

Complete Genomic Sequence of Bluetongue Virus Serotype 16 from China

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Received 23 September 2011/Accepted 29 September 2011

We report here the complete genomic sequence of the Chinese bluetongue virus serotype 16 (BTV16) strain BN96/16. This work is the first to document the complete genomic sequence (segments 1 to 10) of a BTV16 strain. The sequence information provided herein will help determine the geographic origin of BTV16 and define the phylogenetic relationship of BTV16 to other BTV strains.

Bluetongue virus (BTV) is the “type” species of the genus *Orbivirus*, within the family *Reoviridae* (7). It is the etiological agent of bluetongue disease, which is listed as a “notifiable disease” by the Office International des Epizooties (OIE). The genome of BTV consists of 10 linear double-stranded RNA (dsRNA) segments encoding seven structural proteins (VP1 to VP7) and three nonstructural proteins (NS1, NS2, and NS3/NS3a) (5, 6, 8, 9, 11). Twenty-four BTV serotypes have thus far been recognized in the world, and a putative 25th serotype has recently been proposed (BTV25) (2). Seven BTV serotypes (BTV1, BTV2, BTV3, BTV4, BTV12, BTV15, and BTV16) have been isolated in China since the isolation of the first Chinese BTV strain in Yunnan Province in 1979 (3, 10, 12). Worldwide, there has been no report of the full genomic sequence of the BTV16 strain. It is necessary to acquire and analyze the sequence of the complete genome of a BTV16 strain to study the molecular features of this serotype.

In the present study, we report the full genomic sequence of the serotype 16 BTV strain BN96/16, which was isolated from the blood of a sheep that showed obvious signs of bluetongue disease in Yunnan Province, China, in 1996. Viral dsRNA from BN96/16 was prepared according to the protocol described by Attoui et al. (1). Full-length cDNA copies of each genomic segment were synthesized in a sequence-independent manner using the full-length amplification of cDNAs (FLAC) method, and subsequent rounds of PCR amplification were performed as described by Maan et al. (4). The 10 PCR products corresponding to each of the genomic segments of BN96/16 were purified and cloned into the pEASY-Blunt clone vector (Transgen Biotech, China). The cloned inserts were then sequenced by the Invitrogen Company to determine the full genomic sequence of BN96/16.

The nucleotide sequences of the 10 BN96/16 segments were determined. The nucleotide lengths of BN96/16 segments 1 through 10 are as follows: segment 1, 3,944 bp; segment 2, 2,935 bp; segment 3, 2,772 bp; segment 4, 1,981 bp; segment 5, 1,763 bp; segment 6, 1,637 bp; segment 7, 1,156 bp; segment 8, 1,125 bp; segment 9, 1,052 bp; and segment 10, 822 bp. The amino acid (aa) lengths of the seven

structural proteins of BN96/16 (VP1 to VP7) are as follows: VP1, 1,302 aa; VP2, 959 aa; VP3, 901 aa; VP4, 644 aa; VP5, 526 aa; VP6, 330 aa; and VP7, 349 aa. The amino acid lengths of the three nonstructural proteins of BN96/16 (NS1, NS2, and NS3/NS3a) are as follows: NS1, 552 aa; NS2, 354 aa; and NS3/NS3a, 229/216 aa.

The data presented here are the first to report the complete sequence of the 10 genomic segments of a strain of BTV16. It is hoped that these data will facilitate future investigations of the molecular characteristics of this strain and will help elucidate its phylogenetic relationship to other BTV strains.

Nucleotide sequence accession number. The full genomic sequence of BTV16 strain BN96/16 has been deposited in GenBank. Accession no. JN671906 to JN671915 correspond to BN96/16 segments 1 through 10, respectively.

We thank Peter Wilker for editing the manuscript.

This study was supported by grants from the National High-Tech Research and Development Program of China (no. 2011AA10A212), Basic Scientific Research Foundation of Central Research Academies and Institutes (ZGKJ201105), and Heilongjiang Natural Science Foundation of China (no. ZJN-0602-01).

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