

Animal Rabies Surveillance, China, 2004–2018

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Rabies is a severe zoonotic disease in China, but the circulation and distribution of rabies virus (RABV) within animal reservoirs is not well understood. We report the results of 15 years of surveillance of the first Chinese Rabies Surveillance Plan in animal populations, in which animal brain tissues collected during 2004–2018 were tested for RABV and phylogenetic and spatial–temporal evolutionary analyses performed using obtained RABV sequences. The results have provided the most comprehensive dataset to date on the infected animal species, geographic distribution, transmission sources, and genetic diversity of RABVs in China. In particular, the transboundary transmission of emerging RABV subclades between China and neighboring countries was confirmed. The study highlights the importance of continuous animal rabies surveillance in monitoring the transmission dynamics, and provides updated information for improving current control and prevention strategies at the source.

Rabies is a fatal zoonotic disease of humans and almost all warm-blooded animals, causing severe dysfunction of the central nervous system (1). About 99% of human cases occur in developing countries, mainly in Asia and Africa (2). Rabies is a major public issue throughout China, resulting in several hundred human deaths every year during 2015–2018 (3). More than 95% of human rabies cases are caused by rabid dogs (4). In contrast, the numbers of animal rabies cases reported in China are much lower than those

of humans; only several provinces, autonomous regions, or municipalities report animal rabies cases to national veterinary authorities, as disseminated by the Veterinary Bulletin, the only official journal to report monthly information on animal infectious diseases in China (5). Even so, such scattered studies have still shown an increase in wildlife rabies in red foxes (*Vulpes vulpes*), raccoon dogs (*Nyctereutes procyonoides*), and ferret badgers (*Melogale moschata* in the mainland and *Melogale moschata subaurantiaca* in Taiwan). Rabies in dogs and livestock has also increased and expanded geographically to include Heilongjiang, Inner Mongolia, Xinjiang, Qinghai, Tibet, and Taiwan, provincial regions within which rabies had rarely or never been reported previously (6–11). These investigations had monitored the emergence of fox- and raccoon dog-specific RABVs in north China that caused the outbreaks in livestock; some wildlife isolates shared a high nucleotide identity with those circulating in neighboring countries (6,7,10). This similarity is a matter for concern because China is surrounded by 14 contiguous countries, all of which are rabies endemic and within which the genetic diversity and phylogenetic characteristics of RABVs have not been well studied.

An understanding of the status of animal rabies is a prerequisite for control and possible elimination of human rabies. Since 2004, China has implemented annual surveillance of animal rabies, with the National Reference Laboratory for Animal Rabies at the Institute of Military Veterinary Medicine, (Changchun, Jilin Province, China) as the project leader (12). This surveillance focuses mainly on dogs, cats, livestock, and wild animal reservoirs that have the potential to maintain the circulation and transmission of RABVs in China. As part of this program, using the epidemiologic information collected and nucleoprotein (N) gene sequences of RABV isolates obtained during 2004–2018, we investigated the infected animal species, geographic distribution, animal sources, and

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DOI: <https://doi.org/10.3201/eid2612.200303>

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genetic diversity of RABVs in China, as well as their phylogenetic and phylogeographic relationships with those of neighboring countries. Our objective was to provide updated information about the animal rabies situation and its public health impact in China and neighboring countries.

Methods

Sample Collection and Detection of Rabies Virus

Since 2004, the Ministry of Agriculture and Rural Affairs of China has implemented the Rabies Surveillance Plan with a focus on free-roaming and stray dogs and cats, especially those showing abnormal behaviors such as biting humans. The plan also requires the monitoring of suspected rabies outbreaks in livestock and wild animals. During 2004–2018, brain tissues of 185 animals suspected of having rabies (dead dogs, dogs behaving strangely or biting humans, livestock showing rabieslike clinical signs, dead foxes, wolves, and raccoon dogs) were submitted (Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/26/12/20-0303-App1.pdf>). In addition, 10,118 brain tissues were collected for active surveillance from 3 types of apparently healthy dogs, mostly from rabies-endemic rural areas: free-roaming and ownerless dogs, slaughtered dogs (for meat consumption), and dogs killed during emergencies (culled in rabies outbreak areas to prevent further transmission) (Appendix Table 2). All specimens were collected and submitted to the reference laboratory by the regional Centers of Animal Disease Prevention and Control.

The brain tissues were examined by the direct fluorescent antibody test (FAT) using FITC-conjugated anti-rabies monoclonal antibody (Fujirebio Diagnostics Inc., <https://www.fujirebio.com>) (13). To obtain the complete coding sequence of the N gene, rabies-positive specimens were subjected to RNA extraction using TRIzol Reagent (Invitrogen, <https://www.thermofisher.com>), followed by reverse transcription PCR with the SuperScript III First-Strand Synthesis System and the Platinum Taq DNA Polymerase High Fidelity kit (Invitrogen) (6).

Gene Sequencing and Phylogenetic Analysis

Amplified N gene sequencing was performed commercially by the Sanger method and submitted to GenBank (see Appendix Table 3 for accession numbers). Phylogenetic analysis of the complete N gene was performed on these sequences and on representative sequences retrieved from GenBank, covering samples collected in China and its neighboring coun-

tries from the 1940s through 2018 (Appendix Table 3). The MEGA 7 program package was used to construct the phylogenetic trees using the neighbor-joining method with 1,000 bootstrap replicates (14). Trees were visualized using Figtree version 1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree>).

To rank the prevalence of the different RABV phylogroups and to analyze their transmission trends in China, we retrieved the sequences of all RABV strains from China deposited in GenBank. After we removed duplicate sequences and those without clear time information, we phylogenetically classified the remaining sequences, along with those obtained during this study, by the procedure described previously and chronologically sorted them by collection date.

Spatial–Temporal Evolutionary Analysis

To investigate the temporal signal and clock likeness of molecular phylogenies based on the N gene dataset, the linear evolutionary rates of different RABV clades were estimated using the Bayesian Markov chain Monte Carlo in BEAST version 1.8.2 package (15,16). For these analyses, we selected the general time reversible model as the substitution model and gamma plus invariable sites as the site heterogeneity model based on the calculations of Model Generator (17,18). An uncorrelated log normal relaxed molecular clock model and the constant size model as a coalescent tree prior were also selected for the analyses, which were run for 100 million steps with sampling at every 10,000 states (19). The BEAGLE parallel computation library was used to enhance the speed of the likelihood calculations (20). Finally, the resulting log file was checked using TRACER version 1.5 (<http://tree.bio.ed.ac.uk/software/tracer>) to confirm that all effective sample sizes were >200. The tree file was obtained using TreeAnnotator version 1.8.2 with a burn-in of 10%, and the maximum clade credibility tree was visualized by FigTree version 1.4.2 (16). Based on the analyses, estimations were made of the rates of nucleotide substitution and the time to most recent common ancestor (tM-RCA) for each RABV clade.

To investigate the phylogeographic spread of RABVs in China and neighboring countries, we used a Bayesian stochastic search variable selection (BSSVS) approach to analyze transmission routes of RABV subclades, in which we applied a Bayes factor to determine the best supported transmission event between 2 geographic locations. Bayes factors were calculated by Spread3 software with a value >3 as cutoff (21,22).

Results

Current Animal Rabies Situation in China

During 2004–2018, animal brain tissues collected from 185 animals with suspected rabies in 17 provinces were submitted to our laboratory; 144 of them (77.8%) were confirmed by FAT as rabies virus positive (Appendix Table 1). Among the positive species, dogs were the main infected animals, accounting for 68.8% of total cases (99/144), followed by cattle (12.5%), sheep (9.7%), camels (4.2%), foxes (2.1%), pigs (1.4%), raccoon dogs (0.7%), and donkeys (0.7%) (Appendix Table 1). Concurrently, 33 (0.33%) of 10,118 brain tissue samples taken during an active surveillance of apparently healthy dogs from 7 provinces across China were found to be FAT-positive. Of the 33 positive specimens, 31 were from free-roaming and ownerless dogs (including stray dogs) and 2 were from dogs killed during an emergency (Appendix Table 2). For livestock rabies, 29 cattle, sheep, and camel cases were reported in Inner Mongolia and Xinjiang during 2013–2018, all of which were caused by fox bites (Appendix Table 1).

Phylogenetic Analysis and Evolution of Animal RABVs in China

A total of 108 complete N genes were amplified from 177 positive brain tissue samples. Of these, we selected 78, representing different years, animal species, outbreaks, and locations, together with 222 reference sequences from China, as well as from neighboring and other countries, to determine their phylogenetic characteristics (Appendix Table 3). Animal RABVs in China were clustered within 4 major clades: Asian, Cosmopolitan, Arctic-related, and Indian Subcontinent, together with different subclades (Figure 1). The Asian clade, the most prevalent one, widely distributed throughout China and Southeast Asia (SEA) countries, shows abundant genetic diversity and is transmitted mainly by dogs. This lineage was further divided into 5 subclades and different lineages. SEA1, 2, 3, and 5 subclades circulate mainly in populous areas within China; however, some lineages and strains in SEA1 and 3 were also found circulating in some countries in Southeast Asia, whereas SEA4 was restricted to the Philippines (Figure 2). Reported only in China, ferret badger RABVs were found to have abundant genetic diversity and were segregated into different lineages within SEA1, 2, and 5 (Figure 1) (23). Within the Cosmopolitan clade, which includes some vaccine strains, a steppe-type subclade was fox-transmitted and distributed along north and northwest border areas and neighboring Mongolia, Russia, and Kazakhstan, forming 2 major lineages (Figure 1).

