Virus Genomics, Evolution and Bioinformatics
11-13 November 2026

Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details	Location
Wednesday, 11 November 2026			
12:00	**13:00**	**Registration, lunch and networking**	
12:45		*Briefing for Opening keynote speaker, Session 1 speakers, SecureBio, microphone runners, chair, moderator and committee*	*Auditorium*
13:00	**13:15**	**Welcome and introductions** **Wellcome Sanger Institute** Lili Bárbara Arruda, Wellcome Sanger Institute, United Kingdom **Scientific programme committee:** *Deogratius Ssemwanga, LSHTM and MRC-UVRI, Uganda* *Kate Grabowski, Johns Hopkins University, United States of America* *Nick Loman, University of Birmingham, United Kingdom* **SecureBio: sponsored 'AI-enabled Biological Risk' Workshop pitch**	*Auditorium*
13:15	**14:05**	**Opening keynote** *Chair: Nick Loman* *Moderator: Kate Grabowski*	*Auditorium*
13:15	14:05	Viral surveillance at the human animal interface: from response to prediction? *Marion Koopmans, Erasmus University Medical Centre, Netherlands*	
14:05	14:10	Comfort break	
14:10	**15:55**	**Session 1: Animals and zoonoses** *Chair: Deogratius Ssemwanga* *Moderator: Nick Loman*	*Auditorium*
14:10	14:40	Ecology and evolution of North American H5Nx viruses *Louise Moncla, University of Pennsylvania, United States of America*	
14:40	15:10	Viruses get around. Genomic surveillance should too. *Erik Karlsson, Institut Pasteur du Cambodge, Cambodia [virtual]*	
15:10	15:25	From Regional Epicentre to Global Panzootic: Spatiotemporal Reassortment Patterns of H5 HPAI Across Flyways at the Qinghai-Tibet Plateau *James Baxter, Roslin Institute, The University of Edinburgh, United Kingdom*	
15:25	15:40	Cryptic invasion and transmission dynamics of peste des petits ruminants virus across Europe *Claire Guinat, INRAE, France*	
15:40	15:55	Reconstructing the hidden evolutionary history of Andes virus from patchy genomic surveillance *Mahan Ghafari, University Of Oxford, United Kingdom*	
15:55	16:40	Refreshment break and networking	*Event Space*
16:25	*16:40*	*Briefing for Session 2 speakers, chair and moderator*	*Auditorium*
16:40	**17:40**	**Session 2: Epidemics and outbreaks** *Chair: Kate Grabowski* *Moderator: Deogratius Ssemwanga*	*Auditorium*
16:40	17:10	From Pairs to Populations *Christophe Fraser, University of Oxford, United Kingdom*	
17:10	17:25	Phylodynamic comparison of cocirculating Clade I mpox lineages in Kinshasa suggests similar transmissibility and virulence *Kieran Chopra, Imperial College London, United Kingdom*	
17:25	17:40	Phylodynamic reconstruction of Crimean-Congo haemorrhagic fever virus characterizes ecological and anthropogenic drivers across multiple centuries *Ellie Bourgikos, University of Oxford, United Kingdom*	
17:40	**18:20**	**Poster pitch talks for odd number posters**	*Auditorium*
18:20	**19:20**	**Poster session 1 (odd number posters) and networking reception**	*Event Space*
19:20 *19:20*	21:30	Dinner *Bar open (card payments only)*	*Hinxton Hall Restaurant* *Graham Cameron Bar*

