

Electronic Supplementary Material

Genetic Analysis of Human Adenovirus Type 7 Strains Circulating in Different Parts of China

Yali Duan¹ • Changchong Li² • Li Deng³ • Shuhua An⁴ • Yun Zhu¹ • Wei Wang¹ • Meng Zhang¹ • Lili Xu¹ • Baoping Xu¹ • Xiangpeng Chen¹✉ • Zhengde Xie¹✉

1. Beijing Key Laboratory of Pediatric Respiratory Infection Diseases, Key Laboratory of Major Diseases in Children, Ministry of Education, National Clinical Research Center for Respiratory Diseases, Research Unit of Critical Infection in Children, Chinese Academy of Medical Sciences, 2019RU016, Laboratory of Infection and Virology, Beijing Pediatric Research Institute, Beijing Children's Hospital, Capital Medical University, National Center for Children's Health, Beijing 100045, China
2. The 2nd Affiliated Hospital and Yuying Children's Hospital of Wenzhou Medical University, Wenzhou 325027, China.
3. Guangzhou Women and Children's Medical Center, Guangzhou 510623, China
4. Children's Hospital of Hebei Province, Shijiazhuang 050031, China

Supporting information to DOI: 10.1007/s12250-020-00334-y

Table S1. Clinical strains of HAdV-7 in this study.

Strain name	Date of isolation	Place of isolation	Sequences obtained	GenBank accession number
HB016#*	2014	Shijiazhuang	Complete genome	MT367398
HB054#*	2014	Shijiazhuang	Complete genome	MT367397
HB115#*	2015	Shijiazhuang	Complete genome	MT367396
HB128#*	2015	Shijiazhuang	Complete genome	MT367395
HB140#*	2015	Shijiazhuang	Complete genome	MT367394
WZ059#*	2015	Wenzhou	Complete genome	MT367399
GZ042#*	2016	Guangzhou	Complete genome	MT367400
BJ20160228	2016	Beijing	Hexon, penton base, fiber genes	MT332546/MT332489/MT332432
BJ20160237	2016	Beijing	Hexon, penton base, fiber genes	MT332547/MT332490/MT332433
BJ20160286	2016	Beijing	Hexon, penton base, fiber genes	MT332548/MT332491/MT332434
BJ20160429	2016	Beijing	Hexon, penton base, fiber genes	MT332549/MT332492/MT332435
BJ20160442	2016	Beijing	Hexon, penton base, fiber genes	MT332550/MT332493/MT332436
BJ20160617	2016	Beijing	Hexon, penton base, fiber genes	MT332551/MT332494/MT332437
BJ20160773	2016	Beijing	Hexon, penton base, fiber genes	MT332552/MT332495/MT332438
BJ20160789	2016	Beijing	Hexon, penton base, fiber genes	MT332553/MT332496/MT332439
BJ285#*	2017	Beijing	Complete genome	MT367405
BJ293#*	2017	Beijing	Complete genome	MT367404
BJ321#*	2017	Beijing	Complete genome	MT367403
BJ354#*	2017	Beijing	Complete genome	MT367402
BJ355#*	2017	Beijing	Complete genome	MT367401
BJ282#	2017	Beijing	Hexon, penton base, fiber genes	MT332575/MT332518/MT332461
BJ295#	2017	Beijing	Hexon, penton base, fiber genes	MT332578/MT332521/MT332464
BJ322#	2017	Beijing	Hexon, penton base, fiber genes	MT332580/MT332523/MT332466
BJ324#	2017	Beijing	Hexon, penton base, fiber genes	MT332581/MT332524/MT332467
BJ325#	2017	Beijing	Hexon, penton base, fiber genes	MT332582/MT332525/MT332468
BJ326#	2017	Beijing	Hexon, penton base, fiber genes	MT332583/MT332526/MT332469
BJ331#	2017	Beijing	Hexon, penton base, fiber genes	MT332584/MT332527/MT332470
BJ356#	2017	Beijing	Hexon, penton base, fiber genes	MT332587/MT332530/MT332473
BJ20180256#*	2018	Beijing	Complete genome	MT350344
BJ20180570#*	2018	Beijing	Complete genome	MT350345
BJ20180683#*	2018	Beijing	Complete genome	MT350346
BJ20180723#*	2018	Beijing	Complete genome	MT367406
BJ20180728#*	2018	Beijing	Complete genome	MT367407
GZ17059	2018	Guangzhou	Hexon, penton base, fiber genes	MT332588/MT332531/MT332474
GZ17081	2018	Guangzhou	Hexon, penton base, fiber genes	MT332589/MT332532/MT332475
GZ17085	2018	Guangzhou	Hexon, penton base, fiber genes	MT332590/MT332533/MT332476
GZ17094	2018	Guangzhou	Hexon, penton base, fiber genes	MT332591/MT332534/MT332477
GZ17097	2018	Guangzhou	Hexon, penton base, fiber genes	MT332592/MT332535/MT332478
GZ17163	2018	Guangzhou	Hexon, penton base, fiber genes	MT332593/MT332536/MT332479

