



WHO Collaborating Centre for **Modelling, Evolution** and **Control** of **Emerging Infectious Diseases**

In 2012, the University of Cambridge received designation as a World Health Organization (WHO) Collaborating Centre. This designation was primarily in recognition and support of the contribution to public health by the Centre for Pathogen Evolution, in the Department of Zoology. The activities of the Collaborating Centre have subsequently grown to include numerous other groups throughout the University.

Located in the Department of Zoology at the University of Cambridge, the Centre for Pathogen Evolution conducts highly translational scientific research focused on improving our understanding and ability to predict pathogen evolution in humans and other animals. As part of this work we curate a global database of antigenic information, and working with computational, mathematical and laboratory tools for pathogen surveillance and evaluation, we provide essential support to WHO activities in influenza vaccine strain selection, and emergency response for time-critical public health questions.

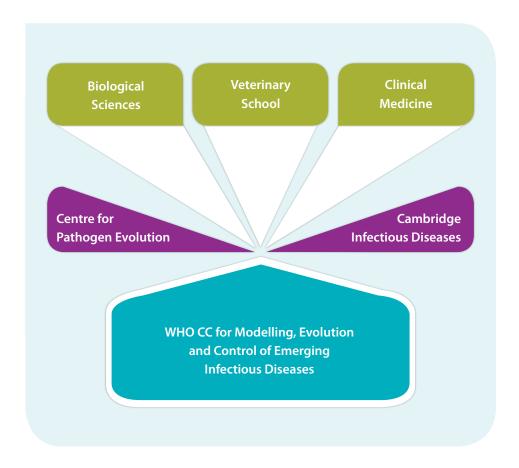
The members of the Centre involved in this work are: Eugene Skepner, David Burke, Leah Katzelnick, Judy Fonville, Ana Mosterin, Gene Selkov, Nicola Lewis, Sarah James, Ramona Mogling, Colin Russell and Derek Smith.



A synergy of academic research, public health and interdisciplinary science

Our WHO Collaborating Centre is in the privileged position of collaborating with Public Health from an academic setting. A tremendous synergy exists between influenza public health and influenza research, due to the necessarily sophisticated surveillance and decision-making processes already in place to track the evolution of influenza viruses and update the influenza virus vaccine. The WHO global influenza surveillance network is the most extensive for any pathogen and provides close to a real-time picture of the global evolution of influenza virus. The detailed insight gained into the dynamics of influenza evolution has informed and expanded our research activities to examine new horizons in public health.

We are a dynamic multidisciplinary team of virologists, immunologists, computational biologists, structural biologists, veterinarians, clinicians, mathematicians, and computer scientists. Alongside a network of world-class collaborators, we combine scientific and experimental excellence to apply antigenic cartography to large complex data sets in a critical public health setting.



Drawing on research groups and institutes within the University's Veterinary, Biological and Clinical Schools, our Collaborating Centre also provides the WHO with expertise in pandemic response, modelling of infectious and vector-borne diseases, clinical management, immunopathology, international/travel medicine, enteroviruses and other emerging encephalitides.

Antigenic Cartography: Mapping the Evolution of Pathogens

Antigenic cartography is a computational and mathematical tool for the analysis of binding assay data, providing a quantification and visualisation—called antigenic maps—of antigenic data. Although its utility was first established in both research and public health in the context of the influenza virus, the techniques of antigenic cartography have subsequently been applied to many other pathogens.

The Haemagglutination Inhibition Assay

Antigenic differences between influenza viruses are routinely measured using the haemagglutination inhibition (HI) assay. The HI assay is a binding assay based on the ability of haemagglutinin (HA), the surface glycoprotein of the influenza virus, to agglutinate red blood cells, and the complementary ability of animal antisera raised against the same or related influenza strains to block this agglutination. Thus an HI titre gives information about the affinity of an antiserum for a virus strain. One can interpret a titre value as a rough measure of distance between the antiserum and the virus. We use this data in an algorithmic way to aid understanding of the evolutionary dynamics of influenza.

Although the HI assay has provided essential antigenic difference information on influenza viruses for over 60 years, HI data are difficult to interpret quantitatively. Assays of the same strain and antiserum will occasionally produce different values, even in the same laboratory.



and the Dutch National Influenza Centre.

There have been attempts to quantify and visualise such binding assay data, but none have been used widely or persistently, nor have they provided an underlying theory that resolves paradoxes in the data. As a result, these data have almost universally been interpreted by eye, and have been considered reliable enough for judging only large antigenic differences. In the case of influenza virus, this means differences of sufficient magnitude to necessitate an update of the vaccine strain (an extensive and expensive procedure).

