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2025 SEA Symposium Abstract

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From Soil to Savior: Discovering LavAbarElk, a Novel Lytic Phage for Bacterial Control

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In the current, rapidly changing world of modern medicine, medical innovations have provided doctors with efficient therapies for many diseases. Yet, as pharmaceutical industries come up with more and more powerful tools against bacterial diseases, bacteria respond by creating resistance mechanisms, rendering traditional therapies less effective. This ongoing "arms race" between medical advances and bacterial development has led scientists to search for alternative methods of therapy, one of the most promising of which is phage therapy.   
   
Phage therapy uses bacteriophages—viruses specifically engineered to infect and kill bacteria—as a prospective solution to combat antibiotic resistance. Bacteriophages, which have existed for billions of years, present a new solution to cure bacterial infections resistant to conventional antibiotics.   
   
While having tremendous potential, bacteriophages are largely unexploited, with millions of phages remaining to be found and characterized. To aid to overcome this lack of knowledge, Metropolitan Community College (MCC) has had the honor of being a participant in the Howard Hughes Medical Institute's (HHMI) Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program to help discover such bacteriophages.   
   
Our work entails the characterization of a novel bacteriophage, LavAbarElk, isolated from soil samples collected in Elkhorn, Nebraska, targeting *Gordonia rubripertincta* NRRL B-16540. Using direct and enriched isolation techniques, three soil samples were subjected to plaque assays, spot tests, and subsequent phage purification, identifying this novel bacteriophage. Sequencing of the LavAbarElk genome, completed at the University of Pittsburgh on January 27, 2025, revealed a genome approximately 66,723 base pairs in length with a GC content of 58.4%. The average sequencing shotgun coverage was reported at approximately 2185, and the genome is circularly permuted. The phage belongs to the DV cluster, with its subcluster and life cycle yet to be determined. The phage's morphological characteristics classify it under the Siphoviridae morphotype based on EM imaging.   
   
Currently LavAbarElk phage genome annotation is underway, with expected completion by Spring. While the genome has not been uploaded to GenBank or archived, the data contributes valuable insights into phage biology and its potential applications. Current Bioinformatics work is focused on phage annotation and genome analysis using PECAAN, DNAMaster, BLAST, Starterator, Phamerator, HHPred, GeneMarkS, and Glimmer, as well as archiving, with plans for publication and broader distribution.