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

Key researchers
Stephanie Waller[1] and Jemma Geoghegan[1]

[1]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.

Key achievements

This programme has delivered significant outcomes and measurable impact beyond the trial itself. It has strengthened workforce capability by training community nurses nationwide in both SCIP administration and cultural safety, ensuring sustainable and culturally responsive delivery of secondary prophylaxis. The project has actively engaged with Māori and Pacific communities through whānau navigators and peer-support hui, fostering trust, empowerment, and greater participation in care. Findings have been disseminated widely through peer-reviewed publications, and conference presentations, contributing to national and international discussions on improving ARF/RHD prevention. Collectively, our achievements demonstrate that SCIP, combined with a rangatahi Māori and Pacific whānau-centred model of care, is a feasible, safe, and culturally responsive alternative to conventional monthly intramuscular injections, with strong potential to transform secondary prophylaxis delivery and reduce health inequities both in Aotearoa and internationally.

Impact

Over the past 18 months, this programme has made major progress in understanding the diversity, ecology, and emergence potential of viruses circulating in Aotearoa's wild bird communities. Since the initial Te Niwha submission, we have published two peer-reviewed papers, released two preprints, and completed a further manuscript on the ecological drivers of viral community structure. Collectively, these outputs demonstrate scientific excellence across genomics, field ecology, and pathogen discovery, and provide new insights central to New Zealand's biosecurity.

Our study in *Influenza and Other Respiratory Viruses* substantially expanded national avian influenza virus (AIV) surveillance. Sampling ~2500 individuals across 33 species from mainland, offshore, and subantarctic regions, we generated one of the most geographically comprehensive datasets for Aotearoa. No high pathogenicity H5N1 (clade 2.3.4.4b) was detected, providing assurance for national biosecurity and confirming New Zealand's continuing HPAI-free status. A single low-pathogenic H1N9 detection in a migratory shorebird highlights the importance of ongoing, targeted surveillance. This work establishes a strengthened baseline against which future incursions can be detected and assessed.

In parallel, our virome-wide work continues to reveal the natural diversity of viruses associated with New Zealand birds. The recent *Journal of Virology* publication and subsequent preprints characterise numerous novel viral families, demonstrating that many viruses are long-standing components of wild bird communities rather than markers of active outbreaks. These studies advance understanding of the "background virosphere" in native and migratory species, a key step toward distinguishing normal ecological processes from signals of disease emergence.

A major conceptual advance is the integration of ecological traits into virome interpretation. Our upcoming manuscript, *Foraging ecology drives viral community structure in New Zealand's aquatic birds*, shows that feeding guild, habitat use, and trophic interactions strongly predict viral diversity and composition. This work establishes an ecological framework for interpreting pathogen distribution and highlights that viral communities are shaped as much by behaviour and environment as by infection dynamics. This represents a shift toward ecological virology, with implications for predicting how environmental change or species movement may alter future disease risk.

These studies collectively deliver significant outcomes for Aotearoa. First, they bolster national preparedness for exotic pathogen incursions such as HPAI, and provide high-resolution genomic and ecological baselines essential for early detection. Second, they enhance conservation management by illuminating how resident viruses interact with taonga species and by identifying ecological factors that may heighten vulnerability. Third, they build national capability in metatranscriptomics, viral discovery, and wildlife genomics, strengthening the scientific platform needed to respond to emerging threats across human, animal, and environmental health.

Looking forward, the ecological insights generated here open clear pathways for predictive models of disease emergence in changing environments. By linking behaviour, habitat, and viral community structure, this work positions New Zealand at the forefront of ecological virology and establishes a foundation for proactive, rather than reactive, wildlife disease surveillance and to better understand New Zealand’s risk of highly pathogenic avian influenza virus incursion.