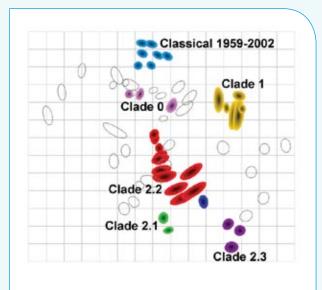
Antigenic Maps

Antigenic cartography is the process of applying mathematical, computational, and statistical techniques to challenging antigenic binding assay data to create antigenic maps. These are not maps in the geographical sense, but in a biological sense: they provide a spatial layout of assay components (virus strains and antisera in the case of influenza), allowing the precise measurement of distances and directions amongst components. This gives a visualisation of the underlying data and, more importantly, provides a concrete mathematical foundation for the quantitative analysis of antigenic data.

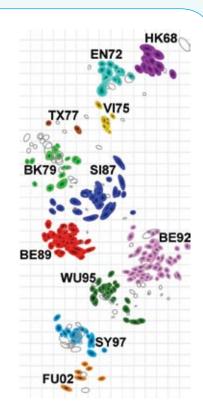
In time, we expect that antigenic maps will become as ubiquitous in the analysis of antigenic data as phylogenetic trees are in the analysis of genetic data. However, importantly, antigenic maps differ from genetic analysis because they reflect antigenic properties of pathogens. While genetic analysis has provided major insights, these insights are of greater impact when related to phenotypic traits. Although antigenic maps themselves are of direct inherent utility—providing intuitive visualisations of assay data, as used to inform the WHO influenza vaccine strain selection process—they also provide a general characterisation that can inform and direct genetic analysis, and make such analysis more immediately applicable.

For example, there is a close relationship between genetic and antigenic change in human influenza A(H3N2) virus, but genetic distance alone is sometimes an unreliable predictor of antigenic distance. Single amino acid changes have been shown to cause large changes in the binding properties of virus strains. Antigenic maps can show precisely when large movements in the antigenic space result from minimal genetic change. Antigenic cartography therefore offers an improved understanding of genetic and antigenic evolution.

Antigenic maps allow us to make sense of vast amounts of difficult binding assay data.
One can see at a glance the global picture of decades of viral evolution.



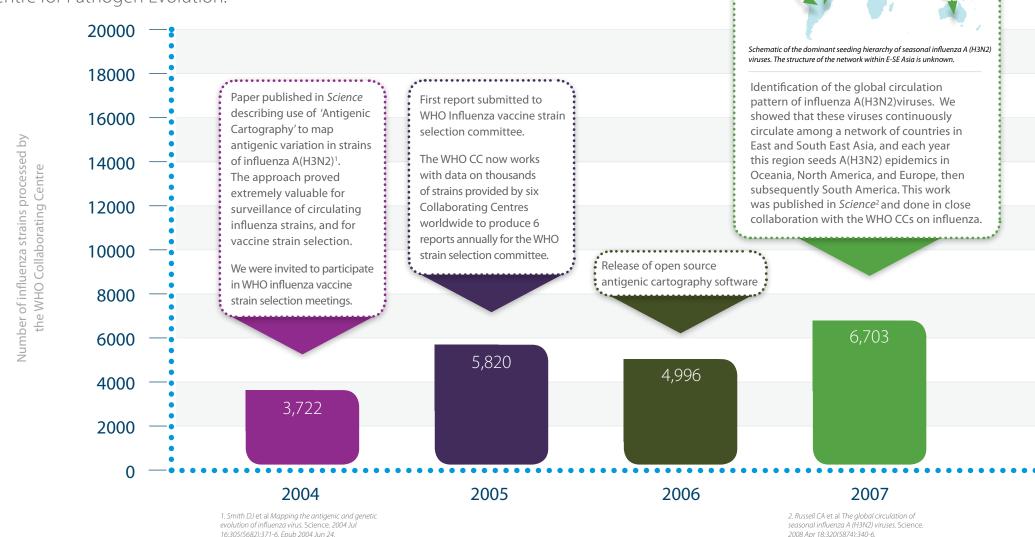
Antigenic map showing antigenic variation between influenza A(H5N1) strains isolated up to 2006.

