



ANNUAL CAMBRIDGE INFECTIOUS DISEASES MEETING OF MINDS

Programme 24th Feb 2017

Organized by Cambridge Infectious Diseases
Interdisciplinary Research Centre

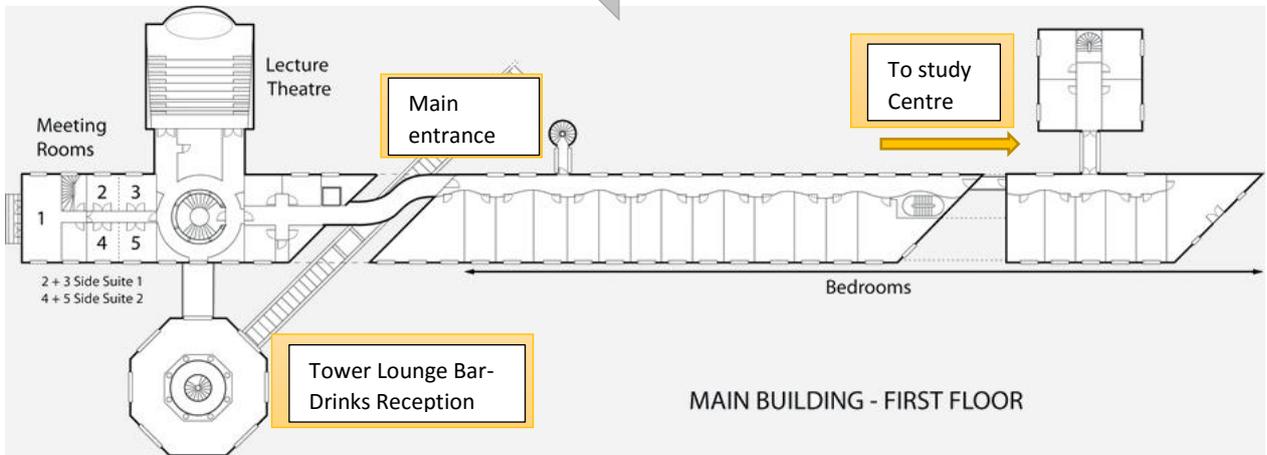
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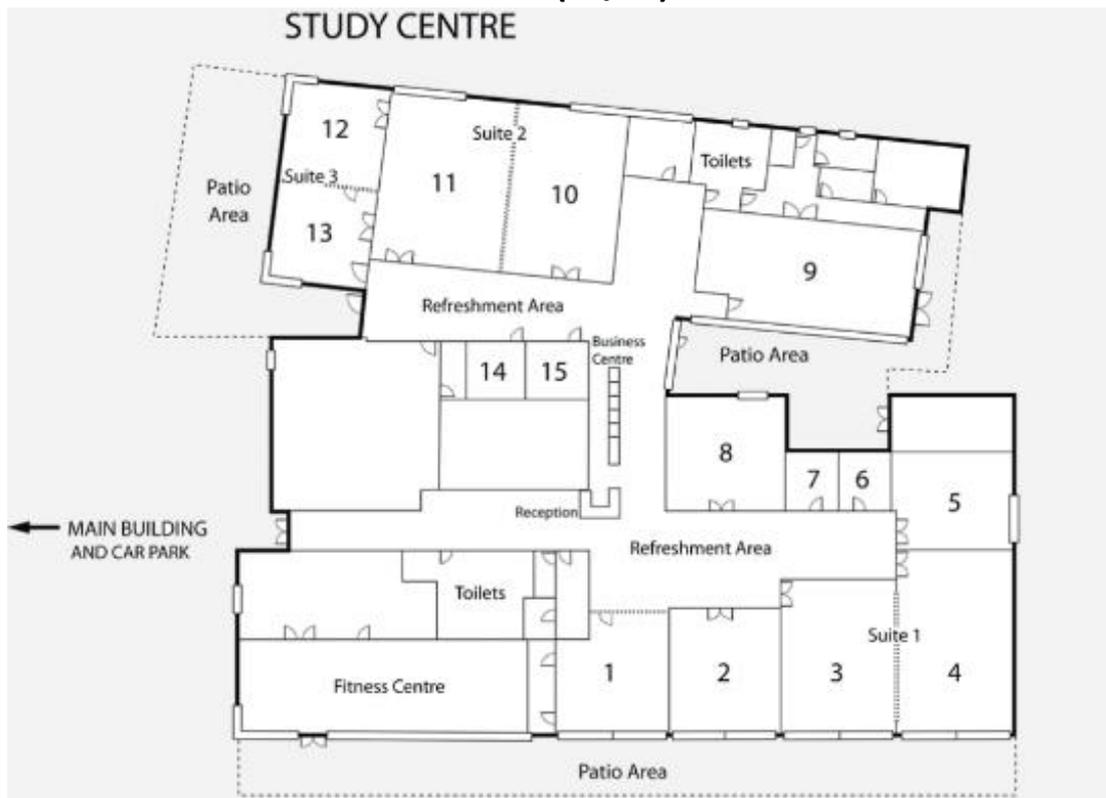
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Møller Centre - Maps

