

Complete Genome Sequence of an Amur Virus Isolated from *Apodemus peninsulae* in Northeastern China

Li-Si Yao,^a Hui Zhao,^b Li-Jun Shao,^c Yong-Xian Liu,^c Xiao-Long Zhang,^a Jing Wang,^a Yong-Qiang Deng,^b Xiao-Feng Li,^b Kong-Xin Hu,^a Cheng-Feng Qin,^b and Bao-Liang Xu^a

Institute of Health, Chinese Academy of Inspection and Quarantine, Beijing, China^a; State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing, China^b; and Jilin Entry-Exit Inspection and Quarantine Bureau, Changchun, China^c

Amur virus was recently identified as the causative agent of hemorrhagic fever with renal syndrome. Here we report the complete genome sequence of an Amur virus isolated from *Apodemus peninsulae* in Northeastern China. The sequence information provided here is critical for the molecular epidemiology and evolution of Amur virus in China.

Hantaviruses within the genus *Hantavirus* of the family *Bunyaviridae* cause hemorrhagic fever with renal syndrome (HFRS) in Eurasia and hantavirus pulmonary syndrome (HPS) in the Americas (3). The viruses are commonly maintained within specific rodent hosts, and human infections occasionally occur through inhalation of aerosolized excreta from infected animals. Recently, Amur virus (AMRV) was identified as one of the causative agents of HFRS in Far East Russia and East Asia (4, 6, 10), together with Hantaan, Seoul, Dobrava-Belgrade, and Puumala viruses (1, 2). HFRS is endemic to many provinces in mainland China (7), and AMRV has been reported in China (2, 9). However, no complete genome sequence of Chinese AMRV has ever been reported.

Here we report the complete genome of the Chinese AMRV strain ApJLCB2011. The virus was isolated from the lung tissue of *Apodemus peninsulae* in Changbai county, Jilin province, China. Total RNA was extracted from virus-infected Vero E6 cells with a QIAamp viral RNA minikit. cDNA synthesis and amplification of complete S, L, and M genomic segments by PCR analysis were carried out as previously described (5). The 5' and 3' termini of each segment were determined by using rapid amplification of cDNA ends. All sequencing was carried out using an ABI 3730 Sanger-based genetic analyzer, and one contig containing a high-quality trace file was assembled using DNASTar version 7.0.

The genome of AMRV strain ApJLCB2011 composes three negative-stranded RNA segments, referred to as S, M, and L. The S segment is 1,695 nucleotides (nt) in length, containing a 1,290-nt open reading frame (ORF) which encodes the nucleocapsid protein. The M segment of 3,595 nt contains a 3,408-nt ORF encoding the glycoprotein precursor. The L segment of 6,477 nt contains a 6,456-nt ORF, which encodes viral RNA-dependent RNA polymerase. The nucleotide sequences at the 5' and 3' termini of each segment are complementary (8). Phylogenetic analysis based on each individual genomic segment was performed by using MEGA 5.05 with the neighbor-joining method, respectively, and the results demonstrated that ApJLCB2011 belongs to AMRV or Soochong virus entities (1). Sequence analysis of S, L, and M segments showed that ApJLCB2011 has 91.1%, 89.4%, and 87.6% nucleotide identities to the AMRV strain AP209 isolated in Russia, respectively. The deduced amino acids (aa) of the G2 regions are methionine at aa 932 and aspartic acid at aa 967, which has been indicated as the signature aa for AMRV (5). Recombination ana-

lyses between newly isolated AMRV and other hantaviruses were performed with SimPlot software, and no obvious recombinant event was detected.

HFRS remains endemic in China and many other countries. The etiological agents in hosts and patients continue evolving, and further field and laboratory investigation should be warranted. The sequence information provided here is critical for the molecular epidemiology and phylogenetic evolution of AMRV in China.

Nucleotide sequence accession numbers. The nucleotide sequence of the genome of AMRV strain ApJLCB2011 has been deposited within the GenBank sequence database under accession numbers JX473002 (L segment), JX473003 (M segment), and JX473004 (S segment).

ACKNOWLEDGMENTS

This work was supported, in part, by the Fundamental Research Funds for the Public Research Institutes (no. 2010jk012) and the Science and Technology Planned Project of General Administration of Quality Supervision (no. 2011K149).

REFERENCES

- Jiang JF, Zhang WY, Wu XM, Zhang PH, Cao WC. 2007. Soochong virus and Amur virus might be the same entities of hantavirus. *J. Med. Virol.* 79:1792–1795.
- Jiang JF, et al. 2007. A new Hantaan-like virus in rodents (*Apodemus peninsulae*) from Northeastern China. *Virus Res.* 130:292–295.
- Jonsson CB, Figueiredo LT, Vapalahti O. 2010. A global perspective on hantavirus ecology, epidemiology, and disease. *Clin. Microbiol. Rev.* 23:412–441.
- Kariwa H, et al. 2012. Isolation and characterization of hantaviruses in Far East Russia and etiology of hemorrhagic fever with renal syndrome in the region. *Am. J. Trop. Med. Hyg.* 86:545–553.
- Lokugamage K, et al. 2002. Genetic characterization of hantaviruses transmitted by the Korean field mouse (*Apodemus peninsulae*), Far East Russia. *Emerg. Infect. Dis.* 8:768–776.

Received 20 September 2012 Accepted 20 September 2012

Address correspondence to Bao-Liang Xu, xubl@caiq.gov.cn.

L.-S.Y. and H.Z. contributed equally to this work.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JVI.02586-12

6. Lokugamage K, et al. 2004. Genetic and antigenic characterization of the Amur virus associated with hemorrhagic fever with renal syndrome. *Virus Res.* **101**:127–134.
7. Ma C, et al. 2012. Hantaviruses in rodents and humans, Xi'an, PR China. *J. Gen. Virol.* **93**:2227–2236.
8. Mir MA. 2010. Hantaviruses. *Clin. Lab. Med.* **30**:67–91.
9. Wang H, et al. 2000. Genetic diversity of hantaviruses isolated in china and characterization of novel hantaviruses isolated from *Niviventer confucianus* and *Rattus rattus*. *Virology* **278**:332–345.
10. Yashina LN, et al. 2000. Genetic diversity of hantaviruses associated with hemorrhagic fever with renal syndrome in the far east of Russia. *Virus Res.* **70**:31–44.