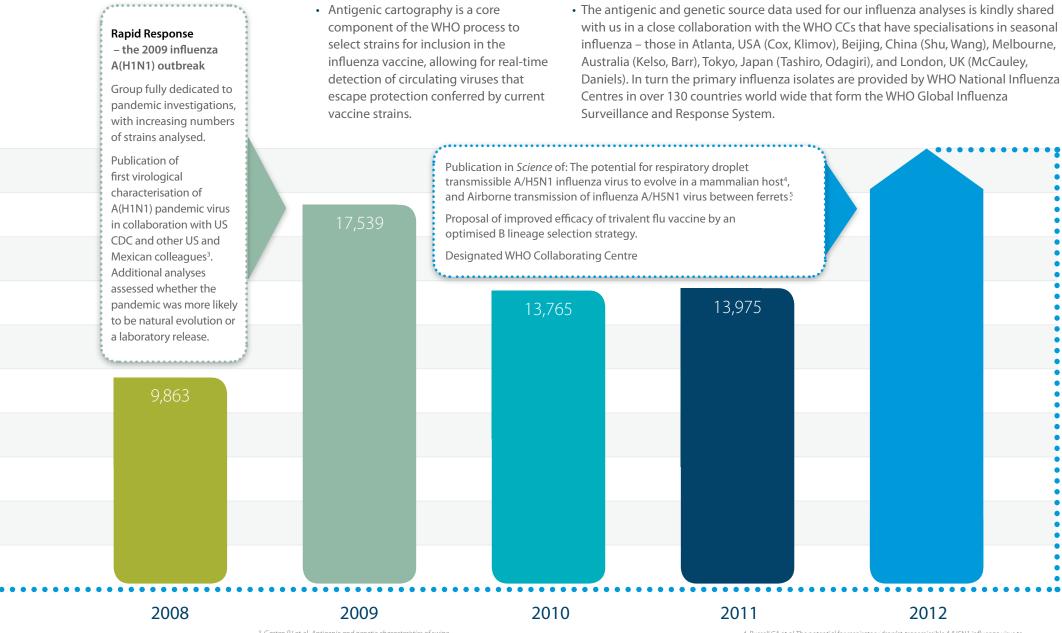


The first antigenic map of the influenza A(H3N2) virus from 1968 to 2003. Each strain is coloured to represent the antigenic cluster to which that strain belongs, while the antisera used in the HI assays are shown as uncoloured open shapes. Clusters are named with two letters referring to the location of the first isolation and two digits refer to year of isolation. Both the vertical and horizontal axes represent antigenic distance; this is similar to the way both axes on a geographical map represent geographic distance.

From academic research to essential provision for global public health

Graph showing number of influenza strains analysed annually by the Centre for Pathogen Evolution.