From Storeys Way, follow Churchill Rd



Suite2 (11/10)



Cambridge Infectious Diseases 6th Annual Meeting

Friday 24th February 2017, The Møller Centre, Churchill College, Cambridge

8.45	<i>Registration and Coffee</i>	
9.15	Introduction	Professor James Wood, Co-Chair of CID
Session 1: Ecology and evolution of infectious diseases		
<i>Chair: Olivier Restif, Department of Veterinary Medicine</i>		
9.30	Evolution of transmissible cancers in Tasmanian devils.	Elizabeth Murchison, Department of Veterinary Medicine
9.50	Dynamics of antibodies against henipaviruses in a captive African bat population.	Romain Garnier, Department of Veterinary Medicine
10.10	Fast-killing parasites can be favoured in spatially structured populations.	Helen Leggett, Department of Genetics
10.30	Keynote: Understanding how epidemic viruses emerge in new hosts - from molecules to landscapes.	Colin Parrish, College of Veterinary Medicine, Cornell University, USA.
11.00	Tea & Coffee -30 mins	
Session 2: Theoretical and real world modelling of infectious diseases		
<i>Chair : Julia Gog, DAMTP</i>		
11.30	Mathematical modelling of the citrus disease Huanglongbing.	Andrew Craig, Department of Plant Sciences
11.50	Facilitators of the geographic transmission of pandemic A/H1N1 influenza in the United States.	Stephen Kissler, DAMTP
12.10	Modelling the within-host adaptation of the influenza virus: measuring the rate of reassortment in a single human host.	Chris Illingworth, Department of Genetics
12.30	LUNCH- 60 mins	
Session 3: Neglected Infectious Diseases		
<i>Chair : Peter Bull, Department of Pathology</i>		
1.30	Immuno-epidemiological investigations into immunity to schistosomes.	Shona Wilson, Department of Pathology
1.50	Social network interventions for mass drug administration.	Goylette Chami, Department of Land Economy
2.10	The 50 Helminths genomes project: searching for targets amongst one million new genes.	Matthew Berriman, Wellcome Trust Sanger Institute
2.30	Flash Talks 5 x 4 mins	See Programme Detail
3.00	Tea & Coffee- 40 mins	Poster session
Session 4: Novel Interventions for prevention and management of infectious diseases		
<i>Chair: Piero Mastroeni, Department of Veterinary Medicine</i>		
3.40	Translating microbial genomics into clinical practice.	Estée Török, Department of Clinical Medicine
4.00	The Ageing Immune System and Vaccination.	Danika Hill, Babraham Institute
4.20	The impact of MenAfriVac in the African meningitis belt.	Caroline Trotter, Department of Veterinary Medicine
4.40	Closing Speech	Lydia Drumright, Co-Chair Cambridge Infectious Diseases
5.00	Drinks & Canapés Reception	
		The Tower Lounge Bar

Programme Detail

Flash Talks

A new session incorporating five short 4 min talks, selected from talk/poster submissions. Please see Poster & Flash Talk abstracts.

1. Human parainfluenza 3: an effective in vitro model for therapeutic candidates. Anna Smielewska
2. How pathogenic bacteria subvert host ubiquitin signalling. J N Pruneda
3. Monitoring influenza epidemics from routinely collected severe case data. A. Corbella
4. Single Cell transcriptomics of malaria parasites. Adam Reid.
5. Single Cell Transcriptomics Using Drop-seq. Andrew Russell.

