Cambridge Infectious Diseases Interdisciplinary Research Centre Meeting of Minds 2017

FRI 24TH NOVEMBER 2017
HOWARD THEATRE,
DOWNING COLLEGE, CAMBRIDGE.

UNIVERSITY OF CAMBRIDGE

CAMBRIDGE INFECTIOUS DISEASES

CAMBRIDGE INFECTIOUS DISEASES IRC

CO-CHAIRS

Professor James Wood
Department of Veterinary Medicine

Dr Lydia Drumright
Department of Medicine

COORDINATOR AND MEETING ORGANISER

Dr Allyson Walsh
Department of Veterinary Medicine

CIDIRC will enable the University of Cambridge to provide a world-leading interdisciplinary research environment for infectious diseases and accelerate solutions to reduce the burden of infectious diseases globally.

CIDIRC focuses on infectious diseases and the impact these have on national and global health. Connecting researchers across Cambridge, we help spark new ideas for collaborative research as well as providing flexibility and expansion possibilities for traditional disciplines to address complex infectious disease problems. Our virtual network has expanded to include over 30 different departments and institutes, representing multiple disciplines in all six schools, from Arts, Humanities and Social Sciences, through to Biological and Physical Sciences and Clinical Medicine.

Joining Cambridge Infectious Diseases is free and is open to Cambridge-based researchers, at any level of their career, with an interest in research relating to infectious diseases. The online researcher directory allows people to search for network members with interests or expertise in particular areas. We encourage everyone based in Cambridge and with an interest in Infectious Diseases to join us at CID events and engage with us. At the core of our activities is grant development support, including focussed meeting series, promoting cross-discipline networking through various meetings, events, and seminars, supporting early career researchers, and providing pathways to impact through organizing public engagement and outreach activities, including active involvement in the Cambridge Science Festival.

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MORNING PROGRAMME

8.30	***Registration and Coffee – Howard Grace Room***
9.15	**Introduction** Professor James Wood, Co-Chair of CIDIRC, Department of Veterinary Medicine.
Session 1: **Molecular biology of infectious diseases** Chair: Dr Paula MacGregor, Department of Biochemistry	
9.30	**Structure, Mechanism and Evolution of Class II Viral Membrane Fusion Proteins** Dr Yorgo Modis, MRC LMB.
9.50	**New drug targets in the SHAPE of HIV-1 RNA** Dr Julia Kenyon, Department of Medicine.
10.10	**Rapid evolution of cell surface receptors in African trypanosomes** Dr Mark Carrington, Department of Biochemistry.
10.30	***Tea & Coffee & Networking - 40 mins***
Session 2: **Engineering innovations for clinical diagnostics** Chair: Professor John Clarkson, Department of Engineering	
11.10	**Engineering Better care** Professor John Clarkson, Department of Engineering
11.30	**Nucleic acid tests with purchasing price parity: pipe dream or possibility.** Professor Lisa Hall, Department of Chemical Engineering and Biotechnology.
11.50	**Acoustic Resonator Sensors for Medical Applications** Professor Andrew Flewitt, Department of Electrical Engineering.
12.10	**Breath Biopsy, chemicals on breath as biomarkers of disease** Chris Hodkinson, VP Business Development, Owlstone Medical Ltd.
12.30	***LUNCH- 60 mins - Howard Grace Room***

ALL PRESENTATIONS TO BE HELD IN HOWARD THEATRE

AFTERNOON PROGRAMME

Session 3: Microbial genomics and antimicrobial resistance Chair: Dr Hendrik van Veen, Department of Pharmacology		
1.30	**Living off the fat of the land - targeting fatty acid metabolism in the opportunistic human pathogen, Pseudomonas aeruginosa** Dr Martin Welch, Biochemistry.	
1.50	**How to build a Google for bacterial genomes** Dr Zamin Iqbal, The European Biofinormatics EBI.	
2.10	**Global Genomics Surveillance of AMR** Dr David Aanensen, WTSI.	
2.30	Flash Talks 5 x 4 mins	Selected *
3.00	***Tea & Coffee- 40 mins***	***Poster session***
Session 4: Disease transmission and response in urban and rural environments *Chair: Dr Lydia Drumright, Department of Medicine*		
3.40	**The hominin STD clinic: the ancient origins of HSV2** Dr Charlotte Houldcroft, Department of Archaeology and Anthropology.	
4.00	**Pathogen Spillover at the core-matrix interface** Professor Hamish McCallum, Environmental Futures Research Institute, Griffith University, Australia.	
4.20	**The trials and tribulations of using field deployable genomics during epidemic response** Dr Ian Goodfellow, Department of Pathology.	
4.40	**Closing Speech** Dr Lydia Drumright, Co-Chair Cambridge Infectious Diseases, Department of Medicine.	
5.00	**Drinks & Canapés Reception** - Howard Grace Room	

