**Preplanned Studies**

# Outbreaks of Acute Respiratory Disease Associated with Human Adenovirus Infection in Closed Camps, China, December 2011–March 2014

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## Summary

### What is already known on this topic?

Human adenovirus (HAdV) was frequently associated with acute respiratory disease (ARD) outbreaks in military camps.

### What is added by this report?

HAdV-B7, HAdV-B14, and HAdV-B55 were determined to be responsible for 3, 2, and 4 ARD outbreaks in military camps, China, respectively, with a total attack rate of 28.0% during 2011 to 2014.

### What are the implications for public health practice?

The findings suggest that vaccine development and administration in military camps must be prioritized. Quarantining among new recruits before entering into the military and the identification of the major responsible genotypes at the current stage is warranted.

Human adenovirus (HAdV) was frequently associated with acute respiratory disease (ARD) outbreaks in closed environment, especially in military camps. In the current study, we investigated the genetic characteristics and epidemiological characteristics of HAdV strains that were responsible for the ARD outbreaks in military camps in China. Among HAdV-related outbreaks that were reported from 2011 to 2014, a total of 3,813 patients were diagnosed from 13,622 camp members, with an overall attack rate of 28.0%. HAdV-B7, HAdV-B14, and HAdV-B55 were determined to be responsible for 3, 2, and 4 outbreaks, respectively. The total attack rate of HAdV-related ARD was 28.0%, ranging from 10.9% to 39.9% among various outbreaks. HAdV-B14 related outbreaks had a higher attack rate than outbreaks of the other two genotypes. Phylogenetic analysis revealed no obvious relationship between outbreak strains and locally circulating strains, indicating the introduction of the strain from a new recruit's hometown might be

responsible for the outbreaks. The findings suggest that vaccine development and administration in military camps must be prioritized. Quarantining among new recruits before entering into the military and the identification of the major responsible genotypes at the current stage is warranted.

Traditionally, there are 51 HAdV serotypes, which are assigned to seven subgroups (A–G) according to biophysical, biochemical, and genetic characteristics. In recent years, new serotypes or subspecies were increasingly recognized by use of phylogenetic analysis, which arised from genome recombination between the hexon gene, fiber, and penton genes. These newly emerged HAdV types resulted in continuous outbreak events on campuses, such as in university campuses or at recruit training centers (*1–2*), posing severe threats to public health. In China, the ARD outbreak had been constantly reported in the closed community, such as in military camps; however, their etiological agents are rarely determined, in part due to the lack of molecular typing in field investigations. The first known HAdV-associated ARD outbreak in the military was reported from a recruit training camp in 2009, which was determined to be caused by HAdV-B55 infection (*3*). In this study, we described the HAdV-related ARD outbreaks that had been reported in military camps from 2011–2014, investigating the genetic characteristics of the responsible HAdV strains and their related epidemiological characteristics.

The field investigation and laboratory tests were carried out in accordance with the approved guidelines. Briefly, after the report of an outbreak, nasopharyngeal aspirate (NPA) samples were collected from the index case and from at least 30% of the ARD patients and tested for the commonly seen viral pathogens, i.e., HAdV, influenza virus, respiratory syncytial virus, human rhinovirus, human enterovirus, human coronavirus, and human metapneumovirus. All tests were performed by polymerase chain reaction (PCR) or

real-time PCR. HAdV infection from the outbreak was identified by PCR assay using HAdV universal and serotype-specific conventional PCR assays (4–5). To validate the causal relationship between HAdV and the outbreak disease, seroconversion evidence was further determined from paired samples using the neutralizing antibody test. For each outbreak, the responsible HAdV strains were isolated. Briefly, NPA specimens were inoculated into A549 cells incubated at 36 ℃ and observed for cytopathic effects (CPEs) for 21 days. Selected paired samples (acute-phase samples and convalescent-phase samples that were collected over one month apart) were tested for the presence of anti-HAdV antibodies by a colorimetric serum microneutralization assay, using the strains isolated from the outbreak event. All the subjects who were residing in the military camps over the outbreak duration were interviewed using a standard questionnaire to acquire the following information: date of birth, sex, clinical symptoms, date of contact with the patients, and date of onset of symptoms. All data were collected as part of the emergency response to the outbreak events. Data were de-identified for analysis, and the informed consent requirement was waived.

During the period from December 2011 to March 2014, 9 HAdV-related outbreak events of ARD were determined from military camps or recruit training centers, based on both molecular and serological evidences. In each of the outbreaks, other respiratory viruses than HAdV, including influenza A virus or parainfluenza virus, was only occasionally tested as positive, and were not considered as the causative agents of the outbreaks. According to the standard criteria to define ARD, a total of 3,813 patients were diagnosed from 13,622 camp members, with an overall attack rate of 28.0%. The attack rates ranged from 10.9% to 39.9% among various outbreaks (Table 1). Four camps had only male recruits. The other four camps had both male and female recruits, where female patients were also reported, but with a lower attack rate than in males (21.0% *vs.* 39.4%, *P*<0.001). The patients were aged from 18 to 24 years. All the HAdV-associated ARD were reported among cold season from December to next March, which coincided with the training period for recruits. The outbreaks were identified to start from 1 to 6 weeks (median 3 weeks) after the initiation of the training activity. The peak outbreak occurred mostly from 11 to 25 days after the disease onset of index case.

HAdV-positive results were further confirmed by

TABLE 1. Epidemiological characteristics of HAdV-related outbreak events of acute respiratory disease in military camps during December 2011—March 2014.

| Characteristic | All participants (N=13,622) | |
| --- | --- | --- |
| | ARD patients (n=3,813) | *P* |
| Gender | | |
| Male | 3,720 (28.35) | <0.001 |
| Female | 93 (18.56) | |
| Age of soldier | | |
| New recruits | 2,722 (31.86) | <0.001 |
| Veterans | 1,091 (21.48) | |
| HAdV genotype | | |
| HAdV-B7 | 688 (24.77) | <0.001 |
| HAdV-B14 | 1,016 (37.70) | |
| HAdV-B55 | 2,109 (25.88) | |
| Outbreaks areas, province | | |
| HuBei/2013/HAdV-B7 | 376 (25.53) | <0.001 |
| ShanXi/2013/HAdV-B7 | 107 (16.54) | |
| HuBei/2013/HAdV-B7 | 205 (31.16) | |
| LiaoNing/2012/HAdV-B14 | 185 (30.32) | |
| GanSu/2013/HAdV-B14 | 831 (39.86) | |
| HeBei/2012/HAdV-B55 | 650 (28.54) | |
| ShanXi/2011/HAdV-B55 | 309 (10.92) | |
| TianJin /2012/HAdV-B55 | 1,150 (37.80) | |
| Total | 3,813 (27.99) | |

