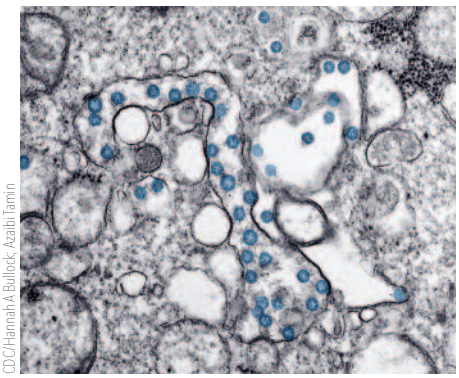
COVID-19: the infection challenging the world – report on a webinar series

The 35th Annual Scientific Conference of the British Society for Microbial Technology (BSMT) took place online on 11–14 May. Not surprisingly, the focus was on one topic, COVID-19, with a particular focus on laboratory aspects of the pandemic. Here, Mark Wilks reports on behalf of the BSMT committee.

In this report we take a look at some of the themes that arose during the week. Because the talks remain accessible online, there seems little point in giving a blow-by-blow summary when you can just as easily visit the BSMT website (www.bsmt.org.uk). We have just pointed out a few features of interest and some of the points that came up in discussion. Hopefully, this will encourage you to register and listen to the talks if you have not already done so.



CDC/Hannah A Bullock, Azaibi Tamin

SARS-CoV-2 and COVID-19 disease, the focus of the BSMT webinar.

COVID-19 pandemic, a global perspective

The first speaker was Dr Michael Head (Senior Research Fellow in Global Health, Clinical Informatics Research Unit, University of Southampton). Throughout this pandemic there has been a tension between an understandably national approach to containing the pandemic and the global perspective that is necessary if the pandemic is to be contained. In particular, the development of vaccines gives us a chance to halt the pandemic if we can be persuaded to adopt a global perspective: vaccines is the theme of our last speaker of the meeting that I will come to later.

Dr Head gave us an overview of how the pandemic is affecting different areas in the world and how South America has become the hardest-hit region. In contrast, even allowing for the lack of testing and quality of data, the picture from Africa seemed relatively good. He drew our attention to a newly published study on West Africa where experience with the recent Ebola virus outbreak has led the development of systems and infrastructure that may have built some resilience and improved responsiveness to the present pandemic, suggesting that the global North could learn a lot about outbreak response from the global South.

Dr Head was particularly critical of the decision to go ahead with the Olympic Games in Japan this year – some 80,000 athletes and support staff, very few of whom will have been vaccinated, descending in one small area. This seemed to him to be a recipe for disaster and indeed is opposed by 80% of the Japanese population. The chances of returning home to every corner of the globe with a 'biological souvenir' seem quite significant. He contrasted this with a look at the UK vaccine roll out which he called a model of how good things can be 'when the grown-ups are allowed to take charge'! He next presented some of his findings from RESIN, a long-running project from the University of Southampton analysing funding trends in health research and the $115 billion that had been spent in research on infectious diseases from 2000 to 2017.

Dr Head pointed out that spending on infectious diseases was in decline from 2006 to 2017, which may not have been unreasonable given the increased problems of non-communicable diseases. However, analysis showed that the spending on infectious diseases pandemics was always a case of 'playing catch up'; for example, with Ebola and the original SARS and MERS outbreaks. Funding is pumped in when there is a problem and not before; a more proactive horizon-scanning approach about what might be coming next is crucial.

Although he thought that the pandemic is probably worse right now than at any point in the last 12 months, he was cautiously optimistic about the outlook over the next 12 months while stressing the need to get more vaccines to low- and middle-income countries. He reserved particular ire for the idea of a naturally acquired herd immunity and the authors of the Great Barrington Declaration, which he thought had a very detrimental effect particularly in the UK last autumn over the decision to avoid a second lockdown.

