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# Complete Genome Sequence of a Street Rabies Virus Isolated from a Rabid Dog in China

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**A rabies virus (RABV) was isolated from a dog in Anhui Province, China, in 2008. The virus was designated DRV-AH08. Its entire genome was sequenced and found to be closely related to RABV recently isolated in China and other Asian countries (homology of 87 to 98%) but distantly related to RABV in the “cosmopolitan” group (homology of 84 to 85%) in the clade I of RABV.**

China has experienced three major rabies epidemics during the past 60 years, with the current one ongoing (12, 14). Rabies remains a public health threat around the world, with an almost invariably fatal encephalomyelitis (3). Although effective vaccines are available, rabies still causes more than 55,000 human deaths annually throughout the world, with most of them in the developing countries in Asia and Africa (10). In recent years, the reported human rabies cases in China surpass 3,000 per year (13). Rabies virus (RABV) belongs to the genus *Lyssavirus* in the family *Rhabdoviridae*. Its genome is a single-strand and negative-sense RNA of approximately 12 kb in length (7, 11). Based on phylogenetic analysis of the nucleoprotein (N) and/or the glycoprotein (G) gene sequences, previous studies have divided all RABVs (genotype 1 of lyssaviruses) into two major clades, one comprising those isolated from terrestrial animals around the world and the other containing viruses isolated from bats and raccoons in the Americas (1, 2, 5, 8). An RABV was isolated in 2008 from a dog in Anhui Province, China, by passaging it in suckling mice and was designated DRV-AH08. To obtain the entire genomic sequence from this virus, total RNA was extracted from an infected suckling mouse brain using TRIzol LS reagent (Invitrogen, Carlsbad, CA). Ten pairs of oligonucleotide primers to amplify regions of the RABV genomes were designed based on the genomic sequences of the HEP-Flury and CVS-11 strains (4, 9). PCR products were purified using the QIAquick gel extraction kit (Qiagen, Germantown, MD) and cloned into the pCR-Blunt II Vector (Invitrogen). Cloned DNA was sequenced using the BigDye Terminator cycle sequencing ready reaction kit and ABI Prism 3730 sequencer. The assembly of genomic sequence was carried out with the aid of SeqMan software (DNASTAR Inc.). Homology searches and comparisons of all the sequences obtained were performed using the Lasergene package (DNASTAR Inc.). Sequences of encoded proteins were aligned with MEGA version 5 (6). The complete genome of the DRV-AH08 is 11,924 nucleotides in length, similar to other street RABV published to date (11). The lengths of the coding sequences are as follows: 1,353 nucleotides (nt) for the N, 891 nt for the phosphoprotein, 609 nt for the matrix protein, 1,575 nt for the G, and 6,384 nt for the RNA-dependent RNA polymerase. Sequence comparison indicates that this virus is closely related to the viruses that have been identified recently in China and other Asian countries, with high homology (86 to 98%) (12, 13). The homologies between this virus and those in the “cosmopolitan” group are only 84 to 85%. This virus, along with those re-

cently identified in China and Asia, although they can still be grouped into clade I of RABV, might represent a distinct lineage from those in the cosmopolitan group that includes all the vaccine strains (except CTN181) and street viruses isolated from terrestrial animals from all over the world.

**Nucleotide sequence accession number.** The complete genome sequence of DRV-AH08 is available in GenBank under accession number [HQ450385](http://www.ncbi.nlm.nih.gov/nuccore/HQ450385).

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