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臺灣禽流感病毒監測現況：

禽場外圍環境調查與高病原性病毒基因體分析

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摘要

2.3.4.4 分支 H5 亞型高病原性禽流感病毒自 2014 年起於全球持續擴散，近年因野生禽類帶毒與頻繁重組，疫情遍及除澳洲外各大陸。臺灣自 104 年起遭 2.3.4.4c 分支 H5N2 亞型、H5N3 亞型及 H5N8 亞型入侵，再於 110 年檢出 2.3.4.4b 分支 H5N2 亞型，以及 111 年 11 月 2.3.4.4b 分支 H5N1 亞型入侵，並於 112 年取代既有病毒株，持續成為禽場主流行株至今。在家禽運銷頻繁、飼養型態多元及高抗體背景下，病毒軌跡與演化日益複雜。114 年研究計畫為禽場外圍環境監測與病毒基因體分析，禽場外圍環境監測於 114 年第四季完成 255 場次環境採樣，檢出 9 場陽性（3.5%），以水禽場風險最高，並成功於蛋雞場檢出 H6N1 亞型，顯示具早期預警效能。同時於基因體分析計畫完成 44 株禽流感病毒次世代定序，確認國內 H5N1 亞型病毒仍流行多種基因型，並解析其親緣關係與重要跨物種位點。整體結果顯示，結合環境監測與高解析度基因體分析，有助於掌握病毒演化趨勢、評估跨物種風險，並作為後續防疫策略與產業鏈監測之科學依據。

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Current Status of Avian Influenza Virus Surveillance in Taiwan: Peripheral Environmental Investigation of Poultry Farms and Genomic Analysis of Highly Pathogenic Viruses

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Abstract

Clade 2.3.4.4 H5 subtype high pathogenicity avian influenza (HPAI) viruses have continued to spread globally since 2014. In recent years, driven by virus carriage in wild birds and frequent reassortment events, outbreaks have been reported on all continents except Australia. In Taiwan, clade 2.3.4.4c H5N2, H5N3, and H5N8 viruses were introduced at the beginning of 2015, followed by the detection of clade 2.3.4.4b H5N2 viruses in 2021 and the incursion of clade 2.3.4.4b H5N1 viruses in November 2022. By 2023, the latter had replaced the previous circulating strains and has remained the predominant lineage in poultry farms to date. Under conditions of frequent poultry movement, diverse farming systems, and a high seroprevalence background, viral transmission and evolutionary trajectories have become increasingly complex. The 2025 research program comprised peripheral environmental surveillance of poultry farms and viral genomic analysis. In the fourth quarter of 2025, environmental sampling conducted on 255 poultry farms were completed, with nine positive detections (3.5%), and the highest risk was found in waterfowl farm; furthermore, an H6N1 virus was also successfully detected in a layer farm, demonstrating the early warning capacity of this surveillance system. In parallel, the project of next-generation sequencing was performed on 44 avian influenza viruses, confirming the continued circulation of multiple H5N1 genotypes in Taiwan. The phylogenetic relationships and key biomarkers associated with cross-species transmission were analyzed. Overall, these results reveal that the integration of environmental surveillance with high-resolution genomic analysis facilitates monitoring of viral evolutionary trends, assessment of interspecies transmission risk, and providing a scientific basis for subsequent prevention strategies and poultry industry–wide surveillance.