Other Cosmopolitan strains were dog-transmitted and mainly distributed in populous inland areas (Figure 2). Arctic-related RABVs in China segregated within the AL2 subclade and formed 2 lineages, one in northeastern China and far eastern Russia, Mongolia, and South Korea with dogs and raccoon dogs as the major hosts, and the other in southwestern China with dogs as the major transmission source (Figures 1,2). The Indian Subcontinent clade had not been identified in China until the first human rabies case caused by this clade was identified in 2017 in the border area of Tibet close to Nepal (24). That human case was caused by the bite of a local stray dog and remains the only Indian Subcontinent clade RABV confirmed so far in China.

For the chronological sorting of different subclades, we retrieved all 2,486 RABV sequences from China deposited in GenBank. After removing repeated sequences and those without date information, 1,118 eligible sequences remained, representing 1,118 Chinese strains isolated during 1969–2018 (including those in Figure 1). These sequences included complete genome ($n = 45$), full length or partial N ($n = 819$), glycoprotein (G; $n = 208$), phosphoprotein (P; $n = 15$), matrix protein (M; $n = 25$) and RNA-dependent RNA polymerase (L; $n = 6$) genes. Figure 3 shows the spatial-temporal trends of different RABV subclades in China, in which the 55 Chinese RABV sequences submitted to GenBank between 1969 (the earliest submission) and 2003 (therefore listed chronologically as “before 2004”) segregated within 3 SEA and 1 Cosmopolitan subclade. Following initiation of official rabies surveillance in 2004, numbers of sequences submitted to GenBank sharply increased and high numbers of submissions have been maintained thereafter. The resulting data showed clearly that most rabies outbreaks have been caused by strains of the Asian clade (93.3%), with limited involvement of strains of the other 3 clades. Within the Asian clade, the subclade SEA1 predominated in rabies endemics in China (70.1%), followed by SEA2 (16.7%). SEA1 is the most widely distributed of the subclades and continues to spread. The steppe-type subclade first emerged in 2011 and has rapidly become predominant among the livestock RABV strains found along border areas in Inner Mongolia and Xinjiang Province (Figure 2). AL2 was first detected in 2007 and has become a common subclade in recent years (10). The Indian Subcontinent clade caused an occasional case in 2017. The result showed that steppe-type, AL2, and Indian Subcontinent strains are emerging RABVs in China. Dog-transmitted Cosmopolitan strains have not been detected during the past decade.

Transmission of Animal Rabies in China and Neighboring Countries

Results of the Bayesian skyline model analysis showed that the mean rate of nucleotide substitution for the tested RABVs was 3.50×10^{-4} substitutions per site per year (95% highest posterior density $2.90\text{--}4.11 \times 10^{-4}$ substitutions per site per year). This finding is consistent with the previous analyses of evolutionary change performed on dog-related RABV N genes (25). Differences in evolutionary rates among the clades

and subclades were not significant. All representative RABVs in China and neighboring countries shared a tMRCA, predicted to merge 349–563 years ago (Figure 4). Further analysis of transmission routes of RABV subclades by BEAST revealed the transboundary transmissions of rabies in different border regions around China. The significant translocation pathway of SEA1 (Bayes factor 76.9) (Appendix Table 4) from China to Indonesia was identified in accordance with our previous analysis of the G gene (Figure 5) (26).

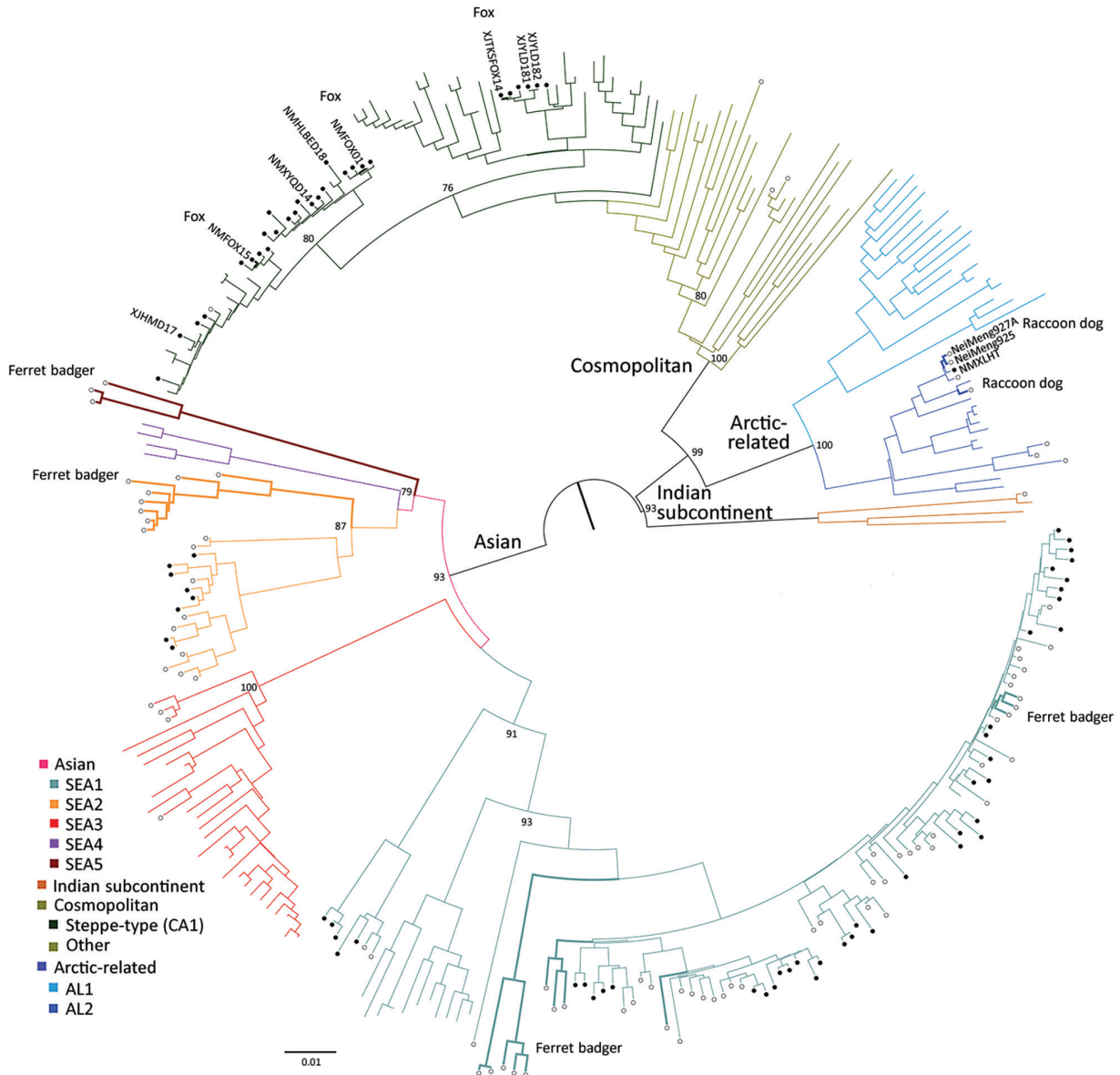


Figure 1. Phylogenetic analysis of 300 full rabies virus nucleoprotein sequences showed that RABVs in China could be classified into 4 major clades and 8 subclades. Bootstrap values = 1,000. Solid circles indicate sequences from this study; open circles indicate representative sequences from China previously published and retrieved from GenBank (Appendix Table 3, <https://wwwnc.cdc.gov/EID/article/26/12/20-0303-App1.pdf>). Unlabeled sequences are from surrounding countries; a few are vaccine sequences in the subclade of another Cosmopolitan clade. Named branches: dog isolates spilling out from wild animals; bold branches: wild animal isolates as indicated. SEA, Southeast Asia.