Note: The information on the ninth outbreak of Liaoning /2013/ HAdV-B55 was missing.

sequencing of hexon gene, penton, and fiber genes. The genotype was determined by alignment and phylogenetic tree analysis. HAdV-B7, HAdV-B14, and HAdV-B55 were reported to be responsible for 3, 2, and 4 outbreaks, respectively. A higher attack rate was identified from HAdV-B14 (37.7%), significantly higher than that of HAdV-B7 (24.8%) and HAdV-B55 (25.9%) (*P*<0.001, Table 1). The mean age of the patients was highly comparable among all the outbreak episodes regardless of the HAdV types. The incubation period ranged from 4 to 8 days, showing no difference among outbreaks associated with various genotypes. Among 3,813 ARD patients, 736 (19.3%) developed pneumonia, and the patients with HAdV-B7 (164, 23.8%) and HAdV-B55 (518, 24.6%) had a higher chance of developing pneumonia than those with HAdV-B14 (54, 5.3%; *P*<0.001).

To investigate the genetic characteristics of the responsible virus, the whole genome sequence of one strain for each outbreak was obtained by deep-

sequencing of the HAdV isolates or the raw positive samples. Previously published sequences of HAdV-B7, HAdV-B14, HAdV-B55, and HAdV-B11 were recovered from GenBank and used for the alignment

with the current outbreak strains. For each genotype, the phylogenetic trees were respectively constructed based on the HAdV complete genome and 3 segments (penton, hexon, and fiber) by maximum likelihood

B HAdV-B14

MG642747/USA/2011
MG642742/USA/2012
MG642752/USA/2009
MG642746/UnitedKingdom/2011
MG642744/USA/2010
MG642748/USA/2010
MG642749/USA/2010
MG642750/Honduras/2008
MG642745/USA/2009
MG642743/USA/2005
MG642756/Nepal/2007
MG905108/USA/2012
MG905102/USA/2012
MG905099/USA/2006
MG905101/Canada/2011
MG905103/USA/2003
MG642753/USA/2010
MG905100/Ireland/2010
MH669072/USA/2009
MG905104/USA/2006
MG905105/USA/2007
MG642754/USA/2012
MG642755/USA/2011
MG905109/USA/2007
MG905107/USA/2012
FJ822614/USA/2007
MG642751/USA/2009
MH669071/USA/2009
MH669073/USA/2009
MG905106/USA/2008
MH669070/USA/2006
JN032132/China/2011
JQ824845/China:Guangdong/2010
MF062484/China:Beijing/2010
JX892927/China:Liaoning/2012 ●
KP896482/China:Gansu/2013 ●
MG905112/Netherlands/1974
MG905111/Netherlands/1957

$3\times10^{-4}$

C HAdV-B55

JX123028/China:Chongqing/2011
KP279748/China:Anhui/2012
KY070248/China:Guangdong/2016
KY780932/China:Guangdong/2016
KC857701/China:Jiangsu/2012
MN052861/China:Jiangsu/2018
KJ883520/China:Hebei/2013
KF908851/China:Tianjin/2013
KP896483/China:Liaoning/2013 ●
KP896484/China:Tianjin/2013 ●
KX289874/China:Jiangsu/2015
JX123029/China:Chongqing/2012
FJ643676/China:Shanxi/2006
MK123978/China:Guangdong/2018
KP896478/China:Hebei/2012 ●
MH256656/China:Sichuan/2018
MH256657/China:Sichuan/2018
MT806174/China:Hebei/2019
MT806175/China:Hebei/2019
KJ883522/China:Shanxi/2011 ●
MK123981/China:Guangdong/2013
KJ883521/China:Hebei/2013
JX491639/China:Beijing/2011
MK886831/China:Beijing/2015
MN654376/SouthKorea/2009
KY471323/SouthKorea/2016
KY471320/SouthKorea/2016
KX494979/SouthKorea/2016
MW053454/SouthKorea/2019
MN654380/Egypt/2000
MN654382/Egypt/2002
MN654384/Egypt/2008
MN654385/Egypt/2000
MN654386/Egypt/2007
MN654387/Egypt/2009
FJ597732/Singapore/HAdVB11/2005
MN654389/Singapore/2005
MN654391/Egypt/2005
MN654392/USA/1997
MN654393/Japan/2012
JX123027/China:Chongqing/2010
MT513753/USA/2006
MN654394/USA/1976
MN654395/Spain/1969
AF532578/Sweden/HAdVB11/
AY163756/USA/HAdVB11/
KF906413/South_Korea/HAdVB11/2010

0.002

FIGURE 1. Phylogenetic tree was constructed based on the full genome sequences using maximum likelihood method with 1,000 bootstraps by MEGA 7.0. (A) HAdV-B7; (B) HAdV-B14; (C) HAdV-B55.
Note: The strains labeled with black dots were obtained from the current study.

method using the MEGA 7 software (version 7.0.26, USA) .

For alignment of HAdV-B7 genotype, a total of 109 sequences were obtained from GenBank. Based on the alignment with these available sequences, most of the Chinese strains could be clustered in 5 branches that were distinct from the strains of other countries (Figure 1A, Supplementary Figure S1A, S2A, and S3A, available in http://weekly.chinacdc.cn/). Interestingly all 3-outbreak related HAdV-B7 strains in the current study and the strains from Hubei in the year of 2012 and 2013 formed a separate cluster within the Chinese lineage, irrespective of the geographic location of the outbreak events, possibly suggesting genetic characteristics specific to outbreaks.

