

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Wednesday, 18 September 2024		
12:00	13:00	Registration, lunch and networking
12:45	13:00	<i>Briefing for session 1 speakers, microphone runners, chair, moderator & committee - Auditorium</i>
13:00	13:15	Welcome
		<p>Wellcome Connecting Science: Tressa Creavin, <i>Connecting Science, UK</i></p> <p>Scientific Programme Committee: Sarah Auburn, <i>Menzies School of Health Research, Australia</i> Deus Ishengoma, <i>National Institute for Medical Research, Tanzania</i> Mara Lawniczak, <i>Wellcome Sanger Institute, UK</i> Daniel Neafsey, <i>Harvard T.H. Chan School of Public Health, USA</i> Vikki Simpson, <i>Wellcome Sanger Institute, UK</i></p>
13:15	14:55	Session 1: Spatiotemporal genomic epidemiology of parasites and vectors
		<p><i>Chair: Sarah Auburn, Menzies School of Health Research, Australia</i> <i>Moderator: Daniel Neafsey, Broad Institute, USA</i></p>
13:15	13:40	The Malaria Vector Genome Observatory – data, tools and training for genomic surveillance of Anopheles mosquitoes <i>Anastasiya Hernandez-Koutoucheva, Wellcome Sanger Institute, UK</i>
13:40	14:05	The utility of parasite population genetic data to monitor transmission dynamics: Insights from 20 years of surveillance in Papua New Guinea <i>Alyssa Barry, Deakin University, Australia</i>
14:05	14:30	Establishing malaria genomic surveillance in far-west Africa <i>Alfred Amambua Ngwa MRC, Gambia</i>
14:30	14:55	Strategic Use of Molecular Data for National Malaria Surveillance and Decision-Making <i>Sarah Volkman, Harvard T.H. Chan School Of Public Health, USA & Daouda Ndiaye, CIGASS, Senegal</i>
14:55	15:30	Refreshment break and networking
15:15	15:30	<i>Briefing for session 2 speakers, chair & moderator - Auditorium</i>
15:30	16:50	Session 2: Drug, diagnostic and insecticide resistance
		<p><i>Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania</i> <i>Moderator: Mara Lawniczak, Wellcome Sanger Institute, UK</i></p>
15:30	15:55	Dissecting malaria parasites drug and diagnostic resistance through large scale genomics: implication for malaria control and elimination in Africa <i>Abele Fola, Brown University, USA [virtual presentation]</i>
15:55	16:20	Embedding mosquito genomics into vector control trials and implementation <i>Martin Donnelly, Liverpool School of Tropical Medicine, UK</i>
16:20	16:35	Unraveling the genetic diversity and resistance profiles of P. falciparum in Southwestern Uganda: A low transmission setting <i>Monica Mbabazi, Infectious Disease Research Collaboration, Uganda</i>
16:35	16:50	The impact of switching first-line antimalarials on drug-resistant Plasmodium falciparum populations in the Greater Mekong Subregion <i>Ethan Booth, Mahidol Oxford Tropical Medicine Research Unit (moru), Thailand</i>
16:50	17:30	Poster pitch talks for odd number posters
		<i>Chair: Vikki Simpson, Wellcome Sanger Institute, UK</i>
17:30	19:00	Poster session 1 - odd number posters
19:00	19:30	Speed networking
19:30	21:00	Dinner
19:30		Bar open (card payments only)

