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Exploration of Possible Translational Frameshifts in Phages of the EA5 Cluster

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Bacteriophages are viruses that only infect bacteria. Due to their specificity, these phages do not harm or negatively interfere with humans. Recently, scientists have discovered the use of bacteriophages to have significant value as they can be used in phage therapy as an alternative treatment to combat bacterial diseases. Bacteriophage research will also further advance the understanding of its genome, indicating the effects of specific proteins on bacteria and shed light on their evolutionary history. Students at Florida International University have researched and annotated a newly discovered bacteriophage, GreenIvy. It belongs to the cluster EA5 (morphotype Siphoviridae), has a genome length of 40,254 base pairs, containing 61 genes. GreenIvy was annotated using bioinformatic tools including PhagesDB, GeneMark, Glimmer, HHpred, Expasy, Starterator, NCBI Blast, Aragorn, tRNAscan-SE, and DNA Master. In our analysis, 18 different sequences matching known slippery sequences were identified in GreenIvy’s genome. However, only two of them are possible slippery sequences. One is well studied in phages, located in tail assembly chaperone (gene 16), with slippery sequence CGGGGGGCG and with the slippage happening at bp 9,420. A second slippery sequence was identified between genes in 38, with sequence GGGAAAT and located at 25,749 base pairs. The frameshift results in a larger DNA Polymerase protein, with the small predicted gene 37 being part of the polymerase gene (gene 38). This recurring sequence is conserved in all members of the EA5 cluster. Last, a possible frameshift was identified in the small gene 23 with unknown function assigned, and preceding endolysin (gene 24). This possible frameshift results in a larger endolysin gene, expanding the N-terminus of this protein. The new size and sequence match well with other longer endolysins in other clusters not related to EA5.