For HAdV-B14, a total of 50 sequences were recovered from GenBank, including 38 full genome sequences, 5 hexon, and 7 fiber gene sequences. The phylogenetic trees based on full genome sequences demonstrated a clear divergence of the 2 lineages that were derived from the year before 2012 and after 2012 for the strains from China, respectively; while for the hexon gene, the 2 lineages from China became 1 lineage, and for fiber and penton genes, the geographical distribution disappeared (Figure 1B, Supplementary Figures S1B, S2B, and S3B). The strains from China between 2010–2011 were clustered with those from the USA between 2006 and 2008. According to alignment 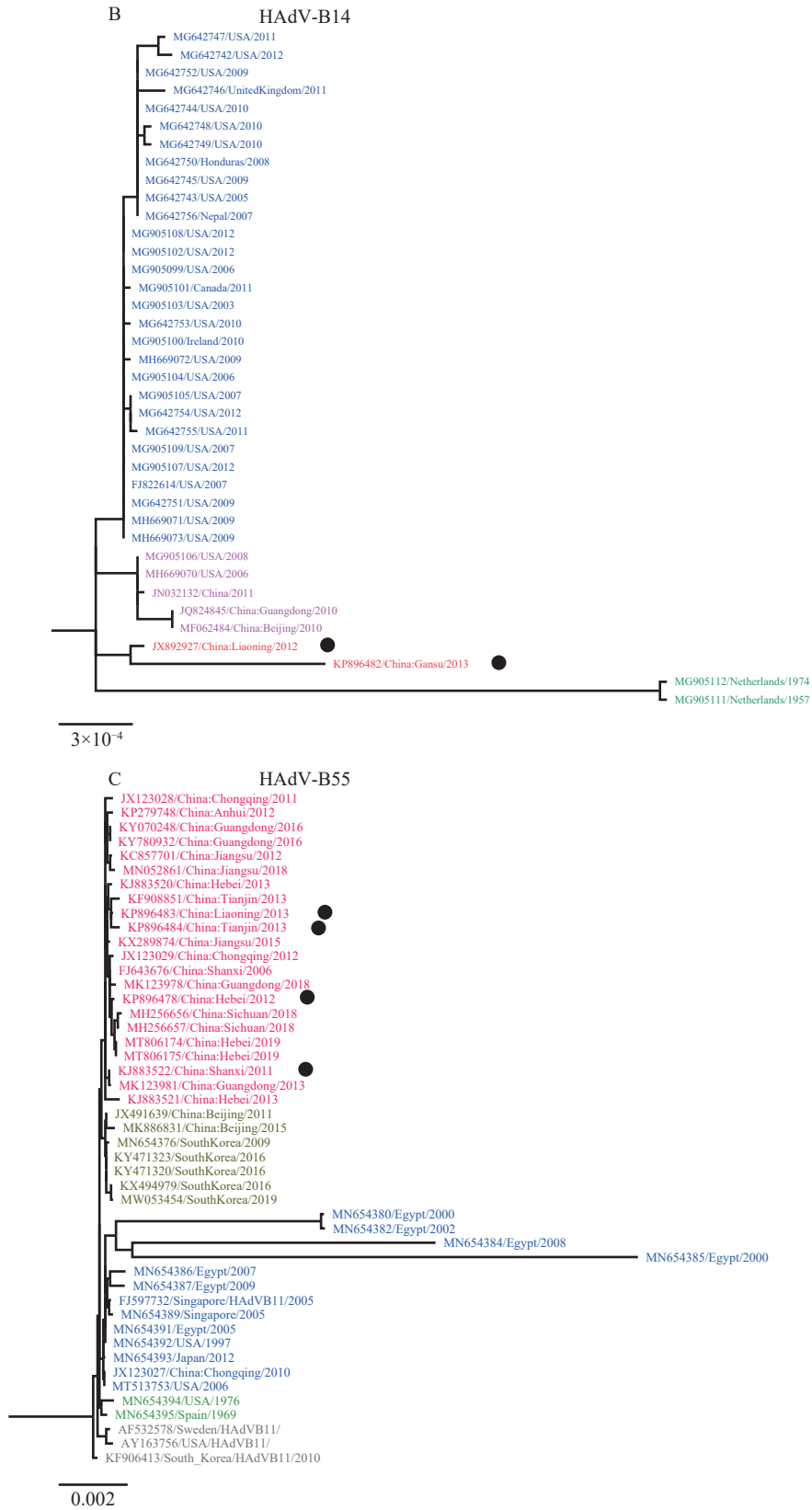of complete genome sequences, the current outbreak strain (KP896482/China:Gansu/2013) was most closely related to the strain from Liaoning (JX892927/China:Liaoning/2012) (99.9% nucleotide similarity and 99.6% amino acid similarity) while differing from the outbreak strain in the same region that were isolated in 2011 (for hexon gene, JX310315/China:Gansu/2011, 99.8% nucleotide similarity and 98.1% amino acid similarity; for fiber gene, JX310316/China:Gansu/2011, 99.7% nucleotide similarity and 98.1% amino acid similarity). This might reflect that the outbreak event was caused by a strain introduced into the camp by recruits and that the strain did not locally circulate.

For HAdV-B55, a total of 59 sequences were recovered from GenBank, including 47 full genome sequences, 6 hexon, and 6 fiber gene sequences. Based on the full genome sequences, all Chinese strains had high homologies, showing spatial specific distribution patterns and clustering into one branch (Figure 1C). Two strains from Beijing were clustered with strains from the Republic of Korea. While for hexon, fiber, and penton genes, the Chinese strains formed several branches (Supplementary Figures S1C, S2C, and S3C). The strains detected during the recent military outbreaks from 2011 to 2013 were interspersed in the strains isolated from the community strains between 2010 and 2012. This might indicate that the most recent descendant from the early isolates were responsible mainly for the current outbreaks in military camps.

## DISCUSSION

In summary, we have determined HAdV-B7, HAdV-B14, and HAdV-B55 to be the most common HAdV genotypes that were responsible for outbreaks in military camps or recruit training centers in China. This is different from the situation in the American military, where HAdV-E4, HAdV-B7, and HAdV-B14 act as the predominant strains sequentially isolated from the outbreaks (6–9). According to prior epidemiological investigation performed in community population in China, HAdV-B3 and HAdV-B7 were most frequently detected among ARD patients, while only in recent years HAdV-B55 emerged with increasing prevalence (10). In the absence of herd immunity against the uncommonly seen HAdV-B14 and newly emerging HAdV-B55 in the local community populations, military recruits were highly susceptible to outbreaks if these 2 types of HAdV were introduced into the susceptible population. An HAdV vaccination program against these three outbreak-related genotypes is urgently needed in this high-risk population.

