

Virtual Conference Agenda

Start Finish Presenter details

(BST) (BST)

Monday, 7 June 2021

13:00 13:10 We	elcome
----------------	--------

Scientific Programme Committee:

Caroline Buckee, Harvard University, USA

Deus Ishengoma, National Institute for Medical Research, Tanzania

Mara Lawniczak, Wellcome Sanger Institue, UK

Dan Neafsey, Broad Institute, USA

13:10	15:00	Session 1: Spatial Epidemiology
		Introduction to the session Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania
13:10	13:30	The host with the most: High-resolution parasite genotyping to identify elusive reservoirs of malaria transmission Wendy O'Meara, Duke Global Health Institute, USA/Moi University, Eldoret, Kenya
13:30	13:50	Spatial analysis of parasite population genomics during malaria elimination efforts in Eastern Myanmar Xue Li, Texas Biomedical Research Institute, USA
13:50	14:00	Novel highly multiplexed Ampliseq targeted NGS assay for P. vivax molecular surveillance achieves geographical differentiation of global isolates from 26 countries and at within-country level in Vietnam. Eline Kattenberg, Institute of Tropical Medicine Antwerp, Belgium
14:00	14:10	Population genetics of the Plasmodium falciparum circumsporozoite protein in two distinct regions with different malaria endemicity in Tanzania Beatus Lyimo, National Institution for Medical Research, Tanzania
14:10	14:20	Fine-scale relatedness analysis reveals the recent epidemiological history of P. falciparum populations in the Pacific Coast of South America Manuela Carrasquilla, Harvard T.H. Chan School of Public Health, USA
		Highly commended lightning talk
		Somya Mehra, Burnet Institute, Australia
		Highly commended lightning talk Hugo Valdivia, NAMRU-6, Peru
		Highly commended lightning talk Sarah Volkman, Harvard T.H. Chan School of Public Health, USA
14:30	15:00	Q&A Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania Moderator: Mara Lawniczak, Wellcome Sanger Institue, UK
15:00	15:20	Break
15:20	15:50	Networking



18:05 Networking

17:35

Genomic Epidemiology of Malaria 7-9 June 2021

15:50	17:35	Session 2: Insecticide Resistance
		Introduction to the session Chair: Dan Neafsey, Broad Institute, USA
15:50	16:10	Genomic structural variations and insecticide resistance in malaria vectors Charles Wondji, Liverpool School of Tropical Medicine, UK
16:10	16:30	Anopheles mosquitoes surveillance and genomics Damaris Matoke-Muhia, Kenya Medical Research Institute, Kenya
16:30	16:40	Genetic variation in insecticide resistance genes - a pan-African perspective from 2,784 wild-caught Anopheles gambiae, coluzzii and arabiensis mosquitoes Chris Clarkson, Wellcome Sanger Institute, UK
16:40	16:50	Mapping the frequency of genetic mutations conferring insecticide target site resistance in African malaria vector species Penelope Hancock, Imperial College London, UK
		Highly commended lightning talk Amelie Wamba Ndongmo Regine, CRID-LSTM unit, Cameroon
		Highly commended lightning talk Naveen Kumar, Tata Institute for Genetics and Society, India
		Highly commended lightning talk Petra Korlevic, EMBL-EBI, UK
		Highly commended lightning talk Eric Lucas, LSTM, UK
17:05	17:35	Q&A Chair: Dan Neafsey, Broad Institute, USA Moderator: Caroline Buckee, Harvard University, USA



Tuesday, 8 June 2021

13:00	14:20	Session 3: Drug Resistance
		Introduction to the session Chair: Dan Neafsey, Broad Institute, USA
13:00	13:20	Genetic surveillance to support national malaria control in Vietnam Nguyen Thanh Thuy Nhien, OUCRU, Vietnam
13:20	13:30	Molecular monitoring of Plasmodium falciparum to evaluate the interventions strategies in Senegal from 2015 to 2019 Yaye Die Ddiaye, Cheikh Anta Diop University, Senegal
13:30	13:40	Comparison of different genotyping methods for differentiating Plasmodium falciparum recrudescence from new infections in antimalarial drug clinical trials Annina Schnoz, Swiss Tropical and Public Health Institute, Switzerland
		Highly commended lightning talk Alfred AmambuaNgwa, MRC Unit The Gambia at LSHTM, Gambia
		Highly commended lightning talk Irene Omedo, University of Oxford, UK
		Highly commended lightning talk Aung Myint Thu, Shoklo Malaria Research Unit, Thailand
13:50	14:20	Q&A Chair: Dan Neafsey, Broad Institute, USA Moderator: Deus Ishengoma, National Institute for Medical Research, Tanzania
14:20	14:50	Break
14:50	15:20	Networking
15.00	17.10	Cassian A. Dialogical Insights from Canamas
15:20	17:10	Session 4: Biological Insights from Genomes Introduction to the session Chair: Mara Lawniczak, Wellcome Sanger Institue, UK
15:20	15:40	Genetic and genomic approaches to inform malaria interventions and vaccine design Amy Bei, Yale School of Medicine, USA
15:40	15:50	The protective effect of sickle haemoglobin against severe malaria depends on parasite genotype Gavin Band, University of Oxford / Wellcome Sanger Institute, UK
15:50	16:00	Plasmodium falciparum histidine-rich protein 2 deletion is under recent positive selection in Ethiopia and threatens malaria diagnostic and control strategies Jonathan Parr, University of North Carolina at Chapel Hill, USA
16:00	16:10	Within host evolution of malaria parasites revealed by single genome sequencing Ian Cheeseman, Texas Biomedical Research Institute, USA



