# 家禽流行性感冒等疾病之次世代定序應用

疾病診斷組

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#### 摘要

次世代定序相較於傳統核酸定序方法,具有通量、成本及速度之 優勢,已廣泛運用在病原鑑定及基因定序領域。近年高病原性家禽流 行性感冒病毒持續於國際造成嚴峻疫情,臺灣亦於104年開始發生禽 場案例。本所為提升定序量能,建立了次世代定序方法,已實際應用 於家禽與野鳥之禽流感病毒基因體定序,包括禽場 H6N1 亞型、墨西 哥株 H5N2 亞型、高病原性 H5Nx 亞型病毒及反向遺傳 H5Nx 亞型疫 苗株,與野鳥 64 種不同亞型之病毒基因體定序。另外也應用於牛結 節疹、牛病毒性下痢及鵝坦布蘇等病毒之基因體定序,並發表於科學 期刊。未來將繼續評估與建立第三代定序,並協助本所其他病原之基 因體定序研究。

## Application of next generation sequencing on studying

### avian influenza and other diseases

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#### Abstract

Compared with traditional nucleic acid sequencing methods, next generation sequencing (NGS) has the advantages of high-throughput, cost and speed, and has been widely used in the fields of pathogen identification and genome sequencing. In recent years, high pathogenicity avian influenza (HPAI) viruses have caused severe epidemics globally, and poultry cases appeared in Taiwan in 2015. Analyzing genomic sequences of avian influenza virus extensively broadens our understanding of biology and ecology of this heavily impacting virus. In order to improve the sequencing capacity, we established the NGS method, which has been actually applied to the genome sequencing of avian influenza viruses in poultry and wild birds, including H6N1 subtype, Mexican-strain H5N2 subtype, HPAI H5Nx subtype, vaccine strains of reverse genetic H5Nx subtype, and those of a variety of subtypes viruses isolated from wild birds. In addition, our laboratory has used NGS in the genome sequencing of lumpy skin disease virus isolated from cattle, bovine viral diarrhea virus isolated from a calf, and Tembusu virus isolated from geese, and these researches have been published in scientific journals. In the future, we will continue to evaluate and establish the third generation sequencing and assist our investigation on other pathogens.