By comparing various outbreaks, a higher attack rate was identified from HAdV-B14-related outbreaks when compared to those from HAdV-B7 and HAdV-B55, possibly indicating a higher susceptibility and transmissibility of HAdV-B14 in closed settings than the other two types. This conclusion, however, could differ in terms of geographic origin and immunity background of the population. Similar with previous findings (8), younger age and male gender were associated with an increased risk for HAdV infection during outbreak events, irrespective of the HAdV genotypes. Although disease severity varied among genotypes, we observed that infection with HAdV-B7 and HAdV-B55 caused more pneumonia than HAdV-B14 from the outbreak events. The infection source of the HAdV outbreak was preliminarily explored by genetic alignment of the viral strains. For HAdV-B14, no obvious phylogenetic relationship was derived between the HAdV responsible for the outbreak and

the locally circulating strain, likely indicating the introduction of the strain from a new recruit's hometown as the major infectious source. However, whether this hypothesis holds true and how the disease was introduced into the camp are hard to be determined, since the infected individual might still be in the incubation period at the time of entering camp, and thus might be missed even with mandatory quarantine for febrile illness. Quarantine among the new recruits before entering into the military and the identification of the major responsible genotype at the current stage is warranted.

This study was subject to some limitations. The severity of ARD caused by different HAdV genotypes was not evaluated as no individual-level data were collected. The study did not include all the outbreaks of HAdV in closed camps during December 2011–March 2014 in China.

**Conflicts of interest**: No conflicts of interest declared.

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A HAdV-B7

MT367402/China:Beijing/2017
MW816001/China:Hubei/2019
MN307146/USA/2018
MN307147/USA/2018
MN307148/USA/2018
MT367406/China/2018
MW815999/China:Hubei/2019
MT941567/China:Guangdong/2019
MT367403/China/2017
MT367400/China:Guangdong/2016
MW816000/China:Hubei/2019
MW816101/China:Hubei/2019
MT350346/China:Beijing/2018
KX897164/China:Hubei/2015
MT920215/China:Guangdong/0
MT367405/China:Beijing/2017
MW816029/China:Hubei/2019
MG923582/SaintPetersburg/2013
MH262326/USA/2017
MN307154/USA/2019
KJ019881/China:Hubei/2012
MT367395/China:Hubei/2015
KC857700/China:Jiangsu/2012
MT350345/China:Beijing/2018
MN307156/USA/2019
JF800905/China:Shanxi/2009
LC530212/Japan/2018
MT367404/China:Beijing/2017
MH262320/USA/2016
MT367397/China:Hubei/2014
KP670855/China:Guangdong/2011
MH910662/USA/1955
MH910667/USA/1999
MH910666/USA/1996
MH910669/USA/1960s
MN936178/USA/2008
MH910663/USA/1997
MH910664/USA/1997
MT367399/China:Zhejiang/2015
JN860677/USA/2009
MH910668/USA/1997
KJ019882/China:Hubei/2012
KJ019883/China:Hubei/2013
KP670857/China:Guangdong/2011
MT950360/China:Guangdong/2019
MT367394/China:Hubei/2015
MH262321/USA/2016
MG736304/China:Jiangxi/2017
MT993342/China:Guangdong/2019
KJ019880/China:Hubei/2012
MG696134/China:Jiangxi/2017
MN135993/China:Guangdong/2018
MT367398/China:Hubei/2014
KP670861/China:Guangdong/2011
MW816028/China:Hubei/2019
MN422293/USA/2019
MH262325/USA/2017
MN307153/USA/2019
MG923581/SaintPetersburg/2013
MT950361/China:Guangdong/2019
KP670856/China:Guangdong/2011
MT367396/China:Hubei/2015
KC440171/China:Guangdong/2011
MH262319/USA/2016
MT350344/China:Beijing/2018
MH355567/China:Beijing/2018
KJ019885/China:Hubei/2012
KP896481/China:Hubei/2013
KP896480/China:Shanxi/2013
KP896479/China:Hubei/2013
MT367407/China:Beijing/2018
KJ019886/China:Hubei/2013
MN164629/China:Guangdong/2018
KP670859/China:Guangdong/2012
KP670858/China:Guangdong/2010
JX625134/China:Chongqing/2010
MH262322/USA/2017
KT963081/USA/2014
MT367401/China/2017
KJ019879/China:Hubei/2013
MN638757/USA/2019
KJ019887/China:Hubei/2013
MN307157/USA/2018
KP670860/China:Guangdong/2012
MT941568/China:Guangdong/2019
MN422292/USA/2019
MH262324/USA/2017
KJ019884/China:Hubei/2012
KU361344/Volgograd/2014
MK492255/USA/2014
MK492256/USA/2014
MK492257/USA/2017
MH697601/USA/2017
MH697602/USA/2017
MH697603/USA/2017
MH697604/USA/2017
MH697605/USA/2017
MH697606/USA/2017
MH697607/USA/2017
MH697600/USA/2017
MH262323/USA/2017
KJ019888/China:Hubei/2012
MW816100/China:Hubei/2019
MH262318/USA/2016
MT325873/China:Jiangxi/2017
MN307155/USA/2019

$3×10^{-4}$

B          HAdV-B14

MG642747/USA/2011
MG642742/USA/2012
MG642745/USA/2009
MG642744/USA/2010
MG642754/USA/2012
MH669071/USA/2009
MG642751/USA/2009
FJ822614/USA/2007
MG905104/USA/2006
MG905103/USA/2003
MG905100/Ireland/2010
MG905109/USA/2007
MG905105/USA/2007
MG905107/USA/2012
MG905101/Canada/2011
MG642753/USA/2010
MH669072/USA/2009
MG642755/USA/2011
MG642752/USA/2009
MG642746/UnitedKingdom/2011
FJ841901/USA/2007
MG642756/Nepal/2007
MG905099/USA/2006
MG905102/USA/2012
MG905108/USA/2012
MG642743/USA/2005
MG642750/Honduras/2008
MH669073/USA/2009
MG642748/USA/2010
MG642749/USA/2010
HQ265808/Ireland/2009
JQ824845/China:Guangdong/2010
MF062484/China   :Guangdong/   2010
JX892927/China:Liaoning/2012
JX310315/China:Gansu/2011
JN032132/China   :Beijing  /2011
MH669070/USA/2006
KC825052/China:Liaoning/2008
KP896482/China:Gansu/2013
MG905106/USA/2008
JF420883/China:Beijing/2010
MG905111/Netherlands/1957
MG905112/Netherlands/1974

