

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	Briefing for session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
13:00	13:15	Welcome
		<p>Wellcome Connecting Science: Treaasa Creavin, Connecting Science, UK</p> <p>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, Broad Institute, USA Vikki Simpson, Wellcome Sanger Institute, UK</p>
13:15	14:55	Session 1: Spatiotemporal genomic epidemiology of parasites and vectors
		<p>Chair: Sarah Auburn, Menzies School of Health Research, Australia Moderator: Daniel Neafsey, Broad Institute, USA</p>
13:15	13:40	Unlocking genetic diversity through the vector observatory, a global collaborative resource on genomic variation for over 20,000 Anopheles mosquitoes Anastasia Hernandez-Koutoucheva, Wellcome Sanger Institute, UK
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 Alyssa Barry, Deakin University, Australia
14:05	14:30	Establishing malaria genomic surveillance in far-west Africa Alfred Amambua Ngwa MRC, Gambia
14:30	14:55	Strategic use of molecular data for national malaria surveillance and decision-making Sarah Volkman, Harvard T.h. Chan School Of Public Health, USA & Daouda Ndiaye, CIGASS, Senegal
14:55	15:30	Refreshment break and networking
15:15	15:30	Briefing for session 2 speakers, chair & moderator - Auditorium
15:30	17:05	Session 2: Drug, diagnostic and insecticide resistance
		<p>Chair: Deus Ishengoma, National Institute for Medical Research, Tanzania Moderator: Mara Lawniczak, Wellcome Sanger Institute, UK</p>
15:30	15:55	Dissecting malaria parasites drug and diagnostic resistance through large scale genomics: implication for malaria control and elimination in Africa Abebe Fola, Brown University, USA
15:55	16:20	Embedding mosquito genomics into vector control trials and implementation Martin Donnelly, Liverpool School of Tropical Medicine, UK
16:20	16:35	Title TBC Speaker TBC
16:35	16:50	Unraveling the genetic diversity and resistance profiles of P. falciparum in southwestern Uganda: A low transmission Monica Mbabazi, Infectious Disease Research Collaboration, Uganda
16:50	17:05	The Impact of switching first-line antimalarials on drug-resistant Plasmodium falciparum populations in the Greater Mekong Subregion Ethan Booth, Mahidol Oxford Tropical Medicine Research Unit (moru), Thailand

17:05	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	<i>Briefing for Session 3 speakers, chair & moderator - Auditorium</i>
09:30	11:20	Session 3: Genomic studies of species interactions
		<i>Chair: Mara Lawniczak, Wellcome Sanger Institute, UK</i>
		<i>Moderator: 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	Title TBC <i>Lucas Amenga-Etego, West African Centre for Cell Biology of Infectious Pathogens, Ghana</i>
10:20	10:35	Defining immune escape polymorphisms in Plasmodium vivax: 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 P.falciparum - sickle haemoglobin association at local and continental scales <i>Gavin Band, Oxford University, UK</i>
10:50	11:05	Plasmodium falciparum establishes chronic infections through high var gene expression switching rate <i>Antoine Claessens, University of Montpellier, France</i>
11:05	11:20	Plasmodium falciparum 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	<i>Briefing for Session 4 speakers, chair & moderator - Auditorium</i>
12:00	13:00	Session 4: Harmonising data standards and analysis resources for public health
		<i>Chair: Bryan Greenhouse</i>
		<i>Moderator: Daniel Neafsey, Broad Institute, USA</i>
		Tools for recurrence classification and marker evaluation <i>Aimee Taylor, Institut Pasteur, France</i>
		Followed by a panel discussion
13:00	14:30	Lunch
14:15	14:30	<i>Briefing for Session 5 speakers, chair & moderator - Auditorium</i>

14:30	15:30	Session 5: Transmission and genetic surveillance of malaria: new methods, analyses and resources
		<i>Chair: Daniel Neafsey, Broad Institute, USA</i>
		<i>Moderator: Mara Lawniczak, Wellcome Sanger Institute, UK</i>
14:30	14:40	Increasing validated artemisinin partial resistance markers confirmed in Ethiopia during national sentinel-based Plasmodium falciparum molecular surveillance <i>Bokretzion Gidey Brhane, Ethiopian Public Health Institute, Ethiopia</i>
14:40	14:50	Talk Title TBC <i>Speaker TBC</i>
14:50	15:00	Molecular surveillance of malaria in endemic regions in Uganda reveals high genetic diversity of Plasmodium falciparum and correlation with transmission intensity <i>Shahiid Kiyaga, Makerere University, Uganda</i>
15:00	15:10	Nanopore sequencing for Plasmodium falciparum genomic surveillance: the pathway to a public health tool <i>William Hamilton, Cambridge University, UK</i>
15:10	15:20	Deconvolving genetic complexity in Plasmodium vivax infections <i>Edwin Sutanto, Exeins Health Initiative, Indonesia</i>
15:20	15:30	A population genomic model for measuring immune selection and predicting antigen serotypes <i>Myo Naung, Burnet Institute, Australia</i>
15:30	15:40	A complex Plasmodium falciparum cryptotype circulating at low frequency across the African continent <i>Olivo Miotto, University of Oxford, UK</i>
15:40	15:50	Decoding Ethiopia's unique and structurally divergent Plasmodium falciparum populations using genomics <i>Ashley Osborne, Menzies School Of Health Research, Australia</i>
15:50	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 Plasmodium falciparum sickle-associated loci across global populations: the functional and evolutionary <i>Annie Forster, University of Oxford, UK</i>
16:40	16:50	Population genomics over the past century in the African malaria vector Anopheles funestus <i>Petra Korlevic Wellcome Sanger Institute, UK</i>
16:50	17:00	Talk Title TBC <i>Speaker TBC</i>
17:00	17:30	Poster pitch talks for even number posters
		<i>Chair: Vikki Simpson, Wellcome Sanger Institute, UK</i>
17:30	19:00	Poster session 2 - even number posters
19:00	21:00	Dinner
19:00		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: TBC

Moderator: TBC

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

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, microphone runners, 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 prize 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, Broad Institute, USA

Vikki Simpson, Wellcome Sanger Institute, UK

13:10 14:10 Lunch and departures

14:00 Coach departures for Stansted and Heathrow airports

14:10 Coach departures for Cambridge train station and city centre