Complete Genome Sequence of Duck Tembusu Virus, Isolated from Muscovy Ducks in Southern China

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We report here the complete genomic sequence of the duck Tembusu virus (DTMUV) WJ-1 strain, isolated from Muscovy ducks. This is the first complete genome sequence of DTMUV reported in southern China. Compared with the other strains (TA, GH-2, YY5, and ZJ-407) that were previously found in eastern China, WJ-1 bears a few differences in the nucleotide and amino acid sequences. We found that there are 47 mutations of amino acids encoded by the whole open reading frame (ORF) among these five strains. The whole-genome sequence of DTMUV will help in understanding the epidemiology and molecular characteristics of duck Tembusu virus in southern China.

In April 2010, an outbreak of the newly emerged duck Tembusu virus (DTMUV) caused a range of symptoms in infected ducks, including retarded growth, high fever, loss of appetite, decreased egg production, and death (3). Complete genomic sequences of DTMUV isolated in eastern China have been reported (2, 4). However, there has been no report of a complete genomic sequence of DTMUV in southern China’s important waterfowl-producing areas, where the majority of production takes place on small-scale farms with low biosecurity levels.

In January 2012, a DTMUV strain was isolated from a duck farm with an outbreak of egg drop problems in Muscovy ducks in Guangdong Province, China. Subsequently, nucleotide sequences of the isolate were amplified and sequenced. Viral RNA and full-length cDNA were amplified through reverse transcription-PCR (RT-PCR). Oligo7.0 was used to design the PCR primers. Amplified products were purified and cloned into the pMD18-T vector (TaKaRa) and sequenced with an ABI 3730XL genome sequencer. Sequences were assembled and manually edited to produce the final genome sequence. The isolated virus was identified as DTMUV and named WJ-1.

Sequence analysis showed that the full genomic length of WJ-1 is 10,990 nucleotides (nt) without the poly(A) tail, and the 5′- and 3′-terminal noncoding regions are 94 and 618 nt, respectively. Additionally, the coding region of WJ-1 included a single open reading frame (ORF), which encoded a polypeptide of 3,426 amino acids. Comparative sequence analysis showed that WJ-1 was 97% to 100% identical to different strains of DTMUV. Specifically, it resembles the DTMUVs isolated in southern China more closely than it resembles the strains that were found in other regions of China.

WJ-1 shows the same genome organization as other DTMUVs: 5′ untranslated region (5′UTR) - C-PrM-E-NS1-NS2A-NS2B-NS3-NS4A-2K-NS4B-NS5-3′UTR (1). Herein, we found that the PrM coding sequence contains 501 nucleotides, encoding a protein of 167 amino acids, which is 10 amino acids more than that encoded by TA. In addition, the NS1 coding sequence contains 1,026 nucleotides, encoding a protein of 342 amino acids, which is 10 amino acids less than that encoded by TA. The amino acid sequences encoded by the entire ORF of WJ-1 and those encoded by four previously reported DTMUV strains (TA, JQ289550; GH-2, JQ314465; YY5, JF270480; ZJ-407, JQ314464) isolated in eastern China were aligned, and 47 mutations of amino acids were found. The most variable region of the protein of WJ-1 is located in NS3. Positions 69 to 116 and 341 to 391 are the hypervariable regions of NS3.

Potential N-linked glycosylation sites (NLGlys) were found in WJ-1, with a distribution of two in the PrM protein, one in the E protein, four in the NS1 protein, two in the NS4B protein, and three in NS5. We found that there is one more N-linked glycosylation site in the NS1 protein of WJ-1 than in those of GH-2, YY5, and ZJ-407.

Therefore, continuing duck Tembusu virus surveillance in poultry is critical to understanding the genesis and emergence of future pandemic strains in southern China.

**Nucleotide sequence accession number.** The GenBank accession number of WJ-1 is JX549382.

**ACKNOWLEDGMENTS**

This work was supported by the International Sci & Tech Cooperation Program (2010DFB33920) and the Modern Agricultural Industry Technology System (CARS-36).

The funding organizations had no role in the study design, data collection and analysis, ownership of the materials, or preparation of the manuscript.

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Received 31 August 2012 Accepted 4 September 2012

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doi:10.1128/JVI.02361-12