$3×10^{-4}$

C          HAdV-B55

JX123029/China:Chongqing/2012
KJ883521/China:Hebei/2013
KP896483/China:Liaoning/2013
KY471320/SouthKorea/2016
MH256657/China:Sichuan/2018
FJ841905/Taiwan/HAdVB11/2002
FJ841906/Taiwan/HAdVB11/2001
FJ643676/China:Shanxi/2006
KC857701/China:Jiangsu/2012
KJ883522/China:Shanxi/2011
KX289874/China:Jiangsu/2015
KY471323/SouthKorea/2016
MK123978/China:Guangdong/2018
JX491639/China:Beijing/2011
MK886831/China:Beijing/2015
JX123028/China:Chongqing/2011
KJ883520/China:Hebei/2013
KP896478/China:Hebei/2012
KY070248/China:Guangdong/2016
MH256656/China:Sichuan/2018
MN654376/SouthKorea/2009
MN654393/Japan/2012
KP896484/China:Tianjin/2013
JX123027/China:Chongqing/2010
KF908851/China:Tianjin/2013
KP279748/China:Anhui/2012
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MN052861/China:Jiangsu/2018
MK123981/China:Guangdong/2013
MT513753/USA/2006
MT806174/China:Hebei/2019
MT806175/China:Hebei/2019
MW053454/SouthKorea/2019
MN654394/USA/1976
MN654395/Spain/1969
FJ841900/Spain/HAdVB11/1969
FJ841899/USA/HAdVB11/1997
FJ841904/Singapore/HAdVB11/2005
FJ597732/Singapore/HAdVB11/2005
MN654380/Egypt/2000
MN654384/Egypt/2008
MN654385/Egypt/2000
MN654386/Egypt/2007
MN654387/Egypt/2009
MN654389/Singapore/2005
MN654391/Egypt/2005
MN654392/USA/1997
MN654382/Egypt/2002
KF906413/South_Korea/HAdVB11/2010
AB330092/Japan/HAdVB11/2000
AF532578/Sweden/HAdVB11/
AY163756/USA/HAdVB11/

0.008

SUPPLEMENTARY FIGURE S1. Phylogenetic tree was constructed based on the hexon gene using maximum likelihood method with 1000 bootstrap by MEGA 7.0. (A) HAdV-B7; (B) HAdV-B14; (C) HAdV-B55.
Note: The strains labeled with black dots were obtained from the current study.

A                                             HAdV-B7

MT367405/China:Beijing/2017
MT325873/China:Jiangxi/2017
MG736304/China:Jiangxi/2017
MG696134/China:Jiangxi/2017
KJ019881/China:Hubei/2012
KX897164/China:Hubei/2015
KJ019883/China:Hubei/2013
MT920215/China:Guangdong/0
JF800905/China:Shanxi/2009
KJ019888/China:Hubei/2012
MT941568/China:Guangdong/2019
MT367404/China:Beijing/2017
MN307146/USA/2018
MW815999/China:Hubei/2019
MH262319/USA/2016
MH262325/USA/2017
MH697604/USA/2017
MT941567/China:Guangdong/2019
KT963081/USA/2014
MT367403/China/2017
MT350346/China:Beijing/2018

MH355567/China:Beijing/2018

MT367399/China:Zhejiang/2015
MH910663/USA/1997
MT367402/China:Beijing/2017
KJ019879/China:Hubei/2013
KJ019887/China:Hubei/2013
MN307156/USA/2019
MN307157/USA/2018
MN638757/USA/2019
KP670860/China:Guangdong/2012
MT950360/China:Guangdong/2019
MW816100/China:Hubei/2019
MK492257/USA/2017
MT367406/China/2018
MG923582/SaintPetersburg/2013
MH262322/USA/2017
MH697602/USA/2017
MH697607/USA/2017
MT950361/China:Guangdong/2019
MN307154/USA/2019
KP670855/China:Guangdong/2011

KP896480/China:Shanxi/2013          KP896481/China:Hubei/2013
KP896479/China:Hubei/2013

MH910664/USA/1997
MT367407/China:Beijing/2018
KJ019886/China:Hubei/2013
MG923581/SaintPetersburg/2013
MT350345/China:Beijing/2018
MH262323/USA/2017
KP670859/China:Guangdong/2012
LC530212/Japan/2018
MW816029/China:Hubei/2019
MK492256/USA/2014
MN307148/USA/2018
MN422293/USA/2019
MH262321/USA/2016
MH697601/USA/2017
MH697606/USA/2017
MT367397/China:Hubei/2014
MN307153/USA/2019
MW816000/China:Hubei/2019
MT367401/China/2017
KU361344/Volgograd/2014
KJ019880/China:Hubei/2012
MN135993/China:Guangdong/2018
JN860677/USA/2009
MT367398/China:Hubei/2014
KP670856/China:Guangdong/2011
KP670861/China:Guangdong/2011
KP670858/China:Guangdong/2010
KC440171/China:Guangdong/2011
MT367394/China:Hubei/2015
JX625134/China:Chongqing/2010
MH262318/USA/2016
MH262324/USA/2017
MH697603/USA/2017
MT350344/China:Beijing/2018
MH697600/USA/2017
MN307155/USA/2019
MW816101/China:Hubei/2019

MH910662/USA/1955
MH910669/USA/1960s
MN936178/USA/2008
MH910667/USA/1999
MH910666/USA/1996
MH910668/USA/1997
KJ019885/China:Hubei/2012
KJ019882/China:Hubei/2012
MT367395/China:Hubei/2015
MN164629/China:Guangdong/2018
MW816001/China:Hubei/2019
KP670857/China:Guangdong/2011
MT367396/China:Hubei/2015
MW816028/China:Hubei/2019
MK492255/USA/2014
MN307147/USA/2018
MN422292/USA/2019
MH262320/USA/2016
MH262326/USA/2017
MH697605/USA/2017
KC857700/China:Jiangsu/2012
KJ019884/China:Hubei/2012
MT367400/China:Guangdong/2016
MT993342/China:Guangdong/2019

