

報告番号	※	第	号
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主 論 文 の 要 旨

論文題目 Movement of bats and genetic correlation with their associated viruses in east Asia
東アジアにおけるコウモリの移動と関連ウイルスの遺伝的相関
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論 文 内 容 の 要 旨

The present study aimed to examine the migration pattern of the eastern bent-winged bat (*Miniopterus fuliginosus*) in order to determine their role in the dispersion of bat adenovirus and bat coronavirus in east Asia, considering their gene flows and genetic structures (based on deep-sequencing data), using bat fecal guano samples. The bats in China moved to Jeju Island and/or Taiwan in the last 20,000 years via the Korean Peninsula and/or Japan. The phylogenies of host mitochondrial D-loop DNA was not significantly congruent with those of bat adenovirus ($m^2_{xy} = 0.07$, $p = 0.08$), and bat alphacoronavirus ($m^2_{xy} = 0.48$, $p = 0.20$). The first divergence time of bats carrying bat adenovirus in five caves studied (designated as K1, K2, JJ, N2, and F3) was approximately 3.17 million years ago. In contrast, the first divergence time of bat adenovirus among bats in the 5 caves was estimated to be approximately 224.32 years ago. The first divergence time of bats in caves CH, JJ, WY, N2, F1, F2, and F3 harboring bat alphacoronavirus was estimated to be 1.59 million years ago. The first divergence time of bat alphacoronavirus among the 7 caves was estimated to be approximately 2,596.92 years ago. The origin of bat adenovirus remains unclear, whereas these findings suggest that bat alphacoronavirus originated in Japan in samples analyzed in this study. Interestingly, bat adenovirus and bat alphacoronavirus appeared to diverge in a few century from now that were occurred much more recently compared to the divergence time of their hosts. It is assumed that cross-species transmission of the viruses between the bats and other animal species might accelerate genetic diversity of the viruses. In addition, gene flow of the greater horseshoe bats (*Rhinolophus ferrumequinum*),

and genetic correlation with the eastern bent-winged bats were investigated. The phylogenies of the two bat species was significantly correlated ($m^2_{XY} = 0.002$, $p = 0.04$). Considering the gene flows and genetic structures, it is possible that the two bat species could serve as important natural reservoirs of both viruses in east Asia.