CONSIDER FOR TALK

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Bioinformatics Analysis of Mycobacterial R Cluster Phages

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Traditionally, antibiotics have been used in medicine to kill bacteria, but due to their overuse, these chemicals have become less effective in recent years. An alternative, phage therapy, relies on bacteriophages- viruses that infect and kill bacteria in the environment. Mycobacteriophages infect organisms in the genus Mycobacterium, a group known for having species that are pathogenic to humans including M. tuberculosis, the causative agent of tuberculosis. Phage therapy is a more effective choice in treatment because bacteriophages are able to evolve along with the bacterial host, whereas traditional antibiotics cannot. However, a deeper understanding of phage biology is needed before phage therapy becomes mainstream. In spring 2016, advanced bioinformatics approaches were used to analyze the five mycobacterial phages in the mycobacteriophage R Cluster family- Nilo, Papyrus, Send513, Weiss13 and Zenon. The goal was to discover more about the phages in this family since they were isolated in geographically distant locations and most are so new that their genomes have only been partially mapped and annotated. All five phages were isolated on M. smegmatis, a less pathogenic relative of M. tuberculosis. Using a variety of experimental approaches, conserved and unique genomic features of the five R cluster phages were ascertained. DNA nucleotide sequences, along with predicted protein sequences were used to build evolutionary trees for ORFs from D, H, R, and U cluster mycobacteriophages, along with phages that infect a different genus of bacteria, Gordonia. Synteny maps reveal the strong conservation of sequence in most regions of the R cluster genomes, and the previous mentioned evolutionary trees show a strong relationship between R and phages from other clusters, especially those with few reverse genes such as D, H, R, and U. Evidence was found for a mycobacterial origin of several open reading frames in R cluster phages. All this in combination contributes to our understanding of the evolutionary history of these R Cluster phages. The study of the Cluster R phages could reveal information that might help in medical applications against more pathogenic species of mycobacteria, such as tuberculosis. This work is also expected to provide new bioinformatics information about the genetics and function of this and other classes of bacteriophages.