How to evaluate test performance for the diagnosis of COVID-19

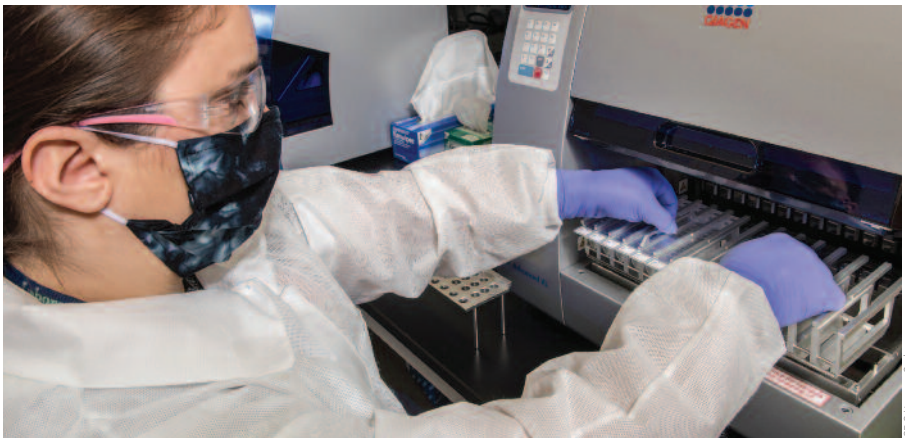
From a global perspective, our next speaker focused entirely on one topic, which might appear narrow but is of crucial importance – the evaluation of test performance in the diagnosis of COVID-19. This was given by Professor Jonathan Deeks (University of Birmingham), an acknowledged world expert on the evaluation of test performance. This area has been neglected up until now but the need to introduce rapid and sensitive tests that are also highly specific for the diagnosis of COVID-19 has focused attention on this area. In fact, here the great advantage of a webinar available for repeated listening is obvious. Although the talk itself was extremely clear, and carefully structured, the subject matter is necessarily complex, and is much easier to take in by listening and pausing at particular slides rather than being in the audience at a normal face-to-face presentation.

He distinguished several standard stages of test evaluation from an initial analytical performance, which is primarily laboratory-based, moving on to clinical performance – seeing how a test performs in the field – and then beyond that determining if a test is clinically effective and indeed cost-effective to introduce.

Unfortunately, in the case of COVID-19 in some cases key stages for the introduction of tests had been omitted. He cited the case of the Abbott ID NOW test, which was glowingly endorsed by President Trump and given emergency authorisation by the US Food and Drug Administration (FDA). This introduction was based on an analytical validity study of only 60 samples with an apparent sensitivity of 100%. Many tests that your laboratory has introduced have probably been subjected to more extensive testing.

He made the important point that although existing biobanks consisting of samples from those known to have had or not had an infection allows fast assessment of the sensitivity and specificity of the test, one question rarely asked is about how representative these groups of specimens are of those in whom the test will eventually be used. Or might antibody and antigen levels be higher than those most likely to be encountered when the test is used under real conditions.

Professor Deeks emphasised that you should evaluate test performance in real-world settings. The important term 'intended use' describes the application of a test in a particular patient or population group used to diagnose a stated condition. Test performance differs with intended use; for example, the people, place and purpose of testing and the target condition that testing aims to detect.



CDC/James Gathany

Polymerase chain reaction methodology plays a vital role in testing during the pandemic.

An excellent illustration of this is how the performance of the Innova lateral-flow test (LFT) widely used in the UK has varied considerably depending on the setting in which it is used. This might be in symptomatic patients or in a Test and Trace centre, or samples might be different; for example, a dry swab or saliva. And the important question about who is doing the actual testing is often ignored. In this case the sensitivity of the test varied from 96% in in-patients with pneumonia who had symptoms for more than five days, down to a mere 3% in asymptomatic students where testing was done by non-healthcare workers.

The role of LFTs for screening is largely based on claims that they are positive when individuals are infectious, but LFTs are known to be only positive when viral levels are high, so their use in the general population has to be questioned. Professor Deeks emphasised that it is always important to look at the consequences of testing – the benefits and the harms – while remembering that it is interventions that change outcomes, not the tests themselves. The impact of any testing will depend upon consequent behaviour. Broader impact includes benefits (ie cases detected, changes in our behaviour) and harms (ie unnecessary isolation, less caution in our behaviour from false negatives, leading to increases in transmission and importantly lost income).

