CONSIDER FOR TALK

2021 SEA Symposium Abstract

George Mason University

Fairfax VA

Corresponding Faculty Member: Anne Scherer (aschere2@gmu.edu)

Annotation and Analysis of Two Gordonia Phage Genomes, TuertoX and ChisanaKitsune

Mikias M Abebe, Jack Z Anderson, Rebecca Burris, Keidra E Carter, Maryam Durrani, Megan N Fetterly, Beccy A Fowler, Andrew A Friedman, Thy M Khuong, Chance A Konnor, Bonnie Madden, Michelle N Makula, Katrina McTigue, Austin R Morgan, Sarah I Qureshi, Mary Rainey, Gaston A Sanchez Quiero, Anne E Scherer, Lulu Singer, Sakshi M Thakar, Phuong Truong, Mustafa Zaeean

Here we describe two novel bacteriophages, TuertoX and ChisanaKitsune. ChisanaKitsune was isolated in Northern Virginia via the enrichment method using *Gordonia rubripertincta NRRL B-16540* as the host. TuertoX was adopted through the SEA-PHAGES genome exchange and was originally isolated by Armari Long at the University of Pittsburgh via direct plating. Both genomes were sequenced using Illumina sequencing at the Pittsburgh Bacteriophage Institute.

TuertoX (tuerto is Spanish for person with one eye) is a temperate phage that forms small clear plaques and is a *Gordonia* phage in subcluster CZ2. While the plaques were described as being clear, the presence of integrase and immunity repressor genes suggests that the phage is temperate. We have also identified the common core sequence used to integrate into the host genome during lysogeny. The TuertoX genome is 46,221 bp in length and has a GC content of 67%. It was isolated from a soil sample taken from the Jefferson Hills borough in the Greater Pittsburgh Region. TuertoX has 75 predicted gene products.

ChisanaKitsune (Japanese for tiny fox) is a cluster DQ *Gordonia* phage that was isolated from a garden located on the George Mason University campus in Fairfax, VA. ChisanaKitsune forms small clear plaques and is likely a lytic phage as it lacks an integrase gene and other genes associated with lysogeny. The genome is 88,657 bp long and has GC content of 60%. ChisanaKitsune has ~120 predicted gene products. Phylogenetic analysis of cluster DQ and related phages will be presented and underscores the remarkable diversity found in the *Gordonia* phages.

A summary of phages found in our phage discovery course (currently underway) will also be presented.