WZ17156	2018	Wenzhou	Hexon, penton base, fiber genes	MT332594/MT332537/MT332480
WZ17158	2018	Wenzhou	Hexon, penton base, fiber genes	MT332595/MT332538/MT332481
WZ17160	2018	Wenzhou	Hexon, penton base, fiber genes	MT332602/MT332539/MT332482
WZ17165	2018	Wenzhou	Hexon, penton base, fiber genes	MT332596/MT332540/MT332483
WZ17169	2018	Wenzhou	Hexon, penton base, fiber genes	MT332597/MT332541/MT332484
WZ17177	2018	Wenzhou	Hexon, penton base, fiber genes	MT332598/MT332542/MT332485
WZ17180	2018	Wenzhou	Hexon, penton base, fiber genes	MT332599/MT332543/MT332486
WZ17183	2018	Wenzhou	Hexon, penton base, fiber genes	MT332600/MT332544/MT332487
WZ17190	2018	Wenzhou	Hexon, penton base, fiber genes	MT332601/MT332545/MT332488
BJ20180270#	2018	Beijing	Hexon, penton base, fiber genes	MT332555/MT332498/MT332441
BJ20180287#	2018	Beijing	Hexon, penton base, fiber genes	MT332556/MT332499/MT332442
BJ20180296#	2018	Beijing	Hexon, penton base, fiber genes	MT332557/MT332500/MT332443
BJ20180593#	2018	Beijing	Hexon, penton base, fiber genes	MT332559/MT332502/MT332445
BJ20180702#	2018	Beijing	Hexon, penton base, fiber genes	MT332561/MT332504/MT332447
BJ20180713#	2018	Beijing	Hexon, penton base, fiber genes	MT332562/MT332505/MT332448
BJ20180733#	2018	Beijing	Hexon, penton base, fiber genes	MT332565/MT332508/MT332451
BJ20180765#	2018	Beijing	Hexon, penton base, fiber genes	MT332566/MT332509/MT332452
BJ20180771	2018	Beijing	Hexon, penton base, fiber genes	MT332567/MT332510/MT332453

Thirty-three HAdV-7 isolated in this study.

* Seventy strains with complete genome sequence.

Table S2. Primers used for amplification of the complete genome, penton base, hexon, and fiber gene.

