CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

Seton Hill University

Greensburg PA

Corresponding Faculty Member: Kristen Butela (kab340@pitt.edu)



Izzy Owen

Isolation and genomic characterization of Mycobacteriophages Wilbur and Romney2012

Kaylee Anderson, Tyler Breth, Hannah Brichacek, Victoria Caruso, Dilveer Chaggar, Delaney Cortazzo, Karlee Criado, Tanner Druck, Denali Espy, April Falkosky, Jusdan Griffith, Cierra Harrington, Briana Kostan, Kaitlyn Kutchman, James LaGrosse, Anna Lasslo, Dustin Martin, Samantha McKee, Izzy Owen, Elizabeth Powell, Corey Pruzinsky, Zachary Sheffler, Emma Snyder, Jackson Towers, Alicia Walsh

Mycobacteriophages Wilbur and Romney2012 (Cluster A4) were isolated from separate soil samples collected from geographically distinct locations on the campus of Seton Hill University in Greensburg, PA via enrichment culture on *Mycobacterium smegmatis* mc2155 and characterized by students at Seton Hill University participating in the SEA-PHAGES research program. Both phages form clear plaques of 2.5 mm in diameter after 24 h incubation at 37°C. Both genomes are highly similar (51.4 kb, 63.9% GC, defined linear ends, 99% nucleotide similarity) despite being isolated from unique soil samples collected on different days. Phage genomes were annotated using DNA Master, HHPred, Phamerator, and the BLAST database suite. Wilbur and Romney2012 each contain 84 predicted protein-coding genes. Several noncoding features in the Wilbur genome were identified and annotated. Various phage characteristics were explored, including the permissive temperature range for plaque formation, ion co-factor requirements, and lysogen formation. Despite having genetic features common to temperate phages, Wilbur forms clear plaques under laboratory conditions, and no lysogens were able to be isolated using this phage. Future directions include examination of Wilbur and Romney2012 under various conditions to assess lysogeny and broader bioinformatic searches for noncoding features and mapping of membrane spanning domains.