

Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details
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Wednesday 9 November 2022

11:30 12:50 Registration, lunch and networking

12:30 12:50 Briefing for Keynote & Session 1 speakers, chair, moderator & committee - Auditorium

12:50 13:00 Welcome

Scientific Programme Committee:

[Kate Grabowski, Johns Hopkins University, USA](#)

[Christian Happi, Redeemer's University, Nigeria](#)

[Katrina Lythgoe, University of Oxford, UK](#)

[Emma Thomson, University of Glasgow, UK](#)

13:00 14:05 Keynote 1

13:00 13:05 Introduction to the session

Chair: Christian Happi

Moderator: Kate Grabowski

13:05 14:05 Title TBC - **VIRTUAL**

[Tulio de Oliveira, Stellenbosch University, South Africa](#)

14:05 16:10 Session 1: Epidemics and outbreaks

14:05 14:10 Introduction to the session

Chair: Oliver Pybus

Moderator: Katrina Lythgoe

14:10 14:40 Hamiltonian steps into phylodynamics: a focus on applications

[Philippe Lemey, KU Leuven, Belgium](#)

14:40 15:10 Empowering new approaches to prevent vampire bat rabies outbreaks using viral sequence data

[Daniel Striecker, University of Glasgow, UK](#)

15:10 15:25 High number of community SARS-CoV-2 long-term persistent infections uncovered through analysis of genetic data from the ONS Covid Infection Survey

[Mahan Ghafari, University of Oxford, UK](#)

15:25 15:40 Tracking COVID-19 in the Philippines: Developing and Implementing Genomic Surveillance across the Country's Public Health Network - **VIRTUAL**

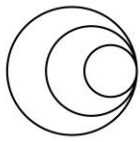
[Angelica Tujan, Research Institute for Tropical Medicine, Philippines](#)

15:40 16:10 The Proximal Origin and Evolution of SARS-CoV-2 - **VIRTUAL**

[Kristian Andersen, Scripps Research, USA](#)

16:10 16:40 Refreshment break

16:20 16:40 Briefing for Session 2 speakers, chair & moderator - Auditorium



16:40 18:15 Session 2: Virus evolution

16:40 16:45 Introduction to the session

Chair: Katrina Lythgoe

Moderator: Kate Grabowski

16:45 17:15 SARS-CoV-2 genomic surveillance and public health response in Botswana - **VIRTUAL**

[*Sikhuilie Moyo, Botswana Harvard AIDS Institute, Botswana*](#)

17:15 17:45 Evolutionary ecology of CRISPR-Cas immunity and phage immunity avoidance

[*Stineke van Houte, University of Exeter, UK*](#)

17:45 18:00 Transcriptome mining extends the host range of the Flaviviridae to the basal Metazoa

Jonathon Mifsud, University of Sydney, Australia

18:00 18:15 Natural influenza A virus outbreak in swine at a county fair reveals relaxed purifying selection and strong genetic drift in an important reservoir

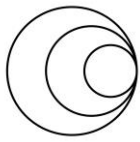
David VanInsberghe, Emory University, USA

18:15 18:45 Lightning talks for even number posters

18:45 19:45 Poster session 1 - even number posters, with refreshments

19:45 21:30 Dinner

Bar open (card payments only)



Thursday 10 November 2022

07:30 09:00 Breakfast

09:10 09:30 Briefing for Session 3 speakers, chair & moderator - Auditorium

09:30 11:35 Session 3: Emerging viral infections and zoonoses

09:30 09:35 Introduction to the session
Chair: Emma Hodcroft
Moderator: Christian Happi

09:35 10:05 Where next for virus genomic epidemiology?
[Oliver Pybus, University of Oxford, UK](#)

10:05 10:35 Pathogen Genomic Surveillance in the Caribbean
[Christine Carrington, University of the West Indies, Trinidad & Tobago](#)

10:35 10:50 The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2
Jonathan Pekar, University of California San Diego, USA

10:50 11:05 Putative APOBEC3 deaminase editing driving short-term evolution of MPXV since 2017
Áine O'Toole, University of Edinburgh, UK

11:05 11:45 Refreshment break

11:25 11:45 Briefing for Session 4 speakers, chair & moderator - Auditorium

11:45 13:20 Session 4: Host-virus interactions

11:45 11:50 Introduction to the session
Chair: Daniel Striecker
Moderator: Emma Thomson