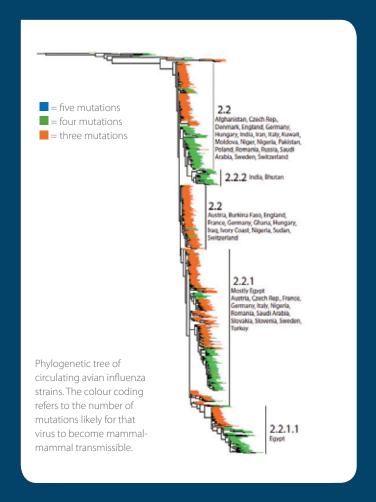




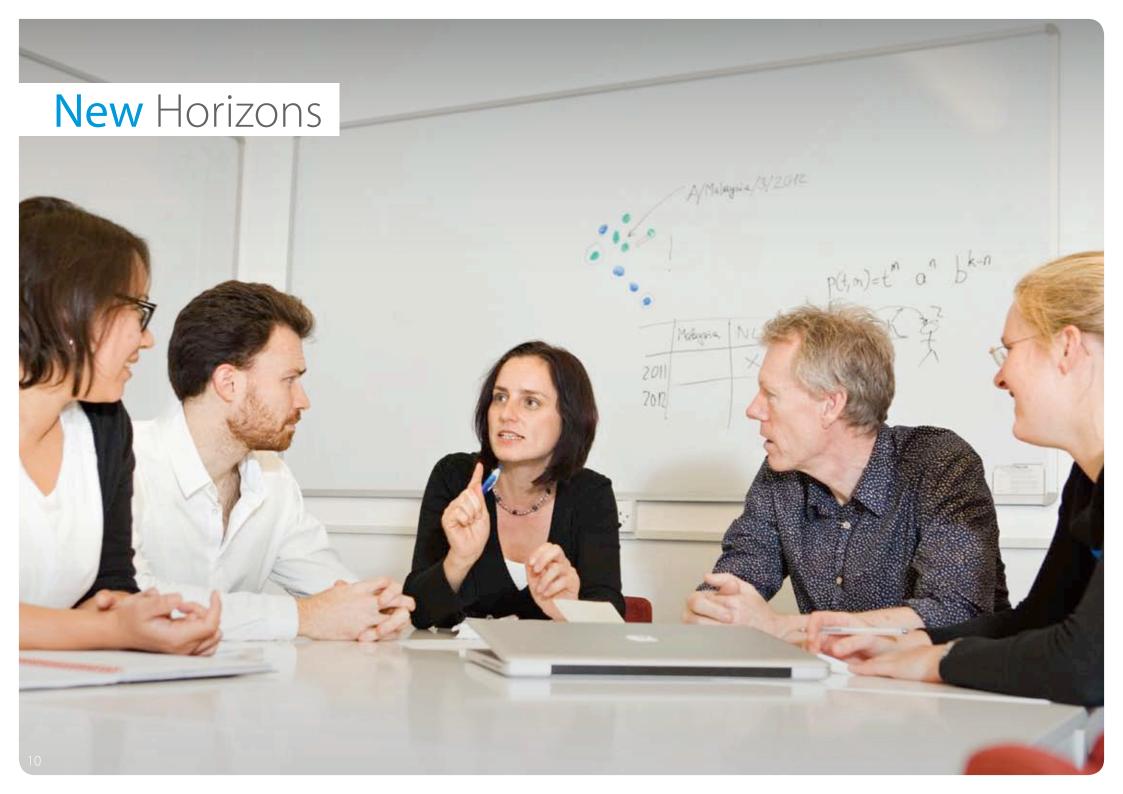
Risk analysis – how close is nature to evolving an aerosol transmissible influenza A(H5N1) virus?

Since 1997, influenza A(H5N1) virus, or 'bird flu', has infected over 1,000 people, killing ~60% of them. However, even with all of these infections the virus has not been seen to transmit between humans – almost all cases have been of individuals in close contact with infected birds. Does this mean the virus is incapable of human to human transmission? In 2012, two papers by the Fouchier and Kawaoka groups revealed that potentially as few as five mutations (amino acid substitutions) in avian H5N1 were necessary to create a strain of H5N1 that could transmit through the air between ferrets, and thus potentially among humans.

A key question is: could such a virus evolve in nature? If so, how soon would such a virus evolve? We performed an analysis of all the available influenza A(H5N1) virus surveillance data, and found that there are viruses that have recently circulated in birds that might require only three additional substitutions to become mammal-to-mammal transmissible. We then developed a mathematical model of within-host virus evolution to study factors that could increase and decrease the probability of the remaining substitutions evolving after the virus has infected a mammalian host. Our work suggested that it is possible for a mammal-to-mammal transmissible A(H5N1) virus to evolve within a single mammalian host and highlighted critical areas of research in which more data are needed for further refining this risk assessment, and potentially averting this threat. This risk analysis was published in *Science* and used by the WHO and US and Dutch governments in critical security decisions related to the original findings.



We now know the risk of these viruses evolving in nature is real, and we now know the further research that needs to be done to more accurately assess and mitigate this risk. Derek Smith



Dengue and Enterovirus-71

The techniques of antigenic cartography are likely to be applicable to all pathogens. To date, these methods have been used for human swine, equine and avian influenza, rabies viruses, foot and mouth disease viruses, and most recently dengue and enterovirus -71, described below.

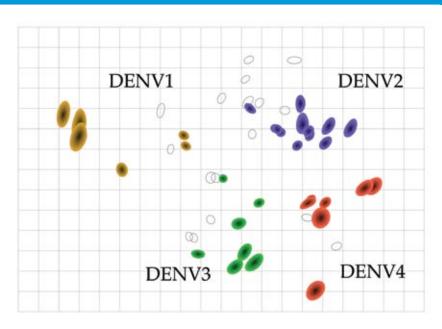
Dengue

Dengue viruses infect around 50-100 million people each year, with an estimated 2.5 billion people at risk, primarily those living in tropical and subtropical countries. The viruses are generally categorised into four different 'serotypes', which can generate a complex of antibodymediated occurrences, such as cross-protection and infection enhancement. Consensus suggests that infection enhancement contributes to the pattern of variable-sized outbreaks observed. Knowledge about the degree of antigenic variability among dengue viruses is limited, as no comprehensive antigenic analysis of dengue viruses has yet been undertaken.