Thursday, 19 September 2024

09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium
09:30	11:20	Session 3: Genomic studies of species interactions Chair: <i>Mara Lawnczak, Wellcome Sanger Institute, UK</i> Moderator: <i>Sarah Auburn, Menzies School of Health Research, Australia</i>
09:30	09:55	Exploring the history of human malaria using ancient DNA <i>Megan Michel, Max Plank, Germany</i>
09:55	10:20	Using multi-prong approaches for tackling antimalarial resistance in Ghana <i>Lucas Amenga-Etego, West African Centre for Cell Biology of Infectious Pathogens, Ghana</i>
10:20	10:35	Defining immune escape polymorphisms in <i>Plasmodium vivax</i> : insights from the analysis of allelic turnover of 16 antigens in a longitudinal cohort of Papua New Guinean children <i>Alison Paolo Bareng, Burnet Institute, Australia</i>
10:35	10:50	Geographical analysis of the <i>P. falciparum</i> - sickle haemoglobin association at local and continental scales <i>Gavin Band, Oxford University, UK</i>
10:50	11:05	<i>Plasmodium falciparum</i> establishes chronic infections through high var gene expression switching rate <i>Antoine Claessens, University of Montpellier, France</i>
11:05	11:20	<i>Plasmodium falciparum</i> infection in the human host and the vector influences natural Anopheline biting behavior and parasite diversity <i>Sophie Berube, University of Florida, USA</i>
11:20	12:00	Refreshment break and networking
11:45	12:00	Briefing for Session 4 speakers, chair & moderator - Auditorium
12:00	13:00	Session 4: Harmonising data standards and analysis resources for public health Chair: <i>Bryan Greenhouse, University of California, USA</i> Moderator: <i>Daniel Neafsey, Broad Institute, USA</i>
12:00	12:05	Introduction <i>Bryan Greenhouse, University of California, USA</i>
12:05	12:20	Tools for recurrence classification and marker evaluation <i>Aimee Taylor, Institut Pasteur, France</i>
12:20	12:50	Interactive scenario: Can you prevent the spread of drug resistant malaria with your data analysis skills? <i>Kathryn Murie, University of California, USA</i> <i>Sofonias Tessema, Africa Centres for Disease Control and Prevention, Ethiopia</i> <i>Amy Wesolowski, Johns Hopkins Bloomberg School Of Public Health, USA</i> and "you, the audience"
12:50	13:00	Discussion and way forward
13:00	14:40	Lunch
14:25	14:40	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:40	15:40	Session 5: Transmission and genetic surveillance of malaria: new methods, analyses and resources Chair: <i>Daniel Neafsey, Broad Institute, USA</i> Moderator: <i>Mara Lawnczak, Wellcome Sanger Institute, UK</i>
14:40	14:50	Molecular surveillance of malaria in endemic regions in Uganda reveals high genetic diversity of <i>Plasmodium falciparum</i> and correlation with transmission intensity <i>Shahid Kiyaga, Makerere University, Uganda</i>
14:50	15:00	Nanopore sequencing for <i>Plasmodium falciparum</i> genomic surveillance: the pathway to a public health tool <i>William Hamilton, Cambridge University, UK</i>
15:00	15:10	Deconvolving genetic complexity in <i>Plasmodium vivax</i> infections <i>Edwin Sutarjo, Exeins Health Initiative, Indonesia</i>
15:10	15:20	A population genomic model for measuring immune selection and predicting antigen serotypes <i>Myo Naung, Burnet Institute, Australia</i>
15:20	15:30	A complex <i>Plasmodium falciparum</i> cryptotype circulating at low frequency across the African continent <i>Olivo Miotto, University of Oxford, UK</i>
15:30	15:40	Decoding Ethiopia's unique and structurally divergent <i>Plasmodium falciparum</i> populations using genomics <i>Ashley Osborne, Menzies School Of Health Research, Australia</i>
15:40	16:20	Refreshment break and networking
16:10	16:20	Briefing for Session 5 speakers, chair & moderator - Auditorium
16:20	17:00	Session 5: Continued
16:20	16:30	Pregnant women as a sentinel population for genomic surveillance of malaria in the Democratic Republic of Congo <i>Varanya Wasakul, Mahidol Oxford Tropical Medicine Research Unit (MORU), Thailand</i>
16:30	16:40	Probing <i>Plasmodium falciparum</i> sickle-associated loci across global populations: the functional and evolutionary implications <i>Annie Forster, University of Oxford, UK</i>
16:40	16:50	Population genomics over the past century in the African malaria vector <i>Anopheles funestus</i> <i>Petra Korlevic, Wellcome Sanger Institute, UK</i>
16:50	17:00	Cryptic diversity among malaria vectors in the Brazilian Atlantic Forest <i>Luisa DP Rona, Federal University Of Santa Catarina, Brazil</i>
17:00	17:40	Poster pitch talks for even number posters Chair: <i>Vikki Simpson, Wellcome Sanger Institute, UK</i>
17:40	19:10	Poster session 2 - even number posters
19:10	21:00	Dinner
19:10		Bar open (card payments only)

Friday, 20 September 2024

09:15	09:30	Briefing for Session 6 speakers, chair & moderator - Auditorium
09:30	11:20	Session 6: Vector and parasites: neglected and emerging species Chair: Alyssa Barry Deakin University, Australia Moderator: Dan Neafsey Harvard T.H. Chan School of Public Health, USA
09:30	09:55	Molecular surveillance of Plasmodium vivax in Vietnam: Initial Findings and Prospective Challenges Nguyen Than Thuy Nhien, OUCRU, Vietnam
09:55	10:20	Molecular surveillance of Plasmodium vivax in remote hard-to-reach communities from the Peruvian Amazon region: the last milestone to eliminate malaria Dionicia Gamboa, Universidad Peruana Cayetano Heredia, Peru
10:20	10:35	Ad1000G: A comprehensive, range-wide evolutionary analysis of over 1000 whole genome sequences of Anopheles darlingi, the primary South American malaria vector Jacob Tennessen, Harvard TH Chan School of Public Health, USA
10:35	10:50	Population genomics of Plasmodium malariae from four African countries Zach Popkin-Hall, University Of North Carolina, USA [virtual presentation]
10:50	11:05	Updating the burden and drug resistance profiles of Plasmodium ovale species: a malaria elimination challenge Hoseah Akala, Kenya Medical Research Institute/WRAIR-A, Kenya
11:05	11:20	A new chapter in the Malaria Cell Atlas: Insights into neglected malaria parasites, Plasmodium ovale and Plasmodium malariae from single-cell RNA-sequencing in Mali Sunil Kumar Dogga, Wellcome Sanger Institute, UK
11:20	12:00	Refreshment break and networking
11:45	12:00	Briefing for session 7 chair, moderator & committee - Auditorium
12:00	13:00	Session 7: What next? Priorities for genomic epidemiology of malaria - panel discussion Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania Moderator: Vikki Simpson, Wellcome Sanger Institute, UK
13:00	13:10	Closing remarks and award presentation Scientific Programme Committee: Sarah Auburn, Menzies School of Health Research, Australia Deus Ishengoma, National Institute for Medical Research, Tanzania Mara Lawniczak, Wellcome Sanger Institute, UK Daniel Neafsey, Harvard T.H. Chan School of Public Health, USA Vikki Simpson, Wellcome Sanger Institute, UK
13:10	14:00	Lunch and departures
14:00		Coach departures for Stansted and Heathrow airports
14:10		Coach departures for Cambridge train station and city centre