DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

Texas Tech University

Lubbock TX

Corresponding Faculty Member: Allie Smith (allie.c.smith@ttu.edu)

Phage on the Range: Exploring the PrairieDogTown Virus

Christian DeLuna, Carson Bellew, Francesca Makilan, Melanie Baires, Olivia Kelly, Theoren Markusson, George Sander, Arya Sreenivas, Libertyann Ward-Polonski, Damian Al Khayatt, Abigail Frank, Sophia German-Kavle, Morgan Reed, Shreya Srivastava, Austen Rowell, Fahareen B Mosharraf, Allie C Smith, Lisa M Bono

Bacteriophages are a vast and diverse set of bacteria-infecting viruses that are largely still unknown, which creates a wide gap of knowledge of these extremely diverse viruses. The SEA-PHAGES program at Texas Tech University isolated the phage PrairieDogTown from wet soil on campus (33.58793 N, 101.87308 W) on the bacterial host Arthrobacter globiformis B-2979. The phage was named in honor of a city park of the same name dedicated to preserving the black-tailed prairie dog. We did this by obtaining a soil sample from the environment then filtered, purified, and amplified the phage, and it was incubated at 30°C for 24 hours. During the process of isolating PrairieDogTown we discovered it created clear plaque morphologies, the cluster life cycle is lytic, and it is morphologically siphoviridae using transmission electron microscopy. We extracted the DNA genome and sent it to Pittsburgh Bacteriophage Institute for sequencing. Once we received its genome sequence, which had an average coverage of 3431, we used several applications to annotate its genome. We found that PrairieDogTown is a member of the FO cluster, which includes 8 members. It has a genome length of 36,233 bp with a 3’ sticky overhang and a GC content of 68.8%. PrairieDogTown was annotated using DNAMaster, GeneMark, Phamerator, HHpred, PhagesDB, and Blastp. We are currently examining the 82 predicted genes to confirm the start and stop locations each gene and identify gene functions, using a combination of DNA Master, Blastp, and GeneMark. Additionally, we used Phamerator to compare our annotated calls with closely related phage within the cluster. While annotating PrairieDogTown, we have noticed it has on average an unusual number of reverse calls compared to its cluster members . After our annotation is reviewed for quality control, we plan on publishing a genome announcement for PrairieDogTown.