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Structural differences between tape measure proteins of unique Actinobacteriophage clusters and two novel Montana Mycobacteriophages

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Within a bacteriophage genome, the tape measure protein (TMP) dictates the length of a bacteriophage tail. In addition, this protein may function in signaling to activate non-replicating bacterial host cells. The gene that encodes for TMP is typically large in size and thus can be identified in a bacteriophage gene map when taking into consideration the size and proximity to specific programmed ribosomal frameshifts in upstream protein coding genes (Pedulla et al., 2003). The function of TMP was determined by a team of researchers in 1984 (Katsura and Hendrix). The team found that upon removing segments of the gene, the bacteriophage exhibited a proportionally smaller tail, suggesting a direct correspondence between TMP gene length and the length of the phage tail. While subsequent studies have supported these data, several bacteriophages have been found to contain portions of the gene that do not contribute to tail length (Pedulla et al., 2003).   
The objective of this study was to compare structural differences in TMPs belonging to different phage clusters. We first annotated the genomes of two novel Mycobacteriophages, MrYolo and Froghopper, and identified the gene encoding tape measure protein in each genome. The putative secondary and tertiary structures of these TMPs were determined using prediction software (PredictProtein, 2017). From the Actinobacteriophage Database we then selected TMP amino acid sequences of 4 phages each from clusters A, B, K, and F, (Russell & Hatfull, 2016), and software was used to predict the secondary and tertiary structures of each TMP selected. Finally, we ran ClustalW alignments, and generated phylogenetic trees showing the relationship among TMPs of the selected phages (Bioinformatics Center, 2017). The results of this study showed that TMPs within clusters are more closely related and structurally similar than those of different clusters.