CONSIDER FOR TALK

2021 SEA Faculty Meeting Abstract

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Novel capsid proteins identified in the actinobacteriophages using cryo-electron microscopy

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The capsid is the protein shell that surrounds the dsDNA bacteriophage genome and protects it from the environment as the phage finds a new host. The actinobacteriophages are almost all tailed bacteriophages that use a major capsid protein to make the capsid, along with the portal protein and tail proteins. However, other proteins can also be found in the capsid, including minor capsid proteins and decoration proteins. These can be challenging to recognize using conserved amino acid sequence identity since their structure can be conserved even when the amino acid sequence has diverged beyond recognition. Cryo-electron microscopy is a structural technique that creates high resolution maps of bacteriophage capsids to determine the protein structure. We have used cryo-electron microscopy to obtain sub 3 angstrom resolution maps for Rosebush (B cluster), Patience (U) and Adjutor (D). Analysis of the capsid structure has revealed previously unannotated capsid proteins with novel protein folds and also identified a potentially common structural motif found in the C-termini of both the major capsid protein of Rosebush and the minor capsid protein of Patience.