Experience with these new antigen tests shows that they raise multiple challenges and emphasise that tests require the same rigorous evaluation as drugs and vaccines. He concluded with two pleas. First, we need better specimen banks that are representative and well maintained. Second, we need a continuous and active dialogue between public health, clinical medicine, laboratory medicine, methodological experts in test evaluation and regulators to agree on evaluation strategies. It is clear that these have been severely lacking in the present pandemic where an *ad hoc* approach has prevailed.

Setting up and running a SARS-CoV-2 testing service

The second day of lectures provided insight into the challenges of increasing testing capacity as the pandemic escalated in the UK. In the first session, Dr Catherine Moore (Consultant Clinical Scientist, Public Health Wales, Cardiff) provided a comprehensive summary of the development of SARS-CoV2 testing in Wales, which focused on the challenges in the development of the laboratory service. The existing pre-pandemic Public Health Wales laboratory network originally consisted of eight sites holding a single cross-site accreditation status. This meant that all sites, including those subsequently incorporated into the service, worked within nationally agreed SOPs and all results fed into a single LIMS.

The role and importance of laboratory developed assays was discussed, as was the development and decision-making behind the selection of appropriate polymerase chain reaction (PCR) targets. The point was raised that reliance on commercial assays has produced a skill shortage in this area and there is a need to address this through laboratory training structures if these skills are to be preserved.

Dr Moore discussed the challenges that were encountered during the drive to increase testing and the ways in which these were overcome. These included difficulties of introducing PCR-based testing in laboratories with limited or no existing PCR experience, shortages of experienced staff and the seemingly constantly shifting and rapidly evolving testing policy. The global shortage in the supply of a key reagent was creatively addressed through coordination with local pharmaceutical and university institutions to support the supply chain of guanidinium isothiocyanate after its

supply was restricted by national allocation.

The rapid introduction, verification/validation and training of staff on new and repurposed platforms was a significant undertaking even within a single department. Coordinating this and introducing a quality control system over an accredited network brought with it additional complications and challenges. Dr Moore indicated that the service, for a period, came under significant media and public scrutiny and throughout had to preserve, as far as possible, routine diagnostic services. This all required a massive effort along with flexibility and creativity to overcome what remains a high-pressure and complex situation. Dr Moore recently received an MBE in the Queen's Birthday Honours List for her work.

Setting up and running a Lighthouse Lab for mass SARS-CoV-2 testing

The second session provided a different perspective on mass SARS-CoV-2 screening and was presented by Professor Alan McNally. Professor McNally is Professor in Microbial Genomics at the University of Birmingham and his day job is working on the evolutionary genomics of pathogenesis and antimicrobial resistance in bacterial pathogens. This mass testing venture was clearly outside his comfort zone but he had been a vocal critic of the lack of capacity for SARS-CoV-2 testing, and so felt he had little choice but to take up the challenge when this was offered!

The Milton Keynes Lighthouse site rapidly moved from less than 1000 tests using manual processing to over 30,000 tests per day as increased automation was introduced. Impressively, this was achieved in less than a month and eventually reaching a peak of around 50,000 tests per day. Many of the problems encountered during this process, such as logistics, training and workflow efficiency, will be familiar to those working in diagnostic laboratories. However, these were magnified by the sheer scale of the undertaking and workload. Logistic support was drawn from the Army logistic corps, and volunteers from a wide range of backgrounds including veterinary laboratories and academia were required to perform testing.

At the end of the first wave of the pandemic, the experience gained in the setting up of the Milton Keynes laboratory was shown to be invaluable as there was the desire to increase testing capacity further. The 'Turnkey' laboratory was set up within the University of Birmingham, which operated throughout the second and third waves, and a summary of this provided an interesting perspective on the role of this facility in the detection of S gene variants, which would be identified as the Kent variant B.1.1.7.