ALL PRESENTATIONS TO BE HELD IN HOWARD THEATRE

SPEAKER & CHAIR BIOGRAPHIES

Dr Yorgo Modis is a Reader in Virology & Immunology, Department of Medicine, University of Cambridge. His group's overarching goal is to gain a mechanistic understanding at the molecular level of how enveloped RNA viruses interact with host cells during infection, employing a complementary set of approaches including X-ray crystallography, electron microscopy, solution biophysics, fluorescence microscopy and cell biological approaches.

Dr Julia Kenyon is an Associate PI in the Department of Medicine and a College Lecturer at Homerton. She also has a visiting position at the National University of Singapore. Julia's interests are in RNA structures in health and disease, in particular the development of new techniques to look at RNA structure.

Dr Mark Carrington is a Research Group Leader in the Department of Biochemistry, University of Cambridge. The aim of his lab is to determine the molecular mechanisms that underlie some of the unique aspects of the biology of trypanosomes and other related protozoa.

Dr Paula MacGregor is a BBSRC David Phillips Fellow in the Department of Biochemistry. Paula is interested in the molecular and cell biology of the interaction between African trypanosomes and their external environment. Current work in her lab aims to experimentally characterise molecular diversity amongst different African trypanosome species and how that affects host-parasite interactions.

Professor John Clarkson FREng is the Director of the Cambridge Engineering Design Centre and Head of the Department of Engineering at University of Cambridge. His research interests are in the general area of engineering design, particularly the development of design methodologies to address specific design issues, for example, process management, change management, healthcare design and inclusive design.

Professor Lisa Hall is Professor of Analytical Biotechnology and Deputy Head of the Department of Chemical Engineering and Biotechnology. The main umbrella of research in the Analytical Biotechnology Group is in heterogeneous analytical systems, with a primary but not exclusive focus on molecular sensors, the latter including both chemical and biological systems.

Professor Andrew Flewitt is a Professor of Electronic Engineering in the Department of Engineering, University of Cambridge. His current research interests include the degradation mechanisms of inorganic thin films transistors and metal oxide thin film transistors. More recently, research activities have included the study of MicroElectroMechanical Systems (MEMS). Of particular interest are sensors and microfluidic pumps devices based on acoustic waves.

Dr Chris Hodkinson is VP of Business Development, Owlstone Medical Ltd. He has over 15 years' experience in the pharmaceutical and biotech industries with the last 6 years in the development and commercialisation of biomarkers for the early detection and screening of cancer.

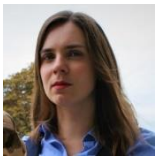
Dr Martin Welch is a Senior Lecturer in The Department of Biochemistry, University of Cambridge. Martin's research focuses primarily on understanding better the molecular basis for pathogenicity in Gram-negative bacteria. His group have established a critical role for certain "metabolic nodes" in the control of virulence, with a particular emphasis on the role(s) played by carbon flux through the glyoxylate shunt and methylcitrate cycle in the opportunistic human pathogen, *Pseudomonas aeruginosa*.

Dr Zamin Iqbal is a Research Group leader at The European Bioinformatics Institute (EMBL-EBI). He leads a computational genomics research group working on genetic variation in microbes, developing methods for representing and understanding complex genetic variation (e.g. surface antigens in *P. falciparum* and the pan-genome in bacteria), and exploring surveillance and diagnostics for antimicrobial resistance.

Dr David Aanensen is Director of the Centre for Genomic Pathogen Surveillance and holds a faculty position within the Department of Infectious Disease Epidemiology at Imperial College London. His group focuses on applied public health bioinformatics research and genomic epidemiology, including providing data and tools for local, national and international utility focused on antimicrobial resistance and genomic surveillance

Dr Hendrik Van Veen is a Reader in Molecular Pharmacology, Department of Pharmacology, University of Cambridge and a teaching fellow at Clare College. His research group study the mechanisms of antibiotic and anticancer drug recognition and transport by multidrug transporters in pro- and eukaryotic cells.

