CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Transcriptional Analysis of Phage Infection Dynamics Using RNA-Seq

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With over 1500 sequenced actinobacteriophages available in the Phages DB database and over 700 submitted to GenBank, there is a growing wealth of DNA sequence data with which to explore actinobacteriophage biology. While this sequence information has led to novel discoveries about actinobacteriophage diversity, structure, evolution, and gene content, there is comparatively little analysis of gene expression. In order to extend our understanding of phages at the RNA level and begin to understand how actinobactiophage regulate the expression of their genes, we performed RNASeq on Kampy, a cluster A4 mycobacteriophage, during various time points during infection of its host, Mycobacterium smegmatis. We show that mycobacteriophage Kampy transcription occurs in roughly two phases, an early phase consisting of genes for metabolism, DNA synthesis, and gene regulation, and a late phase consisting of structural genes and lysis genes. Additionally, we identify the earliest genes transcribed during infection, some as early as five minutes following infection, along with several other possible regulatory units not obvious from inspection of Kampy's genomic structure. Comparing with other RNA-Seq data, we show that the transcriptional profile of Kampy appears similar to that of mycobacteriophage TM4 but unlike that of mycobacteriophage Giles. In order to further expand our understanding of the diversity of mycobacteriophage gene expression programs during infection, we have also performed RNA-Seq on a Rhodococcus phage, WC1, that is closely related to RER2. Performed as part of an upper level continuation class to extend the findings of our freshmen Phage Lab class, we suggest that incorporating RNA-Seq on select actinobacteriophages will not only enhance our knowledge of gene regulation, but will also provide students with an additional level of engaging functional analysis.