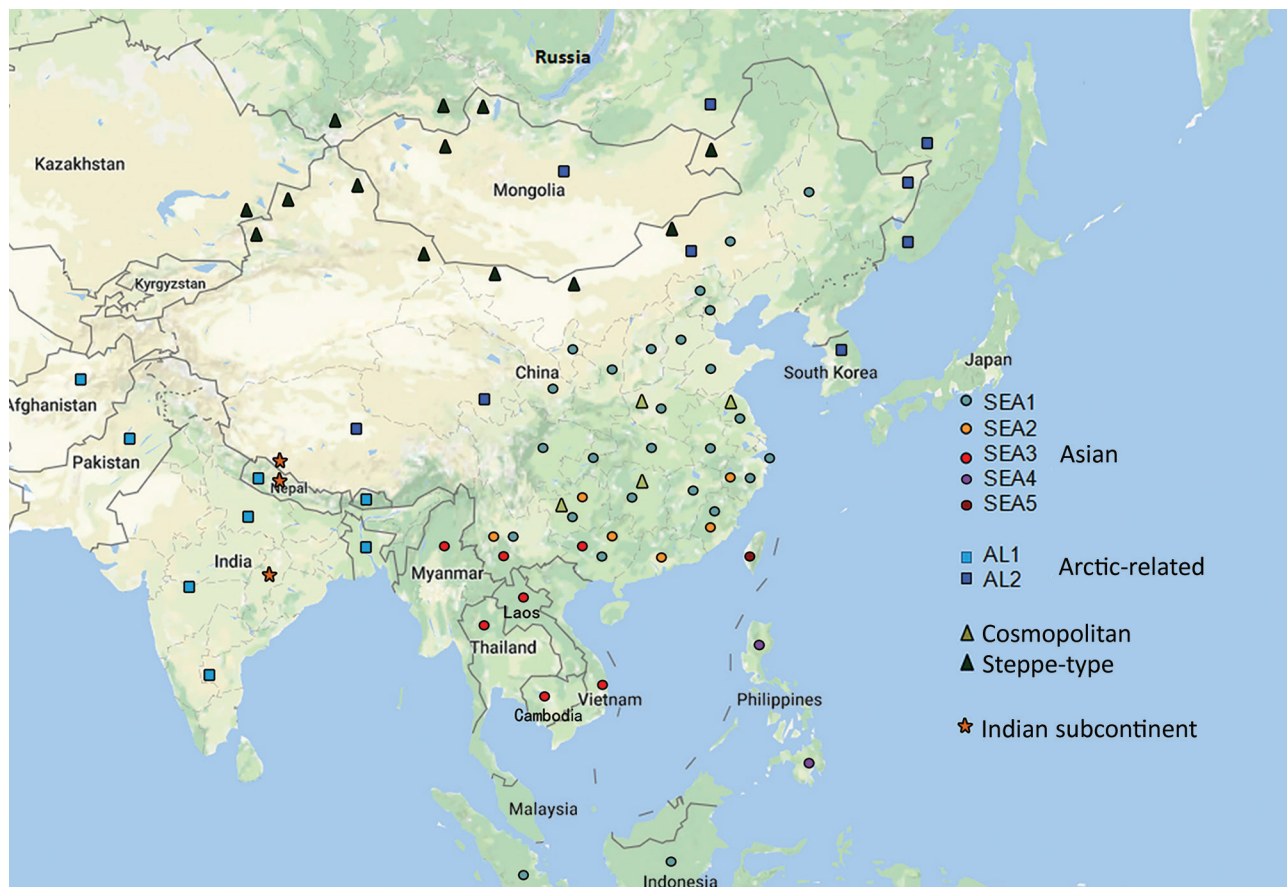


Figure 2. Geographic distribution of rabies virus clades and subclades in China and neighboring countries. The sequence information is from this study and GenBank (Appendix Table 3, <https://wwwnc.cdc.gov/EID/article/26/12/20-0303-App3.pdf>). SEA, Southeast Asia.

Moreover, many SEA3 strains in Myanmar, Thailand, Laos, and Vietnam were genetically close to some strains circulating in Yunnan and Guangxi, China, indicating mutual transmission of SEA3 strains between China and bordering SEA countries (Bayes factor 4.3–85.0), as discussed previously (27). The same transmission was also found for steppe-type and AL2 subclades in border regions between China and Kazakhstan, Russia, Mongolia, and South Korea (Bayes factor 3.17–229.87). The most noteworthy event was the recent cross-border transmission of an Indian subcontinent strain from Nepal to the border region of Tibet, albeit with a lower Bayes factor (0.9), which caused a human rabies death in 2017 (24).

Discussion

There have been studies of the genetic diversity and transmission dynamics of RABVs in China, but the background information was compiled mainly from RABVs collected before 2010 or restricted to several provinces or geographic regions (26,28–30). Information about the molecular epidemiology of RABV

within the past 10 years has been lacking, particularly within the context of the recently increasing animal rabies situation in the north, northwest, northeast, and southwest regions of China (6,7,31,32). In addition, although all the neighboring countries of China are rabies endemic, phylogenetic relationships and transboundary transmission of RABVs between China and these countries have not been systematically investigated; however, a 2013 study based on N gene sequences of RABV isolates collected before 2010 concluded that national borders effectively halted transboundary rabies transmission from China (33). Our study, however, has provided the most comprehensive update of RABV genetic diversity and transmission dynamics in China and has systematically compared these characteristics with those of neighboring countries, using many recent sequences obtained in our continuous surveillance during 2004–2018, along with many representative sequences from GenBank published in the past decade. The results have not only revealed the abundant genetic diversity of RABVs from China with many lineages or strains in most

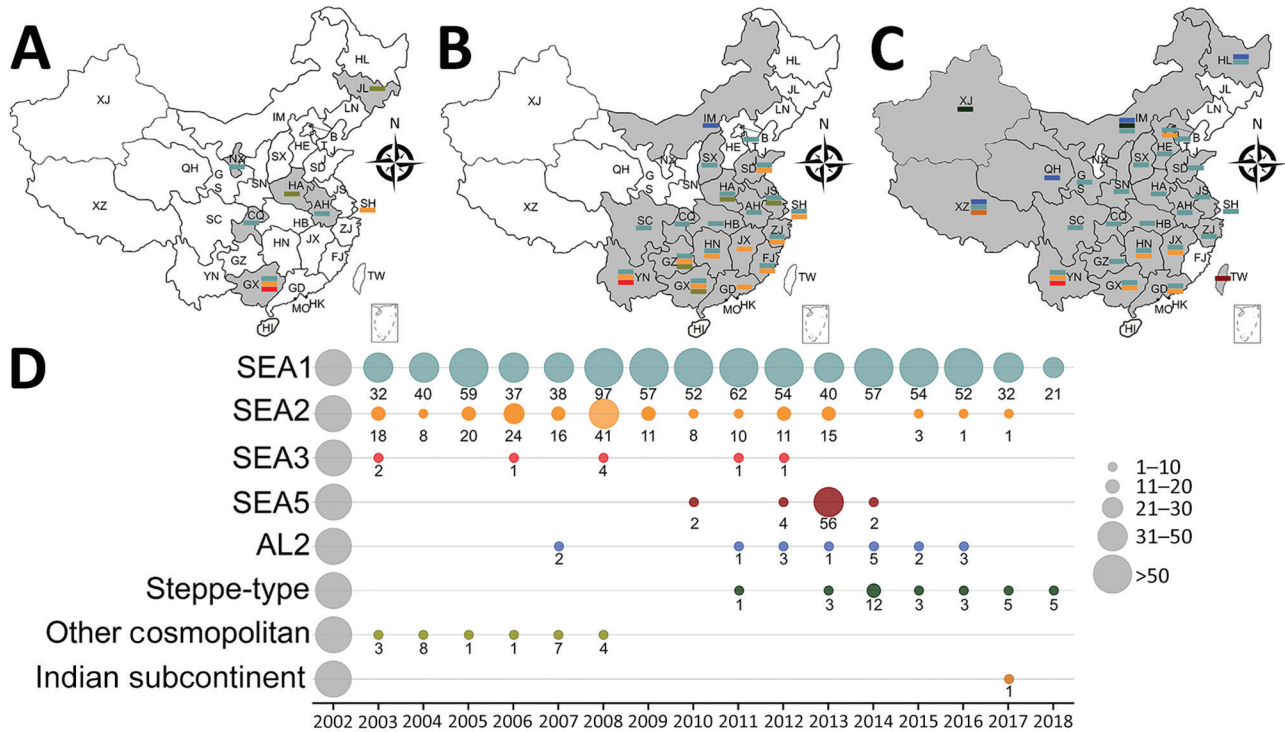


Figure 3. Spatial–temporal dynamics of RABVs in China. Phylogenetic analysis of 1,118 sequences representing 1,118 rabies cases or virus strains, including those obtained in this study using different gene fragments, followed by chronological summation of each subclade. A–C) Distribution of identified subclades during 3 time periods: A) before 2004; B) 2004–2008; C) 2009–2018. D) Quantitative trends of 8 Chinese RABV subclades during 2004–2018. Exact numbers within each subclade are given below the circles. SEA, Southeast Asia.

subclades genetically close to those circulating in neighboring countries (Figure 1) but also delineated the phylogeographic distribution of diverse RABVs in China and neighboring countries (Figure 2). The results have revealed 2 epidemic modes existing in China. The first is the historical dog-mediated rabies epidemic in populous inland provinces mainly in the center, east, and south, in which subclades within the Asian clade, particularly SEA1 followed by SEA 2, play dominant roles. The second consists mainly of outbreaks caused by the emerging subclades AL2, steppe-type, and Indian Subcontinent that have been closely associated over the past decade with cross-border transmission (Figure 5). As determined by analysis of data with a Bayes factor >3 using the BSSVS approach, fox-transmitted steppe-type viruses circulate in north and northwest border areas in Inner Mongolia and Xinjiang Province, with transboundary transmission between China and Mongolia, Russia, and Kazakhstan. Wild foxes have become the main rabies transmitter in these areas (Figure 1; Appendix Table 1). The raccoon dog-transmitted AL2 subclade emerged in the northeast likely through cross-border transmission from Mongolia. The Indian Subcon-

tinent subclade, emerging to cause a human death in Tibet in 2017, is the most recent transboundary transmission event of dog-mediated rabies from a neighboring country (24). Our study has also shown transboundary transmission of the SEA3 subclade, mediated by dogs in the border areas between southwest China and SEA countries (Figure 5).

