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2025 SEA Symposium Abstract

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Discovery and Genome Annotation of Cluster EE Phage HeadMave

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Bacteriophages can potentially be used to combat antibiotic-resistant bacterial infections, which could become a major health crisis if left unsolved. We discovered our phage, HeadMave, in Abingdon, Maryland, and are working to annotate its genome. We carried out plaque assays and full plate titers to isolate and purify our phage HeadMave. We used *Microbacterium foliorum* strain NRRL B-24224 as the host bacteria. After electron microscopy at the University of Maryland, Baltimore County, we discovered that it has a siphovirus morphology. Furthermore, after sending our phage sample to the Pittsburgh Bacteriophage Institute to sequence our phage genome, we discovered that it belonged to the EE cluster and identified that it potentially has 26 protein-coding genes and one tRNA. By completing the genome annotation, we aim to determine the final genes and their associated protein functions using DNA Master, Phamerator, HHPred, DeepTMHMM, and BLASTing the genes using The Actinobacteriophage Database and NCBI. With the discovery of these genes, we could gain a deeper understanding of the phage structure and achieve our goal of potentially finding a use for HeadMave.