Primer	Sequences (5'-3' orientation)	Position ^a
HAdV7-1F	GTGTGGTGATTGGCTGTG	71-88
HAdV7-1R	TAGTCTGTCTGAGGTCTTCC	1,620-1,639
HAdV7-2F	GCTTGAGGACTTGTGGA	1,383-1,400
HAdV7-2R	TCAGGTCTTCAGTCACATC	3,297-3,315
HAdV7-3F	ATGCCTTACCAGTGTAACAT	3,105-3,124
HAdV7-3R	AACTTCTCCTCGCTCCAG	4,942-4,959
HAdV7-4F	GCCACTTCGTTTCATCATT	4,856-4,873
HAdV7-4R	CATATTCCAGAGACCTACTATC	6,777-6,798
HAdV7-5F	GCTCGCACATAGTCATAGA	6,658-6,676
HAdV7-5R	CTACTTCCATCACATCAACAG	7,879-7,899
HAdV7-6F	TGAGGAAGGAGGACCAGA	7,535-7,552
HAdV7-6R	CAACGATACCGAGATTGATTC	8,640-8,660
HAdV7-7F	TTGACATCCTGGATCTGAC	8,565-8,583
HAdV7-7R	CTAGAGCATCAACGACTGT	10,373-10,391
HAdV7-8F	TACTGGTAGCCGATGAGAA	10,131-10,149
HAdV7-8R	CGTCCGAGGAGTTAATGC	12,084-12,101
HAdV7-9F	CATAGAAGAGGTGGATGAAGT	11,944-11,964
HAdV7-9R	TCGTAAGAAGGAGGAGGAC	13,923-13,941
HAdV7-10F	CACAATTACCACCGTCAGT	15,328-15,346
HAdV7-10R	GCAGCGTCAACAGTCATT	17,194-17,211
HAdV7-11F	CCATCCATCATTCCCCTC	16,968-16,986
HAdV7-11R	ACTGAAGTAGGTGTCTGTTG	18,492-18,511
HAdV7-12F	CCTGCTCTATGCCAACTC	21,010-21,027
HAdV7-12R	GGATAATGACCTGAGAACCT	22,940-22,959
HAdV7-13F	TGCTCCTCGTTCACATAC	22,870-22,887
HAdV7-13R	CAGTCTCGGATGTAGTCAC	24,865-24,883
HAdV7-14F	TTATGATGGCTGTAGTGCTA	24,622-24,641
HAdV7-14R	GGTCTTCGCTCTTGTGAT	26,511-26,528
HAdV7-15F	AGGAGGAGGACTGAGGAT	26,347-26,364
HAdV7-15R	TGTTACTAATGCGGATGGAA	28,338-28,357
HAdV7-16F	CGTCTCTGTGGAGTTCTTAT	28,189-28,208
HAdV7-16R	CGTAGGTAGGCAATTCGTA	30,172-30,190
HAdV7-17F	CTTCTTACCATACTCATCTG	29,987-30,007

HAdV7-17R	GTGCTTTCATCTTCATAGGG	31,297-31,316
HAdV7-18F	TTAGAGAAGACGACTGACAA	32,213-33,232
HAdV7-18R	CACAAGAACTGACACGAATA	33,952-33,971
HAdV7-19F	GGAAGAGACGGAAGAATCA	33,663-33,681
HAdV7-19R	GGAATGGTGCCAATATGC	35,193-35,210
HAdV7-20F	CGTGATTAACAACAGCACCGAAAGTT	34,570-34,596
HAdV7-20R	ATAATATACCTTATAGATG	35,210-35,228
HAdV7-21F	CTCTCTATTTAATATACCTTATAGATGG	1-28
HAdV7-21R	CTCAGAAATTCACCTCCTCATTGAGTTT	293-320
HAdV7-Penton-1F ^b	GATGATAGCAGCGTGTGGA	13,699-13,718
HAdV7-Penton-1R ^b	GGTGCTGGGTAGAGCGTATG	15,595-15,614
HAdV7-Hexon -1F ^b	CTGAACAGCATCGTGGGTCT	18,219-18,238
HAdV7-Hexon -1R ^b	ACTCGCCCGTTCATGTACTC	19,837-19,856
HAdV7-Hexon -2F ^b	CGTCGAGGATGAACTGCCTA	19,560-19,579
HAdV7-Hexon -2R ^b	CAGTGTTGACTATGGCGCAG	21,363-21,382
HAdV-7-Fiber-1F ^b	GAAATTTTCTCCCAGCAGCA	31,100-31,119
HAdV-7-Fiber-1R ^b	ATTGGCTCGCTTTGAAACTG	32,392-32,411

^aThe nucleotide positions indicated are those according to HAdV-7 (GenBank accession number MG696136).