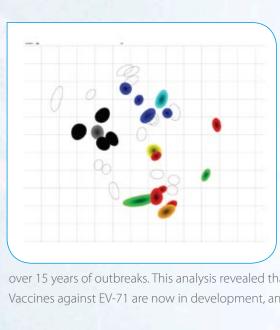
The **Dengue Antigenic Cartography Project** is an international collaborative effort to systematically characterise antigenic variation in dengue viruses. One thousand dengue viruses are being tested with non-human primate antisera to generate a large dataset of neutralisation titres, and antigenic cartography used to probe the forces underlying antigenic evolution. The antigenic map will allow us to test: (1) how well serotypes as currently defined match observed antigenic clusters on the map, (2) if antigenic subtypes (antigenic clusters) exist within serotypes and (3) how quantitatively different antigenic clusters are.

Collaborators donate strains for an antigenic map, including those that reflect genetic, temporal, and geographic diversity among dengue viruses. This project will establish a global picture of the antigenic variation in the dengue virus that will create an antigenic surveillance system similar to the one currently in place to monitor the antigenic evolution of influenza viruses.

This work has potentially profound implications for scientific research on the relationships between the genetic and antigenic evolution of the dengue virus and clinical outcomes of dengue infection, as well as for assessing the current and future protection conferred by prospective dengue vaccine candidates.



Early antigenic map of dengue virus, showing clear clustering and antigenic separations between the four types of dengue viruses.



Enterovirus-71

Enterovirus-71 (EV-71) is another example of an antigenically variable pathogen, where surveillance is critical for early detection and prevention of outbreaks. First isolated in California in 1969, EV-71 has been the cause of numerous outbreaks of hand, foot and mouth disease, which can cause severe neurological disease, most recently becoming prevalent around the Asia-Pacific region. Outbreaks can vary being small and localised ones to large epidemics, with hundreds of thousands of people being infected.

In Taiwan, the reemergence of EV-71 in 2008 resulted in the largest outbreak in the country for the past 11 years. Several molecular epidemiology studies of EV-71 have revealed the genetic evolution of EV-71 isolates by using partial- or whole-genome sequencing. However, little had been reported about the antigenic evolution of EV-71. In a 2009 study in collaboration with colleagues in Taiwan, we used antigenic cartography to analyse samples from

over 15 years of outbreaks. This analysis revealed that the re-emerging EV-71 strains formed a separate cluster which was antigenically distinct from previous strains.

Vaccines against EV-71 are now in development, and we are involved in the evaluation of EV-71 vaccine clinical trials and selection of vaccine strains.



Drawing on 800 years of academic excellence

The University of Cambridge is one of the world's oldest universities and leading academic centres, and a self-governed community of scholars. Comprising 31 Colleges and over 150 departments, faculties, schools and other institutions, the University is committed to achieving excellence in research and scholarship, and to ensuring that its research contributes to the well-being of society.

The WHO CC includes groups across the University in novel and emerging infections and translational science to support its core activities.

The School of Veterinary Medicine at Cambridge is at the forefront of veterinary science and education and is a centre of excellence for teaching and research. The Department undertakes research encompassing basic and applied biomedical and veterinary sciences, ranging from molecular sciences to whole animal research, clinical science and comparative medicine. Most pertinently, work using mathematical modelling, statistics, biocomputing and theoretical biology in infectious disease dynamics have been applied to the study of emerging zoonoses, and transmission studies, particularly in animal-human crossover.

Addenbrooke's hospital, the site of the University's Clinical School and Department of Medicine is one of the UK's finest University teaching hospitals, with an international reputation based soundly on treatment, teaching and research. Research in infection is both clinically and experimentally based, with an emphasis on the understanding of invasion and transmission of pathogens particularly relevant to developing countries such as trypanosomiasis, salmonella, malaria, schistosomiasis and leishmaniasis; and the molecular biology and pathogenesis of herpesviruses, HIV, rotaviruses, influenza and papillomavirus. Pioneering research is being undertaken in the application of whole genome sequencing to understanding the transmission dynamics of hospital acquired pathogens.

The University also has strong links with the Wellcome Trust Sanger Institute, a world leader in genomics research, located in Hinxton, a small village 9 miles south of the city of Cambridge. The Institute uses genomic information to understand the role of genes in health



and disease. Several teams of researchers are dedicated to tackling diseases affecting primarily the developing world, with projects to sequence the pathogens that cause, leishmaniasis, schistosomiasis, sleeping sickness and tuberculosis.

Underpinning the WHO CC and promoting crosslinks between Schools and Departments at the University of Cambridge, Cambridge Infectious Diseases is a university initiative that draws together leading researchers in infectious diseases drawn from across the city into a virtual network of experts available to support the WHO.

