Assessing the impact of new diagnostics technology on global epidemiology

The committee of the British Society for Microbial Technology reports on proceedings of its recent scientific meeting, held at Public Health England, Colindale, in May.

Over 110 biomedical scientists and medical scientists attended the annual British Society for Microbial Technology (BSMT) symposium, with the emphasis this year on the relationship and relevance of laboratories to epidemiology. Professor Brian Duerden CBE and Professor Eric Bolton chaired the meeting.

Professor Bolton opened the meeting with an introductory talk on how next-generation sequencing and metagenomics are already influencing plotting the transmission of certain organisms and looking to future requirements. Professor Crook then discussed the role of the microbiology laboratory in the vision of a National Infection Service and the role of whole-genome sequencing in surveillance.

Other speakers continued and expanded this theme showing how new technologies, and in some cases older technologies, impact on the epidemiological study of infectious agents. These included azithromycin-resistant shigellosis spread globally through sexual contact, Ebola virus and Zika virus.

An interesting presentation illustrated the importance of, and issues around, personalised medicine as new technologies develop. Another speaker showed how disruptive technologies such as the mobile internet, advanced robotics and next-generation genomics are influencing epidemiological fieldwork such as that employed in the African Ebola outbreaks.

The morning and afternoon sessions each concluded with panel discussions which generated much audience participation. A supporting trade show helped to ensure an interesting and informative symposium for delegates.

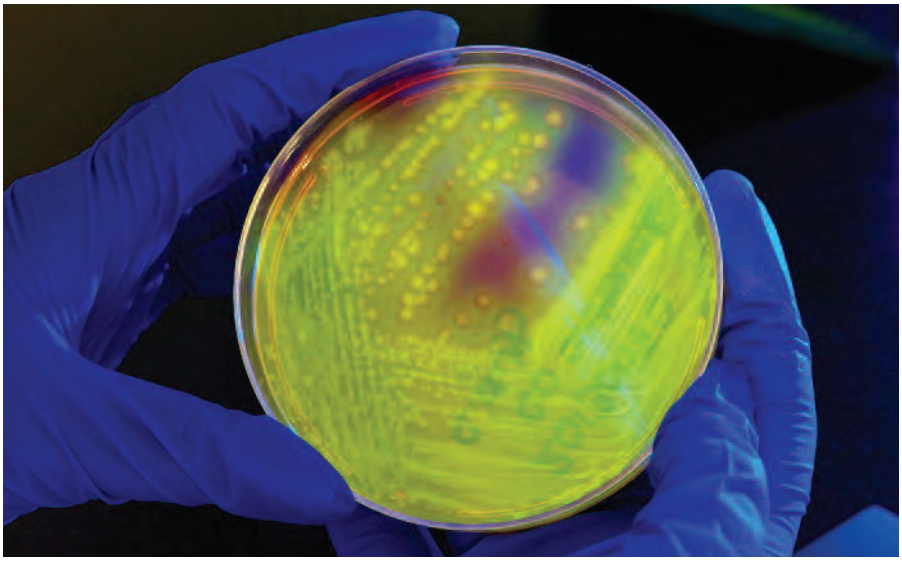
Next-generation sequencing

Professor Eric Bolton (BSMT President) opened this year's annual scientific symposium with 'New Technologies: Diagnosis of Infections and Advances in Epidemiology'. Professor Bolton discussed how next-generation sequencing (NGS) is significant in the future of clinical and public health microbiology. It can be used to identify the fingerprint of bacteria, detect pathogenicity, virulence and resistance genes which have already yielded results in understanding the transmission of *Mycobacterium tuberculosis*, *Clostridium difficile* and *Staphylococcus aureus*, and has proved extremely valuable in tracking hospital-acquired infections.

Professor Bolton then mentioned the impact of metagenomics and the ability of sequencing directly from clinical specimens. This is currently used to study phylogeny and taxonomy but has also been used to evaluate bacterial diversity, allowing researchers to characterise microbiomes from samples that were otherwise difficult to study.

Professor Bolton carried on to discuss a research project by Professor Sarah J O'Brien (Department of Epidemiology and Population Health, University of Liverpool) entitled 'Fully Integrated, Real-Time Detection, Diagnosis and Control of Community Diarrhoeal Disease Clusters and Outbreaks'.