0.002

B               HAdV-B14

JQ815085/Canada/2011
MG642756/Nepal/2007
JQ824845/China:Guangdong/2010
MG905100/Ireland/2010
MF062484/China    :Guangdong   /2010
MG905109/USA/2007
MG905099/USA/2006
MG905103/USA/2003
MG905105/USA/2007
MG905102/USA/2012
MG905104/USA/2006
MG905107/USA/2012
MG905108/USA/2012
FJ822614/USA/2007
MG905101/Canada/2011
JN032132/China   :Beijing  /2011
MG905106/USA/2008
JX892927/China:Liaoning/2012 ●
MG642743/USA/2005
MG642751/USA/2009
MG642745/USA/2009
MH669070/USA/2006
MG642746/UnitedKingdom/2011
MG642747/USA/2011
MG642753/USA/2010
MG642750/Honduras/2008
MG642742/USA/2012
MH669071/USA/2009
MH669072/USA/2009
MH669073/USA/2009
MG642754/USA/2012
MG642755/USA/2011
MG642748/USA/2010
MG642744/USA/2010
MG642752/USA/2009
MG642749/USA/2010
JF420882/China:Beijing/2010
HQ163915/Ireland/2009
FJ841909/USA/2007
JX310316/China:Gansu/2011
JQ815083/Canada/2011
JQ815084/Canada/2011                            KP896482/China:Gansu/2013 ●
MG905112/Netherlands/1974
MG905111/Netherlands/1957

$4 \times 10^{-4}$

C               HAdV-B55

MN654393/Japan/2012
KJ883521/China:Hebei/2013
MK886831/China:Beijing/2015
KY780932/China:Guangdong/2016
KX494979/SouthKorea/2016
KP279748/China:Anhui/2012
FJ841914/Taiwan/HAdV-B11/2001
JX491639/China:Beijing/2011
MW053454/SouthKorea/2019
MN654395/Spain/1969
MN654394/USA/1976
FJ841908/Spain/HAdV-B11/1969
                                         AF532578/Sweden/HAdVB11/
                                         AY163756/USA/HAdVB11/
                                         KF906413/South_Korea/HAdVB11/2010
KP896484/China:Tianjin/2013 ●
MN654391/Egypt/2005
MN654389/Singapore/2005
MN654387/Egypt/2009
MN654386/Egypt/2007
MN654385/Egypt/2000
MN654384/Egypt/2008
MN654382/Egypt/2002
MN654380/Egypt/2000
FJ603103/Singapore/HAdV-B11/2005
FJ597732/Singapore/HAdVB11/2005
MT806175/China:Hebei/2019
MT806174/China:Hebei/2019
MN654392/USA/1997
MK123978/China:Guangdong/2018
KY471323/SouthKorea/2016
KX289874/China:Jiangsu/2015
KJ883520/China:Hebei/2013
FJ841913/Taiwan/HAdV-B11/2002
JX123029/China:Chongqing/2012
MT513753/USA/2006
JX123027/China:Chongqing/2010
MN654376/SouthKorea/2009
MH256657/China:Sichuan/2018
KY471320/SouthKorea/2016
KP896483/China:Liaoning/2013 ●
KF908851/China:Tianjin/2013
FJ841907/USA/HAdV-B11/1997
JX123028/China:Chongqing/2011
MN052861/China:Jiangsu/2018
MK123981/China:Guangdong/2013 ●
KJ883522/China:Shanxi/2011
MH256656/China:Sichuan/2018
KY070248/China:Guangdong/2016
KP896478/China:Hebei/2012 ●
KC857701/China:Jiangsu/2012
AB162822/Japan/HAdV-B11/2001_2005
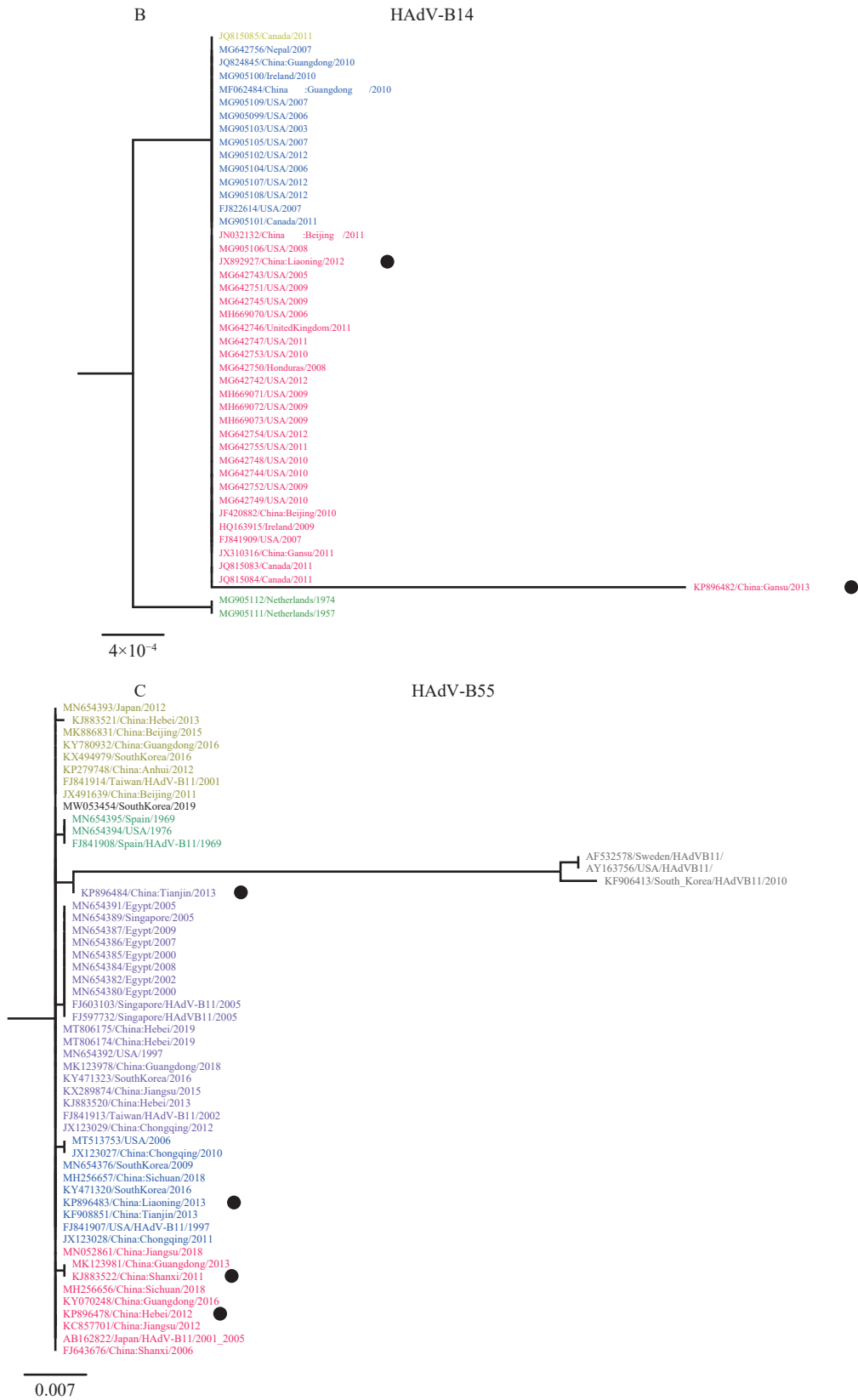FJ643676/China:Shanxi/2006

0.007

SUPPLEMENTARY FIGURE S2. Phylogenetic tree was constructed based on the Fiber gene using maximum likelihood method with 1,000 bootstrap by MEGA 7.0. (A) HAdV-B7; (B) HAdV-B14; (C) HAdV-B55.
Note:The strains labeled with black dots were obtained from the current study.