Talk Abstracts

1. Evolution of transmissible cancers in Tasmanian devils

Elizabeth Murchison, Department of Veterinary Medicine, University of Cambridge.

Tasmanian devils are marsupial carnivores endemic to the Australian island of Tasmania. Tasmanian devils are considered endangered due to the emergence of a transmissible facial cancer that is spread between animals by the transfer of living allogeneic cancer cells by biting. This cancer, known as DFT1, was first observed in 1996, and has spread through devil populations across most of the island. In 2014, a second transmissible facial cancer, DFT2, was observed in devil populations in Tasmania's south-east. Considering the rarity of transmissible cancers in nature, it is surprising to find two transmissible cancers in the same species. We have reconstructed the genomes of both DFT1 and DFT2, and are using these to understand the origins and evolution of transmissible cancers in Tasmanian devils.

2. Dynamics of antibodies against henipaviruses in a captive African bat population.

Romain Garnier, Department of Veterinary Medicine, University of Cambridge.

Understanding the dynamics of immunity is crucial from a disease ecology perspective, particularly at the individual level. This is particularly true in species deemed likely to harbour zoonotic pathogens such as bats. However this also requires the possibility to recapture individuals, which can be challenging in the wild. An alternative is to use captive populations kept in conditions similar to their wild counterparts. With this approach, it was shown that levels of immunity against henipaviruses varied seasonally, potentially in association with the pregnancy in female bats. Here using long term data collected over several years of monitoring and short term data collected weekly for three months, we study the dynamics of anti-henipaviruses antibodies in captive African straw-coloured fruit bats. We show that bats can maintain antibodies, and potentially infection, for a long time in captivity. We also analyse the variations of antibody levels in females in the weeks prior to parturition in relation to body condition. We discuss the importance of these dynamics for the modelling of the circulation of viruses in bat populations in which reproduction results in seasonal influx of susceptible individuals potentially protected by maternal antibodies.

3. Fast-killing parasites can be favoured in spatially structured populations

Helen Leggett, Department of Genetics, University of Cambridge.

It is becoming increasingly clear that the evolution of infectious disease is influenced by host population structure. Theory predicts that parasites should be more 'prudent'—less transmissible—in spatially structured host populations. However, here I (i) highlight how low transmission, the phenotype being selected for in this context, may also be achieved by rapacious host exploitation, if fast host exploitation confers a local, within-host competitive advantage and (ii) test this novel concept in a bacteria–virus system. I found that limited host availability and, to a lesser extent, low relatedness favour faster-killing parasites with reduced transmission. By contrast, high host availability and high relatedness favour slower-killing, more transmissible parasites. Our results suggest high, rather than low, virulence may be selected in spatially structured host–parasite communities where local competition and hence selection for a within-host fitness advantage is high.

4. Keynote: Understanding how epidemic viruses emerge in new hosts – from molecules to landscapes.

Colin Parrish. Cornell University, College of Veterinary Medicine/Baker Institute.

The emergence of viruses as epidemic pathogens in new hosts are rare events, but the outcomes can be dramatic and severe. However, we still lack a basic understanding of the major events that are involved. Here I will provide a summary, with some examples, of what appear to be the key events allowing successful inter-host transfers and spread. Factors that may influence emergence include the interactions of the virus with the host cell receptor, the interactions within the cells and tissues of the different hosts, replication efficiency; route of transmission and stability, and the density and connectedness of the host populations. As well as general examples, some cases to be described include the viruses that my laboratory has been studying – the canine parvovirus, and H3N2 and H3N8 canine influenza viruses, all of which have emerged to cause epidemics in dogs after transfer from other hosts.

5. Mathematical modelling of the citrus disease Huanglongbing

Andrew P. Craig, Nik J. Cunniffe, Matthew Parry, Francisco F. Laranjeira, Christopher A. Gilligan. Department of Plant Sciences, University of Cambridge.