^bThese primers are quoted from reference (Chen *et al.*, 2015).

Table S3. Reference sequences used in this study.

Accession Number	Year	Location	Type*
AY495969	2004 (deposited)	CHN	HAdV-7a
AY594255	1954	USA	HAdV-7p
AY594256	2006 (deposited)	USA	HAdV-7a
AY601634	1997	USA	-
JN860677	2009	USA	HAdV-7d2
JX423383	2006	USA	HAdV-7d2
JX423387	1997	USA	HAdV-7d2
JX423388	1997	USA	HAdV-7b
KF268125	1988	USA	HAdV-7a
KF268134	1988	USA	-
KF268135	unknown	USA	-
KT963081	2014	USA	HAdV-7d
KU361344	2014	RUS	-
MG923582	2013	RUS	-
MH262318	2016	USA	-
MH262319	2016	USA	-
MH262320	2016	USA	-
MH262321	2016	USA	-
MH262322	2017	USA	-
MH262323	2017	USA	-
MH262324	2017	USA	-
MH262325	2017	USA	-
MH262326	2017	USA	-
MH697600	2017	USA	-
MH697604	2017	USA	-
MH697605	2017	USA	-
MH697606	2017	USA	-
MH697607	2017	USA	-
MH910669	1960s	USA	-
MH910662	1955	USA	-
KP670855	2011	CHN	-
GQ478341	2008	CHN	-
HQ659699	2007	CHN	-
JF800905	2009	CHN	HAdV-7d
JX625134	2010	CHN	HAdV-7d
KC440171	2011	CHN	HAdV-7d
KC857700	2012	CHN	-
KF268314	2011	CHN	-

KF268316	2011	CHN	-
KJ019879	2013	CHN	-
KJ019880	2012	CHN	-
KJ019881	2012	CHN	-
KJ019882	2012	CHN	-
KJ019883	2013	CHN	-
KJ019884	2012	CHN	-
KJ019885	2012	CHN	-
KJ019886	2013	CHN	-
KJ019887	2013	CHN	-
KJ019888	2012	CHN	-
KP670856	2011	CHN	-
KP670857	2011	CHN	-
KP670858	2010	CHN	-
KP670859	2012	CHN	-
KP670860	2012	CHN	-
KP670861	2011	CHN	-
KX897164	2015	CHN	-
MH355567	2018	CHN	-

* Types identified by restriction endonuclease analysis.

