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Shining a Beem of Light on Phages

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Every day new information and findings lead to the improvement of biotechnology, such as CRISPR, CAS-9, and phage therapy. This process can start by deducing phage genomes, and in our specific interest, the genome of phage Beem. Novel bacteriophage Beem was isolated from the host *Mycobacterium smegmatis*. Beem was found by Brandon Martinez at the Dominican College of Blauvelt in 2019. Beem was a direct soil sample and is morphotype Siphoviridae. However, of the multitude of phages studied, only about 40% of the typical phage genome functions are known. To solve this, we have to use the information from protein sequences that have already been verified. In addition, Cluster J’s and siphoviridae phage optimal pH’s are unknown. In this study, we seek to annotate Beem’s genome and assign functions for the coded proteins. We also seek to create a phylogenetic tree based on the DNA sequences of other Cluster J phages and compare this to the pH of their soils. This genome was processed on DNA Master, using Glimmer and Genemark for gene prediction, Starterator and Blast to choose start sites, and Phamerator, HHPred, and Blast again to assign functions. The information gathered was then manually confirmed. A phylogenetic tree was created by using Clustal Omega, with PhagesDB for fasta files. Soil acidity was then found with the USDA Web Soil Survey, using coordinates from PhagesDB. Beem was found to have 2 terminase small subunits, possibly due to its large size. Most of the Cluster J phages studied were found in strongly acidic soil, where Beem’s pH rating was 5.3. Through this process, we have added to the expanding database of phage genomes, their functions, and understanding of cluster J. From there, the knowledge of other clusters can be improved and, eventually, the whole of all phages.