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Genomic Analysis of Microbacterium Phage HarperAnne

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Antibiotic resistant bacterial infections are projected to be the leading cause of death by the year 2050. Bacteriophages, viruses that exclusively infect bacterial cells, are a promising solution to this pending health crisis. Phages are the most abundant biological particle on the planet. They are evolutionarily ancient and genetically highly diverse. Studying phage genomes gives valuable insight into the proteins coded for in phage DNA that allow them to infect their host and avoid their hosts’ defenses. HarperAnne was discovered during the wet lab portion of the course in an organic soil sample collected in Pinellas County on September 11, 2018. This lytic phage infects the host *Microbacterium foliorum* NRRL B-24224 SEA, a nonpathogenic relative of infectious bacteria including *Mycobacterium abscessus*. Phage DNA was extracted using HHMI SEA-PHAGES protocols. Sequencing, completed by the Pittsburgh Bacteriophage Institute, revealed that HarperAnne is a Cluster EE phage with a genome length of 17,116 bp, 26 genes, a 9 bp 3’ sticky overhang, and 68.8% GC content. BLAST results indicated the closest annotated phage relatives are Noelani and Miaurora. The purpose of this study was to compare the genome of HarperAnne to phages in the same pham to identify similar and unique gene products. We hypothesized that there would be synteny among structural and assembly function genes and that proteins with the same function would have regions of high amino acid identity. We compared HarperAnne to phages in the pham using several different predictive programs including Phamerator and HHPred. We found a high degree of similarity of structural and assembly function genes. Structural genes identified include terminase, portal protein, major capsid protein, head-to-tail connector complex protein, minor tail protein, tail assembly chaperone, and lysin A. There is one orpham. No tRNAs are present. Our results indicate a high degree of similarity in gene products between HarperAnne and other phages from the same cluster. Our findings will contribute additional information to the relatively limited body of knowledge about the diversity within and between phages that infect different Actinobacterial hosts.