Professor O'Brien plans to create a new paradigm for detecting and investigating clusters and outbreaks of diarrhoea and vomiting in the community by performing NGS. This technology can monitor and type the evolution of pathogens, detect changes in virulence and changes in antimicrobial resistance, which is advantageous when investigating clusters of cases. Metagenomic sequencing studies can also provide valuable information such as detecting the presence/absence of all major



CDC/Melissa Daniel, James Gathany

Findings have shown that only 20% of *C. difficile* infections were transmitted in hospital from another case.

gastrointestinal (GI) pathogens directly from faecal samples, discover 'new' or slightly different pathogens, teach us about pathogen community composition in symptomatic patients, and can characterise pathogens directly to aid rapid epidemiological investigations.

Microbiology and the vision for a National Infection Service

Professor Derrick Crook (Director of Microbiology and Director of the National Infection Service, Public Health England) presented the keynote address. His focus is to lead the translation of genomic technologies to transform microbiology practice across England, and enable PHE to continue to be at the cutting edge of health protection science.

Professor Crook's presentation opened by stating the vision of the regenerated National Infection Service Programme: "To develop a National Infection Service within the PHE that is nationally and internationally recognised, attracting the best people who are led by eminent experts in infectious diseases, who embrace new technology and are driven to continuously improve and ensure best value for the taxpayer. Thereby ensuring within our resources, that the best scientific evidence is available to manage communicable disease and the finest advice is provided to government and the public, to protect the nation from infection and to improve public health outcomes".

A brief but very interesting rationalisation of the need for creation of this new programme followed and outlined the transition of the Public Health Laboratory Services (PHLS) to the Health Protection Agency (HPA) and subsequently the current Public Health England (PHE). The role of the National Infection Service is to be the foundation for integration of microbiological, epidemiological and related functions, and implementation is anticipated in April 2017.

The National Infection Service will consist of consists of all the components that operate to control communicable disease, with services including microbiology reference, specialist microbiology, operations, research, communicable disease surveillance, and field epidemiology. These will be supported by multidisciplinary services which are non-geographically based and scientifically led with strong management support.

Professor Crook emphasised that, in his view, great scientists do not always make great managers. They excel in carrying out the science and small management change, but may not be the best people to manage and coordinate a service. Thus, the formation of a management hierarchy is seen as essential for business planning, leading and developing a successful service.

These major changes are required with the intention of creating a science 'hub' with 'spoke' and 'node' sites across the country, that will adopt whole-genome sequencing (WGS) technology to bring about significant advances in prompt and accurate identification of organisms as well as providing resistance and epidemiological information. The science hub will permit the development of platforms to provide end-to-end automated molecular solutions, but will require convergence of microbiological, epidemiological and analytical capabilities including training of expert staff. These experts will be developed through extensive and specific training with the formation of multidisciplinary teams.

It is envisaged that the redefined service will change the whole diagnostic paradigm as it may be used to predict the genotype of a microorganism and therefore also the possibility to predict resistance. Thus, phenotypic characteristics of bacteria, viruses, fungi and parasites will support genomic identification and prediction of antimicrobial resistance. The transition to genomic sequencing will result in a gradual decrease in typical culture-based clinical microbiology, which will not disappear completely as there will be a continuing need to monitor drug susceptibility, phenotypic changes, reverse genetics and research. It will be essential to manage and direct timely workflows, improve and optimise sample preparation for sequencing, build and maintain knowledge bases, review and assess data generated, organise and archive data, and troubleshoot in order to provide an efficient and successful service.

Professor Crook identified the need to bring together the various aspects of science, including microbes and genes, maths, physics and computer science. Such an enterprise pools specific scientific knowledge, extraction of DNA/RNA, detection of genes, and development of computer software for analysis and recording the data. The impact of implementing WGS in clinical practice for identification of microorganisms and insight into the future, and in surveillance, was highlighted through two scenarios: mycobacterial reference and *Clostridium difficile* surveillance.

The mycobacterial reference data presented showed that in one step, information regarding species identification, resistance prediction and nearest genomic matches for identification and tracking of outbreaks was available swiftly through WGS. The data on the use of WGS for *C. difficile* showed the epidemiology and reservoirs of the organism within a hospital. The findings showed that only 20% of *C. difficile* infections were transmitted in the hospital from another case, with <3% caught from a 'dirty' room. A related scenario looked at the decline in fluoroquinolone-resistant *C. difficile* in England. Data showed that fluoroquinolone-resistant *C. difficile* has declined to 70% since 2006, probably related to the decreased used of quinolones by approximately 50%.

