Complete Genome Sequences of HonestAbe, Anthony, and Taffo16, Three Cluster C *Bacillus cereus* Group Bacteriophages

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ABSTRACT Three cluster C *Myoviridae* bacteriophages that infect *Bacillus cereus* group bacteria were isolated from soil collected in the mid-Atlantic region using *B. thuringiensis* subsp. *kurstaki* as a host. *Bacillus* phages HonestAbe, Anthony, and Taffo16 each shared 90% or higher average nucleotide identities within their subclusters.

Interest in *Bacillus cereus* group bacteria stems from their ubiquity, complications in species identification when examined phenotypically and genetically (1), and the medical relevance of several members of the group, including *B. cereus sensu stricto*, an organism responsible for outbreaks of food poisoning, *B. anthracis*, the causative agent of anthrax, and the agriculturally important entomopathogen *B. thuringiensis* (2–4). Here, we present the genome sequences of three *Myoviridae* bacteriophages, *Bacillus* phages HonestAbe, Anthony, and Taffo16, isolated from soil samples collected from sites in Maryland and Washington, DC, using *B. thuringiensis* subsp. *kurstaki* strain ATCC 33679 as a host (Table 1). This work was completed as part of the SEA-PHAGES (5) and UMBC STEM-BUILD (6) programs.

Sequencing was performed by the Pittsburgh Bacteriophage Institute and the NC State Genomic Sciences Laboratory to approximately 100× coverage with the Illumina MiSeq platform, and the assembly was completed with Newbler and Consed (7). Genome annotation was completed using DNA Master (http://cobamide2.bio.pitt.edu). *Bacillus* phages HonestAbe, Anthony, and Taffo16 all have linear double-stranded DNA genomes that end in direct terminal repeats averaging 2,416 bp (standard deviation [SD], ±164 bp), as determined by examination of Illumina sequencing reads. The mean genome length was 161,784 bp (SD, ±2,203 bp), and the GC content was in the 37.8% to 38.7% range (Table 1). After removal of duplicates in the terminal repeats, the phage genomes had between 284 and 289 protein-coding genes, with an average start codon breakdown of 87% AUG, 6% GUG, and 8% UUG. *Bacillus* phage Anthony encodes seven tRNAs, and HonestAbe encodes three tRNAs; no tRNA genes were identified in the Taffo16 genome (Table 1).

Cluster assignment was based on nucleotide conservation, genomic synteny, and phylogenetic analysis, as described previously (8). Average nucleotide identity (ANI) was determined by OrthoANI (9). HonestAbe shares a mean of 89.7% (SD, ±3.7%) ANI with the other members of cluster C1 ($n = 33$). Anthony shares a mean of 96.6% (SD, ±1.0%) ANI with C2 phages ($n = 10$), and Taffo16 shares a mean of 92.8% (SD, ±5.9%) ANI with C3 phages ($n = 15$). See http://bacillus.phagesdb.org for details on members of clusters C1, C2, and C3.

Transmission electron microscopy showed HonestAbe, Anthony, and Taffo16 to have 158-nm, 219-nm, and 240-nm tails, as well as icosahedral capsids with diameters of 80 nm, 105 nm, and 117 nm, respectively. Both Anthony and Taffo16 were able to infect the nonpathogenic *B. thuringiensis* strain DSM 350 (10) as efficiently as the original host, as well as *B. cereus* strains FDA5 (ATCC 10702) and Gibson 971, but only at multiplicities of infection of 100- to 1,000-fold higher. Neither of them was able to infect or lyse *B. anthracis* delta Sterne.

TABLE 1 Properties of three *Bacillus* phages

Phage name	Genome size (bp)	Terminal repeat size (bp)	GC content (%)	No. of open reading frames	No. of RNAs	Origin	Cluster	GenBank accession no.
Anthony	159,983	2,422	38.0	286	7	Frederick, MD, USA	C2	MF498901
HonestAbe	161,129	2,576	38.7	289	3	Washington, DC, USA	C1	MG763894
Taffo16	164,241	2,249	37.8	284	0	Columbia, MD, USA	C3	MF765814

Accession number(s). The GenBank accession numbers for the genome sequences reported here are provided in Table 1.

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