DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

University of Maine, Honors College

Orono ME

Corresponding Faculty Member: Emily Whitaker (emily.whitaker@maine.edu)

Leaves Are Falling, Phages Are Calling: The Genomic Annotation of November and Applecrisp

Molly Freeman, Britni Osborne, Jacob Mora, Nala Begin, Emily E Whitaker

Growing antibiotic resistance has caused a regression to a “pre-antibiotic” world; which could lead to economic, health, and population crises. An alternative approach to combat antibiotic resistant infections is re-emerging as an option, phage therapy. Phage therapy against non-tuberculosis mycobacteria (NTM) utilizes mycobacteriophage (phage), viruses that can infect and kill bacteria in the genus *Mycobacterium* such as *M. tuberculosis*. November and Applecrisp are novel, temperate *Siphoviridae* phage belonging to cluster K6 that form turbid plaques 1-4 and 1-5 mm in size, respectively. Both phages were isolated from soil samples collected in Orono, ME using the host *M. smegmatis* mc2155. November and Applecrisp have genome lengths of 61,517 and 61,954 bp with GC contents of 67.3% and 67.1%, respectively. The right arm of the genome, typically associated with genes involved in replication, shows more diversity between K6 phage than the left arm. Despite this diversity, there are multiple conserved phams which are unique to Cluster K6 present in the right arm. Additionally, both November and Applecrisp encode unique orphams. Cluster K phages have been shown to have a broad host range and have been useful in phage therapy. Future experiments to determine the host range of November and Applecrisp will be necessary to conclude whether these phages possess a similarly broad host range as other K phage. By analyzing genomic features, we aim to provide valuable insight into November and Applecrisp encoded proteins, including endolysins, and suggest further testing to screen for the presence of virulence factors.