In managing plant diseases, especially those of perennial and plantation crops, there is often a tension between regulators seeking to destroy infected plants to prevent the further spread of the disease and growers seeking to retain infected plants to maximise their yields. This has been the case for Huanglongbing ('citrus greening') in Brazil. In an effort to prevent Huanglongbing's spread, the Brazilian government has regulated that if 28% of an orchard is found to be symptomatic then the whole orchard will be destroyed. This rule is based on the assumption that a 28% detectable prevalence is likely to mean that the actual prevalence is 100%. We use a mathematical model to evaluate this assumption, and show that the relationship between detectable and actual levels of infection is much wider than allowed for in the Government scheme. There is a high probability that orchards with levels of symptomatic plants substantially below 28%, have a very high (> 90%) prevalence of infected plants. Rather than setting an arbitrary prevalence threshold that would be considered acceptable by both growers and the regulator, future regulations should focus on co-ordinated spraying amongst owners to control the insect host of HLB on a regional level.

6. Seasonal variation in the geographic transmission of influenza

Stephen Kissler, Julia Gog, Vivek Charu, Cecile Viboud, Lone Simonsen, Ottar Bjornstad, Bryan Grenfell. DAMTP, University of Cambridge.

Outbreaks of influenza in the United States between 2003 and 2009 varied widely in geographic speed and structure. Detailed geo-tagged data from ICD9-coded medical claims records provide a unique glimpse into the trajectories of these outbreaks. We use a mechanistic mathematical model to characterise the geographic transmission of the 2003-2004 A/Fujian (H3N2) influenza outbreak, the 2007-2008 mixed-strain outbreak, and the 2009 A/H1N1 pandemic influenza outbreak. Model fits provide insight into the relative importance of various drivers of transmission, such as mobility and the mixing of children in schools, between the three outbreaks. Then, by partitioning each outbreak into a set of overlapping "basins of infection", where transmission can be traced back to a distinct geographic introduction site, further differences between the outbreaks emerge.

7. Modelling the within-host adaptation of the influenza virus: measuring the rate of reassortment in a single human host

Chris Illingworth. Department of Genetics, University of Cambridge.

Reassortment is an important factor in the evolution of the influenza virus due to its potential to create novel combinations of viral segments. However, while reassortment has been extensively studied in small animal hosts, studies examining the same parameter in human hosts have been lacking. We here characterise the reassortment rate during influenza infection within a single human host. Viral sequence data were collected at regular intervals from thirteen patients across two challenge studies. Using an evolutionary model, we identify correlated changes in allele frequencies between variants on different viral segments, suggestive of an effective rate of reassortment that is much lower than has been seen in animal studies. Further, and in agreement with previous work, we find evidence that the rate of apparent reassortment is linked to the dose of virus received by the patient; together these results suggest a meta-population model of within-host influenza evolution, whereby discrete sub-populations evolve in spatially separated locations.

8. Immuno-epidemiological investigations into immunity to schistosomes

Rebecca Oettle, Edridah Tukahebwa, Colin M Fitzsimmons, David W Dunne and Shona Wilson. Department of Pathology, University of Cambridge.

Schistosomiasis, a neglected tropical disease (NTD) caused by infection with trematode helminths of the genus *Schistosoma*, is a debilitating disease, second in importance amongst eukaryotic infections only to malaria. Since the mid 2000s, a W.H.O. roadmap, strengthened by the London Declaration on NTDs, of which we have recently celebrated the five year anniversary, have brought control of this parasite higher on the global health agenda; with elimination as a public health problem, and even in some foci, elimination of infection, being called for in the latest World Health Assembly resolution on NTDs. The design of control programmes for schistosomiasis is based upon reproducible epidemiological patterns, in which children carry the burden of infection, regardless of exposure to the parasite, with development of immunity being apparent in adults. Crucially, the current models of infection dynamics on which the potential success of these programmes is predicted, lack relevant immunity parameters. The role of force of transmission in endemic areas, the

targets of immunity, and how these relate to the slow development of immunity will be discussed, along with potential implications for control programme success.

9. Social network interventions for mass drug administration

Goylette Chami, Andreas Kontoleon, Erwin Bulte, Alan Fenwick, Narcis Kabatereine, Edridah Tukahebwa, David Dunne. Department of Land Economy/Department of Pathology, University of Cambridge.

