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2022 SEA Symposium Abstract

Kansas State University

Manhattan KS

Corresponding Faculty Member: Christopher Herren (cdherren@ksu.edu)



Amaya A Delano



Alexa G Heseltine

Flint Hills Phages - Characterization of the HicB-like antitoxin gene in CR2 subcluster actinobacteriophage Arti

Ashlyn S Bugbee, Amaya A Delano, Julie C Freijat, Alexa G Heseltine, Georgia R Kohlhorst, Joe S Moreno, Ashton B Reeves, Brandon N Rider, Tyler C Ringel, Holly A Ross, Amy J Schaulis, Claire M Schmidt, Ruth A Todd, Emily A Tolbert, Martha R Smith-Caldas, Christopher D Herren

Toxin-antitoxin (TA) systems are widely distributed among bacterial and archaeal species. They are composed of a stable toxin that induces stress responses to numerous environmental challenges and a labile antitoxin that is antagonistic to toxin function and restores normal cellular processes. Of the seven TA systems identified thus far, the type II TA system is the most studied and is characterized by a protein toxin and a protein antitoxin that directly binds the toxin. The type II HicAB system has a small monomeric HicA toxin protein and a multimeric HicB protein. HicB has two functional domains, one that directly binds to HicA and another DNA binding region that functions in transcriptional regulation. All currently identified CR2 subcluster *Gordonia terrae* actinobacteriophages (21 examples) contain a truncated *hicB*-like gene at the same location in the genome that potentially codes for the N-terminal domain of the HicB protein. While no other actinobacteriophages in the PhagesDB database have this shortened HicB-like antitoxin gene, there is a longer HicB-like antitoxin gene found in several subclusters (38 examples, including Xeno) that diverges in amino acid sequences from the gene product presented in Arti.