A                                        HAdV-B7



```
MT367407/China:Beijing/2018
KX897164/China:Hubei/2015
MN307157/USA/2018
JF800905/China:Shanxi/2009
MT367396/China:Hubei/2015
MW816029/China:Hubei/2019
MT367394/China:Hubei/2015
MW815999/China:Hubei/2019
MH262320/USA/2016
MT325873/China:Jiangxi/2017
MH697606/USA/2017
MG736304/China:Jiangxi/2017
MN307155/USA/2019
MT350346/China:Beijing/2018
MT350345/China:Beijing/2018
    KC440171/China:Guangdong/2011
KP670856/China:Guangdong/2011
MT367405/China:Beijing/2017
MW816028/China:Hubei/2019
MK492257/USA/2017
JX625134/China:Chongqing/2010
MH262319/USA/2016
MH262326/USA/2017
MH697605/USA/2017
MT950361/China:Guangdong/2019
MN307154/USA/2019
MW816101/China:Hubei/2019
MN135993/China:Guangdong/2018
    MH355567/China:Beijing/2018
MT367395/China:Hubei/2015
MT920215/China:Guangdong/0
KP670857/China:Guangdong/2011
LC530212/Japan/2018
MW816100/China:Hubei/2019
MN307146/USA/2018
MN422292/USA/2019
MH262321/USA/2016
MH697601/USA/2017
MH697607/USA/2017
MH697600/USA/2017
MT367403/China/2017
MT993342/China:Guangdong/2019
MN307156/USA/2019
    MG696134/China:Jiangxi/2017
MN638757/USA/2019
KP670861/China:Guangdong/2011
MT941568/China:Guangdong/2019
MK492256/USA/2014
MT367406/China/2018
MH262318/USA/2016
MH262325/USA/2017
MH697604/USA/2017
KC857700/China:Jiangsu/2012
MN307153/USA/2019
KP670855/China:Guangdong/2011
    MN164629/China:Guangdong/2018
KU361344/Volgograd/2014
MW816001/China:Hubei/2019
KP670859/China:Guangdong/2012
MT950360/China:Guangdong/2019
MT367404/China:Beijing/2017
MN307147/USA/2018
MN422293/USA/2019
MH262322/USA/2017
MH697602/USA/2017
MT350344/China:Beijing/2018
KT963081/USA/2014
MT367400/China:Guangdong/2016
MT367401/China/2017
    MT367398/China:Hubei/2014
    MT367397/China:Hubei/2014
MG923581/SaintPetersburg/2013
MH262323/USA/2017
KP670860/China:Guangdong/2012
KP670858/China:Guangdong/2010
MK492255/USA/2014
MN307148/USA/2018
MG923582/SaintPetersburg/2013
MH262324/USA/2017
MH697603/USA/2017
MT941567/China:Guangdong/2019
KJ019884/China:Hubei/2012
MW816000/China:Hubei/2019
MT367402/China:Beijing/2017
KP896481/China:Hubei/2013
    JN860677/USA/2009
MT367399/China:Zhejiang/2015
MH910663/USA/1997
MH910664/USA/1997
KJ019885/China:Hubei/2012
KJ019879/China:Hubei/2013
KJ019880/China:Hubei/2012
KJ019881/China:Hubei/2012
KJ019882/China:Hubei/2012
KJ019886/China:Hubei/2013
KJ019887/China:Hubei/2013
KJ019883/China:Hubei/2013
KJ019888/China:Hubei/2012
    KP896480/China:Shanxi/2013
    KP896479/China:Hubei/2013
MH910668/USA/1997
MH910667/USA/1999
MH910666/USA/1996
                                    MH910669/USA/1960s
