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Investigating Tail Proteins of Phages That Infect Gordonia terrae 3612

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Bacteriophages, otherwise known as phages, are viruses that infect bacteria and are found ubiquitously in all environments. Phages utilize tail proteins as their initial point of contact to bacteria during infection, and the specific structures of these proteins can greatly impact the types of hosts the phage can infect. However, it is still not fully understood how tail proteins impact host specificity, including phages that infect *Gordonia* bacteria.   
  
In this study, we sought to compare tail proteins from phages that infect *Gordonia terrae* 3612 to find similarities and differences. It was hypothesized there would be conservation of tail protein amino acid sequences across all *G. terrae* phages as they infect the same host. To test this hypothesis, genes were compared across phages and clusters through pham map analysis, amino acid sequences of tails were compared using dotplots, and evolutionary relatedness of conserved tail genes were assessed with phylogenetic trees.   
  
Tail protein sequences were found to not be conserved across all phages with the same host, refuting the hypothesis. However, tail proteins were conserved within and between clusters; tail protein similarities were found between singleton Finkle and cluster CZ phages as well as between clusters DN, DB, and CV. Additionally, tail protein amino acid sequences were found to be distinct across subclusters within the CZ cluster. Overall, these findings further emphasize the diversity of tail proteins within phages infecting the same host. This adds to our understanding of phage tail diversity in the context of host specificity.