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Comparing Tail Assembly Chaperone Composition within and between Bacteriophage Morphotypes

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Bacteriophages may have a myovirus, podovirus, or siphovirus morphotype based on their tail. Tail assembly chaperones (TACs) are protein components that assist in the assembly of bacteriophage tails. Given that different phage morphotypes have different tails, an investigation was undertaken to compare their corresponding TACs. Phages infecting the bacterial host Mycobacterium smegmatis mc2 155 were examined. PhagesDB was used to identify and characterize commonly sequenced phage clusters per morphotype and their corresponding TAC phams. Phages with myovirus morphology had sequenced phages in clusters C and AA and both clusters had TAC phams 411 and 588. Phages with podovirus morphology had no sequenced phages with TAC genes. Phages with siphovirus morphology had sequenced phages in cluster A with phams 58264 and 40671, cluster K and G both with phams 57221 and 51488, and clusters F and E both with phams 60 and 58308. Information on the range of TAC protein base pair lengths for a given pham was collected. A reference TAC amino acid sequence from each pham was taken and aligned with all other TAC amino acid sequences available on PhagesDB for that given pham. Phams 411 and 588 belonging to the myovirus morphotype were found to have a comparatively higher number of top BLASTp hits out of total hits within their phams when compared to phams of the siphovirus morphotype. In another inquiry to compare TAC amino acid sequences across different morphotype phams, a TAC amino acid sequence from myovirus pham 411 was aligned against all TAC amino acid sequences in siphovirus phams 58264, 57221, and 60 using BLASTp. No significant hits were found.