

台灣新城病病毒分子流行病學研究

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摘要

為瞭解台灣家禽與野鳥之新城病病毒分子流行病學，選取 22 株 2012 年至 2016 年分離之新城病病毒進行序列分析。於融合蛋白基因變異區之親緣樹分析結果顯示，5 株新城病病毒株屬 class II 第 I 基因型、4 株屬第 II 基因型、2 株分離自鴿子之病毒株屬第 VI 基因型、4 株屬第 VII 基因型，其餘 7 株歸類於 class I 病毒群。在融合蛋白切割位序列部分 class I 病毒以及 class II 之第 I、II、VI、VII 基因型病毒分別為 E-Q/R-Q-E-R ↓ L、G-K/E-Q-G-R ↓ L、G-R-Q-G-R ↓ L、R-R-Q-K-R ↓ F 及 R-R-K-K-R ↓ F。研究結果顯示目前台灣雞場新城病疫情主要病原仍為第 VIIe 基因型，而野鳥族群檢測出 3 種低病原性新城病病毒基因型，表示野鳥為此類病毒天然宿主之一。

A Molecular Epidemiological Study of Newcastle Disease Viruses in Taiwan

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Abstract

Twenty-two Newcastle disease virus (NDV) isolates from domestic poultry and wild birds during 2012 to 2016 in Taiwan were genetically characterized. The phylogenetic analysis of the variable region of the F gene indicated that there are at least five genotypes of NDV circulating in domestic poultry and wild birds. Five isolates belonged to class II genotype I, four to genotype II, two (isolated from pigeons) to genotype VI, four to genotype VIIe, and the remaining seven isolates belong to class I NDV. At the F0 cleavage site, the class I and class II genotypes I, II, VI, VII NDV isolates had the sequence motifs of E-Q/R-Q-E-R ↓ L, G-K/E-Q-G-R ↓ L, G-R-Q-G-R ↓ L, R-R-Q-K-R ↓ F, and R-R-K-K-R ↓ F respectively. These results suggest that genotype VIIe NDV is the prevalent virulent strains circulating among chicken farms in Taiwan, and the wild bird population carries avirulent NDV with genetic divergence regularly and may act as one of the important reservoirs.