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La Salle University

Philadelphia PA

Corresponding Faculty Member: Nancy Jones (jones@lasalle.edu)



Krystal Thach

Cherrybomb426 is a New Member of the G1 Subcluster of Siphoviridae Phage

Krystal Thach, Sarah Devine\*, Lina M Barrio, Taj Boynton, Andrew M Ciliberto, Courtney A Elliott, Ryan J Guckin, Jay T Jennings, Connor F Merrill, Keyla N Peralta, Christoff P Ras, Christina M Rice, Madeline K Rodahaver, Zachary T Salvatore, Vanessa Ulysse, Mi'Asia S Underwood, Zaire O Whaley, Molly L Wible, Jennifer Chau, Fabian A Bergman, Nancy L Jones, Jason Diaz

\* Smith College, Northampton MA

Antibiotic resistance is a growing crisis in managing bacterial infections. Bacteriophage are a promising alternative as they are uniquely specific to their host and can rapidly evolve in response to bacterial adaptation. Cherrybomb426 is a phage of the Siphoviridae family and infects *Mycobacterium smegmatis*. It was isolated from an enrichment sample by Sarah Devine in 2011. It is a temperate phage, which is different than the lytic phage, because the injected DNA will stay in the bacterium’s genome for an extended period of time, and eventually enter the lytic cycle. Students from La Salle University in the Integrated Science, Business, and Technology Department annotated Cherrybomb426. Programs used in this process included DNA Master, Phamerator, Starterator, Genemark, HHPred, and NCBI Blast. Cherrybomb426 is in the G cluster (G1 subcluster). Phamerator was used to compare the sequence of Cherrybomb426 with other similar phages. One phage in particular was LouisV14 which was found by Jordan Hagerty, another La Salle ISBT student. Cherrybomb426 consists of 60 genes and its genome has a length of 41456 base pairs, and an overhang sequence of CCCCATGGCAT. The GC content is 66.7%. Students worked together to tackle issues such as addressing reverse genes and start sites that were not initially agreed upon in the results from the auto-annotation. Our class determined that Cherrybomb426 has 3 reversed genes 32, 33, and 59. According to BLAST, Gene 32 codes for an integrase protein which produces an enzyme that permits the genetic material to be injected into the DNA of the host. Gene 33 codes for an immunity repressor protein that binds to a short specific DNA sequence and regulates the expression of a host gene. Gene 59’s authenticity was up for debate for multiple reasons. The gene was found in the reverse direction, which is uncommon but when it does occur, is often accompanied by other genes also going in the reverse direction. Gene 59 was not accompanied by any others and overlapped with the entirety of Gene 60, which is incredibly rare. Gene 59 was blasted on multiple programs and was compared with Phamerator to other phages, and it was finally decided that it was not a real gene. After rounds of BLASTing and comparing the sequence of Cherrybomb426 with similar bacteriophages in the G1 subcluster, we deleted gene 59 and added forward gene 61, which matches genes predicted in this region in other Phamily members. Genes 30 and 3 represented another challenge as Glimmer, GeneMark and Starterator had different start-site predictions. Our BLAST results supported the Starterator start as the best one. The majority of genes have only hypothetical functions; however, for some genes, functions have been established such as minor-tail protein, head to tail connector, major capsid protein, and terminase, among others. The annotation of Cherrybomb426 also includes a programmed translational frameshift.