Chief **Scientists**



Professor Derek Smith

Professor of Infectious Disease Informatics, Centre for Pathogen Evolution, Department of Zoology Director, WHO Collaborating Centre for Modelling, Evolution and Control of Infectious Disease

Derek Smith's research is focused on how pathogens evolve, to what extent this evolution is predictable, and determining public and animal health measures against such ever-changing pathogens. Derek is also a member of the Department of Virology at Erasmus Medical Centre in The Netherlands, and is a Senior Research Fellow at the Fogarty International Center at the United States National Institutes of Health. He is a member of the World Health Organization influenza vaccine strain selection committee, and is also involved in vaccine strain selection for other human and non-human pathogens.



Dr Colin Russell

Royal Society University Research Fellow, Centre for Pathogen Evolution, Department of Zoology

Colin Russell's research focuses on understanding how evolution and epidemiology act in concert to generate the population dynamics of infectious diseases. Colin has worked extensively on the global epidemiology of influenza viruses and has close ties with groups throughout India and Southeast Asia. He works with the World Health Organization on influenza vaccine strain selection and pandemic preparedness. He is also a Research Fellow at the Fogarty International Center at the US National Institutes of Health



Professor Sharon Peacock

Professor of Clinical Microbiology, Departments of Medicine and Pathology

Sharon Peacock focuses on the translation of microbial whole genome sequencing technologies into diagnostic microbiology and public health. She is funded to develop tools for transmission tracking and outbreak investigation of MRSA, and is in the process of extending this experience to a range of other human pathogens. Sharon also has strong links with South East Asia, having spent 7 years at the Wellcome Trust Major Overseas Programme in Thailand where she directed a wide-ranging programme of bacterial disease research, including a major interest in *Burkholderia pseudomallei*. In addition to her research, Sharon chairs the Cambridge Infectious Diseases initiative; is co-lead of the Immunity, Infection and Inflammation theme at the NIHR Cambridge Biomedical Research Centre; and is a member of the Medical Research Council Infection and Immunity Board.



Professor David Dunne

Professor of Parasitology, Department of Pathology

David Dunne's research group carries out immuno-epidemiological studies on human parasitic infections in disease endemic settings. This multidisciplinary work not only seeks to inform efforts to control 'neglected tropical diseases' but also provide insights into fundamental aspects of human/pathogen biology. His research programmes are carried in close, long-term, partnership with African researchers and health workers, and currently include studies in rural areas of Kenya, Uganda, Tanzania, Mali, Ghana and Gabon. David has served on numerous advisory boards and funding panels that support African research and scientific capacity strengthening, and he leads the 'Cambridge in Africa' initiative to provide Cambridge institutional support for African research and scholarship across all academic disciplines.



Professor James Wood

Alborada Professor of Equine and Farm Animal Science, Department of Veterinary Medicine

James Wood's research interests centre on the dynamic processes found at the heart of every infectious disease, at scales from the cellular and sub-cellular through to the more traditionally studied epidemiological scales of the population and metapopulation. His group studies the epidemiological dynamics of various virus infections of humans and other animals, including influenza, African horse sickness, rabies and emergent lyssavirus as well as henipavirus infections and the methods needed to study them; bovine tuberculosis is also an important focus. Recently funded studies include the transmission dynamics of mammalian influenza viruses and their variants through natural hosts, the dynamics of emergent viral infections in bats, in particular *Eidolon helvum*, in Ghana, orbivirus dynamics and bovine tuberculosis control. He co-supervises several students working on these broad areas.



Professor Duncan Maskell

Marks and Spencer Professor of Farm Animal Health, Food Science and Food, Department of Veterinary Medicine

Duncan Maskell's research interests encompass all things to do with bacterial infectious diseases, with special emphasis on the food-borne pathogens *Salmonella* enterica and *Campylobacter jejuni*, and also the respiratory pathogens *Bordetella spp.* and *Streptococcus spp.* This work uses various cell and animal models, applying state-of-the-art genomics-based strategies in close collaboration with the Sanger Institute. In addition to an extensive publication record in many different areas of infectious disease research, he has also been a co-Founder of two biotech companies. He continues to work on a variety of bacterial pathogens and how they interact with their host animals.

A Pan-University Centre

Dr Effrossyni Gkrania-Klotsas is a Consultant in Infectious Diseases, and Clinical Director of the Infectious Diseases division of **Addenbrooke's Hospital**. Her research interests focus on the genetic epidemiology of immunity pathways that mediate infection susceptibility, the epidemiology of hospital infections and travel medicine epidemiology. She is also the Director of the Cambridge Geosentinel and the Cambridge EurotravNet sites.



