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GENOME ANNOUNCEMENT

Complete Genomic Sequence of Duck Flavivirus from China

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We report here the complete genomic sequence of the Chinese duck flavivirus TA strain. This work is the first to document the complete genomic sequence of this previously unknown duck flavivirus strain. The sequence will help further relevant epidemiological studies and extend our general knowledge of flaviviruses.

Duck flavivirus is closely related to Tembusu virus, a zoonotic flavivirus (10). The duck flavivirus is the etiological agent of duck egg drop disease, which causes serious economic loss. The flavivirus genome, consisting of single-stranded positive-sense RNA, approximately 10.5 kb, encodes three structural proteins (capsid [C], membrane [PrM and M], and envelope [E]) and seven nonstructural proteins (NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5) in one open reading frame (ORF) with subsequent cleavage (8, 9). Many viruses have been isolated in China since the isolation of the first BYD strain in 2010. However, there has been no report of the complete genomic sequence of this duck flavivirus. It is necessary to obtain new molecular data on duck flavivirus to extend our general knowledge of flaviviruses.

Here we report the complete genomic sequence of Chinese duck flavivirus strain TA, which was isolated from a duck that showed obvious clinical signs of egg drop disease in Shandong Province, China, in 2010. Postmortem examination showed that the most obvious features of the duck are severe ovarian hemorrhage, ovaritis, and regression.

Viral RNA and full-length cDNA were prepared as described by Su et al. (10). The 5′ and 3′ ends of the genomes were amplified using 5′ and 3′ rapid amplification of cDNA ends (RACE) kits (Invitrogen, Carlsbad, CA), respectively. For 5′ RACE, viral RNA was reverse transcribed and then incubated in C-tailing buffer according to the kit's instructions. For 3′ RACE, viral RNA was incubated with poly(A) buffer for poly(A) tailing of the 3′ terminus. Amplified products were cloned into the pMD18-T vector (13). The cloned inserts were then sequenced. The complete genome had 10,986 nucleotides (nt) and the typical flavivirus genome organization: 5′ untranslated region (UTR)-Cv-Ci-prM-M-E-NS1-NS2A-NS2B-NS3-NS4A-2K-NS4B-NS5-3′ UTR. The long ORF encodes 3,425 amino acids (aa; 95 to 10,372 nt). The 94-nt 5′ UTR was of intermediate size and the 614-nt 3′ UTR was the largest size among flaviviruses (4). The lengths of the predicted cleavage proteins are the following: capsid, 120 aa; PrM,177 aa; envelope, 501 aa; NS1, 342 aa; NS2A, 227 aa; NS2B, 131 aa; NS3, 619 aa; NS4A, 126 aa; 2K, 23 aa; NS4B, 254aa; NS5, 905 aa.

Phylogenetic analysis of the TA and 28 3′ UTR sequences from GenBank showed that the TA grouped into mosquito-borne virus clusters and was closely related to African Bagaza virus (accession no. AY632545; 69.9% identity; MEGA4 version 14.0) (see Fig. S1 in the supplemental material), which caused both human and animal diseases (6, 7).

Most flaviviruses are zoonotic, suggesting that they can be transmitted from animals to people. Bird infections by flaviviruses are frequent (1, 2, 3, 5, 11, 12, 14). Although the natural transmission mechanism is still unknown, infection of human beings by this new emerging duck flavivirus cannot be ruled out. Moreover, the widespread farming of ducks in China emphasizes that the disease should be monitored closely. Therefore, large-scale surveillance for understanding the epidemiology of the duck flavivirus is required.

Nucleotide sequence accession number. The complete genomic sequence of the TA strain has been deposited in GenBank (accession no. JQ289550).

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