Wild animals remain the major sources of AL2 and steppe-type subclades and usually transmit the viruses causing human and livestock rabies in the steppes of Mongolia (34,35). Surprisingly, however, the surveillance in our study identified the initial spillover of these 2 subclades into dogs within China. An AL2 strain (NMXLHT) was isolated from an infected dog in 2013 in Inner Mongolia (Appendix Table 1) and grouped together with the first 2 AL2 strains (NeiMeng 927 and 925) isolated from rabid raccoon dogs in 2007 in Inner Mongolia (Figure 1) (10). Their collection sites were ≈200 km apart. Two steppe-type isolates (NMXYQD14 and XJHMD17) were also identified from dogs: the first in Inner Mongolia in 2014 and the second in 2017 in Xinjiang (Appendix Table 1). These dogs had exhibited strange behavior and had bitten some humans or other dogs. In 2018,

another 3 dog steppe-type isolates (NMHLBED18, XJYLD181, and XJYLD182) were detected, 1 from a dog suspected of having rabies in Inner Mongolia (Appendix Table 1) and 2 from apparently healthy dogs in Xinjiang Province (Appendix Table 2). All 5 of these dog isolates had a very close phylogenetic relationship with 3 fox isolates (NMFOX01, NMFOX15, and XJTKSFOX14) (Figure 1). A case of fox-mediated human rabies was diagnosed by reverse transcription PCR in Xinjiang Province in 2016, although the causative virus was not sequenced (9). These results not

only demonstrated the spillover of wildlife RABVs into dogs in the past decade but also indicated that the risk of the spillover is increasing and threatening public health in northern China.

Rabies is still neglected in China, and efforts to increase awareness and strengthen control measures at the animal sources are still insufficient. As a consequence, the number of animal rabies cases officially reported during 2004–2018 (no data are available from before 2004) was only 893 (5), a much lower figure than the 25,424 human cases reported in China over

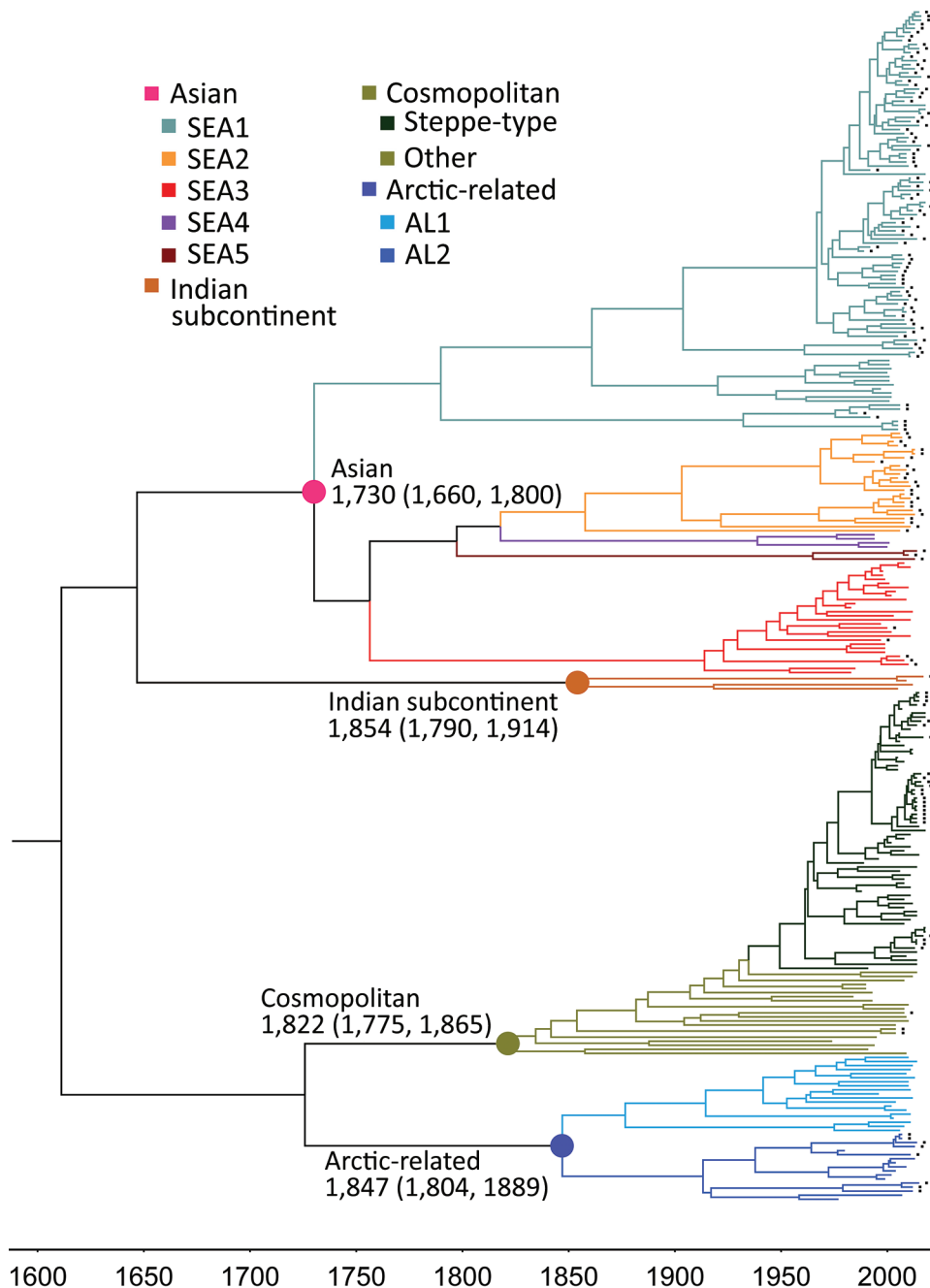


Figure 4. Nucleoprotein gene-based maximum clade credibility tree of rabies viruses. The estimated time to most recent common ancestor of these clades and their 95% highest posterior density values are indicated. The same sequences as in Figure 1 were used, except for those of 5 vaccine strains listed at end of Appendix Table 3 (<https://wwwnc.cdc.gov/EID/article/26/12/20-0303-App1.pdf>). Black solid squares indicate strains from China. SEA, Southeast Asia.

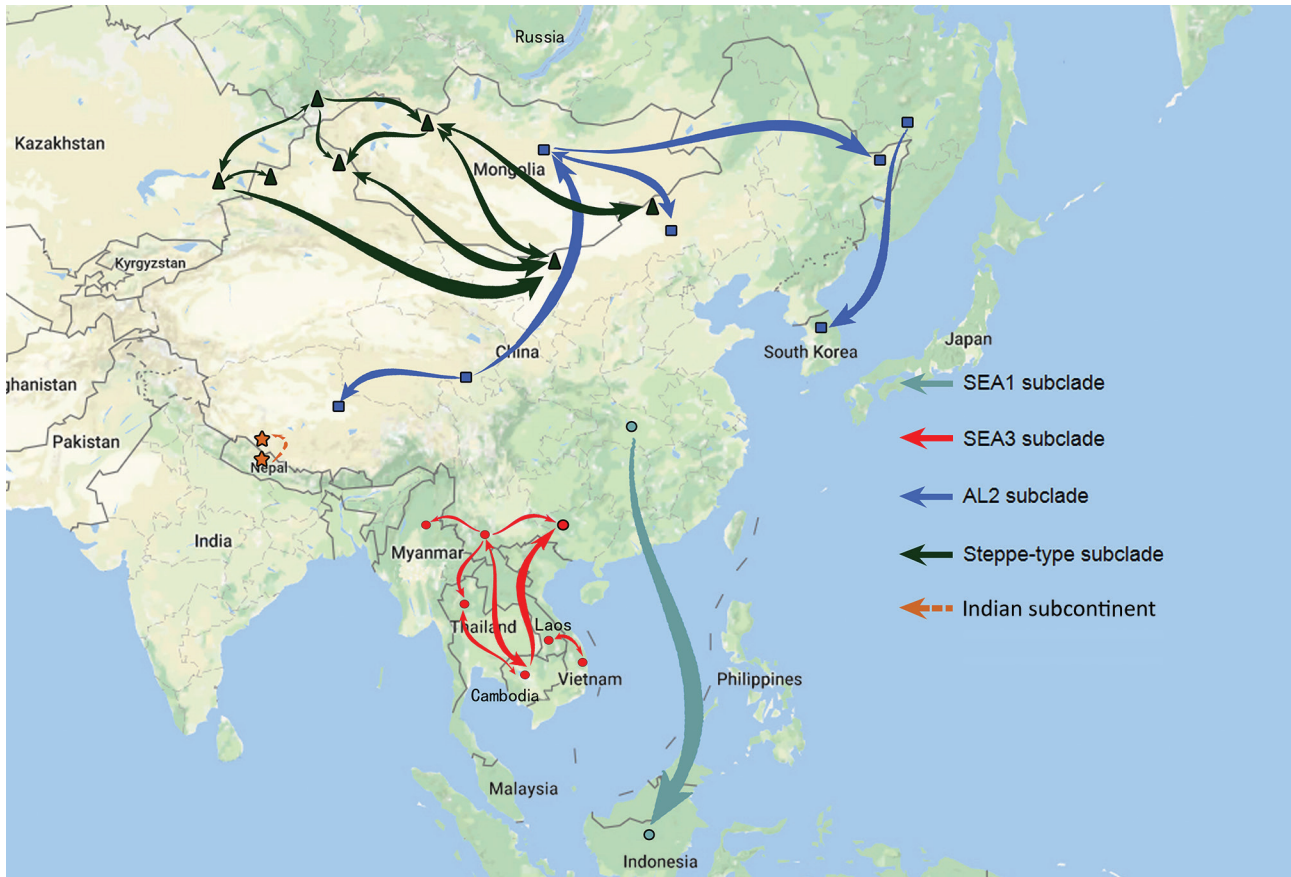


Figure 5. Proposed transboundary transmission of rabies viruses between China and neighboring countries determined by the Bayesian stochastic search variable selection approach. Unbroken lines: transmission events with a Bayes factor >3 ; broken line: transmission event with a Bayes factor <3 . SEA, Southeast Asia.