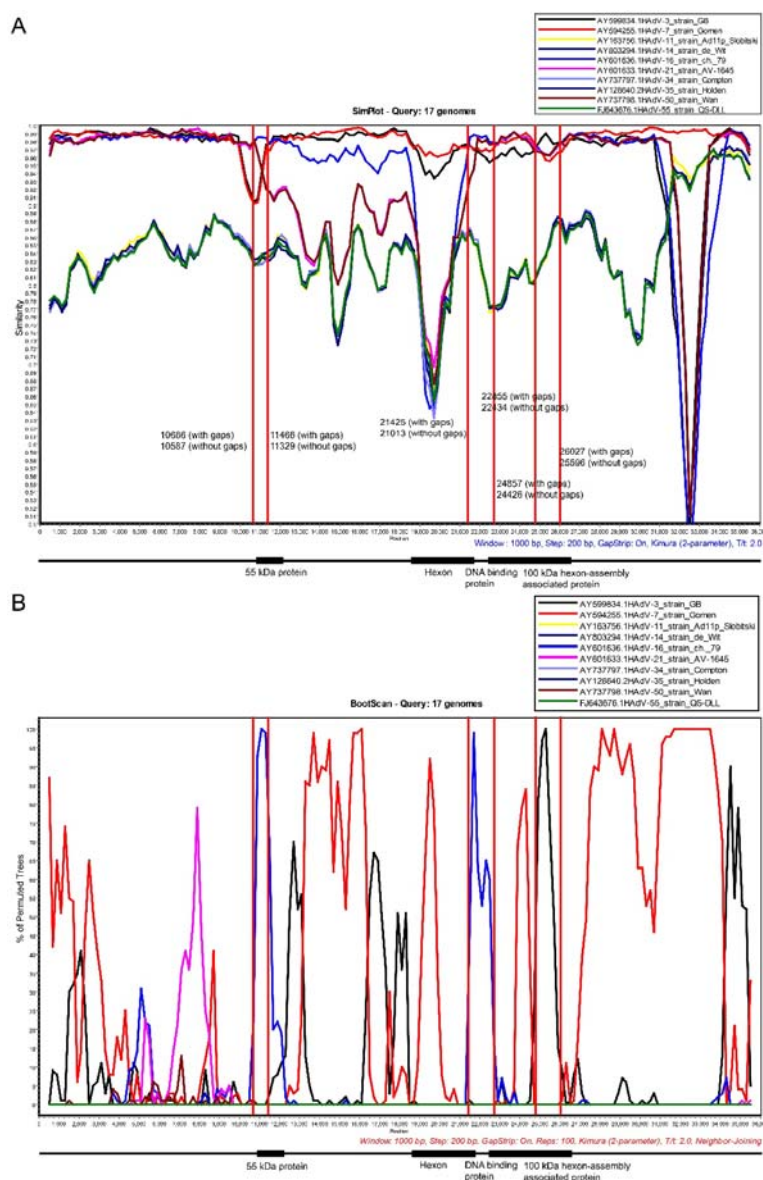


Fig. S1. (A) Simplot and (B) Bootscan analysis of 17 HAdV-7 strains in this study compared with other species B adenoviruses. Recombination analysis was performed by using Simplot with the following input: window size (1000 nucleotides [nt]), step size (200 nt), distance model (Kimura), and tree model (neighbor-joining). The GenBank accession numbers of prototype of each HAdV are as follows: HAdV-3, AY599834; HAdV-7, AY594255; HAdV-11, AY163756; HAdV-14, AY803294; HAdV-16, AY601636; HAdV-21, AY601633; HAdV-34, AY737797; HAdV-35, AY128640; HAdV-50, AY737798; HAdV-55, FJ643676. 55 kDa protein, 10,833–12,002 nucleotide gene location of BJ285, without gaps; 10970–12145 nucleotide gene location, with gaps. Hexon protein, 18,397–21,201 nucleotide gene location of BJ285, without gaps; 18675–21613 nucleotide gene location, with gaps. DNA binding protein, 21,956–23,509 nucleotide gene location of BJ285, without gaps; 22377–23934 nucleotide gene location, with gaps. 100 kDa hexon-assembly associated protein, 23,540–26,029 nucleotide gene location of BJ285, without gaps; 23965–26460 nucleotide gene location, with gaps.

