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Exploring the Characteristics of Bacteriophage Simpson

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Bacteriophages, also known as phages, are viruses that infect, replicate and lyse bacterial cells. Due to the increasing prevalence of antibiotic resistance, phages are emerging as a promising alternative to traditional antibiotics to combat bacterial infections. Our study aims to gain a deeper understanding of the Simpson bacteriophage, which belongs to the AZ cluster of phages that infect Arthrobacter globiformis bacteria. Simpson genome is 43,853 base pairs in length, with 67.6% GC content, and encodes approximately 69 genes. We annotated these genes using different computational tools including PECAAN, HHPRED, Starterator, DeepTMHMM, Phamerator, and BLASTp followed by a detailed quality control of the annotations.

For further analysis, we utilized AlphaFold structure predictions to investigate the function of proteins encoded in Simpson with no known function. Moreover, we have tested if Simpson can infect related Arthrobacter hosts. Recent work has suggested that Sir2-like enzymes play a function in host defenses systems. In eukaryotes, Sir2 encodes an NAD-dependent deacetylase that is inhibited by high concentrations of nicotinamide (NAM), so we are also examining host range in the presence of 5mM and 20mM NAM to test if Sir2-like enzymes may restrict the host range of Simpson.

Lastly, we utilized comparative genomics to compare Simpson to all other AZ phages using dot plots. The analysis revealed a high degree of genomic similarity among Simpson and other AZ phages. In conclusion, our study provides a comprehensive overview of Simpson through multiple approaches including computational predictions, gene annotations, wet lab experiments, and comparative genomics.