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Investigating the Programmed Frameshift in Buttons Gene 22

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In ISBT 104, my class annotated our adopted mycobacterium phage, Buttons. The Mycobacterium phage Buttons was discovered by Christina Jodway in Milbridge, Maine as part of the SEA-PHAGES program. This particular phage was isolated from the bacterial species Mycobacterium smegmatis and its genome was sequenced. Buttons is classified in the subcluster A1. This phage genome length is 49,420 base pairs long. There are 86 genes in Buttons. The predicted life cycle for Buttons is the lysogenic life cycle. Buttons has a “slippery” sequence in gene 22 where the ribosome makes a mistake and changes the reading frame during translation. This causes the ribosome to make a longer protein in Buttons where the first half is approximately aligned to the short-form of the gene but the rest of the sequence is different. Programmed translational frameshifting (PTF) is an alternate process in protein translation. PTF usually happens in the tail-assembly chaperone proteins. The tail-assembly chaperone protein comes in two forms of the small subunit and the large subunit. In genes 22 and 23 of Buttons, gene 22 encodes the small subunit of the tail-assembly chaperone protein, and PTF causes fusion of genes 22 and 23 to create the large subunit. PTF is one way phages can regulate protein levels without the use of a new promoter. Overall, PTF helps the phage maintain the correct proportion of chaperone proteins to efficiently assemble the tail fiber for Buttons.