Mass drug administration (MDA) is the mainstay of treatment delivery for neglected tropical diseases. MDA entails the communitywide distribution of preventive chemotherapies to at-risk populations. Single-dose treatments are required annually or biannually due to imperfect drug efficacy and rapid reinfection. Community-based MDA is a process whereby two individuals are selected by their community to deliver medicines to all eligible village members. It is the only method of administering treatment to both children and adults at risk of helminthic infections. We explore how social networks can be used to evaluate MDA implementation and to design novel interventions for increasing treatment coverage. A routine round of community-based MDA for *Schistosoma mansoni*, hookworm, and lymphatic filariasis was tracked in 17 villages for 16,357 individuals. Friendship networks, socioeconomic characteristics, and treatment outcomes (praziquantel, albendazole, and ivermectin) were collected. Here we show that community medicine distributors (CMDs) with tightly-knit (clustered) friendship connections achieve the greatest reach and speed of treatment coverage. In friendship networks, clustering occurs when the person of interest has two friends who also are friends. Hence, tightly knit, close friends determine the performance of CMDs. Importantly, we demonstrate that clustering predicts treatment diffusion through social networks whilst centrality, e.g. the number of connections, is unrelated to diffusion. Clustering should be considered when selecting seed nodes for large-scale treatment campaigns.

10. Matthew Berriman - not available

11. Translating microbial genomics into clinical practice

Dr Estée Török, Department of Medicine, University of Cambridge.

The ability to perform rapid, high-throughput microbial whole-genome sequencing (WGS) using bench-top platforms represents a step-change in capabilities for diagnostic and public health microbiology laboratories. As the cost of sequencing continues to decline, the challenge will be to define how best to apply this technology in clinical microbiology. I will review the potential clinical applications of WGS (e.g. outbreak investigation, rapid diagnosis of multidrug-resistant organisms, surveillance of antimicrobial resistance and emerging pathogens) and discuss the challenges of implementation.

12. The Ageing Immune System and Vaccination

Danika L. Hill¹, Edward J. Carr¹, James Dooley², Wim Pierson¹, Adrian Liston², Michelle A. Linterman¹ Babraham Institute, Cambridge. ²Department of Microbiology and Immunology, University of Leuven.

Vaccination is one of the most successful, cost-effective interventions for reducing infection-related morbidity and mortality worldwide. With age, function of the immune system declines, rendering older people more susceptible to infections and less able to benefit from vaccination. Indeed, improving vaccine efficacy is key to reducing infection-related morbidity in older people. To date, the complexity of the ageing process has hindered attempts to fulfill this ambition, and there is a critical need to better understand the underlying biology. With a focus on T cell, B cells and the germinal centre, we have identified multiple cellular changes that associate with ageing and poor vaccination responses.

13. The impact of MenAfriVac in the African meningitis belt.

Caroline Trotter, Department of Veterinary Medicine, University of Cambridge.

Since December 2010, nearly 300 million people living in the African meningitis belt have been immunised with MenAfriVac® – an affordable meningococcal group A conjugate vaccine. Mass campaigns targeting 1-29 year olds have been rolled out across the belt, which stretches from Senegal in the west to Ethiopia in the east, with the aim of eliminating meningitis epidemics. Working with the MenAfriCar Consortium and the World Health Organisation, I have been researching the impact of these campaigns. Studies in Chad demonstrated a remarkable effect of vaccination on both meningitis incidence and the prevalence of asymptomatic pharyngeal carriage. Analysis of surveillance data from 9 different countries shows an overall 60% decline in suspected meningitis cases, 60% decline in the risk of districts reaching the epidemic threshold and >99% decline in confirmed cases of group A disease. Future challenges include the maintenance of protection against group A through appropriate long term immunisation strategies and the residual threat of epidemics due to other meningococcal serogroups.

Poster Exhibition & Flash Talks

- 1. MUUI- Makerere University and UVRI Infection and Immunity Research collaboration**
Corinna Alberg Pathology, University of Cambridge.
- 2. THRiVE initiative- Training Health Researchers into Vocational Excellence**
Corinna Alberg, Pathology, University of Cambridge

Two posters summarising the activities off the MUUI plus and THRiVE initiatives which form major components of the Cambridge Africa Programme. The MUUI programme specifically focuses on supporting research excellence in Uganda in the fields of immunity and infection. We would like to publicise the Cambridge Africa programme to infectious disease researchers in Cambridge and interest them in getting involved with the programme.