11:50 12:05 Phylogenomic characterization of a highly divergent new lineage of SARS-CoV-2 from white-tailed deer and associated human case - **VIRTUAL**
Oksana Vernygora, Canadian Food Inspection Agency, Canada

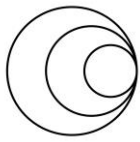
12:05 12:35 Talk title TBC - **VIRTUAL**
[Placide Mbala, Institut National de Recherche Biomedicale, DRC](#)

12:35 13:05 Implementation of HIV Cluster Detection and Response in the United States
[Anne Marie France, CDC, USA](#)

13:05 13:20 Association between disease severity and co-detection of nasopharyngeal pathogens in infants with RSV infection
Tanya Golubchik, University of Sydney, Australia

13:20 14:30 Lunch

14:10 14:30 Briefing for Session 5 speakers, Keynote speaker, chair & moderator - Auditorium



14:30 16:05 Session 5: Vaccines and human virus evolution

- 14:30 14:35 Introduction to the session
Chair: Emma Thomson
Moderator: Katrina Lythgoe
- 14:35 15:05 COVID vaccines and beyond - Lessons learnt
[*Tess Lambe, Oxford University, UK*](#)
- 15:05 15:35 Genomic surveillance for pre-pandemic vaccine preparedness
[*Jonathan Heeneey, University of Cambridge, UK*](#)
- 15:35 15:50 The social lives of DNA viruses: observing HSV populations in humans with a cohort of newly-infected individuals
Moriah Szpara, Pennsylvania State University, USA
- 15:50 16:05 From Vaccine to Pathogen: Modeling Sabin 2 Vaccine Virus Reversion and Evolutionary Epidemiology
Wesley Wong, Harvard TH Chan School of Public Health, USA

16:05 16:35 Refreshment break

16:35 17:40 Keynote 2

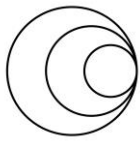
- 16:35 16:40 Introduction to the session
Chair: Kate Grabowski
Moderator: Katrina Lythgoe
- 16:40 17:40 Sentinel: Pandemic preemption in the genomic and information age
[*Pardis Sabeti, Broad Institute, USA*](#)

17:40 18:15 Lightning talks for odd number posters

18:15 19:15 Poster session 2 - odd number posters, with refreshments

19:15 21:30 Dinner

Bar open (card payments only)



Friday 11 November 2022

07:30	09:00	Breakfast
09:10	09:30	Briefing for Session 6 speakers, chair & moderator
09:30	11:05	Session 6: Phylogenetics
09:30	09:35	Introduction to the session <i>Chair: Christian Happi</i> <i>Moderator: Katrina Lythgoe</i>
09:35	10:05	The Promise and Realization of Phylogenetics Emma Hodcroft, University of Bern, Switzerland
10:05	10:20	Towards near-real-time and pandemic-scale Bayesian phylogeny inference <i>Patrick Varilly, Broad Institute, USA</i>
10:20	10:35	Patterns of HIV molecular clustering under varying incidence, sampling coverage, and thresholds <i>Gregory Hart, Bill & Melinda Gates Foundation, USA</i>
10:35	10:50	An ancestral recombination graph for the hepatitis B virus <i>Arthur Kocher, Max Planck Institute, Germany</i>
10:50	11:05	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination <i>Kathryn Campbell, University of Glasgow, UK</i>
11:05	11:45	Refreshment break
11:25	11:45	Briefing for Keynote, chair, moderator & committee
11:45	12:50	Keynote 3
11:45	11:50	Introduction to the session <i>Chair: Kate Grabowski</i> <i>Moderator: Katrina Lythgoe</i>
11:50	12:50	The adeno-associated virus AAV2 is associated with severe hepatitis in children in the UK Emma Thomson, University of Glasgow, UK
12:50	13:00	Closing remarks and prize presentation
		Scientific Programme Committee: <i>Kate Grabowski, Johns Hopkins University, USA</i> <i>Christian Happi, Redeemer's University, Nigeria</i> <i>Katrina Lythgoe, University of Oxford, UK</i> <i>Emma Thomson, University of Glasgow, UK</i>
13:00	13:50	Lunch and departures
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge train station and city centre