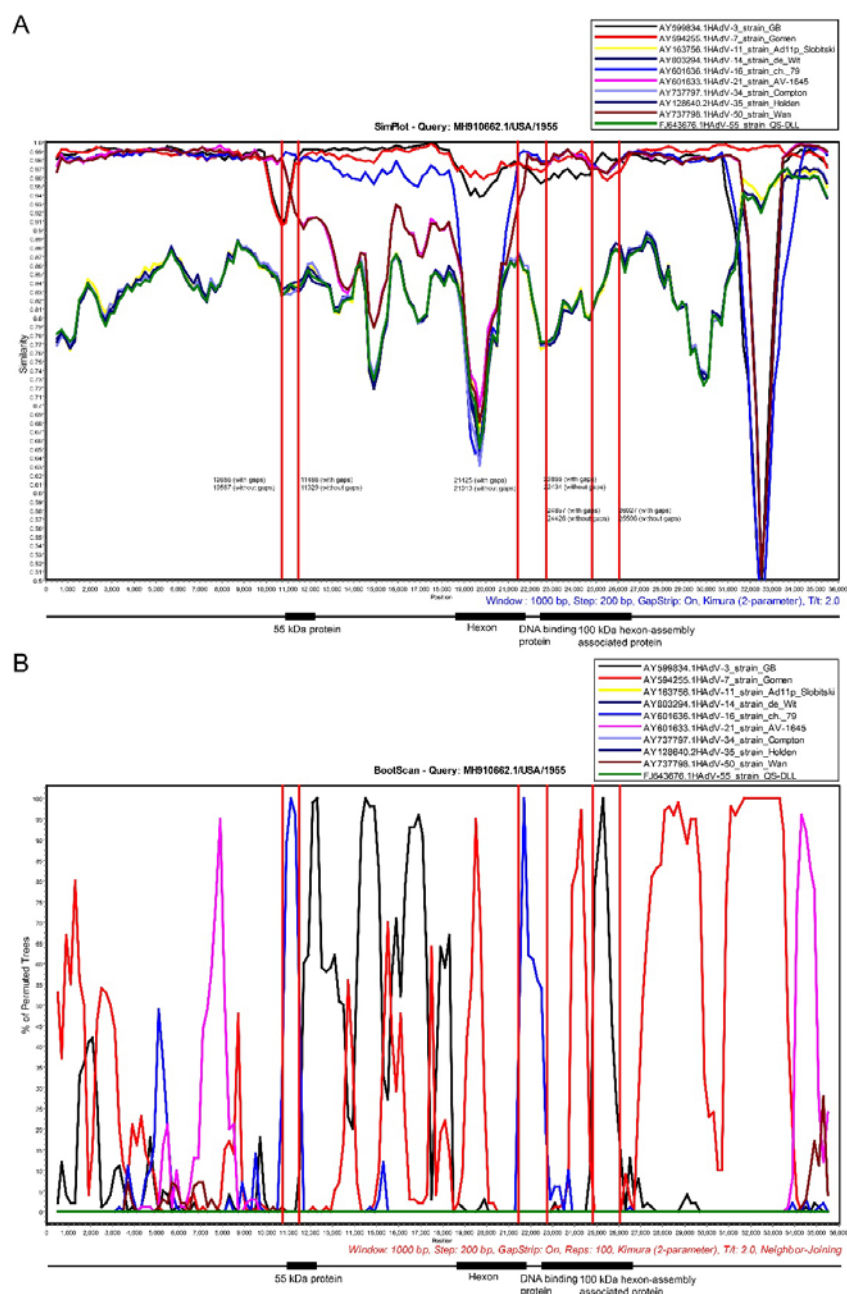


Fig. S2. (A) Simplot and (B) Bootscan analysis of the whole genomes of U.S. strain MH910662 isolated in 1955 compared to other species B adenoviruses. Recombination analysis was performed by using Simplot with the following input: window size (1000 nucleotides [nt]), step size (200 nt), distance model (Kimura), and tree model (neighbor-joining). The GenBank accession numbers of prototype of each HAdV are as follows: HAdV-3, AY599834; HAdV-7, AY594255; HAdV-11, AY163756; HAdV-14, AY803294; HAdV-16, AY601636; HAdV-21, AY601633; HAdV-34, AY737797; HAdV-35, AY128640; HAdV-50, AY737798; HAdV-55, FJ643676. 55 kDa protein, 10,833–12,002 nucleotide gene location of BJ285, without gaps; 10970–12145 nucleotide gene location, with gaps. Hexon protein, 18,397–21,201 nucleotide gene location of BJ285, without gaps; 18675–21613 nucleotide gene location, with gaps. DNA binding protein, 21,956–23,509 nucleotide gene location of BJ285, without gaps; 22377–23934 nucleotide gene location, with gaps. 100 kDa hexon-assembly associated protein, 23,540–26,029 nucleotide gene location of BJ285, without gaps; 23965–26460 nucleotide gene location, with gaps.

