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VIRUSES

Whole-Genome Sequence of Human Rhinovirus C47, Isolated from an Adult Respiratory Illness Outbreak in Butte County, California, 2017

Chao-Yang Pan,[a] Tasha Padilla,[a] Shigeo Yagi,[a] Linda S. Lewis,[b] Terry Fei Fan Ng,[c] Rachel L. Marine,[c] William Allan Nix,[c] Debra A. Wadford[a]

[a]Viral and Rickettsial Disease Laboratory, California Department of Public Health, Richmond, California, USA
[b]Community Health & Sciences, Butte County Public Health Department, Oroville, California, USA
[c]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

ABSTRACT Here, we report the full coding sequence of rhinovirus C47 (RV-C47), obtained from a patient respiratory sample collected during an acute respiratory illness investigation in Butte County, California, in January 2017. This is the first whole-genome sequence of RV-C47 to be reported.

Rhinovirus C (RV-C) is a 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 in patients with influenza-like illness, defined as fever of >38°C with cough and/or pharyngitis (1, 2). RV-C has been associated with more severe respiratory illness (3) than have RV-A and RV-B species and is also distinct from RV-A and RV-B in not being culturable by conventional cell culture methods (4).

In January 2017, an acute respiratory illness outbreak occurred at a long-term care facility in Butte County, California, affecting 12 residents and 4 staff members and causing symptoms, including fever, cough, malaise, and congestion. Three patients were diagnosed with pneumonia, with one requiring hospitalization. Nasopharyngeal (NP) samples from five of the outbreak patients were submitted to the California Department of Public Health Viral and Rickettsial Disease Laboratory (VRDL) for virus testing by real-time PCR. VRDL detected RV-C in four of the five patients by methods previously described (5). No respiratory virus was detected from the fifth patient's specimen. We used a next-generation sequencing (NGS) approach to characterize the RV-C isolate from a single patient. Briefly, the NP sample was clarified, filtered through a 0.45-μM column, and nuclease treated before nucleic acid extraction using the NucliSENS EasyMAG system (bioMérieux, Inc., Durham, NC). Extracted nucleic acid was treated with DNase to remove DNA. Reverse-transcription PCR, cDNA PCR, and PCR were performed using the sequence-independent single-primer amplification method (6). Nextera XT libraries were prepared and sequenced on an Illumina MiSeq 300-cycle paired-end run. Sequence data were processed through a bioinformatics pipeline modified from a previous study (7). The complete genome sequence of RV-C was obtained from the specimen and typed as RV-C47 with the strain designation CA-RGDS-1001.

Based on the VP1 region, CA-RGDS-1001 shares 96% nucleotide identity (NI) with the only other available RV-C47 VP1 sequence (PNG7254-3947) (GenBank accession number JF519760); CA-RGDS-1001 has <80% NI with VP1s from other RV-C genotypes. The rhinovirus genome can be divided into one structural (P1-capsid) and two nonstructural (P2 and P3) regions. The P1, P2, and P3 regions of CA-RGDS-1001 share 67 to 79%, 65 to 79%, and 65 to 80% NI with other RV-C genotypes, respectively.

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Address correspondence to Debra A. Wadford, debra.wadford@cdph.ca.gov.

Accession number(s). The genome sequence of this RV-C47 isolate (CA-RGDS-1001) has been deposited in GenBank under accession number MF806525.

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