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Finding Fun in Fefferhead and Polishing Up the Genome of ShamWow

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Bacteriophages, or phages, are viruses found in abundance around the world that infect various bacterial host species in order to replicate. In our first year participating in the SEA-PAHGES program we ran an entirely online model with students attending class off-campus due to the COVID pandemic. We studied the genome of two Mycobacteriophage discovered previously by other labs, Fefferhead and Shamwow. Fefferhead was discovered in Cary, North Carolina in 2014 by Matthew L Petrovich of Hope College; ShamWow was found in Pittsburgh, Pennsylvania by Norhan Shamloul of the University of Pittsburgh. After isolating, purifying, and amplifying the bacteriophages, their structures were examined through Transmission Electron Microscopy (TEM) images. Through this process, it was determined that these phages are of Siphoviridae morphology, meaning they have non-enveloped capsule heads and have long, non-contractile tails. The phages’ genomic DNA was extracted and sequenced, establishing that were both temperate and part of the K6 and E clusters, respectively. The length of the Fefferhead genome is 61,366 base pairs, while ShamWow contains 75,933 base pairs with approximately 98 and 140 predicted genes in each, respectively. We used the software programs DNA Master, Starterator, Phamerator, GeneMark, Glimmer, Phagesdb BLAST, and BLAST in order to predict the presence of protein-encoding open reading frames (ORFs) and assign each a start codon. Using HHpred, NCBI BLAST and Synteny, we attempted to deduce the function of each gene to find its importance in the genome. Of the 98 genes identified through auto-annotation of Fefferhead, two genes were deleted due to lack of coding potential. Analysis supported assigning functions to 35 of the 98 annotated genes, and one previously unidentified coding regions was discovered during manual annotation: Fefferhead\_68. Fefferhead\_68 is a 267 bp region that contains coding potential and has strong conservation of sequence to other related phage, Beezoo and YoureAdopted, but doesn’t contain a protein with known function as of yet. In addition to protein coding genes, Fefferhead has two tRNA genes contained in its genome. We are currently in the process of annotating ShamWow. The information that we have accumulated or are currently working on through our annotations can hopefully be used by others in the future as they predict the same aspects of their genome.