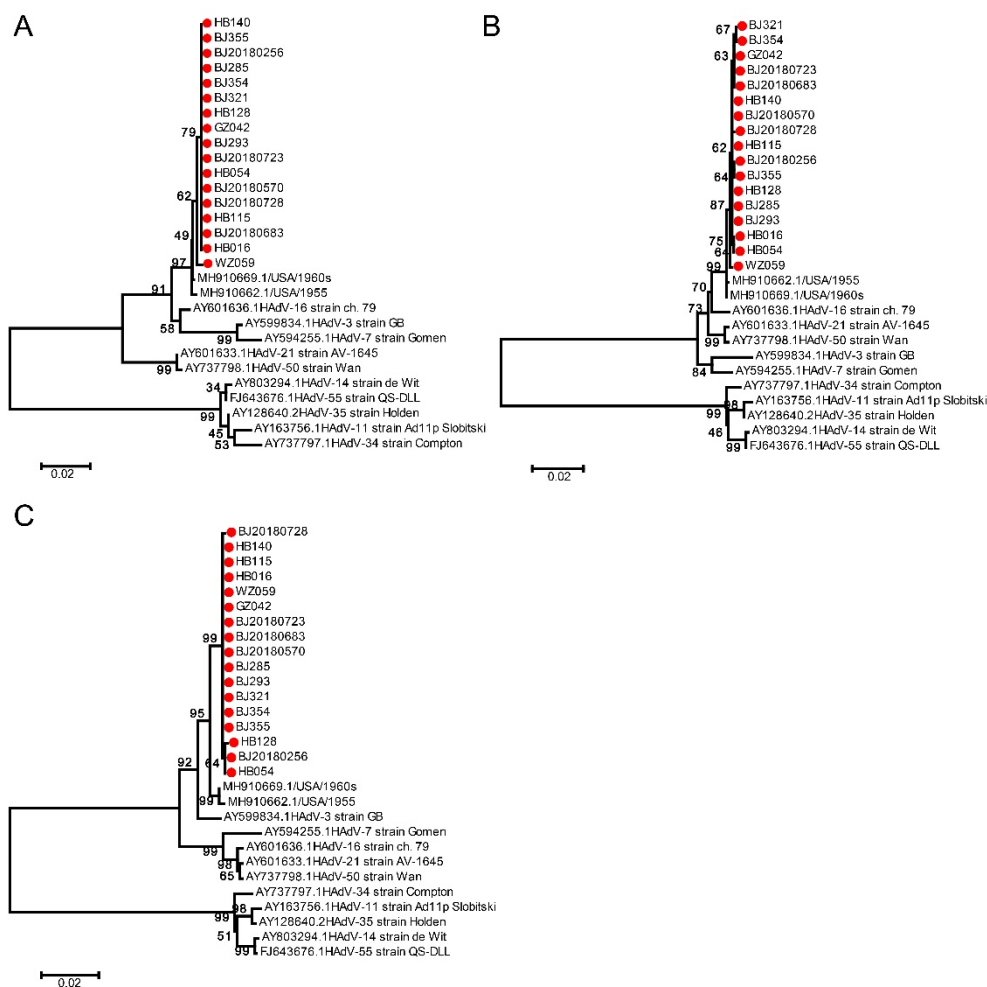


Fig. S3. Phylogenetic analysis of recombinant region 1 (A), recombinant region 2 (B) and recombinant region 3 (C). Recombinant region 1: 10,587-11,329 nucleotide gene location of BJ285, without gaps; recombinant region 2: 21,013-22,434 nucleotide gene location of BJ285, without gaps; recombinant region 3: 24,426-25,596 nucleotide gene location of BJ285, without gaps. The phylogenetic tree was generated by using the neighbor-joining method based on the Kimura two-parameter model with 1000 replicates. The red dots indicate strains obtained in this study.