the same period (3). Of the reported animal rabies cases, only a small proportion was submitted for laboratory diagnosis, and the 185 rabies-suspected animals tested in our study account for most of these. This low figure notwithstanding, 15 years of continuous surveillance have been adequate to reveal the spread of animal rabies (Figure 3) and have highlighted that dog rabies is still widely distributed, accounting for 74.6% (132/177) of total infected animals (Appendix Tables 1, 2). Phylogenetic analyses (Figure 1) have clearly shown that all livestock RABV isolates grouped together with either dog or fox isolates, indicating that dogs and foxes are major transmission sources. These analyses have also shown that some RABV isolates were ferret badger specific, circulating solely in ferret badgers and forming independent lineage (within SEA 2) or even a subclade (such as SEA 5 in Taiwan). Moreover, the ongoing surveillance has also revealed the spillover of fox- and raccoon dog-transmitted RABVs into dogs, which emphasizes the importance of sequence-based analysis in tracking the sources of

animal rabies cases, for which investigation into the retrospective biting history is impossible. In addition, our study has delineated the current status of wildlife rabies in China, emphasizing the roles of the relevant wild reservoir hosts in the current increase of rabies transmission. Altogether, our work has shown that sustained surveillance of animal rabies, combined with sequence-based analysis of collected RABVs, is a robust strategy to track the transmission source.

In conclusion, although animal rabies is largely underreported in China, our continuous surveillance has been able to document the current status and transmission trends of animal rabies within the country, showing that these consist of a combination of historical dog-mediated rabies in populous inland areas and the emergence of wildlife-mediated rabies during the past decade in border areas. We have also completely updated the phylogenetic and phylogeographic characteristics of RABVs in China, with particular attention to the prevalence and transboundary transmission of emerging RABV subclades.

This study was supported by the National Key Research and Development Plan (grant no. 2016YFD0500401) and National Natural Science Foundation of China (grant nos. 31302043, 31972720, and 31902307).

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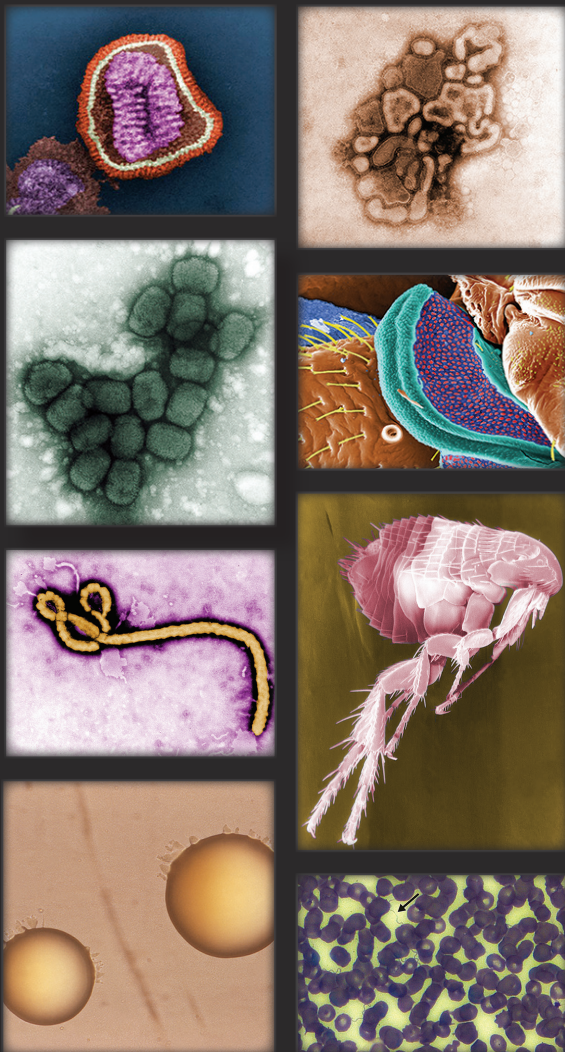
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Animal Rabies Surveillance, China, 2004–2018

Appendix

Appendix Table 1. Detection of suspected rabies in brain samples submitted during 2004–2018 (positive/total)*

Province	Dog	Cattle	Sheep	Camel	Pig	Donkey	Wolf†	Fox	Raccoon dog	Total
CQ	57/70	–	–	–	–	–	0/2	–	–	57/72
HN	6/7	–	–	–	2/2	–	–	–	–	8/9
SD	–	2/2	–	–	–	–	–	–	–	2/2
TJ	4/5	2/2	–	–	–	–	–	–	–	6/7
GD	2/5	–	–	–	–	–	–	–	–	2/5
SX	10/11	1/1	3/3	–	–	1/1	–	–	–	15/16
HE	0/1	–	–	–	–	–	–	–	–	0/1
JS	2/2	–	–	–	–	–	–	–	–	2/2
YN	0/1	–	–	–	–	–	–	–	–	0/1
SH	9/12	–	–	–	–	–	–	–	–	9/12
IM‡	3/3	11/14	5/5	4/4	–	–	–	2/3	1/1	26/30
GS	1/3	–	–	–	–	–	–	–	–	1/3
XJ‡	1/1	1/2	6/8	2/2	–	–	–	1/1	–	11/14
SN	0/2	–	–	–	–	–	–	–	–	0/2
HLJ	0/1	1/1	–	–	–	–	–	–	–	1/2
ZJ	4/6	–	–	–	–	–	–	–	–	4/6
LN	0/1	–	–	–	–	–	–	–	–	0/1
Total	99/131	18/22	14/16	6/6	2/2	1/1	0/2	3/4	1/1	144/185 (77.84%)

*CQ, Chongqing; GD, Guangdong; GS, Gansu; HA, Henan; HE, Hebei; HLJ, Heilongjiang; HN, Hunan; IM, Inner Mongolia; JS, Jiangsu; LN,

Liaoning; SD, Shandong; SH, Shanghai; SN, Shaanxi; SX, Shanxi; TJ, Tianjin; XJ, Xinjiang; YN, Yunnan; ZJ, Zhejiang.

†Two dead wolves were submitted by a zoo.

‡In IM and XJ, 3 dog rabies cases (2 in IM and 1 in XJ) and all livestock and fox rabies cases were caused by a steppe-type subclade during 2013–2018, with foxes being transmission sources. In IM, the remaining dog rabies case and raccoon dog rabies case were caused by AL2 subclade (Figure 1).

Appendix Table 2. Detection of healthy-looking dogs for surveillance during 2004–2018 (positive/total)*

Province	Free-roaming and ownerless dogs	Emergently killed dogs	Slaughtered dogs	Total
GD	7/6085	–	0/265	7/6350
HN	6/1211	2/41	–	8/1252
SN	–	0/112	–	0/112
GX	16/1175	–	0/145	16/1320
ZJ	0/6	–	–	0/6
XJ	2/988†	–	0/7	2/995
QH	0/83	–	–	0/83
Total	0.32% (31/9,548)	1.3% (2/153)	0/417	0.33% (33/10118)

*GD, Guangdong; GX, Guangxi; HN, Hunan; QH, Qinghai; SN, Shaanxi; XJ, Xinjiang; ZJ, Zhejiang.

†These 2 dog rabies cases were caused by steppe-type subclade, according to the phylogenetic analysis in Figure 1.

Appendix Table 3. Information on 300 full N gene sequences of RABVs used in the phylogenetic analyses

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
Afghanistan		04027AFG	Dog	1996	Arctic-related/AL1	EU086162
Afghanistan		02052AFG	Dog	2002	Arctic-related/AL1	KX148225
Afghanistan		04029AFG	Dog	2004	Arctic-related/AL1	KX148227
Afghanistan		09032AFG	Dog	2009	Arctic-related/AL1	JX987739
Afghanistan		BDR6	Cattle	2010	Arctic-related/AL1	AB699218
Afghanistan		ACS11	Human	2011	Arctic-related/AL1	KF992019
Bhutan		Btn115	Cattle	2010	Arctic-related/AL1	AB910532
Brazil		95022BRE	Dog	1995	Cosmopolitan/other	KX148215
Cambodia		9914CBG	Dog	1997	Asian/SEA3	EU086170
Cambodia		9911CBG	Dog	1998	Asian/SEA3	EU086168
Cambodia		I0515204	Dog	1998	Asian/SEA3	KM366251
Cambodia		9908CBG	Dog	1999	Asian/SEA3	EU086167
Cambodia		M0516129	Dog	2002	Asian/SEA3	KM366209
Cambodia		N1011101	Dog	2003	Asian/SEA3	KM366270
Cambodia		O0405536	Dog	2004	Asian/SEA3	KM366206
Cambodia		S1030654	Dog	2008	Asian/SEA3	KM366202
Cambodia		T1002618	Dog	2009	Asian/SEA3	KM366262
Cambodia		U0821622	Dog	2010	Asian/SEA3	KM366267
Cambodia		V0808656	Dog	2011	Asian/SEA3	KM366221
China*	Chongqing	CQWSD01	Dog	2005	Asian/SEA1	KT221095
China*	Chongqing	CQWXD01	Dog	2005	Asian/SEA1	KT221093
China*	Chongqing	CQQJD6	Dog	2006	Asian/SEA1	KT221097

