

2010-2018 年臺灣禽類副黏液病毒第一型

分離株檢測與親緣分析

疫學研究組

劉玉彬助理研究員

摘要

禽類副黏液病毒第一型同義於新城病病毒，廣佈於全球，對於大部分禽鳥均有感受性，並造成重要家禽疾病之新城病疫情發生。本研究將 2010-2018 年由臺灣禽鳥所分離之 40 株病毒株進行融合蛋白基因序列分析，其中 39 株分屬 class I genotype 1 及 class II genotype I、VI 及 VII 等基因型，另有 1 株病毒株依據分類準則應在 class I 項下成立新的基因型。親緣分析顯示臺灣水禽之 class I sub-genotype 1.2 分離株序列與北美野鳥序列具高度相關；臺灣鴿子副黏液病毒近年之主要流行株為 class II sub-genotype VI.2.1.1.2.1 及 VI.2.1.1.2.2 基因亞型；而造成臺灣新城病疫情之病毒為 class II sub-genotype VII.1.1 基因亞型。本研究發現 5 種以上不同基因亞型的禽類副黏液病毒第一型存在於臺灣禽鳥、1 株具特異性之新基因型病毒株及侯鳥對於此病毒之跨洲際傳播可能扮演重要角色。

Detection and phylogenetic analysis of avian paramyxovirus 1 ~~strains Isolated~~ isolated in Taiwan from 2010 to 2018

Yu-Pin Liu

Abstract

Avian paramyxovirus 1 (APMV-1), synonymous with Newcastle disease virus, is a worldwide viral agent that infects various birds that is responsible for outbreaks of Newcastle disease, one of the most important diseases affecting poultry. In this study, 40 APMV-1 isolates collected from poultry, migratory birds, and resident birds from 2010-2018 in Taiwan were characterized phylogenetically. Our phylogenetic analysis of the complete fusion protein gene of the APMV-1 isolates, revealed that 39 of the 40 Taiwanese isolates were either closely related to APMV-1 class I genotype 1, or to class II genotypes I, VI or VII. One ~~one~~ isolate met criteria for its designation as a novel genotype within class I. One sub-clade of sequences, that was nested within the class I sub-genotype 1.2, were closely related to those isolated from wild birds in North America. Viruses placed in class II sub-genotypes VI.2.1.1.2.1 and VI.2.1.1.2.2 were the dominant pigeon paramyxovirus 1 strains circulating during the last decade in Taiwan. All the Newcastle disease outbreak-associated isolates belonged to class II sub-genotype VII.1.1, which has been mainly responsible for the present epizootic in Taiwan. We conclude that at least five sub-genotypes of APMV-1 circulate among multiple avian host species in Taiwan. One genetically divergent group of APMV-1 should be considered as a novel genotype within class I, and migratory birds may play an important role in intercontinental spread of APMV-1.