

Detection of novel coronaviruses from dusky fruit bat (*Penthetor lucasi*) in Sarawak, Malaysian Borneo

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Funding information

Malaysian Ministry of Higher Education (MoH), Grant/Award Number: FRGS/1/2020/STG03/UNIMAS/02/1; Universiti Malaysia Sarawak (UNIMAS)

Abstract

Background: Sarawak has one of the highest diversity of fruit bats species (family Pteropodidae) in Malaysia, with 19 species described. Most coronavirus (CoV) studies have mainly focused on insectivorous bats, resulting in a lack of information on CoVs present in frugivorous bats. In addition, bat CoV surveillance activities are lacking in Malaysia.

Objectives: Our study focuses on determining the presence of bat CoVs in dusky fruit bat (*Penthetor lucasi*).

Methods: Guano samples belonging to *P. lucasi* were collected from Wind Cave Nature Reserve. The samples were screened for the presence of CoVs using validated hemi-nested consensus RNA-dependent RNA polymerase consensus primers.

Results: The bat CoV positivity rate was 38.5% ($n = 15/39$), with the viruses belonging to two subgenera: *Alphacoronavirus* (α -CoV) and *Betacoronavirus* (β -CoV). Phylogenetic analysis revealed that CoVs from 14 samples of *P. lucasi* belong to the genus α -CoV and may represent previously described genetic lineages in insectivorous bats in Wind Cave. However, only one sample of *P. lucasi* was detected with β -CoV which is closely related to subgenus *Nobecovirus*, which is commonly seen in frugivorous bats.

Conclusions: This study provides the first available data on CoVs circulating in *P. lucasi*.

KEYWORDS

Alphacoronavirus, *Betacoronavirus*, coronaviruses, frugivorous, *Nobecovirus*

1 | INTRODUCTION

Coronaviruses (CoVs) are placed under the subfamily Orthocoronavirinae in the family Coronaviridae. They are enclosed with envelope, and are recognised as single-stranded positive-sense RNA viruses. The CoVs constitute the largest continuous RNA genomes among mammalian viruses, with sizes ranging from 25,000 to 32,000 base pairs (Woo et al., 2009). Based on the ICTV nomenclature, CoVs have been classified into four genera, that is: *Alphacoronavirus* (α -CoV), *Betacoron-*

avirus (β -CoV), *Gammacoronavirus* (γ -CoV) and *Deltacoronavirus* (δ -CoV) (Cui et al., 2019).

Currently, there are seven known human coronaviruses (HCoV) that are linked to gastroenteritis, and respiratory illnesses. The HCoV-229E and HCoV-OC43 were among the earliest human CoVs detected in the middle of the 1960s, and only caused mild respiratory problems (Heikkinen & Järvinen, 2003). Subsequently, HCoV-NL63 and HCoV-HKU1 were discovered in 2004 and 2005 (Van Der Hoek et al., 2004; Woo et al., 2005). However, the researchers only developed a strong

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