                                    MN936178/USA/2008
                                    MH910662/USA/1955
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0.002

B         HAdV-B14

MG905100/Ireland/2010
MF062484/China/2010
MG905105/USA/2007
MG905108/USA/2012
MG905106/USA/2008
MG642753/USA/2010

MH669071/USA/2009
MG905103/USA/2003
MG905107/USA/2012
JN032132/China/2011
MH669070/USA/2006
MG642754/USA/2012
MG642755/USA/2011
KP896482/China:Gansu/2013 ●
JQ824845/China:Guangdong/2010
MG905099/USA/2006
MG905104/USA/2006
MG905101/Canada/2011
MG642751/USA/2009
MH669073/USA/2009

MG642748/USA/2010
MG642744/USA/2010
MG642752/USA/2009
MG642756/Nepal/2007
MG642743/USA/2005
MG642745/USA/2009
MG642746/UnitedKingdom/2011
MG642747/USA/2011
MG642750/Honduras/2008
MG642742/USA/2012
MG642749/USA/2010

MG905109/USA/2007
MG905102/USA/2012
FJ822614/USA/2007
JX892927/China:Liaoning/2012 ●
MH669072/USA/2009

MG905112/Netherlands/1974
MG905111/Netherlands/1957

$9\times10^{-5}$

C         HAdV-B55

MW053454/SouthKorea/2019
MK123978/China:Guangdong/2018
KF906413/South_Korea/HAdVB11/2010

AY163756/USA/HAdVB11/
AF532578/Sweden/HAdVB11/

KP896484/China:Tianjin/2013 ●
MT806175/China:Hebei/2019
MT806174/China:Hebei/2019
MN654395/Spain/1969
MN654389/Singapore/2005
MN654382/Egypt/2002
MH256657/China:Sichuan/2018
KX289874/China:Jiangsu/2015
JX123028/China:Chongqing/2011
MT513753/USA/2006
KF908851/China:Tianjin/2013
MN654393/Japan/2012
MN654386/Egypt/2007
MN654376/SouthKorea/2009
KY471323/SouthKorea/2016
KJ883522/China:Shanxi/2011 ●
FJ643676/China:Shanxi/2006
MN654394/USA/1976
MN654391/Egypt/2005
MN654385/Egypt/2000
MK886831/China:Beijing/2015
KY471320/SouthKorea/2016
JX491639/China:Beijing/2011
FJ597732/Singapore/HAdVB11/2005
MN654392/USA/1997
MN052861/China:Jiangsu/2018
KY780932/China:Guangdong/2016
KY070248/China:Guangdong/2016
KP279748/China:Anhui/2012
KC857701/China:Jiangsu/2012
MN654384/Egypt/2008
MK123981/China:Guangdong/2013
KX494979/SouthKorea/2016
JX123029/China:Chongqing/2012
MN654387/Egypt/2009
KP896483/China:Liaoning/2013 ●
KJ883521/China:Hebei/2013
KJ883520/China:Hebei/2013
MN654380/Egypt/2000
MH256656/China:Sichuan/2018
KP896478/China:Hebei/2012 ●
JX123027/China:Chongqing/2010

0.005

SUPPLEMENTARY FIGURE S3. Phylogenetic tree was constructed based on the Penton gene using maximum likelihood method with 1,000 bootstrap by MEGA 7.0. (A) HAdV-B7; (B) HAdV-B14; (C) HAdV-B55.
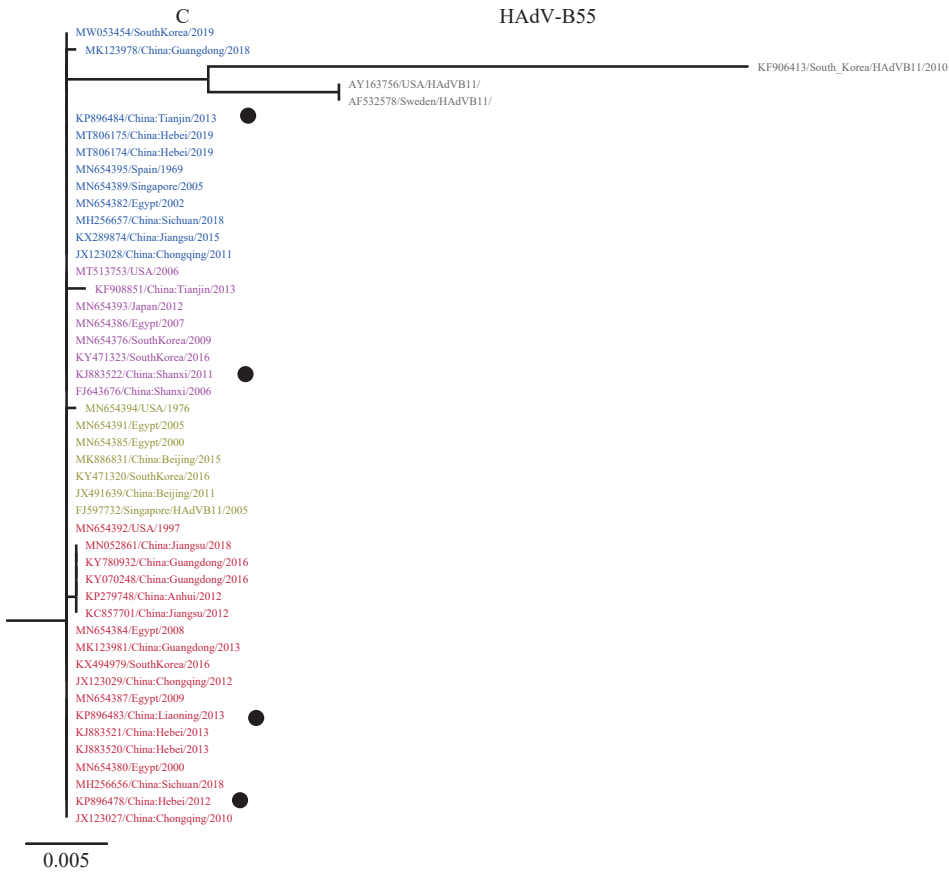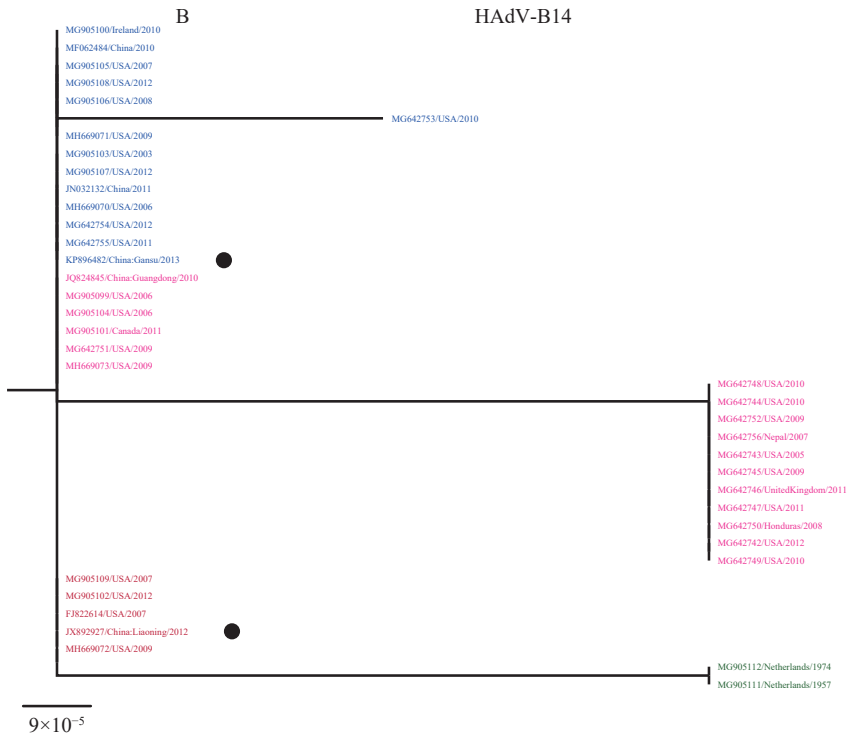Note: The strains labeled with black dots were obtained from the current study.