> The role of the National Infection Service is to be the foundation for integration of microbiological, epidemiological and related functions

In summary, Professor Crook's presentation was an exciting and informative account of the PHE current status in controlling communicable diseases, the role of the new National Infection Service and the huge impact WGS will have on the microbiology diagnostic laboratory in the identification of pathogens and prediction of antimicrobial resistance.

Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission

Dr Kate Baker (Wellcome Trust Sanger Institute, Cambridgeshire) gave an illuminating and informative presentation on intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission. *Shigella flexneri* is a Gram-negative bacterium that causes acute, severe enteritis, often with bloody diarrhoea that confers serotype-specific medium-term (six months to two years) immunity. This pathogen is endemic in developing nations, where it causes a significant diarrhoeal disease burden in children under the age of five years. In high-income nations, *S. flexneri* is typically found in recently-returned travellers, but is also found as a sexually transmissible illness in men who have sex with men (MSM).

In 2009, an MSM-associated outbreak of *S. flexneri* 3a was detected in the United Kingdom and was explored further using WGS. Researchers from the Wellcome Trust Sanger Institute and PHE, as well as other national public health services worldwide, whole-genome sequenced over 330 *S. flexneri* 3a from 29 developing and four high-income nations, including returned travellers and domestically acquired cases.

Using phylogenetics they showed the existence of three distinct lineages of *S. flexneri* 3a: an African-associated lineage comprising isolates from African patients or patients in high-income nations recently-returned from Africa; an Asia-associated lineage with a similar demographic composition; and an MSM-associated outbreak lineage comprising isolates from patients in high-income nations who largely were middle-aged men (rather than the very young and very old who are usually most affected).

The outbreak lineage contained isolates from the UK, France, Canada and Australia indicating ongoing international transmission of the pathogen, and was associated with resistance to azithromycin. Using interview data from some patients, the lineage was shown to be statistically associated with MSM, and repeat isolations showed that

CDC/CDC Connects; Tara Sealy

Two members of the international Ebola epidemic response working in Sierra Leone.

chronic and/or re-infection may have been occurring, which questions our traditional understanding of the clinical course of infection of *S. flexneri*.

Dr Baker concluded her talk by saying that by combining epidemiology and extensive laboratory analysis, the researchers gained greater insight into the clinical syndrome of the disease as well as its global epidemiology.

Disruptive technologies for pathogen diagnostics and epidemiology

Dr Nick Loman (Independent Research Fellow, University of Birmingham) provided an overview of disruptive technologies and infectious surveillance. He quoted the work of American business consultant Clayton M Christensen, who defined and analysed the phenomenon beginning in 1995. A disruptive innovation is an innovation that creates a new market and value network and eventually disrupts an existing market and value network, displacing established market leaders and alliances. An example given was the MiniION device, a DNA sequencer the size of USB stick, which plugs directly into a laptop computer and is capable of very long sequence reads.

He described the use of the MiniION in studying the recent Ebola outbreak in West Africa. The small size of the sequencer meant a whole laboratory including a battery-powered thermal cycler could be carried in a suitcase and set up in a hotel room. Viruses could be sequenced rapidly as soon as isolated without the need for large local laboratories or the need to send isolates back to the UK for sequencing, with all the logistic and safety problems that entails. He presented data from WGS showing real-time analysis of the virus evolution during the outbreak.

Although much of the talk focused on technology, a key part of Dr Loman's message was not technological but looked at the spirit in which the work was done. He stressed the importance of releasing data as early as possible and as often as possible, to use open source tools and to set up as many collaborations as possible; in marked contrast to the way science often works where data are jealously guarded and not shared, to the detriment of science and the individual patient.

He concluded by showing delegates his next venture, which is a laboratory in a caravan to study the Zika virus outbreak in Brazil.

Personalised medicine: one-sized medicine, has it all gone pear-shaped?

Dr Matthew Donati (Consultant Medical Virologist, PHE Microbiology Services, Bristol) gave an enlightening presentation that looked at the current and future state of personalised medicine. In particular, he drew together the relevance and impact of personalised medicine on therapeutics and diagnostics, now and in the future.

