CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

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Identification of two Gordonia phages: SteamedHams and Suerte

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Here we describe two novel bacteriophages, SteamedHams and Suerte, isolated in Northern Virginia via the enrichment method using *Gordonia rubripertincta* NRRL B-16540 as the host. Both genomes were sequenced using Illumina sequencing at the Pittsburgh Bacteriophage Institute.  
  
SteamedHams (named for a famous Albany delicacy) is a lytic phage that forms small clear plaques and is a cluster CT *Gordonia* phage. The genome is 44,571 bp in length and has a GC content of 59.9%. It was isolated from a soil sample taken near a community garden in Alexandria, VA. SteamedHams has 63 predicted gene products.  
  
Suerte (“lucky” in Spanish) is a cluster CZ *Gordonia* phage that was isolated from a busy sidewalk on the George Mason University campus in Fairfax, VA. Suerte forms small clear plaques, though cluster CZ phages are typically temperate. The genome is 47,306 bp long and has GC content of 66.5%. Suerte has 76 predicted gene products including genes consistent with a temperate lifestyle such as a tyrosine integrase. We have also identified the common core sequence used to integrate into the host genome during lysogeny. Suerte has a potential translational frameshift in the tail assembly chaperone. To better identify the slippery site, we developed software, coded in Python, to help characterize the site of the translational frameshift in the tail assembly chaperone gene by searching for conserved slippery sequences across the CZ cluster.