- 3. Human parainfluenza 3: an effective in vitro model for therapeutic candidates**
Anna Smielewska, Edward Emmott, Hamid Jalal, Ian Goodfellow. Pathology(virology), University of Cambridge. (Flash Talk)

Human Parainfluenza Virus 3 (HPIV3) is an enveloped, single-stranded negative-sense RNA virus, member of the family Paramixoviridae. with a significant impact in the transplant and

immunocompromised cohort. At present there is no effective antiviral or vaccine for the management of HPIV infection. This project centers on creating an effective model for the testing of potential inhibitors of HPIV3 using a robust cell culture system and low passage clinical strains as well as the MK9 laboratory strain obtained from Public Health England. The suitability of this system has been evaluated by monitoring the plaque phenotype and sequence evolution of the above strains. A number of inhibitors including zanamivir, favipiravir, epigallocatechin gallate (EGCG) and ribavirin have been trialed using diverse techniques assessing entry and growth inhibition of the virus as well as their combined effects. These drugs have been found to be effective in the laboratory strain and have also been trialed on sequenced clinical isolates from a diverse range of patients.

4. How pathogenic bacteria subvert host ubiquitin signalling.

Pruneda JN, Komander D. MRC Laboratory of Molecular Biology. (Flash Talk)

Pathogenic bacteria rely upon secreted effector proteins to manipulate host signaling pathways, often in creative ways. The CE-clan proteases, specific hydrolases for ubiquitin-like modifications (SUMO, NEDD8) in eukaryotes, can reportedly serve as bacterial effector proteins with deSUMOylase, deubiquitinase, or even acetyltransferase activities. We here characterize bacterial CE effectors, revealing K63-linkage-specific deubiquitinases in Salmonella, Escherichia and Shigella, a ubiquitin and SUMO cross-reactive enzyme in Xanthomonas, and dedicated acetyltransferases in Yersinia and Legionella. We also identify enzymes that perform deubiquitination and acetylation via the same catalytic triad, in a remarkable example of 'protein moonlighting'. Eight crystal structures, including complexes with Ub/Ubl or Coenzyme A, explain substrate and K63-linkage specificity, as well as acetylation activities, and redefine relationships across the CE clan. We further show that accessory domains dictate regulatory effects such as subcellular localization, as exemplified by a ubiquitin-binding accessory domain in Salmonella Typhimurium SseL. Our work both highlights and explains the functional adaptations observed among diverse CE-clan proteins.

5. Monitoring influenza epidemics from routinely collected severe case data

A. Corbella [1], X-S Zhang [2], P. Birrell [1], N. Boddington [2], A. M. Presanis [1], R. Pebody [2], and D. De Angelis [1,2] - [1] MRC Biostatistics Unit, University of Cambridge, School of Clinical Medicine [2] Public Health England (Flash Talk)

Influenza remains a significant burden on health systems. Public health responses should be tailored to the size and timing of any ongoing outbreak. Data on severe cases of influenza in England, which are reported weekly to Public Health England, have the potential to provide powerful information for inferring and predicting the features of seasonal and pandemic influenza. We propose an epidemic model which links the underlying transmission dynamic process with the observational process. Within a Bayesian framework, we infer the parameters of the epidemic model for each seasonal outbreak from 2012 to 2015, including the effective reproduction number, initial susceptibility, the probability of ICU given infection and the attack rate. The epidemic model is also implemented in real time to assess whether early forecasting is possible. Simulation exercises show that the epidemic model is able to forecast the development of seasonal outbreaks once data from the first three months are available. This work suggests that severe case data may be effectively exploited to estimate epidemiological characteristics and to predict the further evolution of an epidemic. Moreover, the results obtained motivate the formulation of a more general evidence synthesis analysis on the joint dynamics of transmission and severity over seasonal influenza.

