

Exploring avian viromes in Aotearoa

Summary Article | Jemma Geoghegan, University of Otago

Our knowledge of the viruses that infect Aotearoa's endemic and introduced bird species is severally limited. Furthermore, little is known about the prevalence of viral transmission between native and introduced birds, and what threats introduced viruses might pose to native species. This project has begun to explore the hitherto undefined virome of Aotearoa's land birds and broaden our knowledge of the diversity of viruses that exist in nature.

In this project we collected cloacal swabs from a range of bird species. Species sampled so far include the North Island kōkako (*Callaeas wilsoni*), weka (*Gallirallus australis*), black robin (*Petroica traversi*) and kakī (*Himantopus novaezelandiae*), among others, with further sampling of other avian species planned. Total RNA was extracted from all samples and subject to RNA Sequencing.

In this study, we explored the avian virome of *Gallirallus australis* – commonly known as weka – a unique host species native to Aotearoa. Using a metatranscriptomic approach, we compared viral abundance and richness between different host age groups. To this end, we observed that viral richness increases with host age in weka. In addition we discovered multiple novel avian viruses falling across many viral families including the *Hepadnaviridae*, *Picornaviridae* and *Astroviridae*.

We also performed a metatranscriptomic study of eighteen kōkako cloaca swab samples taken from three distinct locations in the Northern Pureora Forest Park. Deep RNA sequencing was performed on the samples to reveal the entire virome of the species within each location. From these data, we identified numerous novel viral sequences spanning thirty-seven viral families, eleven of which were determined to have potential vertebrate hosts. Phylogenetic analysis of three of the 11 viral families containing RNA-dependent RNA polymerase sequences revealed six novel kōkako cloacal-associated viruses. In addition, we observed overall differences in virome composition among kōkako viromes sampled from different locations. Overall, the results suggest that the kōkako virome is highly diverse and that the vast majority of viruses discovered in the kōkako cloacal samples are most likely to be environmental or dietary-related. These findings support previous research that wild avian viromes are diverse, and they add to our knowledge of the kōkako virome, which could aid in its conservation.



Overall, our study aims to better inform disease management of Aotearoa's native birds. It also seeks to expand our understanding of the diversity of the unique virosphere here – one that has been isolated for millennia but subject to many host species invasions that have the potential to spread novel infectious diseases.