CONSIDER FOR TALK

2024 SEA Symposium Abstract

La Sierra University

Riverside CA

Corresponding Faculty Member: Arturo Diaz (adiaz@lasierra.edu)



Ana Acosta



Felicity Hernandez



Ruth Montiel



Bridgette Sanchez



Zadie Tsao

Characterization of the 4 HNH Endonucleases encoded within phage Bugger

Ana Acosta, Anheli Franco, Felicity Hernandez, Ruth Montiel, Layla Murillo, Julienne Role, Natallie Ruiz, Annika Samayoa, Bridgette Sanchez, Zadie Tsao, Natasha Dean, Arturo Diaz

Students at La Sierra University annotated the genomes of two siphoviridae phages, Crisis and Bugger, from the genus *Microbacterium* using bioinformatic tools such as PECAAN, BlastP, Pharmerator and HHPred.   
  
Crisis was isolated from *Microbacterium foliorum* on the campus of La Sierra University. Crisis has a 52,949 base pair genome with a 68.9% GC content and was assigned to cluster EC. 39 out of the 90 genes were assigned a function, including eight membrane proteins. A comparison of the 43 phages within cluster EC shows that Crisis is at least 91% similar to the other members within its cluster. Noticeably, differences were found at the beginning or middle of the genome.  
  
Phage Bugger was adopted from the University of Wisconsin Madison-River Falls and annotated by students at La Sierra University. Bugger was assigned to cluster GB, which is composed of four other siphoviridae phages infecting *Microbacterium paraoxydans* NRRL B-14843. Bugger’s genome is 61,511 bp long with a GC-content of 58.1%. 39 out of 126 genes were assigned a function based on sequence similarity, 14 were found to be orphams, and there was 1 tRNA. Genome analysis showed that Bugger contains several endonucleases scattered throughout the genome, including 4 HNH endonucleases, designated HNH-1 through HNH-4, which are all part of PHAM 143768. Multiple sequence alignment revealed that although they all share an NUMOD4 DNA binding motif and an HNH endonuclease motif, the genes were less than 47% similar to each other. Genome comparisons showed that phages Lifes and WaterT did not encode for any HNH endonucleases, whereas Cassita and LeeroyJenkins encode for 1 and 2 HNH endonucleases, respectively. Bugger’s HNH-1 (gene 62) and HNH-3 (gene 87) are not similar to any other HNH endonucleases in Cluster GB. In contrast Bugger HNH-2 (gene 84) is 99% identical to the HNH endonuclease in Cassita and 100% identical to one of the HNH endonucleases in LeeroyJenkins (gene 94). Moreover, Bugger HNH-4 is 99% identical to the second HNH endonuclease in LeeroyJenkins (gene 114). We then used Chimera X to predict the structure of the four HNH endonucleases in Bugger, which further confirmed the difference between the proteins. These variations in size and structure may reflect adaptations that allow these endonucleases to interact with different DNA sequences, or substrates, leading to diverse catalytic activities and biological functions.