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
China*	Chongqing	CQWLD02	Dog	2006	Asian/SEA1	KT221094
China*	Chongqing	CQFJD02	Dog	2007	Asian/SEA1	KT894569
China*	Chongqing	CQBSD01	Dog	2008	Asian/SEA1	KT894564
China*	Chongqing	CQYBD01	Dog	2008	Asian/SEA1	KT221098
China*	Chongqing	CQWLD03	Dog	2009	Asian/SEA1	KT894559
China*	Chongqing	CQD023	Dog	2010	Asian/SEA1	KT894560
China*	Chongqing	CQCSD01	Dog	2011	Asian/SEA1	KT894563
China*	Chongqing	CQJLPD01	Dog	2011	Asian/SEA1	KT894567
China*	Chongqing	CQQJD11	Dog	2011	Asian/SEA1	KT894562
China*	Chongqing	CQWSD11	Dog	2011	Asian/SEA1	KT894561
China*	Chongqing	ZDW046	Dog	2011	Asian/SEA1	KT894571
China*	Chongqing	CQJLPD13	Dog	2013	Asian/SEA1	KT894568
China*	Chongqing	CQCSD17	Dog	2017	Asian/SEA1	MG383887
China*	Chongqing	CQJJD17	Dog	2017	Asian/SEA1	MG383888
China*	Chongqing	CQYCD17	Dog	2017	Asian/SEA1	MK124736
China*	Chongqing	CQYCD18	Dog	2018	Asian/SEA1	MN784133
China*	Gansu	GSHSD14	Dog	2014	Asian/SEA1	KT221103
China*	Guangxi	GXBSD01	Dog	2009	Asian/SEA1	KT894576
China*	Guangxi	GXQZD01	Dog	2009	Asian/SEA2	KT221107
China*	Guangxi	GXRXD01	Dog	2010	Asian/SEA1	KT894575
China*	Guangxi	GXWXD01	Dog	2013	Asian/SEA2	KT894577
China*	Guangxi	GXWXD02	Dog	2013	Asian/SEA2	KT894578
China*	Heilongjiang	HLJC16	Cattle	2016	Asian/SEA1	MG383884
China*	Hunan	HN05	Dog	2005	Asian/SEA2	KT894558
China*	Hunan	HuND02	Dog	2005	Asian/SEA1	KT221100
China*	Hunan	HuND28	Dog	2005	Asian/SEA1	KT221101
China*	Hunan	HN06	Dog	2006	Asian/SEA1	KT894557
China*	Hunan	HNP02	Pig	2006	Asian/SEA2	KT221102
China*	Hunan	HuNPN01	Pig	2006	Asian/SEA2	DQ496219
China*	Hunan	HNYZD01	Dog	2010	Asian/SEA2	KT894572
China*	Hunan	HNNYD03	Dog	2011	Asian/SEA2	KT894573
China*	Inner Mongolia	NMC01	Cattle	2013	Cosmopolitan/ST	KJ152772
China*	Inner Mongolia	NMSH01	Sheep	2013	Cosmopolitan/ST	KJ152774
China*	Inner Mongolia	NMAYC01	Cattle	2014	Cosmopolitan/ST	KJ737435
China*	Inner Mongolia	NMAYCAM03	Camel	2014	Cosmopolitan/ST	KX533959
China*	Inner Mongolia	NMC02	Cattle	2014	Cosmopolitan/ST	KJ748634
China*	Inner Mongolia	NMC03	Cattle	2014	Cosmopolitan/ST	KJ748635

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
China*	Inner Mongolia	NMC04	Cattle	2014	Cosmopolitan/ST	KJ748636
China*	Inner Mongolia	NMCAM01	Camel	2014	Cosmopolitan/ST	KJ748631
China*	Inner Mongolia	NMCAM02	Camel	2014	Cosmopolitan/ST	KJ748632
China*	Inner Mongolia	NMFOX01	Fox	2014	Cosmopolitan/ST	KJ748633
China*	Inner Mongolia	NMXLHT	Dog	2014	Arctic-related/AL2	KU041697
China*	Inner Mongolia	NMXYQD14	Dog	2014	Cosmopolitan/ST	KT894582
China*	Inner Mongolia	NMCAM15	Camel	2015	Cosmopolitan/ST	KX533961
China*	Inner Mongolia	NMFOX15	Fox	2015	Cosmopolitan/ST	KX533960
China*	Inner Mongolia	NMHLBEC16	Cattle	2016	Cosmopolitan/ST	KX533963
China*	Inner Mongolia	NMXYQC16	Cattle	2016	Cosmopolitan/ST	KX533962
China*	Inner Mongolia	NMHLBES17	Sheep	2017	Cosmopolitan/ST	MG383886
China*	Inner Mongolia	NMALSS18	Sheep	2018	Cosmopolitan/ST	MK124741
China*	Inner Mongolia	NMHLBED18	Dog	2018	Cosmopolitan/ST	MK124739
China*	Jiangsu	JSWXD18	Dog	2018	Asian/SEA1	MK124742
China*	Shandong	SDJNC02	Cattle	2007	Asian/SEA1	KT894585
China*	Shanghai	SHCMD01	Dog	2010	Asian/SEA1	KT894579
China*	Shanghai	SHPDD01	Dog	2011	Asian/SEA1	KT894581
China*	Shanghai	SHPDD02	Dog	2013	Asian/SEA1	KT894580
China*	Shanghai	SHBSD16	Dog	2016	Asian/SEA1	MG383885
China*	Shanghai	SHJDD18	Dog	2018	Asian/SEA1	MN784135
China*	Shanxi	SXLFD03	Dog	2007	Asian/SEA1	KT221111
China*	Shanxi	SXD01	Dog	2008	Asian/SEA1	KT221109
China*	Shanxi	SXD01	Dog	2010	Asian/SEA1	KT221108
China*	Shanxi	SXD01	Dog	2013	Asian/SEA1	KT894584
China*	Shanxi	SXYL15	Cattle	2015	Asian/SEA1	KR230090
China*	Tianjin	TJD03	Dog	2008	Asian/SEA1	KT221106
China*	Tianjin	TJC14	Cattle	2014	Asian/SEA1	KT894574
China*	Xinjiang	XJTCS01	Sheep	2013	Cosmopolitan/ST	KJ152773
China*	Xinjiang	XJTKSFOX14	Fox	2014	Cosmopolitan/ST	KU041696
China*	Xinjiang	XJTKSS02	Sheep	2014	Cosmopolitan/ST	MK321229
China*	Xinjiang	XJFYCA15	Camel	2015	Cosmopolitan/ST	MG383882
China*	Xinjiang	XJHMS16	Sheep	2016	Cosmopolitan/ST	MK321230
China*	Xinjiang	XJHMD17	Dog	2017	Cosmopolitan/ST	MK124737
China*	Xinjiang	XJYLC17	Cattle	2017	Cosmopolitan/ST	MK124738
China*	Xinjiang	XJYLD181	Dog	2018	Cosmopolitan/ST	MK124744
China*	Xinjiang	XJYLD182	Dog	2018	Cosmopolitan/ST	MK124745
China*	Xinjiang	XLGLMC18	Cattle	2018	Cosmopolitan/ST	MK124740

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
China *	Zhejiang	ZJZSD1601	Dog	2016	Asian/SEA1	MG383893
China*	Zhejiang	ZJNBD18	Dog	2018	Asian/SEA1	MN784136
China	Anhui	HeF	Dog	1989	Asian/SEA1	HQ118104
China	Anhui	DRV-AH08	Dog	2008	Asian/SEA1	HQ450385
China	Anhui	11AF57	Dog	2011	Asian/SEA1	JQ798950
China	Beijing	BeijingHu1	Human	2007	Asian/SEA1	EU700031
China	Beijing	BJ16-13	Dog	2016	Asian/SEA1	KY214275
China	Beijing	BJ16-51	Dog	2016	Asian/SEA1	KY362747
China	Chongqing	CQ92	Dog	1992	Asian/SEA1	EU159388
China	Chongqing	CQH1202D	Dog	2012	Arctic-related/AL2	KM034905
China	Fujian	FJ004	Dog	2008	Cosmopolitan/Other	FJ561729
China	Fujian	FJ010	Dog	2008	Asian/SEA1	FJ866827
China	Guangdong	CGD0801D	Dog	2008	Asian/SEA2	JN974823
China	Guangxi	GX4	Dog	1994	Asian/SEA2	GU358653
China	Guangxi	N11	Dog	1997	Asian/SEA3	FJ594278
China	Guangxi	GXN119	Dog	2000	Asian/SEA3	DQ866111
China	Guangxi	GXLA	Dog	2003	Asian/SEA2	DQ866116
China	Guangxi	GX304	Dog	2004	Asian/SEA1	DQ866117
China	Guangxi	CGZ0501D	Dog	2005	Asian/SEA1	JN974830
China	Guangxi	GXSL	Cattle	2005	Asian/SEA2	DQ866120
China	Guangxi	CGX0601D	Dog	2006	Asian/SEA1	JN974825
China	Guangxi	CGX0602D	Dog	2008	Asian/SEA1	JN974826
China	Guangxi	CGX0801D	Dog	2008	Asian/SEA2	JN974829
China	Guizhou	Guizhou_A148	Dog	2004	Asian/SEA1	DQ666291
China	Guizhou	gk5	Dog	2006	Asian/SEA1	HQ118102
China	Heilongjiang	TJ11-RD	Raccoon dog	2011	Arctic-related/AL2	KM016898
China	Henan	Henan_Sq10	Dog	2004	Asian/SEA1	DQ666300
China	Henan	Henan_Sq35	Dog	2004	Asian/SEA1	DQ666304
China	Henan	Henan_Sq48	Dog	2004	Cosmopolitan/other	DQ666305
China	Hunan	Hunan_Wg22	Dog	2004	Cosmopolitan/other	DQ666310
China	Hunan	Hunan_Xx35	Dog	2004	Asian/SEA1	DQ666319
China	Hunan	HuNDN16	Dog	2005	Asian/SEA1	DQ515993
China	Hunan	CHN0635H	Human	2006	Asian/SEA2	JN974843
China	Hunan	CHN0504D	Dog	2008	Asian/SEA1	JN974837
China	Inner Mongolia	NeiMeng925	Raccoon dog	2007	Arctic-related/AL2	FJ415313
China	Inner Mongolia	NeiMeng927A	Raccoon dog	2007	Arctic-related/AL2	EU284093
China	Inner Mongolia	CNM1104D	Dog	2011	Asian/SEA1	KC465378