16:10 16:20 Improving statistical power in severe malaria genetic association studies by augmenting phenotypic precision James Watson, MORU, Thailand

Highly commended lightning talk

Kevin Esoh, University of Cape Town, South Africa

Highly commended lightning talk

Emily LaVerriere, Harvard University, USA

Highly commended lightning talk

Alistair Miles, Wellcome Sanger Institute, UK

Highly commended lightning talk

Richard Pearson, Wellcome Sanger Institute, UK

16:40 17:10 Q&A

Chair: Mara Lawniczak, Wellcome Sanger Institue, UK Moderator: Caroline Buckee, Harvard University, USA

17:10 17:40 Networking

Wednesday, 9 June 2021

13:00	14:30	Session 5: Bioinformatics Tools for 21st Century
		Introduction to the session Chair: Mara Lawniczak, Wellcome Sanger Institue, UK
13:00	13:20	Genealogical trees at the population scale Jerome Kelleher, University of Oxford, UK
13:20	13:30	High resolution Anopheles species assignment from a genus-wide sequencing approach Marilou Boddé, University of Cambridge / Wellcome Sanger Institute, UK
13:30	13:40	Fast estimates of IBD from unphased polyclonal malaria infections with Dcifer Inna Gerlovina, EPPIcenter at UCSF, USA
13:40	13:50	A genomic surveillance platform for indel-rich genes from Plasmodium spp. using long-read amplicon sequencing David Plaza, Karolinska Institutet, Sweden
		Highly commended lightning talk Jacob Almagro Garcia, Oxford University, UK
		Highly commended lightning talk Brice Letcher, EMBL-EBI, UK
		Highly commended lightning talk Kevin Wamae, University of North Carolina, USA
14:00	14:30	Q&A Chair: Mara Lawniczak, Wellcome Sanger Institue, UK Moderator: Dan Neafsey, Broad Institute, USA
14:30	14:40	Break



14:40	16:15	Session 6: Transmission
		Introduction to the session Chair: Caroline Buckee, Harvard University, USA
14:40	15:00	SIMPLEGEN: Exploring genetic sampling designs through simulation *Robert Verity, Imperial College, UK*
15:00	15:20	Gene drive for malaria vector control: From lab to application Diabate Abdoulaye, Institut de Recherche en Sciences de la Santé/Centre Muraz, Bobo-Dioulasso, Burkina Faso
15:20	15:30	Plasmodium falciparum genetic diversity associated with continued malaria transmission in pre-elimination settings in South Africa Hazel Beverly Gwarinda, University of Pretoria, South Africa
		Highly commended lightning talk Juliana Cudini, Wellcome Sanger Institute, UK
		Highly commended lightning talk Jason Hendry, University of Oxford, UK
		Highly commended lightning talk Maxwell Murphy, EPPIcenter at UCSF, USA
		Highly commended lightning talk Myo Naung, Walter Eliza Hall of Medical Institute, Australia
		Highly commended lightning talk Abebe Fola, Purdue University, USA
15:45	16:15	Q&A Chair: Caroline Buckee, Harvard University, USA Moderator: Mara Lawniczak, Wellcome Sanger Institue, UK
16:15	16:30	Break
16:30	18:00	Session 7: Genomic surveillance for Elimination and Barriers to Translation
		Introduction to the session Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania
16:30	16:45	Africa pathogen genomics initiative (Africa PGI): beyond COVID-19
16:45	17:00	Sofonias Tessema, University of California, San Francisco, USA Advancing genomics for malaria eradication: What can we learn from COVID-19 Jennifer Gardy, Gates Foundation, USA
17:00	17:15	Putting genomic epidemiology into practice for malaria and covid-19 Dominic Kwiatkowski, Wellcome Sanger Institute, UK
17:15	18:00	Panel discussion - Opportunities and challenges - Where does the field go from here? Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania Moderator: Dan Neafsey, Broad Institute, USA
18:00	18:10	Closing remarks by the Scientific Programme Committee:
		Caroline Buckee, Harvard University, USA

Deus Ishengoma, National Institute for Medical Research, Tanzania

Mara Lawniczak, Wellcome Sanger Institue, UK

Dan Neafsey, Broad Institute, USA