Dr Charlotte Houldcroft is a post-doctoral research associate in the Department of Medicine, working on cytomegalovirus (CMV) infection and reactivation. She has studied Epstein–Barr virus (EBV) latency in B cells, and the role of genomic variation in pathology caused by the three biggest viral killers of paediatric transplant recipients: EBV, CMV and adenovirus. She also has an interest in which infectious diseases afflicted Neanderthals.



Professor Hamish McCallum a Head of School of Environment at Griffith University in Queensland, Australia. He works on modelling wildlife disease, including Tasmanian devil facial tumour, Hendra virus in flying foxes and Chlamydia in koalas. Prior to joining Griffith University, he was the Senior Scientist of the Save the Tasmanian Devil program at the University of Tasmania from 2006 – 2009.

Dr Ian Goodfellow is Head of the Division of Virology, Department of Pathology
University of Cambridge. His group work on cellular pathways involved in norovirus replication and pathogenesis, Hepatitis E virus species selectivity, and novel mechanisms of viral protein synthesis.

Dr Lydia Drumright is a lecturer in Clinical Informatics in the Department of Medicine. Her research utilises epidemiology, statistics, and clinical informatics for understanding infectious disease dynamics. Lydia holds a PhD in Epidemiology and Public Health from University of California, San Diego and an MPH in Health Education from California State University, Northridge.

Professor James Wood is Head of the Department of Veterinary Medicine. He studies the dynamics of emerging infectious diseases, including viral infections of fruit bats in West Africa, focused in Ghana, mammalian influenza, rabies and bovine tuberculosis. Funders include BBSRC, EU FP7 (Antigone Consortium), ESPA, Defra, the RAPIDD program of the Science and Technology Directorate, Department of Homeland Security, Fogarty International Centre, National Institute of Health and the Alborada Trust.

ABSTRACTS

Structure, Mechanism and Evolution of Class II Viral Membrane Fusion Proteins

Monique Merchant, Anna-Albecka Moreau and Yorgo Modis
Department of Medicine, University of Cambridge, MRC Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge, CB2 0QH, UK

Abstract: Enveloped viruses fuse their lipid membrane with a host-cell membrane to deliver the viral genome into the cytoplasm. Viral envelope proteins catalyze this membrane fusion event. They fall into distinct structural classes. Class II fusion proteins have a conserved three-domain architecture and share a common molecular mechanism of fusion. They are found in many important viral pathogens including flaviviruses, alphaviruses and phleboviruses. I will review recent work by my group and others' on the structure, mechanism and fusion activity of class II fusion proteins from flaviviruses and phleboviruses. The evolutionary origin of class II fusion proteins remains unclear but proteins with class II-like folds were recently identified in various eukaryotic species *Caenorhabditis elegans, Tetrahymena, Chlamydomonas* and plants. These eukaryotic proteins have membrane fusion activity, which is used to drive key cell-cell fusion events in various developmental processes including fertilization and syncytia formation. Using bioinformatics approaches, we have identified a set of proteins with predicted class II folds in endogenous retroviruses and transposons in various nematode species including *C. elegans* and the human hookworm parasite *Ancylostoma ceylanicum*. The evolutionary origin of class II fusion proteins remains unclear but we hypothesize that they may have entered eukaryotic genomes by retroviral genome integration.

New drug targets in the SHAPE of HIV-1 RNA

Carin Ingemarsdotter[1], Neil Bell[1], Anne L'Hernault[1], Ziqi Long[1], Jingwei Zeng[1], Andrew Lever[1, 2] and Julia Kenyon[1, 3]
[1], University of Cambridge Department of Medicine
[2], National University of Singapore, Yong Loo Lin School of Medicine, Department of Medicine
[3], National University of Singapore, Yong Loo Lin School of Medicine, Department of Microbiology and Immunology

