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GENOME SEQUENCES

Complete Genome Sequences of Monongahela Hantavirus from Pennsylvania, USA

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ABSTRACT Monongahela hantavirus was first identified in deer mice and was later found responsible for hantavirus pulmonary syndrome cases in Pennsylvania and West Virginia in the United States. Here, we report the complete sequences of Monongahela virus S, M, and L genomic segments obtained from a fatal clinical case reported in 1997.

Several members of the family *Hantaviridae* are responsible for disease in humans (1, 2). In particular, Old World hantaviruses such as Hantaan, Dobrava, Seoul, and Puumala viruses are the causative agents of a severe-to-mild disease called hemorrhagic fever with renal syndrome (HFRS). Seoul virus is an exception in that it can be found worldwide due to the global distribution of its rat host and was recently associated with HFRS cases in the United States (3, 4).

Moreover, after the identification of Sin Nombre virus (SNV) as the causative agent of hantavirus pulmonary syndrome (HPS) in the southwestern United States (5, 6), several other hantaviruses, such as Andes virus, Bayou virus, Black Creek Canal virus, New York virus (NYV), and Monongahela virus (MGLV), have been associated with HPS in different parts of the Americas (7, 8).

In particular, MGLV was first identified in 3 archived samples of Cloudland deer mice (*Peromyscus maniculatus nubiterrae*) captured in West Virginia in 1985 (9). The sequences of the S and M genomic segments obtained from 3 deer mice (designated as MGLV-1, -2, and -3) are highly similar (~83% to 85% identity) to the previously identified SNV and NYV.

In 1997, MGLV was associated with 2 fatal HPS cases in Pennsylvania (10). Partial sequences of S and M segments obtained from one of the patients shared ~96% identity with MGLV-1 and MGLV-2. In 2004, 2 more HPS cases (one of them fatal) were associated with MGLV in West Virginia (11). Partial sequences of the S segment from the deceased patient shared ~98% identity with MGLV-1.

Here, we report the complete sequences of the 3 genomic segments (S, M, and L) from MGLV virus obtained by next-generation sequencing (NGS). Briefly, total RNA was extracted from blood and serum samples of a patient who succumbed to infection in 1997 (10). rRNA was removed using the NEBNext rRNA depletion kit (New England BioLabs), and cDNA libraries were constructed using the TruSeq stranded mRNA kit (Illumina), following a modified version of the manufacturer's protocol that skipped steps necessary for mRNA purification. Sequencing was performed using paired-end 2 × 150-bp chemistry on an Illumina MiniSeq instrument. NGS data, including read mapping, contig assembly, and sequence alignments, were analyzed using CLC Genomics Workbench version 9.1. RNA termini were amplified by rapid amplification of cDNA ends (RACE) and sequenced using standard Sanger methods. Specific regions of each RNA segment were also confirmed by standard reverse transcriptase PCR (RT-PCR). Sequence analysis of MGLV genomic RNA segments and coded proteins are shown in Table 1.

Consistent with previous reports (9–11), the MGLV sequences we obtained are

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TABLE 1 Comparison of MGLV with NYV and SNV

	% identity with:					
	MGLV RNA			MGLV protein		
Virus	L (6,562 nt)	M (3,671 nt)	S (2,081 nt)	L (2,154 aa)	GP (1,141 aa)	NP (429 aa)
NYV	82	81	78	96	96	96
SNV	81	82	77	96	96	93

highly similar to NYV and SNV, the closest related hantaviruses (Table 1). Molecular identification of hantaviruses is routinely performed by our diagnostic laboratory and others using a generic RT-PCR assay that targets a conserved region in the L segment, followed by sequencing of the amplicons (4). The availability of the complete MGLV genome will facilitate our continuous surveillance efforts on hantavirus activity in the United States (7, 8, 12) and will allow future identification of MGLV and its differentiation from other hantaviruses associated with HPS cases in the eastern United States (13, 14).

Data availability. These MGLV genome sequences were deposited in GenBank under the accession numbers MH539865 (L), MH539866 (M), and MH539867 (S).

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