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
China	Inner Mongolia	DG11248	Dog	2013	Arctic-related	KT895593
China	Inner Mongolia	IMDRV-13	Deer	2013	Asian/SEA1	KJ564280
China	Inner Mongolia	WQ14	Cattle	2014	Cosmopolitan/ST	KM016901
China	Inner Mongolia	WQ15	Cattle	2015	Asian/SEA1	KU928249
China	Jiangsu	Jiangsu_Wx1	Dog	2004	Asian/SEA1	DQ666321
China	Jiangsu	CJS0847D	Dog	2008	Asian/SEA1	JN974852
China	Jiangxi	JX08-45	Ferret badger	2008	Asian/SEA2	GU647092
China	Jiangxi	CJX0901D	Dog	2009	Asian/SEA1	JN974853
China	Jiangxi	JX09-17 fb	Ferret badger	2009	Asian/SEA1	GU233765
China	Jiangxi	JX10-37	Ferret badger	2010	Asian/SEA1	KP319222
China	Jiangxi	JX11-05	Ferret badger	2011	Asian/SEA2	KP319193
China	Jiangxi	JX11-30	Ferret badger	2011	Asian/SEA1	KP319225
China	Jiangxi	JX12-150	Ferret badger	2012	Asian/SEA1	KP319228
China	Jiangxi	JX12-244	Ferret badger	2012	Asian/SEA2	KP319196
China	Jiangxi	JX13-09	Ferret badger	2013	Asian/SEA2	KP319201
China	Jiangxi	JX13-345	Ferret badger	2013	Asian/SEA1	KP319235
China	Jiangxi	JX13-418	Ferret badger	2013	Asian/SEA1	KP319220
China	Jiangxi	JX14-717	Ferret badger	2014	Asian/SEA1	KX447687
China	Jiangxi	JX14-719	Ferret badger	2014	Asian/SEA1	KX447689
China	Jiangxi	JX15-475	Ferret badger	2015	Asian/SEA1	KY613018
China	Ningxia	J	Human	1986	Asian/SEA1	GU345747
China	Ningxia	CNX1101H	Human	2011	Asian/SEA1	KC465379
China	Ningxia	NX15	Camel	2015	Asian/SEA1	KU928250
China	Shaanxi	CSX0903D	Dog	2009	Asian/SEA1	JN974876
China	Shaanxi	Shaanxi-HZ-6	Dog	2009	Asian/SEA1	KC977995
China	Shandong	CSD0709D	Dog	2007	Asian/SEA2	HM486381
China	Shanghai	SBD	Dog	1992	Asian/SEA1	EU159393
China	Shanghai	SBH	Human	1992	Asian/SEA1	EU159392
China	Shanghai	SH06	Dog	2006	Asian/SEA1	GU345748
China	Sichuan	CSC0808D	Dog	2008	Asian/SEA1	JN974857
China	Sichuan	Sichuan-BZ-1	Dog	2009	Asian/SEA1	GU591792
China	Taiwan	Nt2702	Ferret badger	2010	Asian/SEA5	KP860155
China	Taiwan	TW-1680	Ferret badger	2013	Asian/SEA5	KF501181
China	Taiwan	2014-3145	Ferret badger	2014	Asian/SEA5	KP892527
China	Tibet	CXZ1201D	Dog	2012	Arctic-related/AL2	KC465372
China	Tibet	CXZ1501H	Human	2015	Arctic-related/AL2	KY175230
China	Tibet	CXZ1704H	Human	2017	Indian Subcontinent	MH671332

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
China	Unknown	FY12	Dog	2005	Asian/SEA1	EU159372
China	Yunnan	CYN0818D	Dog	2008	Asian/SEA3	JF819603
China	Yunnan	CYN1009D	Dog	2010	Asian/SEA3	JX276405
China	Yunnan	CYN1134H	Human	2011	Asian/SEA2	JQ040592
China	Yunnan	CYN1247D	Dog	2012	Asian/SEA1	JX276411
China	Yunnan	CYN14114D	Dog	2014	Asian/SEA1	KP202447
China	Yunnan	Yunnan_Tc06	Dog	2006	Asian/SEA3	EU275243
China	Yunnan	Yunnan_Qj07	Dog	2007	Asian/SEA1	EU275245
China	Zhejiang	F02	Ferret badger	2008	Asian/SEA2	FJ712195
China	Zhejiang	F04	Ferret badger	2008	Asian/SEA2	FJ712196
China	Zhejiang	Zhejiang_Wz1_H	Human	2008	Asian/SEA1	EU700032
China	Zhejiang	ZJF4	Ferret badger	2008	Asian/SEA2	HQ118117
China	Zhejiang	ZJ-LA	Ferret badger	2008	Asian/SEA2	FJ598135
China	Zhejiang	D23	Dog	2010	Asian/SEA1	JX123685
China	Zhejiang	ZJ12-03	Ferret badger	2012	Asian/SEA1	KP319236
China	Zhejiang	ZJ13-66	Ferret badger	2013	Asian/SEA1	KP319237
India		ITN-R148	Dog	2005	Indian Subcontinent	KX434506
India		IAP-R192	Dog	2009	Arctic-related/AL1	KX434512
India		IAP-R194	Human	2011	Arctic-related/AL1	KX434514
India		IUP-R197	Equine	2012	Arctic-related/AL1	KX434517
India		IGU-201	Nilgai	2013	Arctic-related/AL1	KM099392
India		IGU-R202	Mongoose	2014	Arctic-related/AL1	KM099393
Indonesia		FL97-01	Dog	1997	Asian/SEA1	AB154218
Indonesia		SN00-14	Dog	2000	Asian/SEA1	AB154235
Indonesia		FL01-27	Dog	2001	Asian/SEA1	AB154222
Indonesia		SC01-65	Deer	2001	Asian/SEA1	AB154214
Indonesia		SC01-68	Cat	2001	Asian/SEA1	AB154208
Indonesia		SC01-70	Tiger	2001	Asian/SEA1	AB154242
Indonesia		SC01-75	Cat	2001	Asian/SEA1	AB154210
Indonesia		FL02-10	Dog	2002	Asian/SEA1	AB154217
Indonesia		SC02-87	Monkey	2002	Asian/SEA1	AB154224
Indonesia		SW02-22	Dog	2002	Asian/SEA1	AB154240
Indonesia		03003INDO	Dog	2003	Asian/SEA1	KX148266
Iran		87002IRA	Wolf	1984	Cosmopolitan/Other	KX148186
Iraq		RV2516	Cattle	2010	Cosmopolitan/Other	KF155000
Israel		93032ISR	Jackal	1993	Cosmopolitan/Other	KX148191
Japan		Komatsugawa	Dog	1940s	Arctic-related/AL2	AY352494

