



Genome Announcements

Full genome sequencing of the bluetongue virus-1 isolate MKD20/08/Ind from goat in India

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ARTICLE INFO

Article history:

Received 6 January 2016

Accepted 20 January 2016

Available online 22 April 2016

Associate Editor: John Anthony McCulloch

Keywords:

Bluetongue virus-1

Goat

Eastern BTV topotype

Next-generation sequencing

ABSTRACT

This communication reports full genome sequencing of the bluetongue virus-1 (BTV-1) isolate MKD20/08/Ind from goat in northern India. The total BTV-1 genome size was found to be 19,190 bp. A comparison study between the Indian isolate and other global isolates revealed that it belongs to the 'Eastern' BTV topotype. The full genome sequence of BTV-1 will provide vital information on its geographical origin and it will also be proved useful for comparing the Indian isolate with global isolates from other host species.

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Introduction

Diseases caused by the bluetongue virus (BTV) in domestic and wild ruminants are transmitted by certain *Culicoides* species.^{1–3} BTV is the prototype species of *Orbivirus* in the family *Reoviridae*.⁴ The BTV genome consists of 10 linear double-stranded RNA (dsRNA) segments that code for seven structural (VP1–VP7) and four non-structural (NS1, NS2, NS3/NS3a and NS4) proteins.^{5,6} Currently, only 27 distinct BTV serotypes have been identified worldwide.⁷ BTV is endemic in India and approximately 13 different BTV serotypes (BTV-1–4, 6, 9, 10, 12, 16–18, 21 and 23) have been isolated so far.⁸

In this study, we report the full genome sequencing of the BTV-1 isolate MKD20/08/Ind from goat in northern India. The full genome sequence of this isolate is available in the Bluetongue Virus Repository, All Indian Network Program on Bluetongue, Indian Veterinary Research Institute, Mukteswar, India. The complete genome was sequenced by next-generation sequencing (Ion Torrent). After extracting the viral dsRNA using Tri Reagent (Sigma, St. Louis, USA), it was purified by sequential precipitation with lithium chloride. An Ion Xpress plus fragment Library Kit was used to construct the full-length cDNA library, according to manufacturer's protocol (Rev. A, Life Technologies). After multiplexing with different bar-coded adaptors, each library was sequenced on an Ion PI

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<http://dx.doi.org/10.1016/j.bjm.2016.04.022>

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v2 chip (Life Technologies). To establish the complete genome, overlapping sequences were assembled with the Ion Torrent server by mapping closely related genomes (BTV-1 reference genome). The mapped file was viewed with an Integrative Genomics Viewer. The average coverage depth was 127.7 and genome base coverage at 20× was 95.91%.

The segment sizes (1–10) of MKD20/08/Ind were found to be 3944, 2940, 2772, 1981, 1765, 1635, 1154, 1125, 1052 and 822 bp, respectively. These segments encode proteins with amino acid length as follows: VP1 (1302), VP2 (961), VP3 (902), VP4 (644), VP5 (526) VP6/NS4 (330/77), VP7 (349), NS1 (552), NS2 (354) and NS3/NS3a (229/216). The phylogenetic analysis revealed that MKD20/08/Ind belongs to the 'Eastern' BTV topotype. The full genome sequence of the BTV-1 isolate will facilitate future molecular epidemiological investigations and will also help provide vital information on its geographic origin from India and other parts of world.

Nucleotide sequence accession numbers

The full genome sequence of BTV-1 isolate MKD20/08/Ind was deposited in GenBank under accession no. KU234257 to KU234266 corresponding to segment 1 through 10.

Conflicts of interest

The authors declare no conflicts of interest.

Acknowledgements

The authors would like to thank the Director of ICAR-IVRI, Project Director of ICAR-PDFMD and the AINP-BT project for providing facilities.

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