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Exploring the Relationship Between Environment and GC Content in Bacteriophages

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Bacteriophages (phages) are a class of viruses that replicate through infection of specific bacterial hosts. Though still in its early stages, research has shown multiple advantages to using phage therapy in addition to antibiotic use as opposed to just antibiotics alone. To start, phages are easier to mass produce than antibiotics, have fewer side effects, allow for directed treatment at the site of infection, and have a reduced risk of antibiotic resistance when manufactured into phage “cocktails”. Despite these many benefits, use of phages in addition to or in place of antibiotics isn't widely accepted just yet due to lack of public education, disinterest by a thriving pharmaceutical industry, and lack of research. Thus, in an effort to further understand the functional mechanisms of such phages, we decided to do a comparative environmental and genomic analysis of two phages isolated in our lab as a part of the SEA-PHAGE Initiative, Abigail and ManAs. Though both discovered in Worcester, MA, the two phages were found in very different soil environments, with ManAs found in relatively barren soil near the wall of a residential building and Abigail found next to a pond in a park with greater biodiversity and more moist soil. In comparison, Abigail’s genome was much larger than that of ManAs and its GC content slightly lower. We ran Phages DB Blast to determine the 10 most similar viral genomes to each phage and proceeded to search for geographical patterns and environmental similarities in the matches on the Actinobacteriophage Database at Phages DB. By conducting research in this way, we were hoping to find common ground within the morphology of each phage. Whether that be the number of genes present in each phage, the function of each gene or even the type of environment each phage was found in. This research started by looking at websites such as: PECAAN, PhagesDB, and NCBI Blast. PhagesDB revealed all ManAs matches to share a GC content of 68.5%, prompting us to question the relationship between environment and phage GC content. An NCBI Blast revealed ManAs and its closest relative, PaoPu to be related to a strain of “high GC Gram+” organisms, suggesting a possible correlation between GC content and ManAs’ ability to thrive in a less biodiverse environment. Abigail was found to have a GC of 66.5% through PhagesDB and was in the EB cluster. Once the closest relatives to these phages in the same cluster were found, we ran a gene comparison through PECAAN to determine the quantity, direction, and function of the genes in similar phages. With all of these factors in consideration, we hope to learn more about the genetic makeup of these phages and even the clusters that they originate from. In this poster, you will see research conducted to find similarities between the annotated phages and closely related phages in their respective clusters.