Abstract: RNA-protein interactions control many cellular and disease processes and are potential drug targets. By understanding one of the RNA structures involved in HIV-1 packaging (SL3), we previously developed a high-throughput screen for small-molecule inhibitors of the interaction between it and the viral structural protein, Gag (Bell *et al* Biochemistry 2013 Dec 23; 52). Here, we show that one of the inhibitory compounds identified, NSC260594, does specifically block viral genome packaging, providing proof of principle that development of a novel class of RNA targeting antiretroviral drugs is possible. In binding to the viral RNA at SL3, NSC260594 not only prevents Gag binding but also stabilizes the local and distant RNA structure. In order to find further drug targets we have developed a technique to visualise RNA structural changes in individual complexes during an RNA-protein interaction: in-gel RNA-protein SHAPE (selective 2'OH acylation analysed by primer extension). Retroviruses package two copies of their RNA genome and these are linked as a dimer inside the viral particle, but the order in which RNA genome dimerization and the protein interactions that mediate packaging occur is controversial. Using this technique, the HIV-1 Gag protein can be seen to stabilize the RNA into its dimeric structural form.

Rapid evolution of cell surface receptors in African trypanosomes.

Paula MacGregor[1], Harriet Lane-Serff,[2] Matt Higgins[2] and Mark Carrington[1]
[1] *Department of Biochemistry, University of Cambridge* [2]*Department of Biochemistry, University of Oxford*

Abstract: African trypanosomes have complex life cycles comprising at least ten developmental forms, variously adapted to different niches in their tsetse fly vector and their mammalian hosts. Unlike many other protozoan pathogens, they are always extracellular and have evolved intricate surface coats that allow them to obtain nutrients, while also protecting them from the immune defences of either insect or mammal. The

acquisition of macromolecular nutrients requires receptors that function within the context of these surface coats. The best understood of these is the haptoglobin-haemoglobin receptor (HpHbR) of *Trypanosoma brucei*, which is used by the mammalian bloodstream form of the parasite, allowing haem acquisition. However, in some primates it also provides an uptake route for trypanolytic factor 1, a mediator of innate immunity against trypanosome infection. Here, we show that during the evolution of African trypanosome species the receptor has diversified in function from a haemoglobin receptor predominantly expressed in the tsetse fly to a haptoglobin-haemoglobin receptor predominantly expressed in the mammalian bloodstream. Structural and functional studies of homologous receptors from different trypanosome species have allowed us to reconstruct an evolutionary history for how one receptor has adapted to different roles in different trypanosome species.

Engineering Better Care

Prof John Clarkson*, Department of Engineering, University of Cambridge*

Abstract: Over the past two decades, there have been numerous references to the value of a systems approach in calls to transform health and care, without there being a common understanding of what this might mean. However, many people working to improve health and care are aware of and use systems techniques, leading to improved pathways, processes and patient experience in many areas. Healthcare leaders know intuitively that there is a need to involve stakeholders in decisions, think across pathways and deliver integrated care, but lessons can be learned from the analysis and rigour applied in complex engineering systems.John will describe a unique project, led by the Royal Academy of Engineering, in collaboration with the Royal College of Physicians and the Academy of Medical Sciences, to develop a new and integrated approach to guide service design and improvement in health and care. A systems approach will be described as a standalone set of questions, with reference to systems, design, risk and people thinking, and as a design 'spiral' borrowed from the world of ship design.

Nucleic acid tests with purchasing price parity: pipe dream or possibility

Professor Lisa Hall, *Department of Chemical Engineering and Biotechnology, University of Cambridge.*

Abstract: Hall The first sign of infectious disease may be acute fever but could be caused by viral, bacterial and protozoan infection. Diagnostics to distinguish the infections are not available in resource poor countries, mainly as a result of prohibitive cost. So, in the Philippines for example, Clinicians at the University of Santo Tomas Hospital take a comprehensive history and physical examination, when patients present with fever, to elicit symptoms and laboratory tests may be requested to confirm the suspected diagnosis, only if the patients can afford them. For most Filipinos, these tests are not done because they are unaffordable or unavailable. Thus, instead of having accurate diagnosis, the patients are more often managed based on clinical judgment and empiric broad-spectrum antibiotics are often given to cover possible bacterial sepsis, but now antibiotic resistance is so serious that in some regions of the world half the patients with pneumonia do not respond to the first-line antibiotics. A barrier to low-cost diagnostics in the developing world, arises from a value chain that spans the world, without Purchasing Power Parity (PPP). This presentation describes a first tentative step to springing out of the chain of inequalities in PPP with an approach that uses advances in synthetic biology to produce novel components and raw materials can be delivered through robust local production with parity. The outcomes are projected to be better diagnosis, while driving local enterprise, improving technological education and providing a sustainable and expandable long term development.

