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GENOME ANNOUNCEMENT

Complete Genome Sequence of Bluetongue Virus Serotype 16 of Goat Origin from India

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In this article, we document the first complete genome sequence of an isolate of bluetongue virus serotype 16 (BTV16) from a goat in India. The virus was isolated from an in-contact goat from an animal farm in Chennai where clinical disease occurs in sheep. The total size of the genome is 19,185 bp. The information provided for full-length sequences of all 10 segments will help in understanding the geographical origin and transmission of the Indian isolate of BTV16 as well as its comparison with global isolates of BTV16 of sheep, cattle, and other host species origins.

Bluetongue (BT) is vector-borne "notifiable disease" and is endemic in various parts of India (6, 8). The bluetongue virus (BTV) can infect domestic and wild ruminants. The clinical signs are fatal in sheep and white-tailed deer, whereas in cattle, camels, and goats, it appears in a subclinical form (2, 7, 9). *Bluetongue virus* (BTV) belongs to the family *Reoviridae* and genus *Orbivirus* (5). The 10 double-stranded RNA segments encode seven structural proteins (VP1 to VP7) and three nonstructural proteins (NS1, NS2, and NS3/NS3a) (3, 4, 6, 10, 12). So far, 24 serotypes (BTV1 to BTV24) have been recognized globally and a 25th serotype (BTV25) has been proposed (1). Out of these 24 serotypes, 21 have been reported from India (8). Recently, the 22nd isolate, BTV21 has also been isolated in India (11).

We are reporting for the first time the full genome sequence of BTV serotype 16 strain Goat/10/Ind/ABT/Hisar of goat origin from India. The blood was collected from an in-contact goat from an animal farm in Chennai where the disease was prevalent in sheep. The virus was isolated and grown in BHK-21 cells. The infected culture medium was filtered through 0.22-μm-pore filters and treated with DNase and RNase before isolation of the viral RNA by TRIzol reagent (Life Technologies) following the manufacturers' instructions. The double-stranded viral RNA was fragmented by nebulization to prepare a library suitable for whole-genome sequencing on the Ion Torrent Personal Genome Machine (PGM) using a 316 chip and 200-base sequencing chemistry. The sequences were assembled with the Newbler assembler (454 Life Sciences). The GS reference mapper was used to generate contigs (with BTV16 from China used as a reference genome (13)), and the resulting contigs were used for aligning it to the reference sequence (13), which generated a consensus sequence of sample cDNA libraries. The gaps that remained at the ends were filled by Sanger's sequencing. The genome annotation and comparative analysis of the genome were carried out with published genome of BTV16 from China (13).

The total size in nucleotide sequences of the 10 genome segments (seg1 to seg10) of the strain Goat/10/Ind/ABT/Hisar was determined as 19,185 bp, and the sizes of individual segments in base pairs are 3,944, 2,929, 2,772, 1,981, 1,765, 1,637, 1,156, 1,125, 1,053, and 823, respectively. The sizes of the seven structural proteins (VP1 to VP7) of strain Goat/10/Ind/ABT/Hisar are 1,302, 959, 901, 644, 526, 330, and 349 amino acids (aa), respectively. The numbers of amino acids in nonstructural proteins are as follows: NS1, 552; NS2, 354; and NS3/NS3a, 229/216.

The only previous report on the BTV16 full genome sequence is from China (13). The second report of BTV16 strain Goat/10/Ind/ABT/Hisar, from India, would help to understand the origin and spread of the virus to various geographical regions across countries.

Nucleotide sequence accession numbers. The complete genome sequences of all 10 segments (seg1 to seg10) of strain Goat/10/Ind/ABT/Hisar have been deposited in GenBank under accession no. JQ924820 to Q924829.

ACKNOWLEDGMENTS

The work was carried out in the project entitled "All India Network Program on Bluetongue" funded by the Indian Council of Agriculture Research, New Delhi. We also acknowledge the help rendered by the Department of Animal Biotechnology, AAU, Gujarat, for providing the sequencing facility.

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Received 9 May 2012 **Accepted** 11 May 2012

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doi:10.1128/JVI.01128-12

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