Professor McNally's talk was followed by a particularly engaging and interesting questions session in which he was challenged on issues such as UKAS accreditation, quality assurance and training, as well as the potential future application of this testing capacity. It is probably fair to say that the rapid implementation and upscaling of these single-purpose sites with apparently abundant resources has been viewed with some cynicism by those used to working in resource-limited NHS pathology departments. However, Professor McNally proved refreshingly open and provided comprehensive answers on these issues highlighting the significant positive impacts of widespread community testing throughout the pandemic as well as discussing the limitations of such an approach if applied in a clinical diagnostic setting.

Secondary bacterial and fungal infections in COVID-19 patients

The first speaker on the third day of the meeting was Professor Jonathan Edgeworth (Professor of Infectious Diseases and Microbiology, St Thomas's Hospital NHS Foundation Trust), who looked at secondary bacterial and fungal infections in COVID-19 patients. He began with a clear overview on infections in the ICU, the pathogenesis of VAP and BSI and the elusive quest for same-day tests that would rule out or rule in infection. He described the development of a pipeline to rapidly identify bacteria directly from clinical specimens in one day using Oxford Nanopore sequencing.

In fact, there were no particularly unusual bacteria or fungi detected in their work, a pattern that has repeated in many other studies. The fear that very long episodes of VAP involving possible new multiresistant bacteria generally did not happen. In fact, arguably the sudden and unexpected occurrence of large numbers of cases of mucormycosis from India is the most startling microbiological finding of the pandemic, and even then it is not clear, because of the absence of control studies, whether this is the real and dramatic finding that has been reported in the press or whether it has been exaggerated by selective reporting.

This talk is well worth revisiting as an excellent overview of the clinical problem of infections in the ICU and the state that we are at now, with the introduction of same-day sequencing on the cusp of being introduced into clinical practice. The staged approach he described, with each being carefully validated and involving different areas of the laboratory and cooperation with clinicians, provides a very useful model, and it could well be shown at a laboratory meeting where it would be very beneficial.

Whole-Genome Sequencing of SARS-CoV-2 isolates in the COVID-19 pandemic

The second talk on this day was from the opposite end of the spectrum, being about as far removed from the patient as it is possible to be! Professor Nick Loman (Professor of Microbial Genomics, University of Birmingham) spoke on the topic of whole-genome sequencing (WGS) of SARS CoV-2 isolates in the COVID-19 pandemic. He began his talk by paying tribute to the work of Professor Yong-Zhen Zhang from Shanghai who deposited the first sequence of the new virus in Genbank on 10 January 2020, enabling the rapid development of primers for detection by PCR and for vaccine development.

In Birmingham, they were able to rapidly release a sequencing protocol by repositioning their existing work on Ebola virus sequencing to SARS-CoV-2 with Dr Josh Quick by 22 January. He then described the setting up of the COVID-19 Genomics UK Consortium – a national network of NHS organisations, UK public health, academic partners, the Wellcome Sanger Institute, and the Lighthouse laboratories. This is one area where the UK could genuinely claim to be world leading, setting up a sequencing service in March 2020.

Since then nearly half a million isolates have been sequenced. Indeed, at one stage nearly 50% of all sequences worldwide had been obtained in the UK, although this proportion has dropped now that other countries have started large-scale sequencing. This was no stamp-collecting exercise; the whole point of it was to determine how SARS-CoV-2 arrived in the UK and was spreading, the impact of mutations on the course of the epidemic, and whether or not genomics could be used to help prevent a second wave.

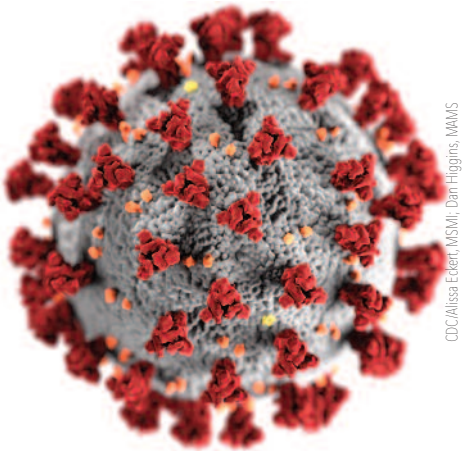
Looking at the question of how and when SARS-CoV-2 arrived in the UK followed. There was limited genetic diversity initially as this was a new virus and there was limited international sampling, with most countries having very few genomes, it was nevertheless possible to accurately date the first cases in the UK to December 2019 with some confidence. Most of the imported lineages just died out, a very few went on with the majority being successfully transmitted to less than 10 other cases. Analysis of over 1300 introductions into the UK in the spring