Acoustic Resonator sensors for medical applications

A. J. Flewitt, E. M. Wajs, G. Rughoobur, L. Garcia-Gancedo, M. de Miguel Ramos
Electrical Engineering Division, *Engineering Department, Cambridge University*

T. Mirea, M. Clement, J. Olivares, B. Diaz-Duran, J. Sangrador, E. Iborra
Universidad Politécnica de Madrid, 28040 Madrid, Spain
V. Gnanapragasam,
Academic Urology Group, Department of Surgery, Cambridge University

Abstract: Thin Film Bulk Acoustic Resonators (TFBARs) consist of a thin film of a piezoelectric material on the surface of a silicon wafer with electrodes above and below the thin film which are designed to overlap in a small area (~100 × 100 μm). By applying an a.c. electrical signal to the electrodes, an oscillating mechanical deformation can be set up in the piezoelectric material to produce an acoustic resonance with a well-defined frequency. Although the thickness of the piezoelectric thin film has primary control of the resonant frequency of the TFBAR, it is also sensitive to mass on the surface of the electrodes. By functionalising the surface of the TFBAR in a specific chemical or biological receptor, it is possible to detect particular chemical or biological species. The engineering of these devices will be discussed along with their application for the detection of prostate-specific antigens.

"Breath Biopsy®, chemicals on breath as biomarkers of disease"

Chris Hodkinson, *Vice President Business Development, Owlstone Medical Ltd, Cambridge, UK*

Abstract: Owlstone Medical are addressing two significant challenges in healthcare, people are diagnosed with cancer when it's too late to cure and expensive drugs that don't work for the majority of the people who take them. Exhaled breath contains over 1,000 Volatile Organic Compounds (VOCs) which are different for different diseases, reflect the current state of the body and are a valuable source of information about the health of an individual. Owlstone Medical are developing a breathalyser for disease which uses its small scale, low cost chemical sensor to detect sub part per billion levels of chemicals in breath and have a mission to save 100,000 lives and $1.5B in healthcare costs.

Living off the fat of the land - targeting fatty acid metabolism in the opportunistic human pathogen, Pseudomonas aeruginosa.

Stephen Dolan, Audrey Crousilles, Andre Wijaya and Martin Welch, *University of Cambridge, Department of Biochemistry.*

Abstract: For many bacterial pathogens, fine dining means fatty acids, and there is no greater connoisseur than Pseudomonas aeruginosa (PA). This organism exhibits an exquisite predilection for consuming fatty acids, which are often abundant at infection sites. In PA, fatty acids are broken down by beta-oxidation to yield acetyl CoA units (if the fatty acid contains an even number of carbon atoms) or acetyl CoA plus a molecule of propionyl CoA (if the fatty acid contains an odd number of carbon atoms). Propionyl CoA is also produced in abundance in polymicrobial infections such as those associated with cystic fibrosis, by the co-habiting microbiota. In PA, the acetyl CoA produced by beta-oxidation is routed through the glyoxylate shunt to generate glucose for biomass production, whereas propionyl CoA is metabolised through the 2-methylcitrate pathway. Inhibition of either pathway leads to cessation of growth and clearance from mammalian infection models, albeit for different reasons. In this talk, I will discuss why this is, and how we are exploiting these observations to target the glyoxylate shunt and 2-methylcitrate cycle enzymes with small molecule blockers.

Building a Google of all bacterial and viral sequence

Zamin Iqbal, *EMBL-EBI*, Phelim Bradley (Oxford Uni), Eduardo Rocha (Pasteur, Paris), Henk den Bakker (Georgia Tech)

Abstract: Most microbial genome sequence data is inaccessible to search, despite being archived centrally. Enabling search for arbitrary DNA sequence (e.g. specific mutations/genes) would unlock this huge dataset both for science and surveillance of infectious disease. I will describe a DNA search-index which can grow

without rebuilding, scaling to millions of genomes, and index a snapshot of all bacterial and viral whole-genome sequence that has ever been archived. I'll apply it to determine the host-range of plasmids, scan for all known antibiotic resistance genes, and measure changes in drug-resistance mutations in tuberculosis.

