Genome Sequences of Rhinovirus Genotype C56 Detected in Three Patients with Acute Respiratory Illness, California, 2016 to 2017

Chao-Yang Pan, Shigeo Yagi, Tasha Padilla, Terry Fei Fan Ng, Rachel L. Marine, W. Allan Nix, Debra A. Wadford

ABSTRACT

We report here two genome sequences of a newly designated rhinovirus genotype, RV-C56, which were obtained from respiratory specimens of three patients with acute respiratory illness in 2016 and 2017. To our knowledge, these sequences represent the first near-complete genomes for RV-C56 strains.

Rhinovirus C (RV-C) is one of three rhinovirus species of the Enterovirus (EV) genus in the Picornaviridae family of nonenveloped, single-stranded, positive-sense RNA viruses. RV-C was first described in 2006 from patients with influenza-like illness (1, 2). RV-C has been associated with more severe respiratory illness than have RV-A and RV-B (3) and is also distinct from RV-A and RV-B in that RV-C is not culturable by conventional cell culture methods (4, 5).

The California Department of Public Health Viral and Rickettsial Disease Laboratory performs diagnostic testing for many respiratory viruses, including RVs and EVs, using real-time reverse transcription-PCR (RT-PCR) assays adapted from the U.S. Centers for Disease Control and Prevention protocols (6). Recently, we detected an increasing number of specimens that tested positive for both EV and RV by these assays. Subsequent viral protein 1 (VP1) and genomic investigations identified RV-C from some specimens, including a recent study of RV-C47 (7).

We generated complete protein-coding sequences (CDSs) of three RV-C strains. Nasopharyngeal swab specimens were clarified by centrifugation, 0.4-/H9262 filtration, and nuclease treatment prior to extraction using the NucliSENS easyMAG system (bioMérieux, Durham, NC, USA). Extracted RNA was treated with DNase, followed by random RT and subsequent PCR (7, 8). Libraries were prepared using a Nextera XT kit (Illumina, San Diego, CA, USA) and sequenced (300-cycle paired-end run) on the MiSeq platform (Illumina). The next-generation sequencing (NGS) data were analyzed by an in-house NGS pipeline performing read quality control, de novo assembly, and BLAST analysis (9). Final consensus genomes were inspected and annotated using Geneious version 11. Average read coverage ranged from 352- to 1,863-fold for the three RV-C genomes.

The genome sequences were confirmed by the Picornaviridae Study Group of the International Committee for the Taxonomy ofViruses (10) as RV-C56. In one instance, twin 1-year-old siblings with a noticeable cough but no fever yielded nearly identical RV-C56 genomes, except for two synonymous nucleotide changes in VP3. We submitted one of the two sequences to GenBank as RV-C56 strain USA/2016/CA-RGDS-1002. We identified a second RV-C56 strain, USA/2017/CA-RGDS-1003, in a 31-year-old female with low-grade fever, shortness of breath, and productive cough who had returned from overseas travel approximately 1 day prior to the onset of the illness. The genome of RV-C56 strain USA/2017/CA-RGDS-1003 shared 99.3% nucleotide identity (NI) to strain USA/2016/CA-RGDS-1002.
No complete CDS of RV-C56 existed prior to this report. Both California RV-C56 strains share 96% NI to a partial capsid sequence reported from Japan in 2014 (GenBank accession number LC004772) (11). Both California RV-C56 strains shared 85% NI and 91% amino acid identity (AI) with VP1 genes from other RV-C genotypes. Compared to the closest full genomes of other RV-C types, the RV-C56 strain USA/2016/CA-RGDS-1002 sequence is missing 26 nucleotides (nt) in the 5’ end and 11 nt in the 3’ end. The rhinovirus polyprotein can be divided into one structural (P1-capsid) and two nonstructural (P2 and P3) regions. The polyprotein regions of the two RV-C56 genomes reported here all share 85% NI (P1, P2, and P3) and 92% AI (P1), 93% AI (P2), and 92% AI (P3) with other RV-C genotypes.

Data availability. The genome sequences of RV-C56 strains USA/2016/CA-RGDS-1002 and USA/2017/CA-RGDS-1003 have been deposited in GenBank under the accession numbers MG950178 and MG950179, respectively.

