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Isolation and Genomic Analysis of Bacillus megaterium Phage 614

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Bacteriophages are the most diverse biological entity on the planet, but like with any other organism, there is a great degree of genomic similarity that can be found among them that indicates relatedness. After initial genome annotation through DNA Master and NCBI Protein BLAST, (bacteriophage 614) appears to exhibit a high level of genomic similarity with other annotated Bacillus phages. Despite this apparent level of similarity, we hypothesize that bacteriophage 614 will still contain several unique and novel elements in addition to known and related features. In our analysis of the phage genome, we utilized DNA Master, the NCBI database, Phyre 2, and HHPRED. We found that bacteriophage shared a high genomic identity with phage 1, phage 2, and phage 3, indicating a close relatedness with the phagenumber family. We also discovered major capsid structural relatedness with phage 4 and phage 5, indicating a more distant relation. 99.5% of the proteins coded in the bacteriophage 614 genome had a strong BLAST protein match (e-value < 10^-5), while only 0.5% of the coded proteins were considered novel. Many of the genes, despite having strong BLAST results, were still ultimately hypothetical proteins in function. Upon further analysis of these proteins and hypothetical folding structure, we discovered functions for several of them. Bacteriophage 614 shares many similarities with other known bacteriophages, but there are several unique elements that make this phage distinct in nature.