

2018~2021 年臺灣蝙蝠麗沙病毒監測成果

疫學研究組

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摘要

本所持續於臺灣蝙蝠群中進行麗沙病毒監測，並於 2016 至 2017 年間，於東亞家蝠檢出臺灣蝙蝠麗沙病毒第一型。持續性應用狂犬病直接免疫螢光抗體染色法及分子生物學方法監測並了解臺灣蝙蝠群中的麗沙病毒流行情形。於 2018 至 2021 年間共計收集 13 種計 407 例蝙蝠檢體，以東亞家蝠(62.7%，255/407)最多，檢體分布範圍涵蓋 18 縣市。期間於東亞家蝠及絨山蝠共計檢出 3 例麗沙病毒陽性，2 例於東亞家蝠檢出之麗沙病毒皆屬第一型臺灣蝙蝠麗沙病毒，1 例於絨山蝠所檢出之麗沙病毒經全長基因定序分析顯示與其他 16 種麗沙病毒及臺灣蝙蝠麗沙病毒第一型相似度皆低於 80%，應為一新型麗沙病毒，並將其命名為臺灣蝙蝠麗沙病毒第二型。依據現有監測結果顯示，目前於臺灣蝙蝠族群至少存在兩種麗沙病毒，本研究結果可促使國內相關單位提高民眾或研究人員接觸蝙蝠之風險意識，以早期預警並降低國人遭蝙蝠感染之風險。

Bat lyssavirus surveillance in Taiwan from 2018 to 2021

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Abstract

Since the identification of Taiwan bat lyssavirus I in the bat *Pipistrellus abramus* in 2016, the lyssavirus surveillance in the Taiwanese bat population has been continuously conducted in Taiwan. To monitor and investigate the epidemiology of bat lyssaviruses in Taiwan, bat populations are routinely surveilled via the direct fluorescent antibody test as well as other molecular techniques. From 2018 to 2021, a total of 407 bat specimens representing 13 species were collected, from geographic regions distributed across 18 cities and counties in Taiwan. The predominant species collected was *P. abramus* which accounted for 62.7% (255/407) of the collected bats. From 2018 to 2021, lyssaviruses were detected in two *P. abramus* specimens and in one *Nyctalus plancyi velutinus* specimen. The lyssaviruses identified in *P. abramus* were similar to Taiwan bat lyssavirus I which was previously identified in 2016-2017. The nucleotide similarities between the lyssavirus identified in *N. velutinus* and other lyssaviruses was less than 80% in the concatenated coding regions, and the newly identified lyssavirus formed a separate branch in the phylogenetic tree. This lyssavirus was thus assumed as a new species of lyssavirus and designated as Taiwan bat lyssavirus II. The current results indicate that two species of lyssavirus exist among bat populations within Taiwan. Therefore, public health awareness and education programs should be undertaken to minimize the risks of bat-to-human infections of lyssaviruses in Taiwan.