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1 Short Communication

2 **Molecular identification of a tentatively novel hantavirus in Malaysian Bronze Tube-**
3 **nosed Bat (*Murina aenea*)**

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15 **Abstract:** In the past ten years several novel hantaviruses were discovered in shrews, moles and
16 bats, suggesting the dispersal of hantaviruses in many animal taxa other than rodents during their
17 evolution. Interestingly, the co-evolutionary analyses of most recent studies have raised the
18 possibility of non-rodents may have served as the primordial mammalian host and harboured the
19 ancestors of rodent-borne hantaviruses as well. The aim of our study was to investigate the presence
20 of hantaviruses in bat lung tissue homogenates originally collected for taxonomic purposes in
21 Malaysia, 2015. Hantavirus specific nested RT-PCR screening of 116 samples targeting the L
22 segment of the virus have revealed the positivity of two lung tissue homogenates originating from
23 *Murina aenea* bat species. Nanopore sequencing of hantavirus positive samples resulted in partial
24 genomic data from S, M and L genome segments. The obtained results indicate the first molecular
25 evidence for hantavirus in *Murina aenea* bat species and also the first discovery of a hantavirus in
26 *Murina* bat species. Sequence analysis of the PCR amplicon and partial genome segments suggests
27 the identified virus may represent a novel species in *Mobatvirus* genus within *Hantaviridae* family.
28 Furthermore, our results provide additional genomic data to help extend our knowledge about the
29 evolution of these viruses.

30 **Keywords:** Mulu mobatvirus, MinION, Tb1-Lu, *Mobatvirus*, one health concept
31

32 **1. Introduction**

33 Hantaviruses (*Hantaviridae*) cause two types of life-threatening human diseases, haemorrhagic
34 fever with renal syndrome (HFRS) in Eurasia and hantavirus cardiopulmonary syndrome (HCPS) in
35 the Americas [1]. To date, as a consensus, wild rodents were believed as natural hosts of hantaviruses.
36 However, recent studies described several novel hantaviruses in shrews, moles and bats, suggesting
37 the dispersal of hantaviruses in several animal taxa during their evolution [2]. To date, 10 bat-borne
38 hantaviruses were described in different bat species from Hipposideridae, Rhinolophidae,
39 Emballonuridae, Nycteridae, and Vespertilionidae families and only one from a flying fox species
40 Geoffroy's rousette (*Rousettus amplexicaudatus*) [3-4].

41 Interestingly, phylogenetic analyses of most recent studies have raised the possibility of bats or
42 other animals (shrews and moles) of the Laurasiatheria superorder may have served as the
43 primordial mammalian host and harboured the ancestors of rodent-borne hantaviruses [3,5].
44 However, complex analyses for the genetic diversity and phylogeography of bat associated
45 hantaviruses are tentative since complete genomic data is available only from Brno virus (BRNV),
46 Dakrong virus (DKGV), Láibín virus (LAIV), Quezon virus (QZNV) and Xuân Son (XSV) viruses.
47 Unfortunately, in case of other bat-associated hantaviruses just partial genomic fragments are
48 available mainly from the conservative L segment hardening the implementation of evolutionary
49 analyses [3-5].