Abstract
Influenza is a major cause of morbidity and mortality in humans and animals. Despite vaccination initiatives and the availability of antiviral drugs, there are an estimated one billion cases of seasonal influenza globally each year, which lead to 300,000 to 500,000 deaths. Influenza is also an archetypal zoonotic disease. Influenza viruses that are endemic in animal populations — particularly poultry and swine — periodically emerge in humans to cause devastating pandemics. Worryingly, an increasing frequency of human infections with avian and swine viruses have been observed globally in recent years. A complex interplay of viral (mutation, recombination/reassortment), host (immune selection, demography, site of infection) and ecological (transmission bottlenecks and environmental factors such as temperature, humidity, UV) factors shape the emergence, evolution and spread of influenza virus and other rapidly evolving pathogens. The improvement of large-scale surveillance and sequencing efforts combined with the recent unification of epidemiology, ecology and evolutionary genetics is beginning to have a profound impact on infectious disease studies with a growing impact on pandemic preparedness. This unification of methods is also playing an important role in the integration of comprehensive virus surveillance data with laboratory based virus susceptibility, pathogenicity, transmission and drug resistance experiments providing insights into the mechanisms that foster transmission at the influenza human-human and human-animal interface. Here, I will provide a summary of my work that has integrated multiple forms of data to understand mechanisms of emergence and transmission of influenza viruses.

Selected Publications