CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

Ouachita Baptist University

Arkadelphia AR

Corresponding Faculty Member: Nathan Reyna (reynan@obu.edu)

Genomic Analysis of Cluster T Mycobacteriophage

Buzz R Hardin, Daniel N Games, Alex Abbott , Meredith Bolin, Rachel Dilatush , AlleaBelle Gongola, Taylor Johnson , Nathan Malone , Hannah Pagan, Nathan Terry , Tyler White , Sam Wilson , Joseph Koon, Colby Smith, Ben Blankenship, Ruth Plymale, Nathan Reyna

Cluster T consists of only phages Mendokysei (UC-Santa Cruz), Bernal13 (University of Florida), and RonRayGun (Ouachita Baptist University). Students at Ouachita Baptist University conducted a bioinformatic analysis of phages in Cluster T in collaboration with both UC-Santa Cruz and U of Florida. At OBU, we focused on characterizing the location of promoters, terminators, integrase, attachment sites, transfer RNA, and repetitive elements found in all three phages. Using either DNAMaster or the web base software PePPER, 6 SigA-like promoters were identified in all members of Cluster T. Seven hair-pin terminators were identified using ARNold and Softberry. Repetitive elements were discovered through the use of Gepard dot plots and MEME logo analysis. Interestingly, only Bernal 13 and RonRayGun contained a potential repetitive motif in Pham 8914 (GP48) However, it appears this pham is deleted from the Mendokysei genome. Nether ARAGORN or tRNAscan-SE found tRNAs in the genomes of phages in Cluster T. However, while all three phage contain Pham 694 (GP25) only in Mendokysei does Pham 694 contain a tRNA like secondary structure. The genomic identification of regulatory sequences in Cluster T has allowed us to begin wet-lab type projects that will lead towards the verification of bioinformatically identified elements in the future.