of 2020 showed that they were mainly from Europe, initially Italy, then overtaken by Spain and then France, with China surprisingly making very little contribution. These sudden changes probably reflect the timing of lockdown in different European countries. At this stage of course our border policy was pretty much mistakenly focused on people flying in to the UK from Wuhan and not Europe – hindsight is a wonderful thing!

During 2020, the virus did not change that much: novel mutations, although constantly occurring, had relatively little impact. However, instead of the usual two mutations a month, around September a new variant B.1.1.7 had accumulated 20 or so mutations in the course of a month and by late Nov/Dec the Kent variant, as B.1.1.7 came to be known, led to a surge of cases in Kent and London. As Professor Loman put in an interview in *The Guardian* "Had everyone in Kent gone on an illegal rave?". Analysis of the mutations showed that many were functional mutations leading to changes in proteins and an increase in transmissibility of up to 70%, leading to it outcompeting other variants when introduced into other parts of the country. The main worry now is of course the Indian variant B.1.617.2, which appears to be spreading faster in the UK than other imported variants, although it is not clear if it will displace the Kent variant. In India, Professor Loman made the point that it is presently hard to know whether the sudden increase is due to changes in epidemiology or changes in the virus itself, as the amount of sequence data and the scale of testing is quite limited. There did not seem to be evidence of immune escape from the Indian variant so far.

Antimicrobial resistance in the time of COVID-19

On the final day of the conference we heard two more talks, first Dr Timothy Rawson (NIHR Academic Clinical Fellow in Infectious Diseases and Microbiology, Imperial College London) spoke on the topic of antimicrobial resistance in the time of COVID-19. About a year ago, it was thought that, as with influenza, secondary infections might lead to large numbers of patients with prolonged VAP and large numbers of possibly novel and resistant pathogens, leading to concern that there would be widespread and unregulated use of antimicrobial agents leading to a sudden escalation in the proportion of antimicrobial resistance. Surprisingly, in the community there was reduced antimicrobial use and a reduction in notifiable infections. Oddly, dental practice showed an increase in prescribing in 2020, although there were wide



CDC/Alissa Eckert, MSMI; Dan Higgins, MAMS

Schematic illustration of the ultrastructural morphology of the SARS-CoV-2 coronavirus.

regional variations. In hospitals there has been high use of empirical treatment but relatively low rates of reported infections. In the ICU again there has been high empirical antimicrobial use but here it has been associated with high rates of reported infections

Dr Rawson described his experience at Imperial where, during the initial surge of COVID-19 in March 2020, critical care capacity was trebled and there was a large number of patients mechanically ventilated (mean of 11 days ventilated), with long periods of paralysis and long ICU stays. However, there was actually a reduction in cases of Gram-negative bacteraemia, possibly as a result of cancellation of surgery and other procedures, and possibly patients were self-isolating and not presenting at hospitals thinking they had mild COVID-19.

What impact will this have in the long-term on antimicrobial resistance is impossible to predict accurately, but Dr Rawson made several important points. We should focus on mechanisms mitigating the impact of the pandemic on antimicrobial resistance, which means gathering evidence that could help shape our understanding and knowledge. We really do not understand the impact of bacterial infection on outcomes in COVID-19 patients. We should probably stratify areas of low risk and limit use of antimicrobials. We need to develop more guidance and clinical decision-making algorithms to limit unnecessary antimicrobial use. At the same time, we have to maintain routine surveillance of antimicrobial resistance and provide continued support for infection prevention and control measures.