Thursday 12 November 2026

09:15		*Briefing for Session 3 speakers, chair and moderator*	*Auditorium*
09:30	**10:30**	**Session 3: Vaccines and treatment** *Chair: Deogratius Ssemwanga* *Moderator: Nick Loman*	*Auditorium*
09:30	10:00	Longitudinal studies of changing susceptibility to emerging and re-emerging viruses *Emily Toth Martin, University of Michigan, USA*	
10:00	10:15	Quantifying uncertainty in HIV-1 transmission risk from persons with low-level viremia *Michael Martin, Johns Hopkins University, United States of America*	
10:15	10:30	Predicting the antigenic evolution of seasonal influenza viruses by measuring phylogenetic convergence *Samuel Turner, University of Cambridge, United Kingdom*	
10:30	11:15	Refreshment break and networking	*Event Space*
11:00		*Briefing for Session 4 speakers, chair and moderator*	*Auditorium*
11:15	**12:45**	**Session 4: Viral metagenomics and microbiome** *Chair: Nick Loman* *Moderator: Deogratius Ssemwanga*	*Auditorium*
11:15	11:45	Sequencing viruses the ARTIC way *Joshua Quick, University of Birmingham, United Kingdom*	
11:45	12:15	The richness of the human virome *Evelien Adriaenssens, Quadram Institute Bioscience, United Kingdom*	
12:15	12:30	Beyond Mpox: Metagenomic Identification of Concurrent Viral Detections in Children with Clade Ib Mpox in Eastern Democratic Republic of the Congo *Ashuza Shamamba Guillaume, Université Catholique De Bukavu, Congo (the Democratic Republic of the)*	
12:30	12:45	Expanding the diversity and host range of the Sarthroviridae *Kate Van Brussel, University of Sydney, Australia*	
12:45	14:15	Lunch and networking	*Event Space*
12:45	**14:15**	**Lunchtime SecureBio sponsored 'AI-enabled Biological Risk' Workshop** *In-person attendees only*	*Barbara McClintock Pavilion*
14:00		*Briefing for Session 5 speakers, chair and moderator*	*Auditorium*
14:15	**16:00**	**Session 5: Adaptation and evolution: virus dynamics within and between hosts** *Chair: Kate Grabowski* *Moderator: Nick Loman*	*Auditorium*
14:15	14:45	The antigenic and genetic evolution of dengue virus *Henrik Salje, University of Cambridge, United Kingdom*	
14:45	15:00	Revealing the deep evolutionary history of orthohepaciviruses *Jonathon Mifsud, KU Leuven, Belgium*	
15:00	15:15	SARS-CoV-2 saltational events are recurrent and trace to persistent human infections *Cécile Tran Kiem, Imperial College London, United Kingdom*	
15:15	15:30	Beyond variant calling: phylogenetic models reveal evolutionary insights from within-host diversity *JT McCrone, Fred Hutch Cancer Center, United States of America*	
15:30	15:45	Compositional diversity and evolutionary dynamics of accessory proteins across the family Coronaviridae *Ash Porter, Dalhousie University, Canada*	
15:45	16:00	One Host, Two Lineages: Population-Scale Detection of SARS-CoV-2 Coinfections *Rosario Evans Pena, University of Oxford, United Kingdom*	
16:00	16:45	Refreshment break and networking	*Event Space*
16:00	**16:45**	**Breaktime SecureBio sponsored 'AI-enabled Biological Risk' Workshop** *In-person attendees only*	*Barbara McClintock Pavilion*

16:30		*Briefing for Session 6 speakers, chair and moderator*	*Auditorium*
16:45	**18:00**	**Session 6: Bioinformatics, machine learning and AI** *Chair: Nick Loman* *Moderator: Deogratius Ssemwanga*	*Auditorium*
16:45	17:15	AI for modeling infectious disease outbreaks *Moritz Kraemer, University of Oxford, United Kingdom*	
17:15	17:30	Prediction of antigenic evolution from single virus sequences using an epistasis-aware protein language model approach *Rubayet Alam, University Of Glasgow, United Kingdom*	
17:30	17:45	Quantum Approximation in Phylogenetic tree Construction *Yeuko Mangenyi, University Of Cape Town, South Africa*	
17:45	18:00	How can we make better phylogenetic tree visualisations? *Gytis Dudas, Vilnius University, Lithuania*	
18:00	**18:40**	**Poster pitch talks for even number posters**	*Auditorium*
18:40	**19:40**	**Poster session 2 (even number posters) and networking reception**	*Event Space*
19:40 *19:40*	22:00	Dinner *Bar open (card payments only)*	*Hinxton Hall Restaurant* *Graham Cameron Bar*

Friday 13 November 2026

09:15		*Briefing for Session 7 speakers, chair and moderator*	*Auditorium*
09:30	**10:45**	**Session 7: Viral genomics and public health** *Chair: Deogratius Ssemwanga* *Moderator: Kate Grabowski*	*Auditorium*
09:30	10:00	Operational perspectives on genomic surveillance of viral pathogens in field settings *Sophie Duraffour, Bernhard Nocht Institute for Tropical Medicine, Germany*	
10:00	10:15	Targeted metagenomic sequencing of respiratory infections from UK healthcare workers in the SIREN study *Marissa Knoll, Wellcome Sanger Institute, United Kingdom*	
10:15	10:30	Estimating epidemic success of viral lineages from population-level wastewater surveillance data *Anika John, ETH Zürich, Switzerland*	
10:30	10:45	Evolutionary promiscuity in norovirus emergence: hidden diversity and multiple routes to persistence and spread *Damien Tully, London School Of Hygiene And Tropical Medicine, United Kingdom*	
10:45	11:30	Refreshment break and networking	*Event Space*
11:15		*Briefing for Closing keynote speaker, chair, moderator and committee*	*Auditorium*
11:30	**12:20**	**Closing keynote** *Chair: Kate Grabowski* *Moderator: Nick Loman*	*Auditorium*
11:30	12:20	Impact of host and pathogen heterogeneities on the epidemiology and phylodynamics of acute viral *Bryan Grenfell, Princeton University, United States of America*	
12:20	**12:35**	**Closing remarks**	*Auditorium*
		Scientific Programme Committee: *Deogratius Ssemwanga, LSHTM and MRC-UVRI, Uganda* *Kate Grabowski, Johns Hopkins University, United States of America* *Nick Loman, University of Birmingham, United Kingdom*	
12:35	13:40	Lunch	*Hinxton Hall Restaurant*
13:45		Coach departure for Stansted and Heathrow airports	*Main entrance*
13:55		Coach departure for Cambridge train station and city centre	*Main entrance*