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doi: 10.4103/1995-7645.243096 ©2018 by the Asian Pacific Journal of Tropical Medicine. All rights reserved. Complete genome sequence of a rodent torque teno virus in Hainan Island, China

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ABSTRACT Objective: Torque teno virus(TTV), are reported in a wide range of mammals. In this study, we sequenced and analyzed the complete genome of a genetic variant of Rodent TTV, RoTTV3-HMU1 (Hainan Medical University). The virus was harbored by a *Rattus norvegicus* in the residential areas of Hainan Island, China. Methods: Torque Teno virus (TTV) was found widely distributed throughout the world infecting an extensively wide range of mammals .We extracted the viral DNA from a Rattus norvegicus liver which was caught from the residential areas of Hainan Island. Purifying the amplicons in the range of 250-500 bp. Then Five hundred nanograms DNA was subjected to high-throughput sequencing. The contigs were compared with the NCBI nucleiotide database, designed the primers to cover the genome by PCR amplification and amplicons of each PCR which have been cloned and sequenced. Finally the genome was annotated by using NCBI ORF finder and FGENESV0. Phylogenetic analysis was implemented by the neighbor-joining method in the MEGA6 software package. Results: We sequenced the complete genome of a genetic variant of Rodent TTV, RoTTV3-HMU1. The genomic sequence of RoTTV3-HMU1 has been deposited in GenBank under accession number MF688246.1. The complete genome of RoTTV3-HMU1 is 2 570 nucleotides (nt) in length with a G+C content of 46.93%. RoTTV3-HMU1 encoded 3 unidirectional overlapping open reading frames (ORF). Sequence analysis indicated that the genome of RoTTV3-HMU1 virus was most closely related to RN_2_15 (GenBank accession no. KM668486.1). Phylogenetic analysis based on both ORF1 and the total genome sequence placed RoTTV3-HMU1 in to the clad RoTTV3 of the RoTTV. Conclusions: Hainan Island faces mainland across the sea, however, the same genotype of RoTTV was identified in both Hainan Island and the other part of China. The detection of RoTTV3-HMU1 contributed to a better understanding about the origin and evolution of RoTTV.

Keywords: TTV; Serotype; Complete Genome Sequence; Rattus norvegicus

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