What of the actual consequences of bacterial infection in patients with COVID-19? Several studies have associated bacterial infection with worse outcomes but these studies are often retrospective observational studies and are often only based on a small number of patients. A large review of post-mortem findings in patients with possible bacterial lung superinfection was published last autumn. Histopathology demonstrated potential 'superbug' infection in 200/621 (32%) patients although they described infection as proven in only 8% of cases. Surprisingly, there were limited data on causative organisms. Overall, bacterial superinfection was assigned as a cause of death in only 3% of patients.

What about the role of early antibiotics in patients with COVID-19? Here, Dr Rawson called attention to a couple of recent trials in the UK. The RECOVERY trial looked at the use of azithromycin in patients with moderate to severe COVID-19 and found there was no clinical benefit either from its anti-inflammatory or antibacterial properties. A weakness of this trial was that the standard of care arm included a lot of patients who had high antibiotic usage anyway as they were in hospital. In contrast, the PRINCIPLE trial looked at community COVID-19 patients and again this showed that azithromycin had no benefit, and did not prevent subsequent hospitalisation or death. In another arm of the PRINCIPLE trial where doxycycline was used there was a low probability of some benefit.

What about the effect of immunosuppression and COVID-19? There are two classes of drugs here: steroids such as hydrocortisone and high-dose dexamethasone and also immunomodulatory drugs such as anti-interleukin-6 (anti-IL-6) agents. Initial fears from observational data have not been borne out by current RCT data and there has been no clear increased risk with the use of steroids or anti-IL-6 drugs.

There have been several important measures focused on antimicrobial stewardship and trying to limit antibiotic use. For example, guidance from the World Health Organization (WHO) has suggested that antibody therapy is not recommended in suspected or confirmed mild-to-moderate COVID-19 cases without direct evidence of bacterial infection. Other groups are focused on developing biomarker prediction rules for COVID-19 patients. For example, in the absence of an elevated white cell count, if there is no decrease in C-reactive protein (CRP) over 48–72 hours during antibiotic treatment this suggests that there is no bacterial infection and treatment can be discontinued. Similarly, many studies used procalcitonin (PCT) in the same way to support the diagnosis of bacterial infection and to avoid antibiotic therapy in patients with low PCT.

Finally, Dr Rawson described some of his work on using artificial intelligence to help guide decision-making and

determine the risk of bacterial infection. Supervised machine learning using routine healthcare data analysed longitudinally – that is over time rather than one point, to give a numerical value of the chances of a bacterial infection at any one time – might enable more accurate and objective decisions to be made about the risk of bacterial infection.

From variola to COVID-19, the development of modern vaccines

In the last talk of the meeting, Professor Sheena Cruickshank (University of Manchester) reviewed the whole topic of vaccines, the area which has surely been an undisputed success story of this pandemic. Appropriately, this talk was given on 14 May, as it was on 14 May in 1796 that Edward Jenner administered his first vaccination. Although, as she rightly pointed out, he was beaten to it by the oft-forgotten work of Lady Mary Wortley Montagu, who vaccinated her own children over 50 years before. She began with a description – really a celebration – of our immune response, capable of responding to thousands of different stimuli from viruses on the nanometer scale to huge parasitic worms and how the innate and adaptive immunity systems work together. This was followed by a lightening tour through Louis Pasteur, Robert Koch and work by Elie Metchnikoff, finishing with the discovery of T cells and B cells and the role of the thymus, which did not happen until 1961.

Professor Cruickshank then moved on to review the different classes of vaccines available. The first and oldest class she described used a related but less harmful infection as the vaccine agent, the best-known example of which is BCG. These are highly effective but dangerous to immunocompromised patients. A step forward was the use of live attenuated pathogens such as MMR, chickenpox and the Sabin oral polio vaccine, all highly effective but still posing some risk of disease in immunocompromised patients.

The next class of vaccines use killed or inactivated pathogens that have been grown in culture. Here, there is still a low risk of disease due to improper inactivation of infectious agent and they often require boosters or adjuvants. Nevertheless, they are relatively simple to produce and often highly effective. Examples include many influenza vaccines, hepatitis A and the Sinovac COVID19 vaccine, which appears to have been successful in large trials in Chile.