Personalised medicine is not new, including genetic polymorphism as the basis of disease in 1902, blood typing for transfusions in 1907, antimalarial primaquine-induced haemolysis in 1956, and long-lasting apnoea following neuromuscular blockade with succinylcholine for electroconvulsive therapy (ECT) in 1957. Bacteriologists have, of course, isolated individual pathogens from individual patients and produced a 'personal' antibiogram for decades, and recent advances in genomics, bioinformatics, robotics, miniaturisation, wireless and the internet are drivers and facilitators of rapid change, and Dr Donati reviewed the impact of these.

If we consider therapeutics, 100,000 Americans die annually and more than 2,000,000 are hospitalised due to adverse reactions to medication – in the UK, 6.5% of hospital admissions are due to adverse drug reactions, although not all are due to genetic predispositions.

Pharmacogenomics is the study of variations in host DNA and RNA impacting on drug response, offering a paradigm shift away from trial and error, and 'one dose fits all'. Next-generation sequencing has enabled new pharmacogenomics applications, including phenotyping cancer and detecting drug-metabolising enzyme polymorphisms.

Human immunodeficiency virus (HIV)-infected patients are routinely screened for abacavir hypersensitivity mediated by HLA-B*5701. Activation of HLA-B*5701-restricted CD8+ T cells results in the secretion of the inflammatory mediators and the escalation of a severe inflammatory response.

Cancer treatment can be personalised by engineering patient T cells to recognise specific tumour antigens, survive immunosuppression and penetrate tissues, with success shown in melanoma and blood cancers. Other applications include 3D-printed organs and stem cell-based transplants that have the potential to revolutionise organ replacement.

Within diagnostics, personalised medicine typically consists of a diagnostic test to determine the utility of a specific treatment; this includes the relatively simple antibiotic sensitivity disc test or the detection of reversions, predispositions and minor population variations of viruses. However, there is no reason to believe that companion diagnostics will not move to the patient/clinic.

Dr Donati suggested that point-of-care testing (POCT) will evolve with nanoparticle diagnostics and other novel systems. Advances in nucleotide sequencing allow rapid data generation for multiple pathogens repeatedly during a treatment course. Collating the detail on host genetics, host response and pathogen character will allow accurate predictions of outcome, and in the future Dr Donati envisages that this could be used to predict vaccine side-effects, or indeed for blood typing.

However, there are significant challenges, for example, regarding regulation and quality control. For instance, what level of accuracy is acceptable for a long nucleotide sequence and how do you quality control the data output and downstream manipulation? Do you quality control every base, each variant or just overall performance? The bioinformatics involved are huge, daunting and present significant security challenges. Another question is about how a trial relevant to a personalised medicine product should be conducted. Standard trial technique designs are too weak for this use, therefore post-marketing surveillance of bespoke treatments will be critical to get sufficient population coverage.

With regard to infection, we are approaching the reality of assessing the

well patient and understanding their predisposition to infectious disease, and applying an appropriate bespoke monitoring mechanism, possibly 'hacked' into the body itself. For the sick, we can identify what pathogen is present, understand any predisposition and if or what treatment will be necessary. With vision backed up by science, and a bit of luck, who knows what could be next.

Integration of public health microbiology into sexually transmitted infection surveillance

