

Identification of a Cardiovirus in Feces of Wild Rats Through Viral Metagenomics

Authors : Shama, Asif Mahmood, Wen Zhang

Abstract : Cardiovirus is a genus of viruses belonging to the family Picornaviridae. Here, we used viral metagenomic techniques to detect the viral nucleic acid in the fecal samples from wild rats in Zhenjiang city in China. Fecal samples were collected from 20 wild rats and pooled into four sample pools and then subjected to library construction, which were then sequenced on the Illumina MiSeq platform. The sequenced reads were analyzed using a viral metagenomic analysis pipeline. A cardiovirus from the feces of a wild rat was identified, named amzj-2018, of which the complete genome was acquired. Phylogenetic analysis based on the complete amino acid sequence of polyprotein revealed that amzj-2018 formed a separate branch located between clusters of Saffold virus and Rat Theilovirus 1 (RTV-1). Phylogenetic analysis based on different regions of the polyproteins, including P1, P2, P3, and P2+P3, respectively, showed discordant trees, where the tree based on the P3 region indicated that amzj-2018 clustered separately between Theiler's murine encephalomyelitis virus and RTV-1. The complete genome of a cardiovirus was determined from the feces of wild rats, which belonged to a novel type of cardiovirus based on phylogenetic analysis. Whether it is associated with disease needs further investigation.

Keywords : viral metagenomics, viruses, cardiovirus, phylogenetic analysis

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