The third class of vaccines she described use protein subunits. Here, purified recombinant components use selected antigens that best stimulate the immune system. This needs a good understanding of the immune system to choose the right protein subunit, but are relatively easy to bulk up and there are many successful examples, such as hepatitis B and the new Novavax vaccine for SARS-COV-2 using the spike protein.

The next class of vaccines are the recombinant viral vector type. Here, a bioengineered virus expresses the target pathogen antigen in vivo. Although relatively new, they have been widely investigated and appear to have a good safety record (eg Ebola vaccine). They often use a non-human virus as a carrier. The best known example is the Oxford AstraZeneca SARS-COV-2 vaccine which appears to give a good level of T- and B-cell response and is cheap to manufacture and store.

The fifth, final and most recent class of vaccines are nucleic acid-based. Professor Cruickshank singled out the extraordinary career of Katalin Kariko, who began writing grants on this topic in 1990, and had many grants and papers rejected but is now rightly credited with the co-invention of mRNA vaccines, of which the Pfizer vaccine is the best known.

Nevertheless, there are no vaccines for diseases such as HIV and malaria. Why is this? Professor Cruickshank identified a number of different factors ranging from a lack of understanding of the agent's basic biology, the variability in pathogen antigens, to the lack of good laboratory models to use to develop the vaccines. Other problems that should be more easily soluble include transport, storage and cost.

In some diseases, such as Zika, there is just a simple lack of research. Although discovered in the 1950s, from the 1960s to 1980s rare sporadic cases of human Zika infections were found across Africa and Asia, typically accompanied by mild illness. It was not until 2007 that the first large outbreak occurred and not until 2015–16 that, as Dr Michael Head showed in the first talk of this meeting, there was significant investment into study of the disease.

One other factor that should be considered is the role Andrew Wakefield, former British gastroenterologist, played in providing a focus for vaccine hesitancy. His hypothesis linking MMR vaccination and autism, which has been repeatedly discredited, had a major impact and is certainly significant in the anti-vaccine movement. Meanwhile, over 80,000 people in Europe contracted measles in 2018, and worldwide over 140,000 died of measles in 2019. Indeed, WHO recently identified vaccine hesitancy as one of the 10 biggest global threats to health.

Nevertheless, even when a vaccine is available and vaccine hesitancy is not a problem, there are still massive problems. A WHO statement from 11 May starkly shows the extent of the inequitable distribution of SARS-COV-2 vaccine. Upper-income countries represent 53% of the world's population and have received 83% of the vaccines, while low- and middle-income countries represent 47% of the world's population and received only 17% of the vaccines.

Professor Cruickshank called our attention to one of the side-effects of the effects of the COVID-19 pandemic, that over 117 million children are thought to be at risk of missing out on measles vaccine as measles vaccination campaigns have been postponed or on the edge of being postponed because of travel bans or because the whole system is overwhelmed by coping with COVID-19. A sobering note on which to finish.

Webinar postscript

The BSMT Committee is very pleased with how well the conference has been received to date with over 800 registrants for the webinar and between 200 and 350 participants joining each day including ~5% from outside the UK. If you did not register for the live meeting you can do so now and gain access to view the recordings by visiting the BSMT website (www.bsmt.org.uk).

We are hugely grateful to our media partner *Pathology in Practice* and to Step Communications, without whose encouragement and support it is unlikely that we would have convened this event. We are also indebted to our 23 sponsor companies and to the four moderators: Professor Eric Bolton, Professor Brian Duerden CBE, Dr Kate Templeton and of course Dr Mark Wilks, the Science Lead for the BSMT, who wrote this report (with input from David Westrip).

The Committee took the decision to give two talks per day in the early afternoon to allow some participants to watch in real time and ask questions of the speakers. However, we also realised (particularly at this time of additional laboratory testing for SARS-CoV2), that watching presentations during the working day would not suit many of the potential audience. To this end the talks and the questions not answered on the day are available on the internet and on YouTube where they will be accessible for several months.

We would really like to know your thoughts on the format for future BSMT conferences. Did you find the webinar a format useful for you and your colleagues? Or would you prefer face-to-face meetings if possible? Do let us know by emailing me at vbevan@bsmt.org.uk.