CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Genome sequence of mycobacteriophage Hammy

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Mycobacteriophage Hammy was isolated from a soil sample collected in Slidell, LA, using *Mycobacterium smegmatis* mc2155 as a host. Electron microscopy revealed that Hammy has an isometric head of 75 nm and a flexible 200-nm long non-contractile tail. The phage was purified and amplified, and its DNA was isolated and sequenced using an Illumina MiSeq instrument. Single-end run reads were assembled to give a contig with 2,914-fold coverage. The 61,812-bp genome is flanked by cos ends with 11-base 3′ extensions of the sequence 5′-CTCGTAGGCAT. The G+C content of Hammy is 67.2% and is similar to that of *M. smegmatis*.  
  
Putative protein-coding genes in the Hammy genome were identified using Glimmer and GeneMark, followed by manual inspection and annotation revision. A total of 94 protein-coding genes were predicted, accounting for a 92.02% coding capacity of the genome. BLASTn analysis revealed that Hammy is a member of the K6 subcluster and closely related to mycobacteriophages DarthP, Cain, Krueger, and Ximenita.   
  
Hammy has features common to temperate phages including a tyrosine recombinase type integrase (gp42), an immunity repressor with the helix-turn-helix DNA binding motif (gp45) and a CRO protein (gp46). Other notable features include a capsid subunit (gp12), a capsid maturation protease (gp9), as well as the lysis system represented by the putative holin (gp31), lysin A (gp29), and lysin B (gp30). Like some other cluster K phages, Hammy encodes a WhiB regulator (gp53), a DnaQ-like exonuclease (gp58), a NrdH glutaredoxin (gp66), a RusA resolvase (gp69), an RNA ligase (gp83), and a tRNA-Trp(CCA) (gp4). Hammy has an *attP* that consists of a 47-bp core flanked by integrase-binding arm-type sites and is predicted to integrate into the *attB* site overlapping a tRNA-Lys gene (LJ00\_23480).