Global Genomics Surveillance of AMR

David Aanensen, *Imperial College London/Wellcome Trust Sanger Institute, Cambridge*.

Abstract: The implementation of routine whole-genome sequencing (WGS) promises to transform our ability to monitor the emergence and spread of bacterial pathogens. The Centre for Genomic Pathogen Surveillance is an initiative based at The Wellcome Genome Campus focussed on genomic epidemiology, laboratory and software engineering for global surveillance of microbial pathogens. The Centre seeks to provide genomic and epidemiological big data and tools to allow researchers, doctors and governments worldwide to track and analyse the spread of pathogens and antimicrobial resistance. Antibiotic resistance is a major international threat to public health and a global problem, which requires co-ordinated responses across multiple countries. The centre, and partners, aims to enhance local capacity for research and active genomic surveillance in the Philippines, India, Nigeria and Colombia. Through sampling and sequencing the DNA of resistant and sensitive bacteria within these strategically relevant countries, we will enhance local research capacity while feeding data into national and international surveillance for monitoring and spotting the emergence of resistance. The information from these units will ultimately help to improve the public health response of entire regions.

The Hominin STD clinic: using genetics, fossils and network analysis to reconstruct the transmission routes of sexually transmitted pathogens

Charlotte Houldcroft [1, 2,] Krishna Kumar[3] and Simon Underdown[4]
[1.] Department of Archaeology, University of Cambridge [2.] Department of Medicine, University of Cambridge [3.] Computational Geomechanics, Department of Engineering, University of Cambridge [4.] Department of Social Sciences, Oxford Brookes University

Abstract: Sequencing of primate and pathogen genomes has revealed that, while many viruses and parasites have co-evolved with their host species, there are some notable exceptions which have jumped the species barrier. I will present our recently published work (doi: 10.1093/ve/vex026) on the chimp-hominin transmission of herpes simplex virus 2 (HSV2). HSV2 is a human herpesvirus found worldwide that causes genital lesions and more rarely causes encephalitis. This virus is most common in central and east Africa, a significant region for the evolution of modern humans. Unlike HSV1 which co-speciated with modern humans, HSV2 jumped from chimps to human ancestors between 1.4 and 3 MYA, through intermediate but unknown hominin species. Using probability-based network analysis, we determined the most probable transmission path between intermediate hosts of HSV2 to the ancestors of modern humans, using paleo-environmental data on the distribution of African tropical rainforest and data on the age and distribution of hominin fossils. Our model identifies *Paranthropus boisei* as the most likely intermediate host of HSV2. I will also present some preliminary data on the gorilla-hominin transmission of pubic lice (*Pthirus pubis*). I will show how archaeology & network analysis can be brought together to show which hominins were engaging in sex, cannibalism and sleeping in other primate's beds.

Pathogen spillover at the core-matrix interface

Hamish McCallum[1], Christina Faust [2], Laura Bloomfield[3], Nicole Gottdenker[4], Andrew P. Dobson[5], Thomas Gillespie[6], and Raina Plowright[7]
[1]*Environmental Futures Research Institute and Griffith School of Environment, Griffith University*
[2]Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow
[3]Emmett Interdisciplinary Program in Environment and Resources, Stanford University
[4]Department of Veterinary Pathology, College of Veterinary Medicine, University of Georgia
[5]Department of Ecology and Evolutionary Biology, Princeton University
[6]Department of Environmental Sciences; Department of Environmental Health, Rollins School of Public Health; Program in Population, Biology, Ecology and Evolution; Emory University

[7]Department of Microbiology and Immunology, Montana State University

Abstract: Spillover of pathogens from wildlife into domestic animals and humans has caused some of the most important epidemics and pandemics in human history. Novel spillover events are often sporadic and difficult to predict. The mechanisms by which land use changes increase spillover risk are difficult to pinpoint from empirical data. We developed a multi-host model that incorporates how land conversion changes carrying capacity, alters inter- and intra-species contacts, and effects spillover risk. We developed general deterministic and stochastic two-host models for the transmission of pathogens from species in intact habitat (core species) undergoing landscape-level conversion. These models were used to predict the risk of spillover into species outside of core habitat (matrix species) and the size of outbreaks in these matrix hosts. Intermediate levels of habitat conversion had the highest probability of outbreaks in the matrix host. The largest epidemics occurred at high levels of habitat conversion, but with decreased frequency. The model also shows that reducing interspecies contacts has the greatest effect on reducing spillover as land conversion commences. Alternatively, when habitat conversion is high, surveillance in matrix hosts is important to prevent rare, but large, outbreaks. This framework can also be adapted to understand pathogen spillover into domestic animals or wild animals that have livelihood and conservation implications.

