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Genomic Analysis of the Mycobacterium Phage Hilltopfarm

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The objective of the research was to analyze and annotate Hilltopfarm, a phage isolated from Mycobacterium smegmatis mc2 155. Hilltopfarm was discovered by Anthony Stewart in 2020 at the University of Pittsburgh in Pittsburgh, Pennsylvania, it was adopted and analyzed by students at Queensborough Community College. The sample was collected from a cluster of filamentous organisms in wood chips at Hilltop Farm, the site where it was discovered, hence the name “Hilltopfarm”. It is of the class Siphoviridae with a double-stranded DNA genome, non-enveloped head, and non-contractile tail. Hilltopfarm has a genome length of 76834 base pairs with 129 genes. It is in the cluster ‘Y’, other phages in this cluster are Bipper, Cracklewink, and Typha. Bioinformatic programs such as Blast, Starterator, Pharmerator, HHpred, DNA Master, and others were used to determine the coding potential, best possible start for a gene, the ribosomal binding site, the function, the tRNAs in the genome, and more. Of the 129 genes in the phage 43 had functions, two were tRNA and the rest had no functions, or their functions could not be determined. The genes that had functions included minor tail protein, tail assembly chaperone, tape measure protein, lysin A, lysin B, head to tail adaptor, head to tail stopper, capsid maturation protease, and other functions typically found in phages. The closest relative to Hilltopfarm is Typha and the majority of the genes have the closest match to the genes of Typha. Hilltopfarm has three genes found only in Bipper and one only in Cracklewink. Hilltopfarm has two tRNAs for Arginine and Methionine just like Typha, while Cracklewink and Bipper have only one for Methionine.