

Programme Genomic Epidemiology of Malaria 2014

8-11 June 2014

Sunday, 8 June 2014

Session I: Setting the Stage

Chair: Victoria McGovern

Welcome and Introduction

Dyann Wirth, Harvard School of Public Health, USA

Genetic signs on the road to malaria elimination

Dan Hartl, Harvard University, USA

Anopheles vectors of malaria: The last kilometer?

Ken Vernick, Institut Pasteur, France

How to use molecular tools in the fight against artemisinin resistant falciparum malaria?

Arjen M Dondorp, Mahidol Oxford Tropical Medicine Research Unit, Thailand

Session II: Introduction to GEM Travel Awardees, supported by BWF, MalariaGEN, CGGH, and WTSC

Chair: Victoria McGovern

The clinical spectrum of childhood severe malaria in eastern Uganda

Peter Olupot-Olupot, Busitema University Faculty of Health Sciences (BUFHS), Mbale Campus, Uganda

Investigation of regulatory SNPs in the promoter region of TNF- α , INF- γ and IL-10 genes and their association with malaria clinical outcomes in a Brazilian Amazonian population

Simone Da Silva Santos, Fiocruz (Oswaldo Cruz Institute), Brazil

Contribution of HRP2 polymorphism in Senegalese isolates in RDT detection

Awa Bineta Deme, Hospital Aristide Le Dantec, Senegal

Relationship between malaria incidence and IgG levels to Plasmodium falciparum merozoite antigens in Malian children: impact of hemoglobins S and C

Mahamadou Diakite, University of Bamako, Mali

Analysis of the DNA sequence of Ace.1 gene in Anopheles gambiae s.s: duplication and recombination history

Luc Djogbenou, Institut Régional de Santé Publique / Université d'Abomey-Calavi, Benin

Molecular antimalarial SP resistance in Plasmodium falciparum parasites from Lubango, Angola

Maria de Fatima Ferreira de Cruz, Fundação Oswaldo Cruz, Brazil

Kinetics of anti-malarial antibodies in children with common haemoglobinopathies in a Tanzanian population

Alphaxard Manjurano, NIMR, Tanzania

Genetic determinants of asexual proliferation rate in Plasmodium falciparum

Jonathan Mwangi, Mount Kenya University, Kenya

Isolation and characterization of the merozoite surface protein family from P. malariae

Supatchara Nakeesathit, Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand

Modeling response and progression of delayed parasite clearance to Artemisinin Combination Therapies (ACTs) in Cameroonian children

Akindeh Nji, University of Yaounde, Cameroon

Association of an Arabiensis time of feeding behaviour using single nucleotide polymorphisms in circadian rhythm genes

Deodatus Maliti, University of Glasgow, UK

A platform for comparative analysis of Plasmodium vivax genotyping data

Hidayat Trimarsanto, Eijkman Institute for Molecular Biology, Indonesia

Session III: Genomes and Genome Variation

Chair: Chris Newbold

Diversity of genome content and organisation across the Plasmodium genus

Matthew Berriman, Wellcome Trust Sanger Institute, UK

Evolution before our eyes: Genome mutation in cultured P. falciparum

William Hamilton, Wellcome Trust Sanger Institute, UK

Genomics of Plasmodium vivax

Elizabeth Winzeler, University of California San Diego, USA

The wonderful world of Anopheles gambiae genome variation – insights from deep sequencing of mosquitos from colony crosses and natural populations

Alistair Miles, University of Oxford, UK

Monday, 9 June 2014

Session IV: Genomic Epidemiology of the Parasite

Chair: David Conway

Temporal analysis of Plasmodium falciparum genotypic infection complexity in the SeneGambian region of West Africa

Alfred Amambua Ngwa, Medical Research Council, Gambia Unit, The Gambia

Using Genomic tools to monitor Artemether-lumefantrine (Coartem) drug response in Plasmodium falciparum field isolates in Senegal

Daouda Ndiaye, University Cheikh Anta Diop de Dakar, Senegal

Population analysis of surface antigens with extremely diverged haplotypes: MSP3.4 and MSP3.8

Zamin Iqbal, University of Oxford, UK

Session V: Artemisinin Resistance

Chair: Rick Fairhurst

K13: A gene involved in artemisinin resistance

Frederic Arieu, Institut Pasteur du Cambodge, Cambodia

Genetic architecture of artemisinin resistant Plasmodium falciparum

Olivo Miotto, Mahidol-Oxford Tropical Medicine Research Unit, Thailand

Independent emergence of artemisinin resistant Plasmodium falciparum in Southeast Asia

