CONSIDER FOR TALK

2021 SEA Symposium Abstract

Brigham Young University

Provo UT

Corresponding Faculty Member: Julianne Grose (julianne\_grose@byu.edu)

Characterizing Gordonia phage AJGECKO Through LIfecycle Analysis

Madilyn Brandt, Cierra Green, Alex Rolfson, Caleb Parker, Mitchell Whitten, Hunter Griffin, Emilee Carr, Hayden Ayers, Julianne H Grose

According to the Center for Disease Control, antibiotic resistance infections will be the leading cause of death by the year 2050. With antibiotics being unreliable, bacteriophages have been researched as a solution to killing resistant bacteria. Even with the progress in phage research, there remains many uncharacterized phage proteins. Determining the function of phage proteins is essential to ensuring safe treatment. The purpose of this project was to isolate and sequence mRNA encoded by AJGECKO to characterize unknown proteins. After discovering and isolating a Gordonia phage from raw sewage, we performed a one-step infection curve to determine the burst time and amount of phage released at each burst. Using the information of the burst time, we isolated RNA at certain times during the beginning, middle, and end of bacterial infection in order to correlate expression time with possible functions in the phage’s life cycle. Time points were determined based on observations about the burst time. The mRNA was depleted of ribosomal RNA and an RNA strand specific library prepped for Illumina Next Generation Sequencing. Our results should provide us with information about 1) the accuracy of our annotation, 2) the possible function of proteins, 3) the timing of events in the phages’ lifecycle, 4) the intensity of expression of phage proteins to find potential promoters/Shine-Dalgarnos that could be used for high protein expression. The data from the one-step infection study combined with RNAseq could also be used to identify whether AJGECKO would be a good candidate for phage therapies, including modeling of phage therapy timing.