Although the initial long-standing connection with the WHO was with the Centre for Pathogen Evolution in the Department of Zoology, our Collaborating Centre has become a university-wide multi-disciplinary activity including groups in the Medical School, Veterinary School, Pathology (which includes virology, bacteriology, and parasitology), Architecture and the Computer Laboratory.

Both Cambridge University and the WHO expect this pan-university activity to continue to grow. Here we give an overview of the activities of some of these groups and of the Cambridge in Africa program.

Professor Jim Kaufman is Professor of Comparative Immunogenetics in the **Department of Pathology.** His research focuses on the evolution of immunity, particularly the major histocompatibility

complex (MHC). As part of this work, his group examine chickens for resistance to infectious pathogens and response to vaccines. Long-term plans include whole genome studies in chickens, development of chickens as a system with a smooth transition between field and laboratory for study of natural pathogens in a natural host, and work on other vertebrates.





Professor Koen Steemers, Head of the Department of Architecture is involved in the architectural design of facilities in resource-poor settings. In particular, his work will contribute to and review the development of models for healthcare facilities for communicable diseases using natural ventilation and sustainable energy sources.

Advisory Board

Prof Ab Osterhaus

Professor of Virology, Erasmus MC, Rotterdam

Prof Jeremy Farrar

Professor of Tropical Medicine, Director of the Oxford University Clinical Research Unit in Vietnam

Prof Ron Fouchier

Professor of Molecular Virology, Erasmus MC, Rotterdam

Prof Yoshi Kawaoka

Professor of Virology, University of Wisconsin, Madison USA and the University of Tokyo and Kobe University, Japan

Dr Simon Frost leads the Population Biology group in the **Department of Veterinary Medicine.**

His research interests focus on the use of mathematical and statistical modelling to understanding the dynamics and evolution of infectious diseases, predominantly RNA viruses such as HIV, hepatitis C and influenza A. Simon's current projects include the statistical modelling of evolutionary processes acting on genetic sequences, modelling viral and immune dynamics, designing diagnostics for viral infections, mining of large clinical databases, and investigating novel means of capturing social, sexual and disease transmission networks, particularly in the context of emerging infectious disease. He is also involved in modelling retroviral transmission in western Uganda and the transmission dynamics of leptospirosis in the Peruvian Amazon.



Dr Alan Blackwell in the Computer

Laboratory is a specialist in the deployment of computing and communication systems for use in challenging professional contexts such as critical care and low-resource settings. Locally customisable and adaptable computing and communication systems are a key priority for the clinical and data collection tools addressing severe emerging diseases.



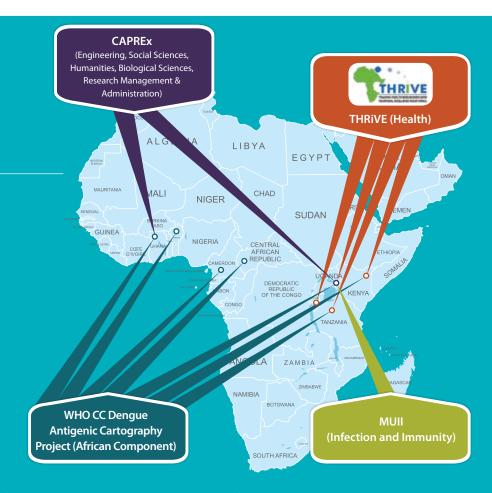
Professor Jonathan Heeney is Professor of Comparative Pathology and Head of the Laboratory of Viral Zoonotics in the Department of Veterinary Medicine. His research interests focus on cross species transmission of viruses, and the coevolution of viruses and their hosts including the evolution of immune mechanisms of disease protection in naturally infected but disease resistant species. Ongoing projects include the evolution of primate retroviruses, the search for novel hepatitis viruses and the dynamics of norovirus infections, and the rational design of novel vaccines for the prevention of diseases caused by notoriously variable viral pathogens.

The Cambridge in Africa Programme: Supporting African Research

As one of the world's leading research-based multi-faculty universities, the University of Cambridge is committed to using its outstanding research capabilities and influence to support the development of African science. Cambridge has a wide-ranging and long-term strategy of holistic engagement with African higher education institutions, through coordinated, cross-faculty research strengthening and scientific training activities, named the Cambridge in Africa Programme (CiA). It works in partnership with African universities and research institutes in Ghana, Kenya, Nigeria, Rwanda, South Africa, Tanzania and Uganda, among others. The CiA is led by Professor David Dunne of the Department of Pathology, who has over 25 years' experience of collaborative research with African partners on neglected diseases in various parts of Africa.