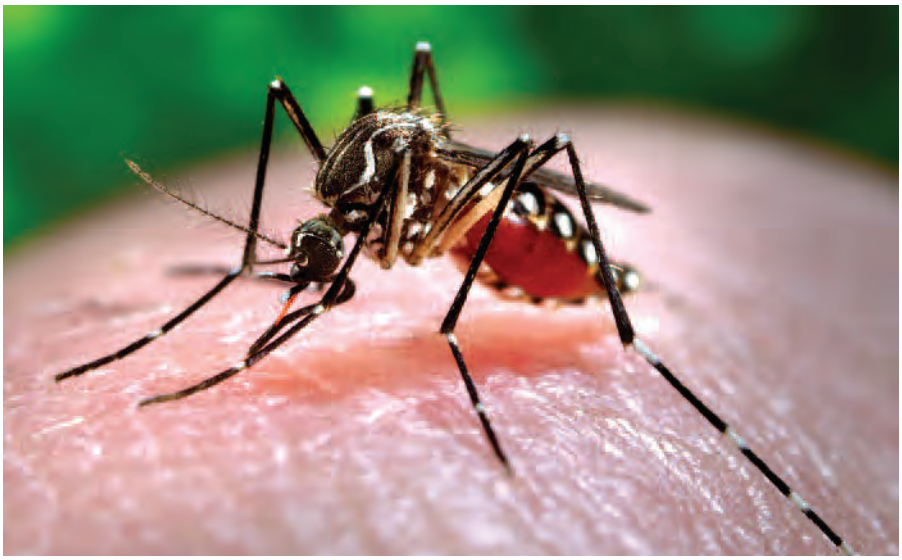
Dr Gwenda Hughes (Consultant Scientist in Epidemiology, Head of Sexually Transmitted Infection Surveillance, National Infection Service, PHE) gave an interesting presentation on how laboratory test results can be linked with clinical sociodemographic and behavioural data to give better intelligence, which can then inform and direct public health response to new infections as they emerge.

Data submitted by all genitourinary medicine (GUM) clinics and greater than 80% of other sexual health services submit a total of over one million records per calendar quarter, and about half a million STI diagnoses per annum to the Genitourinary Medicine Clinical Activity Dataset (GUMCAD) (for England). As the data are pseudo-anonymised, they provide a rich resource of clinical sociodemographic and behavioural information.

Dr Hughes illustrated the use of this database through several different examples. The Gonococcal Resistance to Antimicrobials Surveillance Programme (GRASP) showed how antibiotic resistance was developing by gender and sexual orientation. For example, decreased susceptibility to cefexime was shown to be largely clonal and strongly associated with the MSM group who are HIV-positive and have high rates of partner change. High-level azithromycin resistance first emerged with 16 cases in Leeds among heterosexuals, but since then there is concern that it may spread rapidly in MSM networks, and interestingly partner notification seems to be of only limited success in preventing spread.

Lymphogranuloma venereum (LGV) caused by *Chlamydia trachomatis* serovars L1, L2 and L3 is endemic to parts of Africa, Latin America and Asia, but only occurred sporadically in Europe in 2003. The symptoms can be complex and severe, causing ulcerative proctitis and fever, and untreated infection can result in lymphatic obstruction and fibrosis. The epidemic is associated with MSM (99% cases) and has a concentrated distribution with three-quarters of the cases appearing in London, and there are high rates of STI co-infection.

In 2010, the HPA launched an initiative to improve awareness of LGV at sexual and social venues and internet sites used by MSM diagnosed with LGV. This intensive intervention in London appeared to show immediate results, although this may have been short-lived as the trend is once more rising, with 4400 LGBT diagnoses by the end of 2015.



CDC/Professor Frank Hadley Collins, James Gathany

***Aedes aegypti*, one of the main mosquito vectors of the Zika virus.**

Understanding the evolution and transmission of Ebola virus in Sierra Leone

As a non-clinical virologist, Professor Ian Goodfellow (Head of Virology, Department of Pathology, Addenbrooke's Hospital, Cambridge) works on gastrointestinal viruses, animal studies and novel therapeutics. Recently, for a period of six or seven months, he worked in Sierra Leone, originally in the PHE diagnostic laboratories during the emergency response, and latterly leading a research programme using NGS working in a tent within an Ebola treatment centre in order to study the evolution of the Ebola virus.

In a fascinating presentation, Professor Goodfellow described how Ebola is rare in humans and it is thought that bats are the natural reservoir, although the evidence to substantiate this is limited. There are five types of Ebola virus, of which four are lethal to humans. The origins of the recent epidemic involving Sierra Leone, Guinea and Liberia are thought to have begun in December 2013, and epidemiological evidence suggests that patient zero was a two-year-old boy from Maliandou Village in Guinea, who picked up the virus from bats living in a tree. Evidence is, however, circumstantial in that the tree was burned out but bat DNA was found in the ashes.

In November 2014, following discussions with Dr Tim Brooks from RIPL, Professor Goodfellow was deployed to the diagnostic laboratory in Makeni working alongside others deployed with PHE. However, they first had to build the laboratory and the team was responsible for helping to build and set up the Mateneh Ebola Treatment Centre (ETC) with funding from DFID and built by Royal Engineers. The laboratory eventually opened on 13 December 2014, supported by the non-governmental organisation IMC.

