

**Mathematics of
Evolution-Phylogenetic Trees and Networks**
Workshop 3: Evolution of viruses
(25–27 Sep 2023)



Venue

IMS Auditorium
Institute for Mathematical Sciences
3 Prince George's Park
Singapore 118402

ORGANIZING COMMITTEE

Co-Chairs

Daniel Huson
University of Tübingen

Louxin Zhang
National University of Singapore

Members

Michael Fuchs
National Chengchi University

Simone Linz
University of Auckland

Sebastien Roch
University of Wisconsin-Madison

Mathias Weller
CNRS at Université Gustave Eiffel

Rohan Williams
National University of Singapore

Taoyang Wu
University of East Anglia

**Workshop 3:
Evolution of viruses
(25–27 Sep 2023)**

Monday, 25 September 2023

Time	Title	Speaker
0845–0900	Registration	
0900–0910	Opening Remarks	
0910–0940	Estimating viral mutation rates in the post-genomic era	Mark M. Tanaka University of New South Wales, Australia
0940–1010	Evolutionary dynamics and lineage designation of SARS-CoV-2 genomes	Jian Lu Peking University, China
1010–1040	<i>Coffee Break</i>	
1040–1110	Exploring the antibiotic resistance potential of the virome in infant metagenome	Anupam Gautam University of Tübingen, Germany
1110–1200	<i>Keynote</i> Drug Resistance Mutations in HIV	Olivier Gascuel ISYEB UMR7205– CNRS Muséum National d'Histoire Naturelle, France
1200–1230	A network approach for studying HIV molecular epidemiology	Tsz Ho Kwan The Chinese University of Hong Kong, China

Tuesday, 26 September 2023

Time	Title	Speaker
0845–0900	Registration	
0900–0930	Phylodynamics of SARS-CoV-2 in Hong Kong, 2020–2022	Vijaykrishna Dhanasekaran The University of Hong Kong, China
0930–1000	Genomic epidemiology for estimation of serial intervals in COVID-19 transmission clusters	Jessica E Stockdale Simon Fraser University, Canada
1000–1030	<i>Group Photo & Coffee Break</i>	
1030–1100	Synthetic control methods for infectious disease epidemiology: applications to Wolbachia interventions	Jue Tao Lim Nanyang Technological University, Singapore

Tuesday, 26 September 2023		
Time	Title	Speaker
1100–1150	<i>Keynote</i> Clinical research during the COVID-19 pandemic. What do we need to do better next time?	Barnaby Edward Young National Centre for Infectious Diseases, Singapore
1150–1220	Levels of SARS-CoV-2 population exposure are considerably higher than suggested by seroprevalence	Siyu Chen Oxford University, UK

Wednesday, 27 September 2023		
Time	Title	Speaker
0845–0900	Registration	
0900–0930	Detection and surveillance for genomic variation of SARS-CoV-2	Aiping Wu Chinese Academy of Medical Sciences Peking Union Medical College & Suzhou Institute of Systems Medicine, China
0930–1000	Phylogenetic Supertree of Virus	Jie Feng Lanzhou University, China
1000–1030	The value of high coverage whole genome sequencing of SARS-CoV-2 in Denmark	Mark P. Khurana University of Copenhagen, Denmark
1030–1100	<i>Coffee Break</i>	
1100–1130	Genomic characterization and epidemiology of P.1 and Delta SARS-CoV-2 Variants	Swapnil Mishra National University of Singapore, Singapore
1130–1200	The origin tracing and tracking of emerging influenza A virus and SARS-CoV-2	Yifei Xu Shandong University, China
1200–1230	Zika virus transmission dynamics and characterisation of naturally occurring mutations in a paediatric cohort during the 2016 Nicaragua epidemic	October M. Sessions National University of Singapore, Singapore

This schedule is accurate as of 15 September 2023. It is subjected to changes