



Brief Report

Molecular Identification of a Novel Hantavirus in Malaysian Bronze Tube-Nosed Bats (Murina aenea)

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Abstract: In the past ten years, several novel hantaviruses were discovered in shrews, moles, and bats, suggesting the dispersal of hantaviruses in many animal taxa other than rodents during their evolution. Interestingly, the coevolutionary analyses of most recent studies have raised the possibility that nonrodents may have served as the primordial mammalian host and harboured the ancestors of rodent-borne hantaviruses as well. The aim of our study was to investigate the presence of hantaviruses in bat lung tissue homogenates originally collected for taxonomic purposes in Malaysia in 2015. Hantavirus-specific nested RT-PCR screening of 116 samples targeting the L segment of the virus has revealed the positivity of two lung tissue homogenates originating from two individuals, a female and a male of the *Murina aenea* bat species collected at the same site and sampling occasion. Nanopore sequencing of hantavirus positive samples resulted in partial genomic data from S, M, and L genome segments. The obtained results indicate molecular evidence for hantaviruses in the *M. aenea* bat species. Sequence analysis of the PCR amplicon and partial genome segments suggests that the identified virus may represent a novel species in the *Mobatvirus* genus within the Hantaviridae family. Our results provide additional genomic data to help extend our knowledge about the evolution of these viruses.

Keywords: Sarawak mobatvirus; MinION; Tb1-Lu; Mobatvirus; one health concept

1. Introduction

Hantaviruses (Hantaviridae) cause two types of life-threatening human diseases, haemorrhagic fever with renal syndrome (HFRS) in Eurasia and hantavirus cardiopulmonary syndrome (HCPS) in the Americas [1]. To date, as a consensus, wild rodents were believed to be the natural hosts