



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

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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 in the hexon gene 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](https://www.ncbi.nlm.nih.gov/nuccore/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](https://www.ncbi.nlm.nih.gov/nuccore/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 0.35 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](https://www.ncbi.nlm.nih.gov/nuccore/MT513753)) is phylogenetically distinct from the two

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

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

^aThe complete genome sequence of HAdV-55 strain QS-DLL/China/2006 (GenBank accession number [FJ643676](#)) was used as the mapping reference.

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](#).

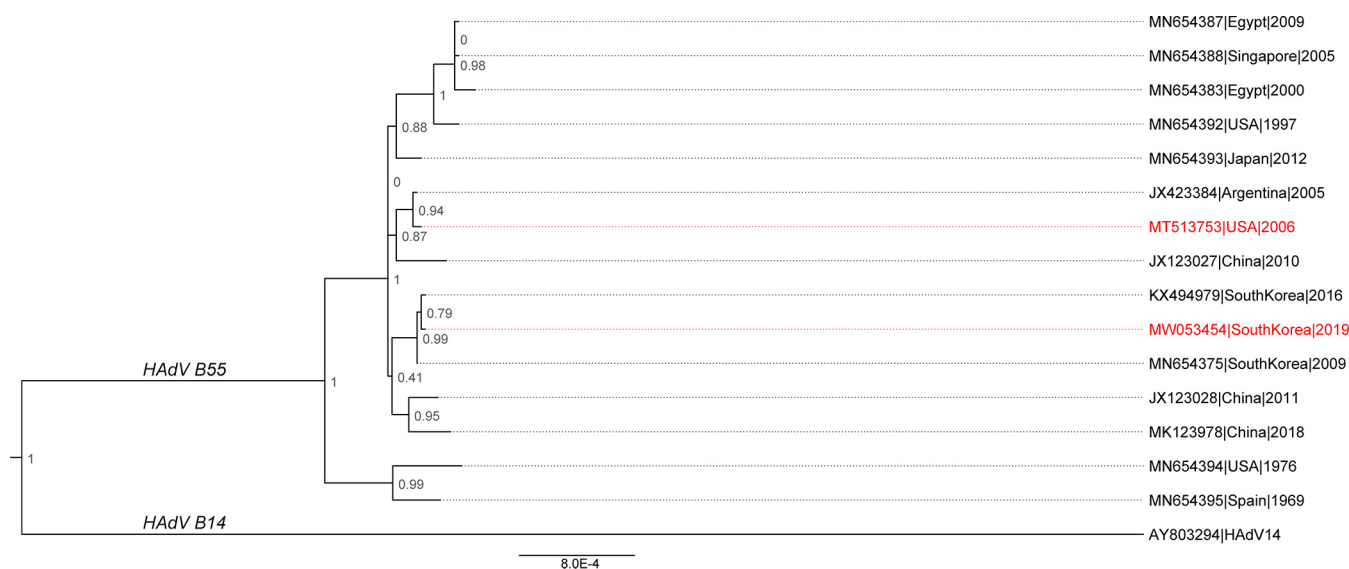


FIG 1 Whole-genome phylogenetic analysis of human adenovirus type 55 isolates. The maximum-likelihood method was used with the sequence of human adenovirus 14 strain de Wit (GenBank accession number [AY803294](#)) as the root. Node confidence values estimated using approximate likelihood ratio test Shimodaira-Hasegawa (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.

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