

As well as publishing in GenBank, students in previous years have presented their work at the Association for Microbiology Society's regional meetings, the Association of Southeastern Biologists Conference, Winthrop University's annual undergraduate research conference (SOURCE) and at the Department of Biology's annual spring research showcase. In June each year, representative student(s) present the work at HHMI's national SEA-PHAGES conference near Washington, DC.