In December 2014, Professor Jeremy Farrar (Director of the Welcome Trust) visited Sierra Leone and discussed with Professor Goodfellow and Dr Books the need for real-time sequencing of the Ebola virus. The need for a real-time in-country genetic sequencing capability was recognised early in the response, as it can be used rapidly to identify and/or confirm epidemiological links in a 'valuable' time frame. At the same time it is able to confirm that the various polymerase chain reaction (PCR)-based tests used at the numerous laboratories testing for Ebola, often using different assays with different primer sets, were still able to detect circulating strains. This was also considered essential during the final stages of the epidemic, and over Christmas 2014, Professor Goodfellow submitted an application for funding to the Wellcome Trust to place a sequencer within the treatment centre to work alongside the PHE diagnostic laboratory.

The platform chosen for sequencing needed to be easy to install, low-maintenance, have a simple and robust workflow, yet still provide high-quality data and have a high throughput. It was also essential that the company selected was willing to engage fully with the project and provide innovative solutions to practical problems. The aim was to sequence 2000 samples and the platform chosen was the ThermoFisher Ion torrent Personal Genome Machine (PGM), which would be combined with the Ebola AmpliSeq workflow and an Ion Chef liquid-handling robot.

In March 2015, the team received training on the use of the instrument and learned how to take it apart, fix it and put it back together again. The AmpliSeq workflow uses multiple primer sets in a multiplex reaction to provide a simple-to-use and robust workflow. The Ebola AmpliSeq panel has two pools, producing 125–275 bp amplicons, and the number of amplicons totals 145. It can be used for nucleic acids extracted from plasma, swabs, semen and breast milk, and can easily deal with degraded samples. The process requires only 5–7 µL of sample

and results are obtained typically within 24–48 hours from sample arrival.

Particular challenges included the practical issues associated with getting six canisters of nitrogen gas to Makeni. In total, over 1200 samples were sequenced, leading to the production of over 600 Ebola genomes, more than a third of the total genomes generated during the entire epidemic.

Sequencing quickly became a core component of the emergency diagnostic response, and the team would sequence, report and feed this information to the District Ebola Response Committee (DERC) and Sierra Leone Ministry of Health to inform on transmission routes. The data was very quickly shared with the scientific community in real time using a number of websites (http://virological.org/c/ebolavirus [Andrew Rambaut]; http://ebola.nextflu.org [Richard Neher, Trevor Bedford]).

Data were not always easy to transfer due to poor internet access and limited bandwidth. Towards the end of the epidemic, sequencing was essential for the identification of possible sources of 'orphan' cases, which are those that are not known to be linked to any ongoing chains of transmission. During the final stages of the epidemic, it was essential to place cases within transmission chains to ensure: i) they were not new introductions from human (or animal) sources; ii) determine if they were part of known transmission chains currently being monitored; iii) confirm they were geographically confined, confirming that control and surveillance systems were working.

As an example, in July 2015, following no recorded cases for 130 days, a single case occurred in Tonkolili. Sequencing within a 48-hour time period aligned this case as being clustered with viruses circulating in Freetown, fitting with the reported travel history; however, the individual did not report any contact with an infected individual. The ability to sequence rapidly excluded the possibility of an unknown transmission chain, the movement of the virus from Guinea, or a new zoonosis.

A number of examples of sexual transmission were also characterised. In one case, a 67-year-old female contracted the virus from a survivor who had been infected 50 days previously, and this led to five others in her household becoming infected.

The epidemic was declared over on 15 January 2016 following a 42-day period of surveillance; however, a few hours later a new case was identified. It was imperative that the laboratory was able to detail whether this was a new introduction, an ongoing hidden chain of transmission, or due to exposure from a survivor. Thankfully, local scientists from Sierra Leone were now trained in sequencing and their work revealed the genome was one nucleotide different to a sample isolated in November 2014 and hence probably linked to persistence in a survivor, ruling out a new introduction or an unmonitored transmission chain.

