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Visualizing Bacteriophage Evolution through Sequence and Structural Phylogeny of Lysin and Terminase Proteins

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A critical part of viral genomics is understanding how genes evolve and persist. Because bacteriophages are so abundant and their history remains largely unexplored, they can provide unique insight on viral evolution. Traditionally, phylogenetic trees have been used to visualize evolution using DNA sequence comparison between organisms. However, sequence similarity may fail to capture key alterations to product structure, and therefore function. Structural phylogenetic trees based upon predicted protein structure may provide a more robust view of the way in which new protein structures and functions arise. Structural prediction models could provide an alternative lens through which to view evolutionary paths.  
Here, mycobacteriophage proteins Lysin A and Terminase were studied. A variety of phage genomes were selected in triplicate from the 10 largest clusters. Protein structural predictions generated by I-Tasser and Phyre2 from amino acid sequence were compared using PyMol. Structural alignment scores were used to quantify the structural homology between proteins of the same function call across different clusters. Five phylogenetic trees were constructed: one based on structural homology of Lysin A, one on structural homology of Terminase, two on genomic sequence of these individual genes, and one on overall genomic sequence alignment. These trees were compared to evaluate differences between sequence and structural homology. Visualizing the relationship between sequence and structures of phage proteins would provide a new perspective on the evolution of the virosphere.