臺灣野生動物狂犬病之再浮現

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摘要

狂犬病為一種神經系統性疾病，主要會造成急性進展性且致死性的腦脊髓炎病變，狂犬病病毒具親神經性為彈狀病毒科（*Rhabdoviridae*）之麗沙病病毒屬（*Lyssaviruses*）。過去 50 年來臺灣曾被認為是狂犬病非疫區國家，但在民國 102 年，野生動物疾病監測中發現鼬獾存在有狂犬病病毒，截至目前 1,416 例鼬獾中，共檢測出 711 例狂犬病陽性病例。為了瞭解臺灣鼬獾感染狂犬病的疫情，尤其是為何僅在鼬獾族群中長期隱密循環感染。以醣蛋白及核蛋白基因分析臺灣鼬獾狂犬病病毒之親緣關係，並探討病毒在時間及空間上的地理演化關係。經分子時鐘及親緣地理分析，臺灣鼬獾狂犬病病毒群與中國狂犬病病毒群有共同分化的祖先，約起源 19 世紀，而臺灣鼬獾狂犬病病毒長期在臺灣獨立演化成為兩種不同基因分群(TW-CS 病毒群分佈在臺灣的西部；TW-E 病毒群分佈在臺灣的東部)，而不同的分群與地理分具有相關性。分析兩種不同基因群之族群波動歷史，TW-E 基因群於民國 102 年時有顯著性的病毒族群擴張，而相對於 TW-CS 基因群則病毒族群則比較穩定，但於民國 99 年時有輕微族群擴張。

Re-emergence of rabies amongst wildlife in Taiwan

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Abstract

Rabies is a neurological disease characterized by acute, progressive, fatal viral encephalomyelitis. The disease is caused by a highly neurotropic rabies virus (RABV) belonging to the genus *Lyssavirus* of the family *Rhabdoviridae*. Taiwan had been considered rabies-free for more than 50 years. However, in 2013, Formosan ferret badger (TWFB) rabies was discovered via routine monitoring of wildlife diseases. Since this recent rabies outbreak, 711 of 1,416 TWFB sputum samples test positive for rabies using the direct fluorescent antibody test. In order to more fully understand TWFB rabies infections, especially the origins of this cryptic infection. Phylogenetic and phylogeographic analyses of the glycoprotein (G) and nucleoprotein (N) genes were conducted to investigate the temporal and spatial evolution of RABV in Taiwan. The results of molecular clock and phylogeographic analyses indicate that TW-RABV strains were derived from China rabies isolates around the beginning of the 19th century, and that the virus then evolved within the Taiwan to form two major clades (TW-CS and TW-E) and that the variation is congruent with geographical distribution. The population expansion analyses showed that TW-E strains rapidly increased in population in 2013. For TW-CS strains, a relatively constant population size has been maintained with only a small peak occurring in 2010.