2022~2024 年臺灣蝙蝠冠狀病毒監測成果

疾病診斷組

胡書佳副研究員

摘要

本所持續於臺灣蝙蝠群中進行冠狀病毒監測,與台北市蝙蝠保育 協會及各縣市動物防疫機關合作收集蝙蝠檢體,並應用分子生物學方 法監測臺灣蝙蝠群中的冠狀病毒流行情形。於 2022 至 2024 年間共計 收集 16 種計 452 例蝙蝠檢體(包含個體、口拭、排遺等),蝙蝠品種 以高頭蝠最多(42.9%, 194/452), 其次為東亞家蝠(29.6%, 134/452)。 冠狀病毒於 5 種蝙蝠檢出(高頭蝠、東亞家蝠、堀川氏棕蝠、臺灣狐 蝠及山家蝠)。以部分 RNA-dependent RNA polymerase 基因序列建構 親緣關係樹,結果顯示高頭蝠檢出之冠狀病毒皆屬於 alpha 冠狀病毒 屬下 Pedacovirus 亞屬;東亞家蝠、山家蝠及堀川氏棕蝠檢出之冠狀病 毒皆屬於 beta 冠狀病毒屬下 Merbecovirus 亞屬;臺灣狐蝠檢出之冠狀 病毒屬於 beta 冠狀病毒屬下 Nobecovirus 亞屬。未來須持續進行臺灣 蝙蝠族群冠狀病毒監測,以了解並早期預警可能人畜共通傳播的疾病 發生。

Bat coronavirus surveillance in Taiwan, 2022-2024

Shu-Chia HU

Abstract

Coronavirus surveillance project in the Taiwanese bat population has been continuously conducted. In this project, Veterinary Research Institute cooperates with Bat Conservation Society of Taipei and local animal disease inspection authorities to collect bat samples. To monitor and investigate the epidemiology of bat coronaviruses in Taiwan, the collected samples are surveilled via molecular techniques. From 2022 to 2024, 452 bat samples from 16 species were collected across various cities and counties in Taiwan. The predominant species of collected samples were Scotophilus kuhlii (42.9%, 194/452), followed by Pipistrellus abramus (29.6%, 134/452). Coronavirus was detected in five species of bats (S. kuhlii, P. abramus, Eptesicus pachyomus horikawai, Pteropus dasymallus formosus, and P. sp.2 (montanus)). The results showed that the coronavirus detected in S. kuhlii belonged to the subgenus Pedacovirus in the genus Alphacoronavirus; the coronavirus detected in P. abramus, P. sp.2 (montanus) E. p. horikawai belonged to the subgenus Merbecovirus in the genus Betacoronavirus; and the coronavirus detected in P. d. formosus belonged to the subgenus Nobecovirus in the genus Betacoronavirus. Current surveillance results show that no coronaviruses related to human infection have been detected in Taiwanese bat. This project of long-term coronaviruses surveillance is required to understand and early warning of the possible zoonotic diseases among Taiwanese bat population.