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University of Maine, Honors College

Orono ME

Corresponding Faculty Member: Melody Neely (melody.neely@maine.edu)

The Duality of Double Agent Agent47

Kirin Guay, Jacob A Bunszel, Andrew D Crisafulli, Ian M Plourde

Bacteriophage (phage), viruses that exclusively infect specific bacterial hosts, are the most numerous entity on the planet with an estimated 1031 viruses, covering all surfaces where bacteria are present. Phage therapy, using phage to treat lethal antibiotic-resistant infections, offers promising solutions to address challenges posed by antibiotic resistance. Phages have highly mosaic, diverse genomes that contain a wealth of biomedical potential, but only a small fraction of phages have been isolated and analyzed. Out of the 25,203 Actinobacteriophages identified in the PhagesDB data base that documents phages collected in the SEA-PHAGES Program, only 4,861 have annotated genomes (5.18%). Agent47 is a temperate mycobacteriophage that was isolated in Orono, Maine using the host M. smegmatis strain mc2155. The Agent47 phage genome has 61,143 bp, a GC-content of 65.6%, and encodes 95 putative genes. Agent47 is a cluster K5 phage, along with phages such as Kratio, InvictusManeo, and Collard. Through genome analysis, we have determined that Agent47 contains a diverse array of genes, including a serine integrase, a dpdA-like tRNA-guanine transglycosylase, a Brn-T toxin-antitoxin system, HNH endonucleases, and a tryptophan tRNA. However, over a third of the genes do not have a known function, therefore further research into the protein products is needed. As instances of antibiotic resistance increase, the research into phages like Agent47 may offer new knowledge for development of treatment plans when all other options have failed.