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臺灣高病原性家禽流行性感冒及其病原性變化

疾病診斷組

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摘要

由於高病原性家禽流行性感冒的 H5N1 亞型（A/goose/Guangdong/1/ 1996，Gs/GD）病毒株經歷多次疫情波已在全球各大陸上蔓延，而 2.3.4.4c 分支 H5 亞型高病原性禽流感終於在 2015 年入侵了臺灣。儘管多年來已經實施了多種控制措施，但這些病毒仍於後續將近 7 年的時間，持續在臺灣傳播、進化和重新組合。由於過去的動物試驗結果顯示 2.3.4.4c 分支 H5 亞型高病原性禽流感於水禽多為不顯性感染，在部份文獻中推論水禽為自然儲主，為疾病持續循環的原因。而自從 2021 年 8 月後臺灣家禽場發現 2.3.4.4b 分支 H5N2 亞型高病原性禽流感，在 6 個月內成為臺灣主要的流行株。由於自 106 年起截至目前為止，為執行計畫將 3 種分支暨 7 株之 H5Nx 亞型高病原性禽流感病毒接種於臺灣重要之家禽，其對家禽之自然感染點鼻途徑感染病原性不完全相同，但仍以水禽常見感染後存活時間較長。因此持續建議防疫單位應對水禽加強禽流感病毒的監測。在高病原性禽流感持續檢出的地區，應採取結合多項感預防和控制措施，以減輕病毒對家禽產業和公共衛生的影響，同時避免病毒再重組對防疫工作帶來的挑戰。

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The pathogenicity changes of High Pathogenicity Avian Influenza in Taiwan

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Abstract

The H5N1 subtype of high pathogenicity avian influenza (HPAI), originated by the A/goose/Guangdong/1/1996 (Gs/GD) strain, has spread across continents globally through multiple waves of outbreaks. The H5 subtype HPAI viruses of clade 2.3.4.4c invaded Taiwan in 2015. Despite the implementation of various control measures over subsequent years after the outbreak, these viruses have continued to spread, evolve, and reassort in Taiwan for nearly seven years. Animal experiments have indicated that H5 HPAI viruses of the clade 2.3.4.4c often cause subclinical infections in waterfowl, reckoning them as natural reservoirs, as mentioned in some literature. Since August 2021, the H5N2 HPAI virus of clade 2.3.4.4b has emerged as the predominant strain in Taiwan's poultry farms within six months. From the year 2017, three different clades and seven strains of H5Nx subtype HPAI viruses have been examined through experimented infection in Taiwan's important poultry species. Although the pathogenicity of these viruses via natural infection routes in poultry, waterfowl typically exhibited longer survival times in comparison to those of land fowls. Hence, intensified monitoring of avian influenza viruses in waterfowl is recommended so as to suspend virus circulation in the population. In areas where high pathogenicity avian influenza persists, a combination of preventive and control measures should be adopted to mitigate the impact on the poultry industry and public health, while also avoiding the challenges posed by viral reassortment to the ongoing efforts in epidemic prevention.