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GENOME ANNOUNCEMENT

Escherichia coli O157:H7 Typing Phage V7 Is a T4-Like Virus

Andrew M. Kropinski,[a,b] Erika J. Lingohr,[a] Dianne M. Moyles,[b] Andrew Chibeu,[a] Amanda Mazzocco,[a] Kristyn Franklin,[a] Andre Villegas,[a] Rafiq Ahmed,[c] Yi-Min She,[d] and Roger P. Johnson[a]

Public Health Agency of Canada, Laboratory for Foodborne Zoonoses, Guelph, Ontario, Canada[a]; Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada[b]; Public Health Agency of Canada, National Microbiology Laboratory, Enterics Research Section, Winnipeg, Manitoba, Canada[c]; and Centre for Vaccine Evaluation, Biologics and Genetic Therapies Directorate, Health Canada, Ottawa, Ontario, Canada[d]

The complete genome sequence of the *Escherichia coli* O157:H7 typing phage V7 was determined. Its double-stranded DNA genome is 166,452 bp long, encoding 273 proteins and including 11 tRNAs. This virus belongs to the genus T4-like viruses within the subfamily *Tevenvirinae*, family *Myoviridae*.

Interest in bacteriophages has increased greatly of late because of their potential as typing, therapeutic, and decontaminating agents. We have tested several of the phages from the *Escherichia coli* O157:H7 typing set (1) in an effort to minimize the carriage of this pathogen by animals destined for the food chain (10). In this publication, we describe the host range and genomic and proteomic characteristics of phage V7.

When 10^8 PFU of this virus was spotted onto fresh lawns of the 12 most common phage types of *E. coli* O157:H7/NM, confluent or semiconfluent lysis resulted. When tested on members of the ECOR collection, V7 lysed 22 of the 72 strains.

The virus was negatively stained with 2% uranyl acetate, revealing an elongated head (108 by 85 nm) and a contractile tail of 110 by 19 nm in length. These values compare favorably with those of coliphage T4 (head is 111 by 78 nm; tail is 113 by 13 nm [5]). Tail fibers were observed lying parallel to the phage tail and in extended kinked conformation.

The complete genome sequence of V7 was determined using 454 DNA sequencing technology at the McGill University and Génome Québec Innovation Centre (Montreal, QC, Canada) and was annotated using AutoFACT (2) followed by manual curation in Kodon (Applied Maths, Austin, TX). A variety of online tools, including tRNAscan-SE, BLAST, Pfam, and TMHMM, were employed in the analysis (http://molbiol-tools.ca).

This virus has a circularly permuted genome of 166,452 bp encoding 273 proteins and including 11 tRNAs. Its proteins exhibited homology to those of T4-like phages such as T4 and RB32 of the genus T4-like viruses (http://www.ictvonline.org) within the newly recognized myoviral subfamily *Tevenvirinae* (5, 6). V7 shares primary protein sequence with 122 T4 proteins and 125 RB32 proteins (3, 12). In addition, it contains the full suite of enzymes necessary to synthesize glycosylated hydroxymethylcytosine, indicating both the advantage and problem associated with pyrosequencing—we can now sequence genomes which are not readily clonable, but we may possibly miss important biochemical features such as hypermodification (11). The latter would have been suspected from a mol% G+C discrepancy found on the basis of melting-temperature and CsCl buoyant-density analyses (9).

To confirm the annotation, this phage was subjected to whole-phage shotgun proteomics (4, 7), and these results along with the electron micrographs are presented as additional material (http://lfz.corefacility.ca/phage_v7/). One of the interesting features of V7, which it shares with enterobacterial phages AR1 (8), RB30 (GenBank accession number AAM52483), and ime09 (GenBank accession number AEK12435), is that the Hoc gene product is significantly longer than that of T4. No evidence exists that the 96-amino-acid insert corresponds to an intein, but it may actually correspond to an internal duplication.

Nucleotide sequence accession number. The nucleotide sequence of the genome of bacteriophage V7 has been deposited with GenBank under accession number HM997020.

ACKNOWLEDGMENT

We thank the Public Health Agency of Canada for financial support.

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Received 27 June 2012 **Accepted** 28 June 2012

Address correspondence to Roger P. Johnson, Roger.Johnson@phac-aspc.gc.ca.

doi:10.1128/JVI.01642-12