6. Single-cell transcriptomics of malaria parasites

Adam J. Reid, Arthur M. Talman, Hayley M. Bennett, Ana R. Gomes, Mandy Sanders, Christopher J. R. Illingworth, Oliver Billker, Matt Berriman, Mara K. N. Lawniczak. Wellcome Trust Sanger Institute. (Flash Talk)

Single-cell RNA-sequencing (scRNA-seq) offers the opportunity to examine transcriptional variation within populations of seemingly homogeneous cells. We developed a method to assess variability across individual malaria parasites, and used scRNA-seq to uncover variation in unicellular eukaryotic organisms for the first time. We find that gene families critical for immune evasion in the mammalian host are also transcribed in sex-specific manners during transmission to the mosquito.

7. Single Cell Transcriptomics Using Drop-seq

Andrew Russell, Lia Chappell, Thierry Voet and Julian Rayner. Wellcome Trust Sanger Institute. (Flash Talk)

Drop-seq is a novel droplet microfluidic technology that is capable of sequencing the transcriptome of thousands of single cells in a single run, increasing the throughput by 2 orders of magnitude compared to many FACS or micromanipulation based methods. This allows single-cell analysis at a fraction of the cost that previous methods such as Fluidigm C1 autoprep permitted (~ 10p/cell). Developments in this technology at the Sanger Institute to date will be presented along with its application to generating single-cell transcriptomic data from malaria-causing Plasmodium parasites.

Speaker Bios

	<p>Elizabeth Murchison is Reader in Comparative Oncology and Genetics at the University of Cambridge, Department of Veterinary Medicine. Her laboratory, the Transmissible Cancer Group, studies the genetics, evolution and host interactions of clonally transmissible cancers in dogs and Tasmanian devils. Elizabeth performed her undergraduate studies at the University of Melbourne and was awarded her PhD from Cold Spring Harbor Laboratory in 2007. After periods of postdoctoral research at the Australian National University and the Wellcome Trust Sanger Institute, she joined the University of Cambridge in 2013. In 2014 she was the recipient of the Cancer Research UK Future Leaders in Cancer Research Award.</p>
	<p>Romain Garnier is a veterinarian, graduated from Nantes Veterinary School in France (2008) and a disease ecologist. I defended my PhD in 2011, having worked on the evolutionary ecology of the transfer of maternal antibodies with Dr. Thierry Boulinier and Dr. Sylvain Gandon. I then joined the group of Pr. Andrea Graham at Princeton University in September 2012 and worked on the nutritional and immunological ecology</p>

	<p>of a wild Soay sheep population. I joined Cambridge in November 2015, having received an AXA Postdoctoral Fellowship to work with Dr. Olivier Restif and Pr. James Wood on African fruit bats immunity.</p>
	<p>Helen Leggett did her MbiolSci at the University of Sheffield with Mike Boots working on honeybee viruses before moving to Oxford for my Dphil with Angus Buckling and Stu West. My Dphil on social evolution and virulence in parasites was awarded the Thomas Henry Huxley Award and Marsh Prize by the Zoological Society of London for the best PhD thesis in the UK in the general area of Zoology. Helen is currently a research fellow for the Royal Commission for the Exhibition of 1851, based in Frank Jiggin's Lab, Department of Genetics (Cambridge), where she is continuing her research on the evolution of parasite virulence by way of experimental evolution with bacteriophage, bacteria and C.elegans, in addition to comparative analyses.</p>
	<p>Colin Parrish is the John M. Olin Professor of Virology in the Baker Institute for Animal Health, at the College of Veterinary Medicine at Cornell University, and currently the Fulbright Visiting Professor at the University of Glasgow. He grew up in New Zealand, and has a BSc (Hons.) from Massey University in Palmerston North, New Zealand, and then gained a Ph.D. in Virology from Cornell University. He completed postdoctoral studies of flaviviruses at Monash University with Drs. Ed Westaway and Peter Wright. He has been on the faculty at Cornell University since 1988. His research focuses on the study of viruses, of virus structures, and the evolution of new viral host ranges. The model systems that his laboratory investigates are the canine parvovirus, which is a cat virus that transferred into dogs in the 1970s to cause a global pandemic of disease, and the H3N8 and H3N2 canine influenza viruses, which transferred from horses or ducks to dogs to cause two epidemics of canine disease that are still continuing. His studies are also examining the general basis of viral emergence, in particular the risk factors associated with origins of new viruses in humans.</p>
	<p>Andrew Craig did his PhD at the University of New South Wales in Sydney, Australia, applying mathematical and computational models to human and animal diseases. Since 2015 he has been a Postdoctoral Research Associate working with Chris Gilligan in the Department of Plant Sciences Epidemiology and Modelling Group. His research is currently focussed on spatial modelling of the plant diseases Huanglongbing and Phytophthora.</p>

