



Genomics in antimicrobial resistance and infectious disease transmission

by

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Venue : Room S1B, G/F Jockey Club Building for Interdisciplinary Research, 5 Sassoon Road

Abstract:

Modern genome sequencing provides a uniquely powerful and relatively cheap means to rapidly characterise the microbial and host composition of any sample without bias. These sequencing techniques provide important new information on the microbial composition, the fundamental patterns and mechanisms of microbial evolution and epidemiology, and are able to determine disease agents and antimicrobial disease status on clinically actionable time-scales. In this talk, I will showcase some of our work on infectious disease genomics and illustrate how genomic analysis has enhanced all of these areas. The genomic data has provided new information of a diverse array of pathogens, ranging from a *Klebsiella* outbreak in a NICU in China, in-host evolution of avian influenza, as well as population level dynamics of several human and animal pathogens.

Bio-sketch:

[Vijay Dhanasekaran](#) obtained his PhD in 2005 from The University of Hong Kong in the Department of Ecology and Biodiversity, and continued as a postdoctoral fellow at the State Key Laboratory of Emerging Infectious Diseases before being appointed to the Duke-NUS Graduate Medical School in Singapore in 2010. Since 2016, he has been a faculty member at Monash University, in the Department of Microbiology, co-director of the Computational Biology Initiative of Monash Biomedicine Discovery Institute, as well as faculty member at the World Health Organisation Collaborating Centre in Influenza Research and Surveillance at the Peter Doherty Institute, Melbourne. His lab applies molecular genetic techniques to study factors that shape the emergence, evolution, and incidence of rapidly evolving viral pathogens such as Influenza; as well as bacterial pathogens such as *Klebsiella*. Members of his team apply established population genetics methods as well as develop new mathematical models to study within-host and population level genomic changes.