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
Kazakhstan		RV259	Red fox	1988	Cosmopolitan/ST	AY352491
Kazakhstan		4867	Cattle	2014	Cosmopolitan/ST	KT965738
Kazakhstan		5300	Jackal	2014	Cosmopolitan/other	KT965733
Kazakhstan		5303	Cat	2014	Cosmopolitan/ST	KT965734
Kazakhstan		5304	Cattle	2014	Cosmopolitan/ST	KT965735
Kazakhstan		5317	Dog	2014	Cosmopolitan/ST	KT965736
Kazakhstan		5328	Cattle	2014	Cosmopolitan/ST	KT965737
Laos		02001LAO	Dog	2002	Asian/SEA3	EU086194
Laos		Lao2	Dog	2011	Asian/SEA3	AB981663
Laos		Lao7	Dog	2011	Asian/SEA3	AB981668
Laos		Lao23	Dog	2012	Asian/SEA3	AB981677
Madagascar		04033MAD	Dog	2004	Cosmopolitan/ other	KX148209
Mexico		91010MEX	Mouse	1991	Cosmopolitan/ other	KX148112
Mongolia		MGL/34	Cat	2005	Cosmopolitan/ST	AB571016
Mongolia		MGL/35	Sheep	2005	Cosmopolitan/ST	AB571017
Mongolia		MGL/36	Dog	2005	Cosmopolitan/ST	AB571018
Mongolia		MGL/26	Cattle	2006	Cosmopolitan/ST	AB571008
Mongolia		MGL/28	Cattle	2006	Cosmopolitan/ST	AB571010
Mongolia		MGL-10	Cattle	2006	Cosmopolitan/ST	AB570997
Mongolia		MGL/22	Dog	2007	Arctic-related/AL2	AB571004
Mongolia		MGL/30	Cattle	2007	Cosmopolitan/ST	AB571012
Mongolia		MGL/25	Dog	2008	Cosmopolitan/ST	AB571007
Morocco		RV2627	Cattle	2009	Cosmopolitan/ other	KF155001
Myanmar		9909BIR	Dog	1999	Asian/SEA3	EU086164
Myanmar		9913BIR	Dog	1999	Asian/SEA3	EU086165
Myanmar		9915BIR	Dog	1999	Asian/SEA3	EU086166
Nepal		4403-13_09030NEP	Human	2003	Arctic-related/AL1	JX944565
Nepal		4403-17	Dog	2009	Indian Subcontinent	JX944597
Nepal		11016NEP	Dog	2011	Arctic-related/AL1	JX987742
Nepal		NPBUF12-1	Cattle	2012	Arctic-related/ AL1	KM979366
Pakistan		Pk 23	Mouse	2010	Arctic-related/AL1	HE802675
Philippines		94270PHI	Dog	1994	Asian/SEA4	EU086200
Philippines		94281PHI	Dog	1994	Asian/SEA4	KX148261
Philippines		03006PHI	Human	2000	Asian/SEA4	EU086203
Philippines		03007PHI	Human	2001	Asian/SEA4	EU086204
Russia		304c	Steppe fox	1977	Arctic-related/AL2	AY352459
Russia		857r	Raccoon dog	1980	Arctic-related/AL2	AY352458

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
Russia		686Cattle	Cattle	1989	Cosmopolitan/ST	AY352482
Russia		RV1596	Red fox	1990	Cosmopolitan/other	AY352474
Russia		RV245	Human	1990	Cosmopolitan/other	AY352475
Russia		RV1589	Cat	1991	Cosmopolitan/ST	AY352456
Russia		3561d	Dog	1996	Cosmopolitan/ST	AY352481
Russia		wolf-kras	Wolf	2002	Cosmopolitan/ST	JX423819
Russia		Rus_YamaloNenets _7405rdr	Deer	2006	Arctic-related/ AL1	KY002910
Russia		1350KRA	Dog	2008	Cosmopolitan/ST	JQ944705
Russia		1352KRA	Dog	2008	Cosmopolitan/other	JQ944706
Russia		1564NNO	Red fox	2008	Cosmopolitan/other	JQ944708
Russia		7445f	Fox	2008	Cosmopolitan/ST	KJ958248
Russia		7461f	Red fox	2008	Cosmopolitan/ST	KJ958249
Russia		7466Cattle	Cattle	2008	Cosmopolitan/ST	KJ958257
Russia		7499fA	Red fox	2008	Cosmopolitan/ST	KJ958231
Russia		7504f	Red fox	2008	Cosmopolitan/ST	KJ958237
Russia		7514f	Red fox	2008	Cosmopolitan/ST	KC794011
Russia		7548f	Red fox	2008	Cosmopolitan/ST	KC794014
Russia		Rus_YamaloNenets _7557af	Fox	2008	Arctic-related/ AL1	KY002909
Russia		7604c	Cat	2009	Cosmopolitan/ST	KJ958251
Russia		7891Cattle	Cattle	2011	Cosmopolitan/ST	KJ958225
Russia		7894w	Wolf	2011	Cosmopolitan/ST	KJ958228
Russia		8000f	Red fox	2011	Cosmopolitan/ST	KJ958254
Russia		8052f	Red fox	2011	Cosmopolitan/ST	KC595280
Russia		8057f	Red fox	2011	Cosmopolitan/ST	KC595283
Russia		8060c	Cat	2011	Cosmopolitan/ST	KJ958262
Russia		Rus_Altai_8041		2011	Cosmopolitan/ST	KY172632
Russia		Rus_Sakha/Yakutia _7985rdr	Deer	2011	Arctic-related/ AL1	KY002904
Russia		8061Cattle	Cattle	2012	Cosmopolitan/ST	KC538853
Russia		fox-2012	Red fox	2012	Cosmopolitan/ST	JX423818
Russia		wolf-bur	Wolf	2012	Cosmopolitan/ST	JX423817
Russia		PO- 01_2014_Primorye	Bear	2014	Cosmopolitan/ST	KP997032
Russia		Kha-f1-15	Fox	2015	Cosmopolitan/ST	KY242672
Russia		Zbk_ct12-15	Cattle	2015	Cosmopolitan/ST	KY242676

Country	Location	Virus name	Species	Year	Phylogenetic clade/subclade	GenBank accession no.
South Korea		BV9901PJ	Raccoon dog	1999	Arctic-related/AL2	KC171645
South Korea		SKRDG0203CW	Dog	2002	Arctic-related/AL2	DQ076124
South Korea		BD0406CC	Raccoon dog	2004	Arctic-related/AL2	KC171644
South Korea		KRH3-04	Dog	2004	Arctic-related/AL2	AY730596
South Korea		KRVB0910	Cattle	2009	Arctic-related/AL2	KJ476821
South Korea		KRVC1305	Dog	2013	Arctic-related/AL2	KF709096
Sri Lanka		H-1218-12	Human	2012	Indian Subcontinent	LC110310
Tajikistan		Tajik_FTA	Dog	2012	Cosmopolitan/ other	KY765901
Tanzania		RV2772	Dog	2010	Cosmopolitan/ other	KF155002
Thailand		8738THA	Human	1983	Asian/SEA3	EU086208
Thailand		8743THA	Human	1983	Asian/SEA3	EU086207
Thailand		THA1015	Dog	1985	Asian/SEA3	AB178893
Thailand		THA1017	Dog	1985	Asian/SEA3	AB178894
Turkey		93100TUR	Dog	1993	Cosmopolitan/other	KX148164
USA		CASK2	Striped skunk	1974	Cosmopolitan/other	JQ685970
USA		CA982	Striped skunk	1994	Cosmopolitan/other	JQ685894
USA		A10-0511	Gray fox	2009	Cosmopolitan/other	JQ685943
Vietnam		01017VNM	Dog	2001	Asian/SEA3	EU086210
		Flury_LEP	Vaccine	1985	Cosmopolitan/other	GU992324
		CVS-11	Vaccine	ND	Cosmopolitan/other	GQ918139
		SAD_Bern_Sana fox	Vaccine	ND	Cosmopolitan/other	EF206720
		PV-2061	Vaccine	ND	Cosmopolitan/other	JX276550
China (CN)		CTN-1	Vaccine	1956	Asian/SEA2	FJ959397

*Discussed in this study. ND, no date.

Appendix Table 4. Predicted transmission events of rabies virus subclades by BEAST

From	To	Bayes factor†	Posterior probability	Clade	Subclade
China (IM)	China (XJ)	229.87	0.98	Cosmopolitan	Steppe-type
China (XJ)	Kazakhstan	167.9	0.98	Cosmopolitan	Steppe-type
China (IM)	Russia	153.93	0.97	Cosmopolitan	Steppe-type
China (YN)	Thailand	84.99	0.94	Asian	SEA3
China	Indonesia	76.91	0.73	Asian	SEA1
Mongolia	China (HLJ)	15.59	0.75	Arctic-related	AL2
Russia	China (IM)	13.63	0.76	Cosmopolitan	Steppe-type
Russia	South Korea	6.85	0.56	Arctic-related	AL2
Mongolia	China (XZ)	5.93	0.53	Arctic-related	AL2
China (XJ)	China (IM)	5.81	0.58	Cosmopolitan	Steppe-type
Cambodia	China (YN)	5.35	0.5	Asian	SEA3
South Korea	Russia	5.2	0.5	Arctic-related	AL2
China (YN)	China (GX)	5.18	0.5	Asian	SEA3
Mongolia	China (IM)	4.97	0.49	Arctic-related	AL2
Cambodia	Myanmar	4.65	0.47	Asian	SEA3
Cambodia	China (GX)	4.61	0.47	Asian	SEA3
Kazakhstan	China (IM)	4.59	0.52	Cosmopolitan	Steppe-type
China (YN)	Myanmar	4.56	0.46	Asian	SEA3
Russia	China (XJ)	4.39	0.51	Cosmopolitan	Steppe-type
China (YN)	Cambodia	4.31	0.45	Asian	SEA3
Russia	Mongolia	4.11	0.49	Cosmopolitan	Steppe-type
China (XZ)	Mongolia	3.62	0.41	Arctic-related	AL2
China (IM)	Mongolia	3.41	0.39	Arctic-related	AL2
Laos	Vietnam	3.33	0.39	Asian	SEA3
Kazakhstan	Russia	3.18	0.43	Cosmopolitan	Steppe-type
Vietnam	Laos	3.17	0.38	Asian	SEA3
China (IM)	Mongolia	3.17	0.43	Cosmopolitan	Steppe-type

*GX, Guangxi ; HLJ, Heilongjiang; IM, Inner Mongolia; XJ, Xinjiang; XZ, Tibet; YN, Yunnan.

†Bayes factor was used to determine the best supported transmission event between two geographic locations, which is calculated by SpreaD3 software with a value >3 as the cutoff value.