



Complete Genome Sequences of a Hantavirus Isolate from New York

 L. K. McMullan,^a C. G. Albariño,^a T. G. Ksiazek,^b S. T. Nichol,^a C. F. Spiropoulou^a

^aVirus Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

^bDepartment of Pathology, Galveston National Laboratory, University of Texas Medical Branch, Galveston, Texas, USA

ABSTRACT We report here the complete genome sequences for all three segments of the New York hantavirus (New York 1). This is the first reported L segment sequence for hantaviruses maintained in *Peromyscus* spp. endemic to the eastern United States and Canada.

In the order *Bunyvirales*, *Hantaviridae* have an RNA genome with three segments, S, M, and L, and infect specific rodent host species. While hantaviruses were known to cause a disease with hemorrhagic fever and renal symptoms, in 1993, hantavirus pulmonary syndrome (HPS) was found to be caused by Sin Nombre hantaviruses (SNV) in individuals exposed to infected deer mice, *Peromyscus maniculatus* (1). In 1994, a fatal HPS case was identified in Rhode Island from a 22-year-old who had traveled to New York. The sequence of the S segment from autopsy lung tissue revealed a genetically distinct hantavirus, sharing only 74% nucleotide identity with SNV, and it was named RI-1 (2–4) (GenBank accession number U09488).

To find the host of the SNV-like New York virus, rodents were trapped on Shelter Island, NY, and several captured *Peromyscus leucopus* mice were antibody positive for hantavirus (5). M segment sequences were determined from lungs of two positive mice, NY-1 and NY-2 (GenBank accession numbers U36802 and U36803) (6). Lung homogenate from one mouse (NY-1) was serially passaged in laboratory-bred *P. leucopus* mice. The S segment sequence was determined and named Shelter Island-1 (GenBank accession number U29210) (7). The only New York virus isolate, Shelter Island-1, was renamed NY-1 and later passaged on VeroE6 cells (8). In 1995, a second fatal HPS case was identified from a 25-year-old man in Long Island, NY, and the complete S segment, HNY-1, was sequenced (GenBank accession number U47135) (9).

The complete sequences for all three genome segments, S, M, and L, of the New York 1 isolate are reported here. New York 1 was received from U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID) and passaged once on VeroE6 cells (VSPB identification ID 808914). Total RNA was extracted from cell culture media using MagMAX viral isolation, and a 100-nucleotide (nt) single-end (SE) library constructed and sequenced using the Illumina HiSeq 2000 platform. Sequence reads were assembled with CLC Genomics Workbench version 10.1. The termini were amplified with 3'- and 5'-rapid amplification of cDNA ends (RACE) and sequenced using Sanger methods. The New York 1 isolate differs from the original *P. leucopus* lung M segment at 8 nucleotides and at 2 amino acids in the glycoprotein (GP): at position 447, the New York 1 isolate contains a leucine, while both rodent GPs have phenylalanine. The New York 1 isolate has serine at amino acid 11, which is identical to one mouse sequence but different from the other, which has phenylalanine.

The isolate presented here (New York 1), mouse NY-1 and NY-2, and human HNY-1 and RI-1 sequences are highly homologous and share 94% nucleotide identity. Hanta-

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virus species also found in New York are Prospect Hill and Seoul viruses, but they are maintained in different rodent hosts and differ by >50%. Other hantaviruses from *P. maniculatus* and *P. leucopus* found in the eastern United States are Monongahela (VA, WV, and PA), TN and NC viruses, and Blue River virus (10). These differ from New York 1 by 10%, 14%, and 20%, respectively. New York 1 and SNV can differ by 16% to 37%.

Hantaviruses are not easily isolated in cell culture, so the identification of a new hantavirus often relies on sequencing alone. A commonly used panhantavirus diagnostic assay, which identifies hantaviruses from all rodent hosts, analyzes conserved regions of the L segment (11). The complete genome of New York 1 will facilitate future identification of hantaviruses found in the eastern United States and Canada.

Accession number(s). The complete genome sequences for the 3 segments of the *Orthohantavirus* sp. strain New York 1 have been deposited in GenBank under the accession numbers [MG717391](#) (S segment), [MG717392](#) (M segment), and [MG717393](#) (L segment).

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