Complete Genome Sequences of Two Human Adenovirus Type 55 Isolates from South Korea and the United States

J. M. Hughes, a Yu Yang, b Anthony C. Fries, c Irina Maljkovic Berry, a Adam R. Pollio, a Christian K. Fung, a Nicos Karasavvas, a Richard G. Jarman, d Robert A. Kushner, e Adriana E. Kajon, a Natalie D. Collins, b Elizabeth Macias, b Jun Hanga

a Walter Reed Army Institute of Research, Silver Spring, Maryland, USA
b U.S. Air Force School of Aerospace Medicine, Wright-Patterson AFB, Ohio, USA
c Lovelace Respiratory Research Institute, Albuquerque, New Mexico, USA
d Walter Reed National Military Medical Center, Bethesda, Maryland, USA

ABSTRACT
Here, we report two complete genome sequences of human adenovirus 55 (HAdV-55) isolates, from a patient in Pennsylvania in 2006 and a U.S. military member in South Korea in 2019. The findings demonstrate the continued global transmission of HAdV-55 viruses in both military and civilian populations.

Adenoviruses (family Adenoviridae), nonenveloped double-stranded DNA viruses, are classified into five genera. Human adenovirus (HAdV) (genus Mastadenovirus) contains more than 70 recognized HAdV types (1, 2). HAdVs are associated with mostly mild, occasionally fatal, acute respiratory infections and can also cause infections in the eyes, intestines, urinary tract, and nervous system. The disease severity is dependent on the type of virus and the host immune status (1, 3–6). Human adenovirus type 55 (HAdV-55) is an emerging adenovirus that evolved from an intertypic genetic recombination between HAdV-11 and HAdV-14 (7–15). HAdV-55 is considered a significant threat to respiratory health for both civilian and military populations.

Here, we report two new HAdV-55 isolates and their complete genome sequences. Isolate CHOP6887 (GenBank accession number MT513753), from a pediatric patient in Pennsylvania in 2006, was first isolated from a nasopharyngeal swab at the Lovelace Respiratory Research Institute (16) and then was plaque purified at the Walter Reed Army Institute of Research. Isolate 21962_S4TF53 (MW053454), which originated from a U.S. military member stationed in South Korea in 2019, was isolated at the U.S. Air Force School of Aerospace Medicine (16).

The genomic DNA samples purified as previously described (16) from viral culture supernatants of CHOP6887 and 21962_S4TF53 were sequenced utilizing next-generation sequencing (NGS) technology with a QIAseq FX DNA library kit (Qiagen) using a QIAseq FX 96-plex adaptor, fragmentation for 5 min at 32°C, and ligation for 15 min at 20°C and a MiSeq system and reagent kit v3 (600-cycle paired ends) (Illumina). FASTQ data were preprocessed using the Trimmomatic 0.33 paired-end mode application (17), followed by reference mapping sequence assembly using Geneious R9 (Biomatters Ltd.). Phylogenetic analysis was conducted using PhyML in MEGA7 (http://www.megasoftware.net) with a substitution model according to the jModelTest2 (GTR + G + I). Node confidence values were estimated using the approximate likelihood ratio test Shimodaira-Hasegawa (aLRT-SH).

The complete genome sequences of strains CHOP6887 and 21962_S4TF53 are both 34,781 nucleotides long with 48.8% G+C content (Table 1). CHOP6887 (GenBank accession number MT513753) is phylogenetically distinct from the two

Citation

Editor
Kenneth M. Stedman, Portland State University

This is a work of the U.S. Government and is not subject to copyright protection in the United States. Foreign copyrights may apply.

Address correspondence to Jun Hang, jun.hang.civ@mail.mil.

Received 25 November 2020
Accepted 14 January 2021
Published 4 February 2021
known U.S. strains (MN654394 and MN654392) (16) (Fig. 1). The sequence is identical to that of strain ARG/ak36_AdV11a/2005 (JX423384) from Argentina, except for a 13-nucleotide deletion in an untranslated region of the genome at position 1461, two synonymous nucleotide differences, and one amino acid difference at residue 39 of the E3 14.3-kDa protein (nucleotide position 27566), which is a Pro for CHOP6887 and a Leu for ARG/ak36_AdV11a/2005. It represents the most recent HAdV-55 identification in the United States since 1997 (18) and the first report of an infection caused by an HAdV-55 strain that may have originated outside the United States. The sequence of isolate 21962_S4TF53 (MW053454) is identical to that of South Korean strain AFMC 16-0011 (KX494979), collected in 2016, except for one synonymous nucleotide difference, which suggests continued transmission of a similar strain in South Korea.

These two isolates are unique new additions to existing genomic and epidemiologic knowledge of HAdV-55 from our recent work and other studies (16). Human adenovirus infections are commonly tested in clinical and surveillance labs without being specifically typed. More comprehensive genomic research is warranted to detect emerging HAdV infections and achieve true understandings of the genetic diversity and genomic evolution.

**Data availability.** The complete genome sequences for HAdV-55 isolates CHOP6887 and 21962_S4TF53 were deposited in GenBank under the accession numbers MT513753 and MW053454, respectively. The raw read data were deposited under BioProject PRJNA689556.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Total data mapped (Mb)</th>
<th>No. of reads mapped</th>
<th>Depth of coverage (×)</th>
<th>GenBank accession no.</th>
<th>Genome size (bp)</th>
<th>G+C content (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHOP6887</td>
<td>163.2</td>
<td>1,093,086</td>
<td>345–6,171</td>
<td>MT513753</td>
<td>34,781</td>
<td>48.8</td>
</tr>
<tr>
<td>21962_S4TF53</td>
<td>114.8</td>
<td>514,425</td>
<td>262–4,532</td>
<td>MW053454</td>
<td>34,781</td>
<td>48.8</td>
</tr>
</tbody>
</table>

*The complete genome sequence of HAdV-55 strain QS-DLL/China/2006 (GenBank accession number FJ643676) was used as the mapping reference.*

---

**TABLE 1** Assembly of complete genome sequences for two HAdV-55 isolates

![FIG 1 Whole-genome phylogenetic analysis of human adenovirus type 55 isolates. The maximum-likelihood method was used with the sequence of human adenovirus 14 strain de Wit (GenBank accession number AY803294) as the root. Node confidence values estimated using approximate likelihood ratio test Shimodaira-Hasegawa (aLRT-SH) and the branch length scale bar (the number of nucleotide substitutions per site) are shown. The two new isolates are shown in red.](image-url)
ACKNOWLEDGMENTS

Funding was provided by the Defense Health Agency Immunization Healthcare Division (DHA-IHD), grant HBISP-17-14, and the Global Emerging Infections Surveillance Branch (GEIS) of the Armed Forces Health Surveillance Division, grant ProMIS ID P0140_20_WR_01.Global. The opinions expressed are the private views of the authors and are not to be conveyed as official or signifying the views of the Department of the Army or the Department of Defense.

REFERENCES