> Epidemiological evidence suggests that Ebola patient zero was a two-year-old boy from Maliandou Village in Guinea, who picked up the virus from bats living in a tree

Professor Goodfellow concluded that during the early stages of the epidemic the lack of laboratory support contributed to the expansion of the epidemic; the international response was essential to controlling the epidemic, but in reality was too slow; real-time sequencing during an epidemic can play an important role, but there are a number of important bottlenecks to be addressed including what samples should be sequenced and when; how to access samples readily; the requirement for 'field-ready' diagnostic centres such as mobile units rather than building ETCs, simple portable equipment and reagents and staff who can be mobilised rapidly in order to provide a timely 'emergency' response.

Epidemiology and entomology of the Zika virus outbreak

Professor Matthew Baylis (Chair of Veterinary Epidemiology, Research Strategy Lead, Institute of Infection and Global Health, University of Liverpool) shared an excellent overview of the recent headline-grabbing Zika virus. Part of the family Flaviviridae, the virus is closely related to dengue virus and the causative agents of West Nile fever, Japanese encephalitis and yellow fever, all of which are transmitted to humans via mosquito bites.

Zika was discovered in monkeys in Uganda in 1947, with the first recognition of human illness seen in Nigeria in 1953. Only 13 more cases were reported over the next 57 years and it disappeared off the radar until 2007 when 5000 infections were noted in Yap (Micronesia) in 75% of the population, then, in 2013–14, 32,000 infections were seen in French Polynesia. There was not much concern until a surge of reports, in 2015 in Brazil, with an associated marked rise in infants born with microcephaly. It is now present in 33 countries in the Americas and is the first major infectious disease causing human birth defects reported in over 50 years. Alarm has also been raised about a strong association between Guillain-Barré syndrome and previous Zika infection. Studies continue in both these areas.

The main vectors of Zika are the mosquitoes *Aedes aegypti* (yellow fever mosquito) and *Aedes albopictus* (Asian tiger mosquito). Transmission may occur either in a sylvatic cycle, between infected non-human primates and the mosquito species found in the forest canopy, from which the virus may be transmitted by mosquitoes to humans visiting or working in the jungle; or in an urban cycle involving transmission of the virus between humans and urban mosquitoes

It is known that climate is important to spread and global warming is putting the world at increasing risk, with *A. aegypti* getting closer to our shores, currently being found in south-eastern Turkey and Madeira; and also *A. albopictus* spreading northwards in Europe, being detected in Paris within the past two years. At the moment, however, neither species has been discovered in the UK, and it is not known if UK mosquitoes are competent to transmit the virus, so work is continuing.

An overview of methodology for detection of Zika was touched upon. Currently, the virus can be detected by a combination of RT-PCR which detects viral RNA within the first week of clinical onset during the transient low-level infection, and IgM-capture enzyme-linked immunosorbent assay (MAC-ELISA) to detect IgM, which persists for approximately one week after clinical onset as the viraemia wanes. A cautionary observation noted cross-reactivity with dengue and Zika when using ELISA.

Professor Baylis drew his fascinating talk to a close with new thoughts on the control of Zika, as vaccines take 10–20 years to develop, and resistance to insecticides is widespread with no evidence to show an ensuing reduction in mosquito populations. Will endemic stability control the disease? Will use of the 'sterile insect technique' work? The latter involves mating a female mosquito with a sterilised male, resulting in a subsequent mass release of sterile males, meaning that females cannot produce offspring. Or will a related technique using intracellular bacteria called *Wolbachia* be the answer? *Wolbachia* is introduced into males and sterilises them and reduces their ability to spread viruses; as females are not sterilised, they pass the *Wolbachia* in their eggs resulting in the spread of *Wolbachia* through the mosquito population. As microbiologists, the thought of bacteria helping to keep us healthy has a certain appeal.

The BSMT is grateful to the following companies who provided financial support for the conference: Alpha Laboratories, Becton Dickinson UK, BioConnections, bioMérieux UK, Bruker UK, Don Whitley Scientific, Launch Diagnostics, Mast Diagnostics, Medical Wire and Equipment, Oxoid (Thermo Fisher), Pro-Lab Diagnostics and Werfen (Instrumentation Laboratory).

The next BSMT Annual Scientific Conference, entitled 'Hot Topics in Microbiology: Join the Grapevine', will be held on Friday, 12 May 2017. It will include a comprehensive trade show, and speakers will include Dr Stephanie Dancer, Dr William Wade and Dr Silke Schlenze. Once again, Professor Brian Duerden CBE and Professor Eric Bolton will chair the conference.