CONSIDER FOR TALK

2021 SEA Symposium Abstract

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Beeming Across the World of Phages

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Throughout the world and in various environments, more than trillions upon trillions of phages are estimated to exist, but most of them have yet to be discovered, let alone isolated or have their genomes annotated. Once new phages have been located and identified, the goal is to annotate their genome to add to the bank of phage genomes. The specific phage we have annotated is named Beem. Beem is related to other actinobacteriophages in cluster J, but it is not identical to them. By annotating Beem, further information was gathered on cluster J and the bacteria they infect. This allows for a better understanding of Beem and similar phages which can be used in future research and other tasks. To address this need for understanding, Beem’s genome was annotated to determine the sequences of DNA that contain genes, what their correct start sites were, and their likely functions. Our team specifically investigated the function of 48 genes, between genes 81-129, most of the functions were determined to be “no known function,” but there were also some peculiar genes. To further study this region, different sections of the genome were also compared to the entire genome for codon bias, to determine any general trends since there is evidence that codon bias is associated with gene expression. Further investigation will be needed to understand these regions of genes, but throughout this process, we were able to identify some of Beem’s close relatives such as Yeet, Baka, Zelink, and others. If any of these phages are significant, whether for bacteria in general or for medical purposes, then the finding and annotation of Beem will be significant as well.