CONSIDER FOR TALK

2025 SEA Faculty Meeting Abstract

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Is Pham 210844 of EA1 Cluster Bacteriophages an ASCE Superfamily ATPase?

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Annotation of novel bacteriophage genomes includes assigning, where possible, putative functions to the encoded gene products on the basis of predicted structural similarity and significant sequence identity/similarity to proteins of experimentally-determined structure and/or function. Functional assignments based upon predicted structural similarity and measured sequence identity alone however may fail to identify conserved amino acid sequence motifs, comprised of amino acids essential for enzyme structure and/or active site function. Pham 210844, identified to date in genomes of EA cluster bacteriophages, is almost invariably annotated as a member of the ASCE-ATPase Superfamily. Here we examine if deeply conserved amino acid motifs of ASCE-ATPases can be unambiguously identified in Pham 210844 sequences of EA1 cluster bacteriophages. Analysis of aligned Pham 210844 sequnces reveals that a cannonical Walker A motif is identifiable only in a subset of Pham 210844 sequences, while a Walker B motif cannot be identified in any Pham 210844 sequences. This suggests that while Pham 210844 likely originates in the ASCE ATPase/KG superfamilies, it is premature to ascribe an ATPase function to Pham 210844 on the basis of predicted structural and/or sequence homology alone.