The trials and tribulations of using field deployable genomics during epidemic response

Ian Goodfellow, *Division of Virology, Department of Pathology, University of Cambridge*.

Not available.

FLASH TALKS (+ POSTER)

1. A novel strategy to target antibiotic resistant intracellular pathogens. Dr. Vikash Singh, Department of Pathology, University of Cambridge. ECR Post Doc.

2. Meningococcal carriage by age in the African meningitis belt: a systematic review and meta-analysis. Laura Cooper, Disease Dynamics Unit, Department of Veterinary Medicine, University of Cambridge. ECR PhD Student.

3. Immune Cells of Anopheles gambiae are Involved in Immunity and Memory Against Malaria Parasites. Gianmarco Raddi, Wellcome Trust Sanger Institute, University of Cambridge, National Institutes of Health. ECR PhD Student.

4. Understanding the genomes and proteomes of Mycobacteria: impacts of drug resistance and identification of drug targets. Dr. Sony Malhotra, Department of Biochemistry, University of Cambridge. ECR Post Doc.

5. Remapping the Antigenic Space via an Unconventional Competition Assay. Longzhu Shen, Department of Zoology, University of Cambridge. ECR PhD Student.

POSTERS ONLY

6. Battlefield between pathogen and host: the role of iron. Dr. Dora Pereira, Department of Pathology, University of Cambridhe. PI

7. Mitochondrial mechanisms in an ancient cancer. Máire Ní Leathlobhair Department of Veterinary Medicine, University of Cambridge. ECR PhD Student

8. Killing two viruses with one Transposon: The doc transposable element mediates anti-viral function of genes. Dr. Daniel Fabian, Department of Zoology, University of Cambridge. ECR Post Doc.

9. Optimisation of a pan-fungal qPCR assay for the molecular diagnosis of Microbial Keratitis. Linda Loterh, London School of Hygiene and Tropical Medicine, ECR Medical yr5 student.

10. Epidemiology of invasive infections caused by vancomycin sensitive and resistant enterococcal strains among oncology patients at the National Cancer Institute of Sri Lanka. Dr.Lasantha Sawani Athukorala. ECR Post Doc.

11. High-throughput bacterial phenotyping and genotyping to investigate antimicrobial action and resistance. Sushmita Sridar, Wellcome Trust Sanger Institute, Department of Medicine, University of Cambridge. ECR PhD Student.

12. Single-cell RNA sequencing to understand developmental decision making in malaria parasites. Andrew Russell, Wellcome Trust Sanger Institute. ECR PhD Student.

13. Tools for exploring the appropriateness and robustness of antigenic maps. Dr. Sarah James, Department of Zoology, University of Cambridge. Academic Clinical Fellow.

14. Multi-resistant NDM-1 and MRC-1 Klebsiella pneumoniae and Eschericia coli: phages, engineered plasmids and enzymes that could serve as novel antibacterial tools. Dr. Matti Jalasvuori. Department of Genetics, University of Cambridge. Early Career PI.

15. The use of clinical informatics to understand the epidemiology of invasive fungal infection (IFI) among hospitalised high-risk patients. Vivian Sze-To, Department of Medicine, University of Cambridge. ECR PhD Student.

16. Trachoma in Northeast Africa: A descriptive epidemiology of the scope of the problem and a review of surveillance efforts using m-Health strategies. Kian Madjedi, Wellcome Trust Sanger Institute, University of Cambridge. ECR PhD Student.

17. A new method for statistical clustering of influenza sequence data. Edyth Parker, Department of Veterinary Medicine, University of Cambridge. ECR

18. Interleukin-22 signalling promotes epithelial protection against Salmonella enterica serovar Typhimurium in human and murine intestinal organoids. Emily Lees, Department of Medicine, University of Cambridge.

19. **Cambridge Academy of Therapeutic Sciences: Entrepreneurs in Residence** Andrea Walker & Paula Frampton. CATS.

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