Initiatives of the CiA include **THRiVE** (Training Health Researchers into Vocational Excellence in East Africa) and **MUII** (Makerere University-UVRI Infection and Immunity Research Training Programme), both sponsored by the Wellcome Trust. Through these research capacity-building programmes, Cambridge is making an important contribution to training African scientists in seven East African institutions (in Uganda, Kenya, Tanzania and Rwanda) to tackle regional health problems and to develop their own regional centres of excellence for scientific education and training. Central to these programmes is the principle of supporting African PhD and post-doctoral research on African priorities, in Africa. African researchers register for PhD and post-doctoral research fellowships in their home universities with local supervisors, but receive support in the form of mentorship and training from leading Cambridge researchers. African fellows can spend up to one year of their research programmes in their Cambridge mentor's laboratory. Supervisors or mentors from Cambridge and Africa take part in exchange visits to provide maximum support and mentorship.

A Cambridge register of more than **95 world-class research groups** is currently available to provide a wide range of mentorship expertise for African researchers. This exceptional resource has been incorporated into a searchable and easily accessible website to provide



African researchers and students with a menu of Cambridge expertise within clinical medicine, veterinary medicine, biological sciences, social sciences, mathematics, engineering and the Wellcome Trust Sanger Institute. This expertise is being combined with taught courses and training modules to develop personal training portfolios for visiting MUII and THRiVE African Fellows. Both the THRiVE and MUII Pogrammes also provide expert visiting lecturers for neuroscience workshops and infection and immunology courses in Uganda, respectively.

The CiA Programme moved into its next phase in October 2012, with the award of a three-year \$1.2 million grant by the Carnegie Corporation of New York and a four-year \$1 million grant by The Alborada Trust, to enhance funding already provided by the Isaac Newton Trust, the A.G. Leventis Foundation, and the University of Cambridge for the establishment of the Cambridge-Africa Partnership for Research Excellence (CAPREx) Programme. CAPREx aims to strengthen Africa's capacity for sustainable excellence in research by supporting the region's

most talented post-doctoral and early-mid career researchers. Building on successful partnerships with the University of Ghana and Uganda's Makerere University, CAPREx's goal is to extend Cambridge's research capacity building programmes into West Africa, and focus on a wider range of subject areas: social sciences, humanities, engineering and biological sciences. Training and mentoring will also be provided to African research management and administration staff, in Cambridge and Africa.

These innovative capacity-building and knowledge-exchange partnerships between Cambridge and African Universities are helping to establish equitable and sustainable, North-South and South-South institutional networks to:

- build critical masses of local research capacity for African priorities
- support human resources and infrastructure for African research excellence, and
- contribute to research training and career pathway development for the best African researchers; and support individual, institutional, and national scientific leadership in African universities.

Professor Dunne said: "I am delighted that the Cambridge in Africa Programme is enabling African academics to engage with Cambridge researchers. The linking of the WHO Collaborating Centre with the Cambridge in Africa programme and its African collaborations/ partnerships enables the Centre to network with African researchers and help to develop African research capacity. This can be achieved by, for example, providing training and technical support to enable disease survey networks and emerging infectious disease surveillance to be developed throughout the African continent. The building of such relationships between the brightest researchers in both Africa and Cambridge is proving to be mutually beneficial not just for Cambridge and Africa, but for tackling global issues."

One example of how CiA and the WHO Collaborating Centre in Cambridge work together is the connection of dengue virus researchers across Africa (e.g. in Kenya, Uganda, Tanzania, Ghana, Nigeria, Cameroon, Central African Republic and Sudan). Through networking and sharing of information, this project is characterising the antigenic and genetic variation in dengue viruses across the African continent, assessing how effectively current vaccine candidates might protect against dengue strains circulating in Africa, and increasing surveillance. Another outcome is to integrate the priorities of African researchers for the study of dengue viruses with the objectives of the global dengue antigenic cartography project.

For more information, please contact Dr Pauline Essah (pae21@cam.ac.uk), Coordinator for the Cambridge in Africa Programme, or visit www.thrive.cam.ac.uk.



Professor Ashley Moffett (Department of Pathology) teaching on a MUII Infection & Immunology course.

Dr Annettee Nakimuli in her Cambridge mentor's (Professor Ashley Moffett – above) lab. Annettee's research focuses on immune interactions in pre-eclampsia, which is a major cause of maternal mortality in Uganda.



The linking of the WHO Collaborating Centre with the Cambridge in Africa programme and its African collaborations/partnerships enables the Centre to network with African researchers and help to develop African research capacity.







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