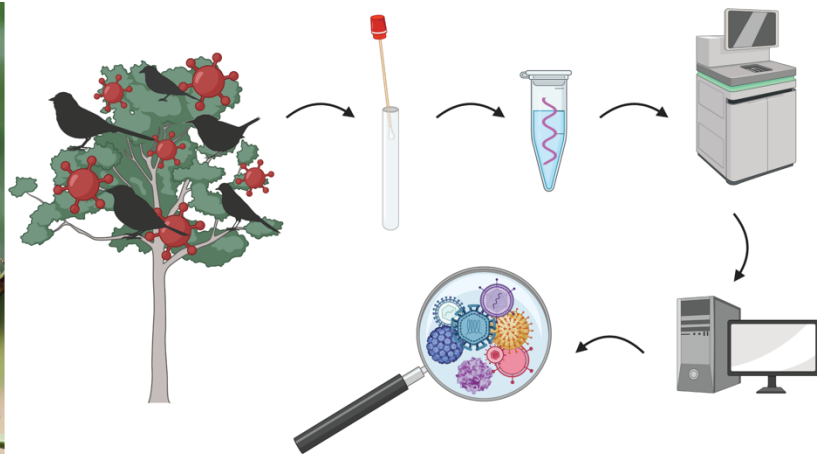




Photo Credit: Tama Robertson



Project Overview

Surveying the Viromes of Aotearoa's Native and Introduced Passerines

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Like all species, birds fall victim to illness from viral infection. Our knowledge of the viruses that infect Aotearoa's endemic and introduced birds is severely limited. We know almost nothing about the prevalence of viruses, the frequency of transmission between native and introduced birds, and what potential viral threats introduced birds might pose to native birds. Passerines are numerous and diverse in New Zealand, and their habitats overlap urban, agricultural, and native areas. This makes passerines ideal for initiating an inventory of avian viruses in Aotearoa, studying the effects of land use on avian virus abundance and diversity, and exploring cross-species virus transmission among these bird species. Our study will sample locations throughout Coastal Otago, cataloging the viruses which infect passerine birds therein, and looking for evidence of cross-species transmission between native and introduced birds. Sampling across land uses (urban, rural, and native) will help identify environmental influences these habitats have on viral prevalence in bird populations.

Through consultation with local iwi, the Department of Conservation, and the University of Otago, we have obtained permission to capture and sample 19 passerine species. These species include native birds like the tauhou, tūī, korimako, and pīwakawaka; and introduced birds such as the house sparrow, blackbird, and dunnock. Birds will be caught with mist nets, measured, banded, and have their viromes sampled using cloacal swabs. The total RNA extracted from these virome samples will be genomically sequenced and the resulting "metatranscriptomes" analysed for viral sequences. In this way, we will identify all viruses present in a bird's virome simultaneously and can use these data to investigate cross-species transmission and the impact of habitat on virus abundance and diversity. We will also use the viral genomic sequences recovered to design rapid molecular biology tests for use in future viral surveying of birds.