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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Highly Virulent Rabies Virus Isolated from a Rabid Pig in South China

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A virulent rabies virus (RABV) strain, GD-SH-01, was isolated from brain tissue of a rabid pig in China. This report describes the first complete genome sequence of a swine-origin RABV strain, and this information will provide important insights into the transmission cycle and genetic diversity of RABV from different hosts in China.

Rabies virus (RABV), a member of the genus *Lyssavirus* in the family *Rhabdoviridae*, is a neurotropic virus that causes fatal encephalitis in warm-blooded animals (3). RABV has a nonsegmented, single-stranded, negative-sense RNA genome that is approximately 12 kb, comprising five genes that encode the nucleoprotein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), and RNA-dependent RNA polymerase (L) (7, 11). The domestic dog is the primary reservoir and vector of rabies transmission in China, although RABV has been isolated or detected in other animal species, such as cat, ferret-badger, fox, pig, cattle, and donkey (2, 4, 13–15). An outbreak of pig rabies emerged in a rural pig farm in Sihui of southern China's Guangdong Province in March 2011 and resulted in the death of 14 pigs. A virulent wild RABV strain, GD-SH-01, was isolated from the brain tissue of a rabid pig, and its complete genomic nucleotide sequence was determined.

The entire genome was generated by reverse transcription-PCR with 10 pairs of primers for amplifying 10 overlapped fragments of RABV. The primers for obtaining both ends of the genomic sequence were designed based on the first 11 nucleotides (nt) at the 3′ and 5′ terminals, which are considered to be highly conserved in RABV (5, 6). The PCR products were purified and cloned into the pMD18-T vector (TaKaRa) and sequenced on a 3730 DNA analyzer (Applied Biosystems). The genome was assembled using DNAStar (version 7.0). The complete genome of strain GD-SH-01 is 11,923 nt in length, with a GC content of 45.42%. The genomic organization is typical of RABV, including a 58-nt 3′ leader, the N gene (nt 59 to 1483), P gene (nt 1486 to 2475), M gene (nt 2481 to 3283), G gene (nt 3289 to 5355), L gene (nt 5380 to 11853), and a 70-nt 5′ trailer. The intergenic regions, N-P, P-M, M-G, and G-L, contain 2, 5, 5, and 24 nt, respectively.

Compared with the vaccine and street strains, the complete genome sequence of GD-SH-01 has 83 to 94% and 84 to 98% nucleotide identity, respectively. Transcriptional initiation and termination signals in the GD-SH-01 strain are conserved as consensus sequences AACAYYHCT and $G(A)_7$ (10). The G protein is known to play a predominant role in the pathogenesis of rabies virus (1, 8, 9). Similar to other virulent strains, Ala_{242}, Asp_{255}, Ile_{268}, and Arg_{333}, which are involved in viral pathogenicity (9, 12), are conserved in the G protein of GD-SH-01. Compared with attenuated vaccine strains (CTN181, CTN-1, HEP-Flury, SAD, RV-97, and RC-HL), G of GD-SH-01 has 7 unique amino acid variations, of which 2 variant loci were identified in the ectodomain.

The sequence data indicated that GD-SH-01 has the characteristics of virulent strains and belongs to genotype 1 of RABV. Several amino acid substitution sites identified in this strain provided evidence of genomic modifications during the transmission of RABV in different hosts. Complete genome analysis of the swine-origin RABV will provide information that may help in understanding the transmission cycle and genetic variations of RABV from different hosts in China.

Nucleotide sequence accession number. The complete genome sequence of RABV strain GD-SH-01 has been deposited in GenBank under accession number JX088694.

ACKNOWLEDGMENTS

This work was supported by grants from the National Natural Science Foundation of China (numbers 31172322 and 31101842) and the Key Program on the Integration of Production, Education and Research of Guangdong Province and Ministry of Education (number 2010A090200083).

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Received 22 August 2012 **Accepted** 23 August 2012

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doi:10.1128/JVI.02234-12

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