

Genome Sequence of a Novel Hobi-Like Pestivirus in China

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Hobi-like pestivirus is a novel pestivirus species first isolated in 2004. Here, we report the genome sequence of a Hobi-like pestivirus strain isolated from contaminated MDBK cells in China. The sequence information is important for surveillance of this emerging animal infectious disease worldwide.

In 2004, an atypical pestivirus named D32/00_‘Hobi’ was first isolated from fetal calf serum (FCS) originating from Brazil (7). It differed from previous pestivirus species (bovine viral diarrhea virus type 1 [BVDV-1] and BVDV-2) based on genetic and antigenic properties. The virus was proposed and accepted as a novel species of the family *Flaviviridae*, genus *Pestivirus*, named Hobi-like pestivirus. A few years later, some closely related Hobi-like viruses were detected in Thailand, Italy, the United States, and Australia (1, 3, 4, 6, 8). According to the conserved 5′ untranslated region (UTR), Hobi-like pestivirus can be divided into two subgroups, Brazilian origin and Thai origin (8). Some reports indicated that viruses were associated with natural infectious and clinical diseases, including diarrhea, abortion, and respiratory disease in cattle (1, 2, 3, 4, 8).

In this paper, the near-full-length genome sequence of one atypical pestivirus, JS12/01, is reported. It was detected and identified in contaminated MDBK cell cultures before the cells were used for clinical sample isolation. The total RNA of the contaminated cells extracted by using TRIzol (Invitrogen) was reverse transcribed and amplified by PCR, and PCR fragments were purified and cloned into the pJET1.2 vector (Thermo) and sequenced.

The complete genomic sequence of JS12/01 comprises an open reading frame of 11,700 nucleotides (nt) flanked by 5′- and 3′-end untranslated regions (UTRs). BLAST results showed that the virus should be one of the novel Hobi-like pestiviruses. The 5′ UTR sequence was analyzed by Clustal X tools and MEGA 4.0.2 software with reference sequences, and phylogenetic analysis demonstrated that it was more strictly related to the viruses from Brazil than to those of Thai origin. A similar cluster displayed the same result in the trees constructed on E2 and N^{pro} sequences. By sequence analysis of the full-length genome, strain JS12/01 displayed the closest relationships to Italy-83/10-ncp and Italy-1/10-1, which had been detected from naturally infected bovines, with nucleotide homologies of 95.4% and 94.8%, respectively. Considering that the virus has been repeatedly detected in batches of FCS (5, 7, 9) and that there has been no report of bovines infected with Hobi-like virus in China, the results indicated that the strain from the MDBK cells was possibly contaminated in a lab, because the cells had been passaged in different labs and might have come into contact with contaminated FCS or other biological products. At present, it is not certain whether the virus is present in the cattle of China or imported from other countries.

Since the first case of natural infection in cattle caused by a Hobi-like strain, Th/04_KhonKaen, in Thailand (9), continuous outbreaks have been reported in Europe (1, 4). The emerging virus may have important implications for enhancing pestivirus control programs. The results of complete genome sequencing will contribute to the understanding of the evolutionary characteristics of Hobi-like pestivirus and the surveillance of the virus transmission.

Nucleotide sequence accession number. The near full-length genomic sequence of JS12/01 was deposited in GenBank under accession no. [JX469119](https://doi.org/10.1093/jvi/1128/JVI.02159-12).

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