Seoul virus (genus Hantavirus; family Bunyaviridae) is an emerging pathogen associated with cases of acute kidney injury in several countries across the globe. We report here the whole-genome sequence of the Tchoupitoulas strain of Seoul virus isolated in New Orleans, LA.

Hantaviruses are members of the Bunyaviridae family; as such, they are enveloped negative-sense single-stranded RNA viruses with a trisegmented genome. The large (L) segment encodes a viral RNA polymerase, the medium (M) segment encodes a glycoprotein precursor, and the small (S) segment encodes the nucleocapsid protein (1). Seoul virus (SEOV) is a globally spread hantavirus linked with the worldwide presence of its reservoir, *Rattus norvegicus* (brown rat) (2). SEOV presents a significant public health risk as a cause of hemorrhagic fever with renal syndrome, which is associated with acute kidney injury (AKI) (2). Six cases of hantavirus-associated AKI were diagnosed in the United Kingdom between 2012 and 2014 (3). Within Europe, SEOV has recently been isolated from brown rats in Yorkshire, Wales, and Sweden, and human SEOV infections were identified in Wales and France (4–7). Despite their worldwide spread, SEOV strains are closely related and have low genetic diversity (8). SEOV strain Tchoupitoulas (TCH) was isolated from the pancreas of a brown rat trapped near the Mississippi River in New Orleans, LA (9). Currently, only the S segment sequence has been published (10). Here, we report the first full-genome sequence of TCH.

The virus was isolated in 1984, propagated in Vero E6 cells by the staff of the Rare and Imported Pathogens Laboratory in 1992, and deposited into the National Collection of Pathogenic Viruses in 2001, under catalog no. 0107221v. Viral RNA was extracted using the QIAamp viral RNA minikit (Qiagen), following the addition of 10 ng/μl GenElute-linear polyacrylamide (Sigma-Aldrich). The sample was digested with Turbo DNase I (Thermo Fisher Scientific) and purified using the RNA Clean & Concentration kit (Zymo). Single-primer isothermal linear amplification (SPIA) cDNA was prepared for sequencing, according to the Illumina Nextera XT protocol, and the 2 × 150-bp paired-end library was run on a MiSeq (Illumina).

Reads were quality trimmed to a minimum score of Q30 across the read. BWA (version 0.7.5) (11) was used to map 1,797,246 reads to the SEOV strain 80-39 reference genome (NCBI GenBank accession numbers NC_005238.1, NC_005237.1, and NC_005236.1), with 99.9% L, M, and S genome coverage, and the TCH S segment reference (NCBI GenBank accession no. AF329589), with 99.9% genome coverage. A consensus genome sequence was produced at a minimum depth of five reads. All analyses were performed using a local instance of the Galaxy Project (12–14). The previously reported TCH S segment contained an additional 16 bp close to the 3′ terminus that is not seen in the 3′ regions of other SEOV sequences (10). Mapping of the reads from this study to the TCH S segment reference revealed no support for the additional 16 bp.

**Nucleotide sequence accession numbers.** The whole-genome sequences have been deposited in GenBank under the accession numbers KU204958 to KU204960. This paper describes the second version of the sequences.

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**REFERENCES**

1. Krüger DH, Schönrich G, Klempe B. 2011. Human pathogenic hantaviruses and prevention of infection. Hum Vaccin 7:683–693. http://dx.doi.org/10.4161/hv.7.6.15197.

2. Jonsson CB, Figueredo LTM, Vapalahti O. 2010. A global perspective on hantavirus ecology, epidemiology, and disease. Clin Microbiol Rev 23: 412–441. http://dx.doi.org/10.1128/CMR.00062-09.

3. Duggan J, Close R, McCann L, McCarthy N, Mannes T, Walsh A, Keys M, Wright D, Charlet A, Brooks T. 2010. Hantavirus infection in people with contact with wild and pet rats in England—preliminary results of a sero-surveillance study. PHE publications gateway:2014321. Public Health England, London, United Kingdom. https://www.gov.uk/government/publications/hantavirus-infection-in-people-sero-surveillance-study-in-england.

4. Jameson LJ, Logue CH, Atkinson B, Baker N, Galbraith SE, Carroll MW, Brooks T, Hewson R. 2013. The continued emergence of hantaviruses: isolation of a Seoul virus implicated in human disease,
5. Jameson LJ, Taori SK, Atkinson B, Levick P, Featherstone CA, van der Burgt G, McCarthy N, Hart J, Osbourne JC, Walsh AL, Brooks TJ, Hewson R. 2013. Pet rats as a source of hantavirus in England and Wales. Euro Surveill 18:pii=20415. http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20415.

6. Lundkvist A, Verner-Carlsson J, Plyusnina A, Forslund L, Feinstein R, Plyusnin A. 2013. Pet rat harbouring Seoul hantavirus in Sweden. Euro Surveill 18:pii=20521. http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20521.

7. Macé G, Feyeux C, Mollard N, Chantegret C, Audia S, Rebibou JM, Spagnolo G, Bour JB, Denoyel GA, Sagot P, Reynes JM. 2013. Severe Seoul hantavirus infection in a pregnant woman, France, October 2012. Euro Surveill 18:pii=20464. http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20464.

8. Tsai TF, Bauer SP, Sasso DR, Whitfield SG, McCormick JB, Caraway TC, McFarland L, Bradford H, Kurata T. 1985. Serological and virological evidence of a Hantaan virus-related enzootic in the United States. J Infect Dis 152:126–136. http://dx.doi.org/10.1093/infdis/152.1.126.

9. Shi X, McCaughey C, Elliott RM. 2003. Genetic characterisation of a hantavirus isolated from a laboratory-acquired infection. J Med Virol 71:105–109. http://dx.doi.org/10.1002/jmv.10446.

10. Lin XD, Guo WP, Wang W, Zou Y, Hao ZY, Zhou DJ, Dong X, Qu YG, Li MH, Tian HF, Wen JF, Plyusnin A, Xu J, Zhang YZ. 2012. Migration of Norway rats resulted in the worldwide distribution of Seoul hantavirus today. J Virol 86:972–981. http://dx.doi.org/10.1128/JVI.00725-11.

11. Li H, Durbin R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 25:1754–1760. http://dx.doi.org/10.1093/bioinformatics/btp324.

12. Goecks J, Nekrutenko A, Taylor J, Galaxy Team. 2010. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. Genome Biol 11:R86. http://dx.doi.org/10.1186/gb-2010-11-8-r86.

13. Giardine B, Riemer C, Hardison RC, Buhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, Taylor J, Miller W, Kent WJ, Nekrutenko A. 2005. Galaxy: a platform for interactive large-scale genome analysis. Genome Res 15:1451–1455. http://dx.doi.org/10.1101/gr.4086505.

14. Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. 2010. Galaxy: a Web-based genome analysis tool for experimentalists. Curr Protoc Mol Biol Chapter 19:Unit 19.10.1–Unit 19.10.21. http://dx.doi.org/10.1002/0471142727.mb1910s89.