ACKNOWLEDGMENTS

The contributions of the California Department of Public Health Viral and Rickettsial Disease Laboratory were supported in part by the Epidemiology and Laboratory Capacity for Infectious Diseases Cooperative Agreement number 6 NU50CK000410 from the U.S. Centers for Disease Control and Prevention. This work was partly funded by federal appropriations to the Centers for Disease Control and Prevention through the Advanced Molecular Detection Initiative line item.

The findings and conclusions in this report are those of the author(s) and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

REFERENCES

1. Arden KE, McErlean P, Nissen MD, Sloots TP, Mackay IM. 2006. Frequent detection of human rhinoviruses, paramyxoviruses, coronaviruses, and bocavirus during acute respiratory tract infections. J Med Virol 78:1232–1240. https://doi.org/10.1002/jmv.20689.
2. Lamson D, Renwick N, Kapoor V, Liu Z, Palacios G, Ju J, Dean A, St George K, Briese T, Lipkin W. 2006. MassTag polymerase-chain-reaction detection of respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like illness in New York state during 2004–2005. J Infect Dis 194:1398–1402. https://doi.org/10.1086/508551.
3. Louie JK, Roy-Burman A, Guardia-Labar L, Boston EJ, Kiang D, Padilla T, Yagi S, Messenger S, Glaser CA, Schnurr DP. 2009. Rhinovirus associated with severe lower respiratory tract infections in children. Pediatr Infect Dis J 28:337–339. https://doi.org/10.1097/INF.0b013e31818ffc1b.
4. Lee W-M, Kiesner C, Pappas T, Lee I, Grindle K, Jartti T, Jakiela B, Lemanske RF, Jr., Shult PA, Gern JE. 2007. A diverse group of previously unrecognized human rhinoviruses are common causes of respiratory illnesses in infants. PLoS One 2:e966. https://doi.org/10.1371/journal.pone.0000966.
5. McIntyre CL, Knowles NJ, Simmonds P. 2013. Proposals for the classification of human rhinovirus species A, B and C into genotypically assigned types. J Gen Virol 94:1791–1806. https://doi.org/10.1099/vir.0.053686-0.
6. Shahkarami M, Yen C, Glaser C, Xia D, Watt J, Wadford DA. 2015. Laboratory testing for Middle East respiratory syndrome coronavirus, California, USA, 2013–2014. Emerg Infect Dis 21:1664–1666. https://doi.org/10.3201/eid2109.150476.
7. Pan C-Y, Padilla T, Yagi S, Lewis LS, Ng TFF, Marine RL, Nix WA, Wadford DA. 2018. Whole-genome sequence of human rhinovirus C47, isolated from an adult respiratory illness outbreak in Butte County, California, 2017. Genome Announc 6(5):e01579-17. https://doi.org/10.1128/genomeA.01579-17.
8. Ng TFF, Marine R, Wang C, Simmonds P, Kapusinszky B, Bodhidatta L, Oderinde BS, Wommack KE, Delwart E. 2012. High variety of known and new RNA and DNA viruses of diverse origins in untreated sewage. J Virol 86:12161–12175. https://doi.org/10.1128/JVI.00869-12.
9. Montmayeur AM, Ng TFF, Schmidt A, Zhao K, Magana L, Iber J, Castro CJ, Chen Q, Henderson E, Ramos E, Shaw J, Tatusov RL, Dybdahl-Sissoko N, Endegue-Zanga MC, Adeniji JA, Oberste MS, Burns CC. 2017. High-throughput next-generation sequencing of polioviruses. J Clin Microbiol 55:606 – 615. https://doi.org/10.1128/JCM.02121-16.
10. Picornaviridae Study Group. Rhinovirus C. http://www.picornastudygroup.com/types/enterovirus/hrv-c.htm. Accessed 26 July 2018.
11. Kuroda M, Niwa S, Sekizuka T, Tsukagoshi H, Yokoyama M, Ryo A, Sato H, Kyotou N, Noda M, Kozawa K, Shirabe K, Kusaka T, Shimojo N, Hasegawa S, Sugai K, Obuchi M, Tashiro M, Oishi K, Ishii H, Kimura H. 2015. Molecular evolution of the VP1, VP2, and VP3 genes in human rhinovirus species C. Sci Rep 5:8185. https://doi.org/10.1038/srep08185.