	<p>Stephen Kissler is a PhD candidate in the Department of Applied Mathematics and Theoretical Physics. He holds BS and MS degrees in Applied Mathematics from the University of Colorado Boulder. He uses statistical models to trace the geographic spread of infectious diseases, and is especially interested in unifying epidemiological and genetic data to make inferences. He currently focuses on the 2009 A/H1N1 influenza pandemic in the United States.</p>
	<p>As an undergraduate, Chris Illingworth studied maths in Cambridge before moving into the world of computational chemistry, studying polarisation effects in molecular models of drug binding. Via postdoc positions at the University of Oxford and the Wellcome Trust Sanger Institute he developed an interest in the potential of sequence data to provide insights into rapid evolutionary processes. Since 2013 he has led a group in the Department of Genetics developing population genetic methods that produce new insights into pathogen evolution.</p>
	<p>Shona Wilson is a Lecturer in Parasitology Her groups' research interests concern the interaction between helminth infections and the human host, in particular the mechanisms of immunity to, and immunopathology associated with, schistosome infections. Major emphases include the ecology of transmission and its influence on the development of human immunity, and the role of co-infection in modulating the human host response to these neglected diseases of great public health importance.</p>
	<p>Goylette (Juliette) Chami is a Junior Research Fellow in medical sciences at King's College, Cambridge and an Isaac Newton Trust Fellow in global health economics. Her work combines field biology with quantitative and computational approaches from the physical and social sciences. Currently, she is developing social network interventions to improve <i>en masse</i> treatment for intestinal schistosomiasis and hookworm infections.</p>
	<p>Matthew Berriman leads a team that is undertaking major projects to sequence the genomes of parasites that are responsible for diseases prevalent throughout the developing world and poorer countries, including malaria and other neglected tropical diseases with a particular focus on helminths such as Schistosomes, tapeworms, roundworms, hookworms, threadworms and whipworms. This work helps shed light on how these parasites live and grow, and could eventually lead to the development of new and specific medicines</p>

	<p>to help eradicate the parasites and the diseases they cause.</p>
	<p>Dr Estée Török qualified in Medicine from the Universities of Oxford and London. From 2004 to 2008 she was a Wellcome Research Training Fellow at the Oxford University Clinical Research Unit in Vietnam, where she did her PhD research in HIV and tuberculosis. Appointed as a Consultant in Infectious Diseases at Addenbrooke’s Hospital in 2009, she set up two new clinical services – a bacteraemia consult service and an outpatient parenteral antibiotic therapy (OPAT) service. In 2011 she joined Professor Peacock’s research group at University of Cambridge, and was awarded a Clinician Scientist Fellowship by the Academy of Medical Sciences and the Health Foundation in 2014. Her current research focuses on translating microbial genomics from a research tool into clinical practice, and she has a particular interest in multidrug-resistant organisms and healthcare-associated infections.</p>
	<p>Dr Danika Hill is a Postdoctoral research scientist in the Laboratory of Lymphocyte Signaling and Development at the Babraham Institute, Cambridge. Danika joined the Linterman group in 2015 after completing a PhD in malaria immunology at the University of Melbourne. Her current research interests are in T cell-dependent antibody responses to vaccination, with a particular focus on the cellular and molecular factors responsible for reduced vaccine efficacy in the elderly.</p>
	<p>Caroline Trotter is a Senior Lecturer in Epidemiology at the University of Cambridge and an honorary epidemiologist at Public Health England. Her research examines the potential and actual impact of immunisation using a range of methods from classic epidemiology to mathematical modelling and health economics. Her work has been used to inform national and (as a consultant to the World Health Organisation) international vaccine policy. While much of her research is focussed on meningococcal disease and carriage in the UK and Africa, she also has current projects on group B streptococcus, pneumococcus, norovirus and rabies.</p>

Notes
