Te Niwha

Research Project Impact Case Study

Genomics-informed detection, surveillance and capacity building to prepare Aotearoa for the existential threat of highly pathogenic avian influenza virus

Short Research Title

A genomics-informed approach to avian influenza virus surveillance

Stephanie Waller and Jemma Geoghegan
Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand

Introduction

New Zealand's risk of highly pathogenic avian influenza (HPAI) virus incursion has historically been considered low due to New Zealand's geographic isolation and the absence of migratory waterfowl. However, the expansion of both susceptible hosts and geographic spread of HPAI subtype H5N1, including to Antarctica, means that New Zealand is on high alert for its arrival.

Results

In collaboration with the Department of Conservation and many others, we investigated avian viruses in wild aquatic birds during the 2023-2024 migration season. Waller *et al.* (2025) collected oral and cloacal samples from 700 birds across 33 species. Sampling took place across New Zealand and, for the first time, included New Zealand offshore islands and subantarctic territories. Researchers used metatranscriptomic sequencing to detect viruses. No HPAI viruses were found, however, they identified a near-complete genome of low pathogenic avian influenza (LPAI) virus H1N9 in red knots (*Calidris canutus*) from the Firth of Thames. Phylogenetic analysis showed that the LPAI H1N9 virus belongs to an Oceania/Asian clade. The long branch length and time to a last common ancestor suggests this virus has been in New Zealand for some time. These findings highlight the need for continued surveillance, especially in migratory shorebirds, due to the global spread of HPAI H5N1.

Impact

This study establishes a framework for broader avian influenza surveillance using advanced genomic techniques. Migratory birds are currently being resampled during the 2024-2025 migration season as New Zealand is currently facing another high-risk migratory period. This work will help assess changes in viral composition between migratory seasons and determine the presence of avian influenza viruses. Nevertheless, the study aims to identify all avian viruses, not just avian influenza virus. Their goal is to track transmission dynamics, evolution, and prevalence of avian viruses in New Zealand. Another research focus for the group is developing environmental monitoring methods. These methods would detect avian influenza virus in samples such as water and sediment, providing a more accessible alternative to direct bird sampling. Ongoing monitoring is critical to detect incursions, track viral evolution, and improve understanding of avian influenza virus in New Zealand.

Reference: Waller *et al.* (2025). Avian influenza virus surveillance across New Zealand and its subantarctic islands detects H1N9 in migratory shorebirds, but not 2.3. 4.4 b HPAI H5N1. *Influenza and Other Respiratory Viruses* (in press).