Shannon Takala Harrison, University of Maryland School of Medicine, USA

Expression profiling of artemisinin resistant P. falciparum isolates reveals association with parasite developmental age and modulation of unfolded protein response

Pedro Ferreira, Nanyang Technological University, Singapore

K13 propeller polymorphism in communities of the Plasmodium Diversity Network: a network for investigating and using plasmodium genetic diversity to inform malaria elimination policies in sub-Saharan Africa

Abdoulaye Djimde, Malaria Research and Training Centre (MRTC)

Session VI: Genomic Epidemiology of the Parasite Cont'd

Chair: Ivo Mueller

Genetic diversity in a global sample of Plasmodium vivax isolates

Jane Carlton, Center for Genomics & Systems Biology, USA

A molecular approach to map P. vivax transmission and epidemiology

Ric Price and Sarah Auburn, Menzies School of Health Research, Australia

A targeted linkage group selection analysis identifies a locus associated with chloroquine resistance in the NIH Plasmodium vivax cross

Jonathan Juliano, University of North Carolina, USA

Population genetic structure of the zoonotic malaria parasite Plasmodium knowlesi in Malaysia

Paul Divis, London School of Hygiene and Tropical Medicine, UK

Session VII: Genomic Epidemiology of the Host

Chair: Kirk Rockett

Genetic susceptibility to severe malaria and mechanisms of ancient natural selection

Chris Spencer, University of Oxford, UK

Genetic scans of hematological traits in human populations

Nicole Soranzo, Wellcome Trust Sanger Institute, UK

Functional analysis of red blood cell and parasite determinants of plasmodium invasion

Manoj Duraisingh, Harvard School of Public Health, USA

The role of admixture and natural selection in establishing African population structure

George Busby, Wellcome Trust Centre for Human Genetics, UK

Tuesday, 10 June

Session VIII: Genomic Epidemiology of the Vector

Chair: Ken Vernick

Genomic evolution of the Anopheles genus: insights from new reference genome assemblies for 16 species

Daniel Neafsey, Broad Institute, USA

Through the lens darkly: A genomic portrait of radiation and introgression in a species complex of malaria vectors

Nora Besansky, University of Notre Dame, USA

Functional speciation genomics of the Anopheles gambiae complex

Frederic Tripet, Keele University, UK

Adaptive introgression eliminates a major genomic island of diversity but not reproductive isolation between Anopheles gambiae sibling species

Chris Clarkson, Liverpool School of Tropical Medicine, UK

Session IX: Genomic Epidemiology of the Vector Cont'd

Chair: Igor Sharakov

The genetics of human host preference in Anopheles gambiae

Michel Slotman, Texas A&M University, USA

Variation in male mating success across spatial scales in Anopheles gambiae: influence of swarms attributes

Abdoulaye Diabate, IRSS/Centre Muraz, Burkina Faso

From population genomics to plasmodium susceptibility, what dense genotyping reveals about a deeply sampled local A. gambiae population

Michelle Riehle, University of Minnesota, USA

The Anopheles gambiae 1000 genomes project

Martin Donnelly and Tiago Antao, Liverpool School of Tropical Medicine, UK

Session X: Transmission and Elimination

Chair: Arjen Dondorp

Using genomics to understand malaria transmission: toward elimination and eradication

Sarah Volkman, Harvard School of Public Health, USA

Mobilis in mobile: malaria transmission dynamics

Philip Bejon, KEMRI-WTRP, Kenya

Hacking networks of malaria transmission for targeted control and elimination

Bryan Greenhouse, University of California, San Francisco, USA

Artemisinin-resistant Plasmodium falciparum and diverse Anopheles vectors in Cambodia

Brandyce St. Laurent, NIH NIAID Laboratory of Malaria and Vector Research, USA

Session XI: Transmission and Elimination Cont'd

Chair: Dyann Wirth

Modelling the transmission and control of artemisinin resistance

Lisa White, Mahidol-Oxford Tropical Medicine Research Unit, Thailand

Assessing the human infectious reservoir of malaria

Chris Drakeley, LSHTM, UK

Next-Gen MalariaGEN

Dominic Kwiatkowski, Wellcome Trust Sanger Institute and Wellcome Trust Centre for Human Genetics, UK